



# IN VIVO

The Publication of the Metropolitan Association of College and University Biologists

Winter 2015

Volume 36, Issue 2

## 47th Annual MACUB Conference Molloy College Rockville Centre, New York November 1, 2014



# The Metropolitan Association of College & University Biologists

Serving the Metropolitan New York Area  
for 48 Years

## MACUB 2014-2015 EXECUTIVE BOARD MEMBERS

### PRESIDENT

Dr. Kathleen Nolan  
Saint Francis College

### VICE-PRESIDENT

Dr. Dirk Vanderklein  
Montclair State University

### TREASURER

Dr. Margaret Carroll  
Medgar Evers College

### CORRESPONDING SECRETARY

Dr. Paul Russo  
Bloomfield College

### RECORDING SECRETARY

Dr. Carol Biermann  
Kingsborough Community College

### MEMBERS-AT-LARGE

Dr. Tin Chun Chu  
Seton Hall University  
Dr. Fernando Nieto  
SUNY College at Old Westbury  
Dr. Christopher Corbo  
Wagner College  
Dr. Donald Stearns  
Wagner College

### 2015 CONFERENCE CHAIRS

Dr. Dirk Vanderklein  
and  
Dr. Quinn C. Vega  
Montclair State University

### 2014 CONFERENCE CHAIR

Dr. Pamela Monaco  
Molloy College

### *IN VIVO* EDITOR

Dr. Edward Catapane  
Medgar Evers College

### AWARDS CHAIR

Dr. Anthony DePass  
Long Island University

### ARCHIVIST

Dr. Kumkum Prabhakar  
Nassau Community College

### PAST PRESIDENT

Prof. Gary Sarinsky  
Kingsborough Community College

### TREASURER EMERITUS

Dr. Gerhard Spory  
Farmingdale State University

### MEMBER-AT-LARGE EMERITUS

Dr. Michael Palladino  
Monmouth University

## Instructions for Authors

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

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

## IN VIVO Editorial Board

**Editor:** Dr. Edward J. Catapane,  
Medgar Evers College

**Associate Editors:** Dr. Ann Brown,  
Dr. Margaret A. Carroll,  
Medgar Evers College

## In This Issue:

MACUB 2014-2015 Executive Board	inside cover
Instruction for Authors	inside cover
Student Perceptions of Anatomical Case Studies in Clinically-Based Programs by Patrick R. Field	37
MACUB 2014 Conference Poster Presentation Award Winners	44
MACUB 2014 Conference Highlights	51
MACUB 2014 Conference Poster Abstracts	54
MACUB 2014 Conference Member Presentations	103
Affiliate Members	inside back cover

## Save the Date

**The 2015 MACUB Conference will be at  
Montclair State College, Montclair, NJ**

**Nov. 7, 2015**

---

# Student Perceptions of Anatomical Case Studies in Clinically-Based Programs

Patrick R. Field

School of Natural Sciences/ Biological Sciences  
Kean University  
1000 Morris Avenue, Union, NJ 07083

---

## Abstract

Perceptions of anatomical case study practice in Occupational Therapy (OT) and Athletic Training Programs (AT) was analyzed through surveys involving case studies in the gross anatomy classroom/laboratory. The survey is composed of two distinct parts: ten statements about the case study method that require ranking using a Likert scale (quantitative), and questions that inquire about strengths and weaknesses of the method (qualitative). The results support a positive relationship between case study pedagogy and skills necessary for clinical practice. Specifically, statistical analysis revealed that the majority of students ( $n = 106$ ) perceive anatomically-based case studies as real world applications of clinical concepts, a valuable evaluation tool and an important preparation for clinical reasoning in the profession (critical thinking skills gained through guided learning of information via discussion, feedback and assessment). Although students expressed concern that case studies with typical presentations, in which rote memorization of facts would suffice for a diagnosis, does not apply to the anomalous patient, development of clinical reasoning skills through case study practice increases the ability to approach the anomalous, non-typical case. Case studies that incorporate anomalous structures, that reflect the holistic approach of considering both physical and cognitive symptoms when evaluating subjects, without immediately revealing the diagnosis, can contribute to this preparation.

Keywords: case study, clinical reasoning skills, anomalous

---

## Introduction

Lecturing of clinical information alone breeds passive learning and, in turn, rote memorization of facts, denying students the opportunity to determine the clinical significance of the information presented<sup>1</sup>. Rather, providing students with a clinical case study including the history, physical presentation, symptoms, results of sensory and motor testing, as well as, accompanying case study questions, allows students to actively determine/verify the diagnosis and the eventual treatment<sup>2,3</sup>. Input from the instructor (on the case) in the forms of facilitated

discussion, feedback and assessment creates a supportive, non-threatening environment in which students make mistakes and then learn from them<sup>1,4</sup>, preparing them for cases in the actual clinical environment<sup>5</sup>. Purposeful thinking from students that incorporates criteria systematically and intellectually demonstrates a mode of critical thinking<sup>6</sup>, and when combined with feedback, their reasoning process fosters clinical reasoning. Paper cases that reflect these principles, that eventually translate theory into practice, are essential in clinically-based programs<sup>7-9</sup>. My goal for this study is to collect and analyze data reflecting

the perceptions that students in clinically-based programs have about working with case studies and their perceived application in the clinical environment.

### **Materials and Methods**

The gross anatomy courses at Kean University, graduate level Human Gross Anatomy (HGA) and undergraduate level Basic Gross Anatomy (BGA), offered to students pursuing clinical degrees in Occupational Therapy (HGA) and Athletic Training (BGA), are classes in which students utilize clinically-based case studies to improve proficiency with clinical reasoning. There is no distinction between the case studies used in the graduate level HGA and undergraduate BGA, however, the discussion format of the presentation, deficits and prognosis is very different. OT students mainly focus on the physical and cognitive deficits as they relate to the activities of daily life (ADL). For example, if the case involves deficits to the dominant upper extremity: How is the client/patient going to be able to brush their teeth, feed themselves, tie their shoes, or put a shirt on? These "occupations" must be considered in addition to employing rehabilitative procedures to increase function. Whereas, when the same case was approached by the ATs, they would focus on evaluating the type of injury to the upper extremity (and the accompanying deficits), immobilizing the upper extremity for further medical evaluation, and then designing a rehabilitative/strengthening program to improve function and get the athlete back on the playing field.

Participation in this study involves completion of a survey composed of two distinct parts: statements about the case study method that require ranking using a Likert scale (quantitative data) and

questions that inquire about strengths and weaknesses of the method (qualitative data). Students (n = 106) from four separate sections of HGA (fall 2011/2012) and two sections of BGA (fall 2011/2012) were given a copy of this survey to complete at the end of the course. Within this survey, "Assessment of case study practice in anatomy for clinically-based programs," students are asked to read and numerically rate the value of ten statements involving the use of clinically-based case studies in gross anatomy (general use and specific components of cases) using a basic Likert scale: 1 (completely disagree), 2 (mostly disagree), 3 (neutral, no opinion), 4 (mostly agree), and 5 (completely agree) (Figure 1). Students were also encouraged to submit opinions about the use of clinical case studies in HGA/BGA including strengths, weaknesses, and future use in their chosen professions (Figure 1). The quantitative data from these 10 statements illustrates the perceptions that students have of clinically-based case studies in gross anatomy and their perceived contribution to the skills of clinical practice/reasoning. Written comments to specific questions (qualitative data) are also utilized to determine the value of clinical case studies in this manner. SPSS was used to obtain descriptive statistics (mean, median and standard deviation) on the quantitative data and determine any correlations (Pearson Correlation 2 tailed t-test,  $p < 0.05$ ) between the ten statements. Qualitative data was aggregated thematically, reporting only on the most common themes. Research protocol and study design have been approved by the Institutional Review Board of Kean University (IRB #11-121202).

## Figure 1. Assessment of case study practice in anatomy for clinically-based programs

Rank each of the following statements using this Likert scale of 1-5:

- |   |                                    |
|---|------------------------------------|
| 1 (completely disagree with statement),   | 2 (mostly disagree with statement) |
| 3 (neutral, no opinion on the statement), | 4 (mostly agree with statement)    |
| 5 (completely agree with statement)       |                                    |

\_\_\_\_ 1. Case studies are valuable examples of real-world applications of concepts learned in lecture/lab.

\_\_\_\_ 2. Critical thinking skills (higher-order reasoning skills) are improved by answering conceptual questions for clinical case studies.

\_\_\_\_ 3. When answering the questions included in a clinical case study, the students should have most of the information to answer those questions presented previously.

\_\_\_\_ 4. When I answer case study questions concerning symptoms/presentations, I basically use the same method to derive the answers.

\_\_\_\_ 5. While discussing case study questions, it is important to present **all** of the possible symptoms and presentations before narrowing down to the most critical.

\_\_\_\_ 6. Discussing cognitive aspects (depression, anger, frustration etc.) associated with trauma or pathology in a case study is equally important as discussing the physical aspects resulting from the trauma/pathology.

\_\_\_\_ 7. I try to predict the diagnosis of each case study through the analysis of elements in the case study related to the diagnosis (e.g. type of accident/trauma) before reading the actual diagnosis.

\_\_\_\_ 8. It is necessary to have the diagnosis included in case studies to reinforce comprehension of clinical issues.

\_\_\_\_ 9. Including clinical case studies and accompanying questions in exams is a valuable method of evaluation of clinical information.

\_\_\_\_ 10. I am confident that I will use case studies in the future in my professional career.

Written Opinions:

1. In your opinion, what are the major strengths of using clinical case studies in HGA/BGA? Weaknesses?

2. If you believe you will use clinical case studies in the future, predict how you will use them, and in what capacity?

## Results and Discussion

### Quantitative Data

The means of the ten statements on the survey indicated that participants (n =106) appear to highly value the many uses of clinically-based case studies in gross anatomy. All means were between the ranking of 4 and the ranking of 5, except statement 4 (mean = 3.96, SD 0.72 ) (Table 1). Statements 1, 2 and 9 yielded the highest means (Table 1). Statement 1 inquired whether case studies are valuable examples of real-world applications of concepts learned and had the highest mean (mean = 4.76, SD 0.47). For statement 2 (mean = 4.63, SD 0.56), students overwhelmingly agreed that critical thinking/higher-order reasoning skills are improved by answering conceptual case study questions. Based on the results of statements 1 and 2, students appear to believe that clinical case studies improve conceptual knowledge (application, analysis, and evaluation in Bloom's Taxonomy of Cognition) in gross anatomy. Guided learning involving discussion, feedback and assessment, three vital components of answering clinical case study questions, empowers students to learn, apply and analyze clinical situations<sup>7-9</sup>. An example of conceptual knowledge in gross anatomy involves the comparison of the regional approach to trauma/pathology vs. damage of individual structures. The regional approach describes the deficits of damaged structures of different tissue types and the interrelationship of those structures towards the function of that anatomical region: e.g. injury in the dorsal scapular region could affect the suprascapular nerve, the dorsal scapular nerve, muscles innervated by these

nerves, vasculature supplying these muscles, and the scapula, compromising the actions of external rotation, abduction and hyper-abduction of the arm at the shoulder joint and weakening elevation and retraction of the scapula. Whereas, learning the function/deficit of an individual structure exemplifies basic rote memorization e.g. solely learning the action of supraspinatus (innervated and supplied by the suprascapular nerve and artery, respectively) and the ensuing deficit of hyper-abduction at the shoulder joint. Results from statement 9 (mean = 4.57, SD 0.63) indicated that answering questions about clinical case studies in exams is an important evaluation tool. Summative assessment (assessment of learning that develops over a period of time) of the clinical knowledge/reasoning acquired for each portion of the gross anatomy courses is evaluated via case studies/questions on exams. Clinical reasoning case studies on exams present medical chart data such as the history, physical presentation, symptoms and sensory/motor testing; and then test the student's knowledge of the deficits described in the scenario, forcing the student to call on previous discussions and utilizing critical thinking skills to make decisions regarding the diagnosis and eventual treatment plan<sup>10,11</sup>.

Pearson Correlation analysis of the data reveals several significant correlations (based on p value,  $p < 0.05$ ) between the results of the statements for both groups calculated individually: group 1 composed of 54 students from 2 sections of HGA and 1 section of BGA in fall 2011 (Table 2); and group 2 composed of 52 students from 2 sections of HGA and 1 section of BGA in fall 2012 (Table 3). As stated, mean responses to statements 1-10 indicates that students are in agreement with the statements that

Statements	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10
Mean	4.76	4.63	4.38	3.96	4.29	4.27	4.13	4.33	4.57	4.50
Median	4.00	4.00	3.50	3.50	3.00	3.50	3.00	3.50	3.50	3.50
Std. Dev.	.47	.56	.72	.72	.92	.83	.94	.78	.63	.75

	Statements	S2	S3	S4	S5	S6	S7	S8	S9	S10
Pearson Correlation Sig. (2-tailed)	S1	.363* .007		.295* .032	.268^ .050				.380* .005	.502* .000
Pearson Correlation Sig. (2-tailed)	S2								.414* .005	.330^ .015
Pearson Correlation Sig. (2-tailed)	S5			.340^ .013		.363* .007				

\* Correlation is significant at the  $p < 0.01$  level (2-tailed),  
^ Correlation is significant at the  $p < 0.05$  level (2-tailed)

	Statements	S2	S3	S4	S5	S6	S7	S8	S9	S10
Pearson Correlation Sig. (2-tailed)	S1	.353* .010							.484* .000	.287^ .039
Pearson Correlation Sig. (2-tailed)	S2			.304^ .030					.437* .001	.444* .001
Pearson Correlation Sig. (2-tailed)	S5			.403* .003		.277^ .046				

\* Correlation is significant at the  $p < 0.01$  level (2-tailed)  
^ Correlation is significant at the  $p < 0.05$  level (2-tailed)

support the use of clinically-based case studies in gross anatomy courses; therefore, the correlations between statements can also be interpreted as being supportive (Tables 2 and 3 details the Pearson correlations and significance-2-tailed, that appears for both groups).

The most significant correlations (based on  $p$  values,  $p < 0.05$ ) for both groups are between the data from statement 1 (case studies as real-world applications) and statements 9 (case study

questions in exams;  $p < 0.005$ , group 1 and  $p < .000$ , group 2 ) and 10 (use of case studies in future professional career;  $p < 0.000$ , group 1 and  $p < .039$ , group 2 ).These correlations point to the importance of clinical case studies as a pedagogical method for learning clinical concepts/ reasoning, both in patient/client/athlete care and evaluations in preparation for clinical internships/professions; the next best method of acquiring clinical knowledge to actually treating patients/

clients/athletes<sup>12</sup>. There also appears to be strong correlations between statements 1, 9 and 10 and statement 2 (case questions improve critical thinking/higher-order reasoning skills): statement 1, real world applications ( $p < .007$ , group 1 and  $p < .010$ , group 2), statement 9, evaluation tool ( $p < 0.002$ , group 1 and  $p < 0.001$ , group 2) and statement 10, future career ( $p < 0.015$ , group 1 and  $p < 0.001$ , group 2). These participants reported that critical thinking skills improve as a result of clinical case study practice, first theoretically (statements 1 and 9), and in turn, professionally (statement 10). In other words, the conceptual questions in these clinical case studies require students to use clinical reasoning skills (acquired from guided feedback discussions) (9) to solve the dilemmas, rather than simply regurgitating factual knowledge learned in lecture. There also appear to be significant correlations between responses in statement 5, considering all possible symptoms/presentations in case questions before narrowing down, and statements 4, using the same method to answer case study questions ( $p < 0.013$ , group 1 and  $p < 0.003$ , group 2) and 6, considering cognitive aspects of trauma is as important as physical aspects ( $p < 0.007$ , group 1 and  $p < 0.046$ , group 2). These results point to vibrant connections between consistently using a process of clinical reasoning that encompasses all of the possible symptoms/presentations, including the mental aspects of trauma/pathology, or the "holistic approach" (a hallmark of clinical reasoning case studies), and narrowing them down (via previous feedback /discussions) to the most critical (Neistadt, 1998), for the purpose of designing a treatment plan.

### **Qualitative Data**

The questions included in the written comments section of the survey are designed to illicit three types of

information from case study use: strengths, weaknesses and predictions of how they could be used in future professions. Similar answers are grouped together, counted and then recorded. A majority of students commented that clinical case studies help prepare for real life experiences (66/101 responses, 66%), and are a useful practical application of knowledge/critical thinking skills (52/101, responses, 52%), responses that resonate with the quantitative data. In addition, fourteen percent of the students stated that clinical case studies reinforce their anatomical knowledge foundation. Among the reported weaknesses, students are most concerned that the typical clinical case studies are not sufficient preparation for the anomalous (non-typical) patient (18/46 responses, 39%). In all likelihood, these clinicians will encounter such a patient/client/athlete in their future careers. This is why development of higher-order/clinical reasoning skills from case studies is important, as opposed to plain rote memorization of facts (damaged structure -deficit), which is sufficient for answers to typical "textbook" case studies<sup>1,12</sup>. If the student can employ clinical conceptual reasoning in addition to the factual knowledge he/she has learned, the better they will be equipped to handle that "non text-book" patient/client/athlete. It is the difference between memorizing (not comprehending) the components of a diagram, labeled photograph or model (i.e. learning the key) for purposes of examination vs. understanding the concepts of those resources, so that when an unfamiliar diagram, photograph or model is presented, the student is able to apply the learned concepts to the novel representation and determine the answers.

The top three predictions for future use of case studies included: to reinforce anatomical knowledge (20/72 responses,

28%), to complete the understanding of a client's presentation/situation (15/72 responses, 21%) and to treat clients/patients/athletes with similar damaged structures/symptoms as those exhibited in previous clinical case studies (14/72 responses, 19%). Although a number of students expressed reservations about case studies built around the non-anomalous subject, some still believe that they would be using typical case studies for the purposes of professional knowledge and treatment.

### Conclusion

Quantitative results show that clinical case studies are valuable for several purposes: as examples of real-world applications of clinical concepts for future professions, for the improvement of critical thinking/clinical reasoning skills, and as important pedagogical tools for formal evaluations/examinations. Reported weaknesses and correlations concerning the holistic method to determine the correct diagnosis/treatment (physical symptoms, cognitive aspects and presentation) reveals that students are anxious about being prepared for the anomalous case that does not follow the typical diagnostic path. In an attempt to remedy this situation, anatomically-based case studies should include: anomalous characteristics (i.e. innervation, vasculature not observed in the majority of the population) extracted from real clinical cases; case study questions that encompasses group discussion of all diagnostic possibilities (guided feedback and assessment); and a diagnosis appearing on a different page from the narrative, so that those students that want to use clinical reasoning to determine the diagnosis will be able to do so and then only refer to the actual diagnosis at their convenience.

### References

- <sup>1</sup>Popil, I, 2011. Promotion of critical thinking by using case studies as teaching method. *Nurse Education Today* **31(2)**: 204-207.
- <sup>2</sup>Herreid, C.F., 1997/1998. What makes a good case study? *Journal of College Science Teaching*. **27(3)**: 163-165.
- <sup>3</sup>Herreid, C.F., 1999,2000. Cooking with Betty Crocker: a recipe for case writing. *Journal of College Science Teaching* **29(3)**:156-158.
- <sup>4</sup>Billings D.M. and J.A. Halstead, 2005. *Teaching in Nursing: A Guide for Faculty*, W.B. Saunders, Philadelphia, PA.
- <sup>5</sup>Clark D.J. and J. Hott, 2001. Philosophy: a key to open the door to CT. *Nurse Education Today* **21(2)**:177-178.
- <sup>6</sup>Paul R., 1995. Critical thinking how to prepare students for rapidly changing world. *Foundations of Critical Thinking*, Santa Rosa, CA.
- <sup>7</sup>Kilminster S., D. Cottrell, J. Grant and B. Jolly, 2007. AMEE Guide No. 27: Effective educational and clinical supervision. *Medical Teacher* **29**: 2-19.
- <sup>8</sup>Ernstzen D.V., E. Bitzer and K. Grimmer-Somers, 2009. Physiotherapy students' and clinical Teachers' perceptions of clinical learning opportunities: a case study. *Medical Teacher* **31(3)**:102-115.
- <sup>9</sup>Nendaz M., A. Rudaz, A. Gut, M. Louis-Simonet, A. Perrier and N., Vu, 2013. Acquisition of clinical competence: added value of clerkship real-life contextual experience. *Medical Teacher* **35**: 957-62.
- <sup>10</sup>Rikers R., S. Loyens and H. Schmidt, 2004. The role of encapsulated knowledge in clinical case representations of medical students and family doctors. *Medical Education* **38(10)**: 1035-1043.
- <sup>11</sup>Durak H., 2007. Use of case-based exams as an instructional teaching tool to teach clinical reasoning. *Medical Teacher* **29(6)**:170-174.
- <sup>12</sup>Neistadt M., J. Wight and S. Mulligan, 1998. Clinical reasoning case studies as teaching tools. *American Journal of Occupational Therapy* **52(2)**: 125-132.

# MACUB 2014 Conference

## Poster Presentation Award Winners

### COMMUNITY COLLEGE

#### Biochemistry, Biophysics and Biotechnology

##### *First Place*

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

#### Developmental Biology and Genetics

##### *First Place*

Artem Gordon and Farshad Tamari  
*Proteomic Investigation of Style Development in Petunia hybrida: An SDS-PAGE Study of  
Total Proteins in Styles of Buds and Mature Flowers*  
Kingsborough Community College, Brooklyn, NY

##### *Second Place*

Yi Jiang and Urszula Golebiewska  
*Analysis of Genes Coding for tRNA in the Genome of Mycobacteriophage Littleton*  
Department of Biological Sciences, Queensborough Community College, Bayside, NY

##### *Third Place*

Weily Lang, Min Shin and Preethi Radhakrishnan  
*Antioxidants Boost Male Fertility: the Role of Reactive Oxygen Species  
in Modulating Fertility and Sperm Viability in D. melanogaster*  
LaGuardia Community College, Long Island City, NY

## **Environmental Biology and Ecology**

### **First Place**

Stephan Smith<sup>1</sup>, Sunil Dehipawala<sup>1</sup> and Harry Gafney<sup>2</sup>

*Characterization of Iron in Petroselinum crispum (Parsley) Using Mossbauer Spectroscopy*

<sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>Queens College, Flushing, NY

### **Second Place**

Safinaz Mashali and Christina P. Colon

*The Impact of Beach Renourishment on Spawning Habitat of the Atlantic Horseshoe Crabs (Limulus polyphemus) on Plumb Beach (Brooklyn NY)*

Department of Biological Sciences, Kingsborough Community College, CUNY, Brooklyn, NY

### **Third Place**

Washington Ramirez<sup>1</sup>, Jinnette Tolentino<sup>2</sup>, Ruel Z. Desamero<sup>2</sup>

*Determining the Structure of Citrate, Glycine and Zinc Complex in Aqueous Solution Using Vibrational Spectroscopy*

<sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>York College, Jamaica, NY

## **Microbiology and Immunology**

### **First Place**

Hyo Jung Shin, Maryam Khan and Susan McLaughlin

*The Effect of PKD2 Inhibitors on the Feeding Behavior of Hydra*

Biology Department, Queensborough Community College, Bayside, NY

### **Second Place**

Paula Delos-Reyes, Kimberly Deleon, Kanchanpreet Kaur, Chung Tse, Monica Trujillo and Mangala Tawde

*Preliminary Characterization of a Streptomyces Strain Collection*

Biology Department, Queensborough Community College, CUNY

### **Third Place**

Elizabeth Kulko, Elyssa Baron, and Luis Jimenez

*Cloning and Sequencing of 16S rRNA and ITS Genes Isolated from Compost DNA to Describe the Microbial Community of a Composting System*

Biology and Horticulture Department, Bergen Community College, Paramus, NJ

## **Physiology, Neuroscience and Clinical**

### **First Place**

**Loren Dubose<sup>1</sup>, Kurt Loney-Walsh<sup>1</sup>, Edward J. Catapane<sup>2</sup> and Margaret A. Carroll<sup>2</sup>**  
***p-Aminosalicylic Acid (PAS) Reverses the Neurotoxic Effects of Manganese  
on Dopamine Post-Synaptic Receptors***

**<sup>1</sup>Kingsborough Community College, Brooklyn, NY and <sup>2</sup>Medgar Evers College, Brooklyn, NY**

### **Second Place**

**Shanique Martin<sup>1</sup>, Juan Mosquera<sup>1</sup>, Jamel Travis<sup>2</sup> and Francisco Villegas<sup>2</sup>**  
***Spatial Learning and Memory in a Rat Model of Sporadic Alzheimer's Disease***  
**<sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>York College, Jamaica, NY**

**MACUB 2014 Conference**  
**Poster Presentation Award Winners**

**SENIOR COLLEGE**

**Biochemistry, Biophysics and Biotechnology**

**First Place**

**Brittany Dhital, Elizabeth Kolmus and Jeremy Seto**  
*Protein Interaction Networks and Novel Isoforms in Schizophrenia and Concordance  
in a Murine Model*  
New York City College of Technology, CUNY, Brooklyn, NY

**Second Place**

**Maria Carvalho, Dena Restaino, Nashali Ferrara, Zachary Fetske, Isabella Pastore,  
Paul A.X. Bologna, and John J. Gaynor**  
*Use of qPCR to Map the Distribution and Seasonal Changes in Early Developmental Forms  
of the Atlantic Sea Nettle (*Chrysaora quinquecirrha*) in Barnegat Bay, New Jersey*  
Dept. of Biology & Molecular Biology, Montclair State University, Montclair, NJ

**Third Place**

**Cynthia Xu, Joseph Frezzo and Jin Montclare**  
*Fluorinated Protein Block Polymers for Drug Delivery*  
New York University Polytechnic School of Engineering, Brooklyn, NY

## Developmental Biology and Genetics

### First Place (Tie)

Anum Aftab, Lee H. Lee and Sandra D. Adams  
*Effect of Black Tea Extract on Herpes Virus Type-2 Infection of A549 cells*  
College of Science and Mathematics, Department of Biology and Molecular Biology,  
Montclair State University, Montclair, NJ

Victor Leon, Jermin Adrawy and Terry L Kamps  
*Identifying Candidate Reproductive Genes from Apomictic Pistils of *Cenchrus ciliaris* (Buffelgrass) Using Genomic Methods*  
Biology Department, New Jersey City University, Jersey City, NJ

### Second Place (Tie)

Bushra Ali, Hassan Tahir, and Lee H. Lee  
*The Effects of Lipophilic Green Tea Polyphenols in Controlling Endospore Germination in *Bacillus cereus**  
Department of Biology and Molecular Biology, Montclair State University, NJ

Marc Philzaire<sup>1</sup>, Shiraz Mujtaba<sup>1</sup>, Kerry Burnstein<sup>2</sup> and Alice Levine<sup>3</sup>  
*MYST1 is the New Co-activator that Regulates the Proliferation of PCa Cells*  
<sup>1</sup>Department of Biology, Medgar Evers College, CUNY, Brooklyn, NY 11225, <sup>2</sup>Department of Molecular and Cellular Pharmacology, Miller School of Medicine, University of Miami, Miami, FL 33136 and, <sup>3</sup>Department of Medicine, Mount Sinai School of Medicine, NY, NY

## Environmental Biology and Ecology

### First Place

Sana Baig and Daniela Shebitz  
*Using Ethnobotanical Indicators for in vitro Antimicrobial Screening of Medicinal Plant Leaves from the Lowland Wet Forests of Costa Rica*  
Kean University, Union, NJ

### Second Place

Katherine Andrade<sup>1</sup>, Martha Jane Peters<sup>2</sup>, Alessa Vindas-Cruz<sup>1</sup> and Daniela Shebitz<sup>1</sup>  
*Causes of *Bromelia pinguin* Dominance in Lowland Wet Forests and its Effects on Plant Diversity in Costa Rica*  
<sup>1</sup>Kean University, Union, NJ and <sup>2</sup>Northwestern University, Evanston, IL

### Third Place

Hasani Douglas, Kortni Garcia, Shellyann Clarke-Lambert, Karl Ruddock and Dereck Skeete  
*Manganese Accumulation in Leaves and Radishes Grown in Manganese Supplemented Soils*  
Medgar Evers College, Brooklyn, NY

## **Microbiology and Immunology**

### **First Place**

James Stamos, Sandra D. Adams and Lee H. Lee  
*Inhibition of HSV-2 in Vero Cells by EGCG and EGCG-Stearate*  
Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ

### **Second Place**

Kirsten Simmons, Nicolle Segarra, Leslie Landy, Jonathan Valsechi-Diaz and Tin-Chun Chu  
*Synergistic Antibacterial Activity of Turmeric and Garlic with Selected Antibiotics*  
Seton Hall University, South Orange, NJ

### **Third Place**

Christopher Chen, Hassan Tahir and Lee H. Lee  
*Study the Effect of Different Tea Polyphenols on the Biofilm formation  
in Pseudomonas aeruginosa*  
Montclair State University, Montclair, NJ

## **Physiology, Neuroscience and Clinical**

### **First Place**

Giancarlo Perez, Reed C. Carroll and Anthony Torres  
*Role of Glutamate Receptor Interacting Protein 1 (GRIP1) in Pseudophosphorylated CaMKII  
Targeting Inhibitory Synapses*  
Biology Department, New Jersey City University, Jersey City, NJ

### **Second Place**

Mina Youssef, Jan Osea, Katrin Llanos and Natalia Coleman  
*The Role of NMDA Receptors in Cancer*  
New Jersey City College, Jersey City, NJ

### **Third Place**

Isaac Beaubrun<sup>1</sup>, Jalissa Wynder<sup>2</sup>, Tyler Bauman<sup>2</sup>, Jonathan Ewald<sup>2</sup>, Kimberly Keil<sup>2</sup>,  
Chad M. Vezina<sup>2</sup> and William A. Ricke<sup>2</sup>  
*Dioxin Exacerbates Prostatic Disease by Increasing Collagen Deposition in Mice Prostates*  
<sup>1</sup>Medgar Evers College, Brooklyn, NY and <sup>2</sup>University of Wisconsin-Madison, Madison, WI

**MACUB 2014 Conference**

**Poster Presentation Award Winners**

**MASTERS/DOCTORIAL**

Elizabeth Y. Flores and Quinn C. Vega  
*Transcriptional Changes that Occur in Response to the Activation  
of Receptor Tyrosine Kinase RET*  
Department of Biology and Molecular Biology, Montclair State University  
Montclair, NJ

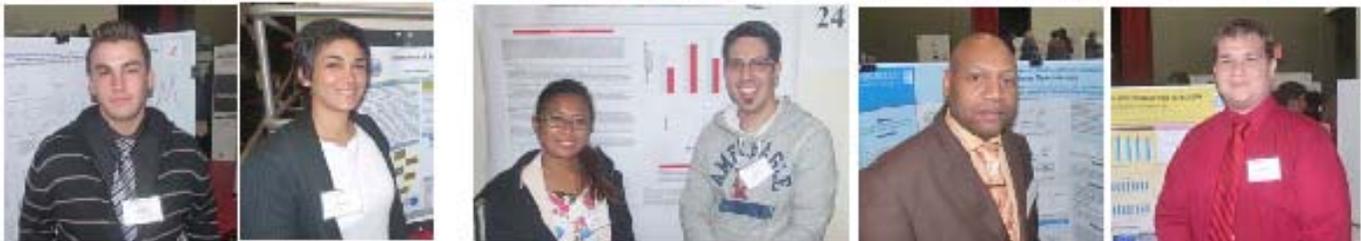
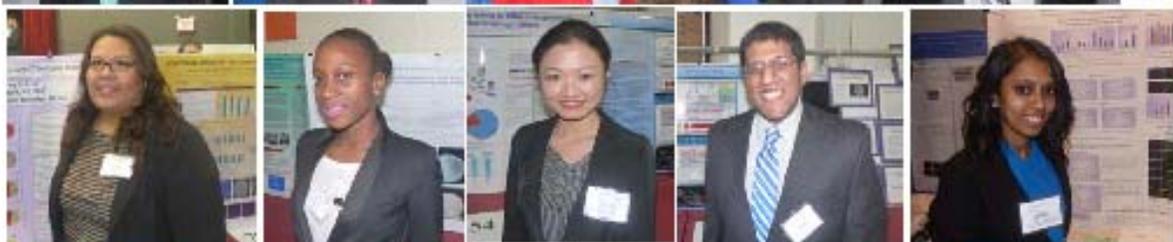
Zain A. Alvi, Tin-Chun Chu and Angela V. Klaus  
*Putative Transition Proteins in 12 Sequenced Drosophila Species*  
Department of Biological Sciences, Seton Hall University, South Orange, NJ

Ayuni Yussof, Syed Samy and Lee H. Lee  
*Synergistic Effect of Green Tea Polyphenols with Antibiotics on  
Escherichia coli and Staphylococcus aureus*  
Department of Biology and Molecular Biology, Montclair State University  
Montclair, NJ

Robert Newby Jr. and Tin-Chun Chu  
*Physiological and Molecular Analyses of ZnCl<sub>2</sub> Stress Response in Cyanobacterium  
Synechococcus sp. IU 625*  
Seton Hall University, South Orange, NJ

Cody Berkefeld, Sandra D. Adams, and Lee H. Lee  
*In Vitro Synergistic Antiviral Activity of Black Tea Theaflavins and Acyclovir on  
Herpes Simplex Virus Types 1 and 2 in A549 Cells*  
Department of Biology and Molecular Biology, Montclair State University  
Montclair, NJ.

Derek Prince and Tin-Chun Chu  
*Antiviral Activity of Polygonum multiflorum*  
Seton Hall University, South Orange, NJ







## MACUB 2014 Conference Poster Abstracts

**Determinants of Repressor Function: Analysis of Clustering through Immunity Assays.** Patrick M. Abbazia, Rhadames Acosta, Emily E. Barner, Jacob Bennett, Anthony Campbell, Darren Chew, Christopher Clemente, Kiara Cornejo, Caitlin Cox, David Del Grande, Zachary DeLong, Bethany DeVault, Andrew Hamm, Donyelle Harrigan, Jordan Huffman, Zachary Kameron, Colleen Kelly, M. Dalton Kern, Deborah Kim, Christine Kline, Hee Jae Ko, Brian Laxamana, Isamar Lopez, Joshua Lim, Sarah Mam, Genesis Martinez, Stephen Masi, Greg Mastrangelo, Aesha Newton-Ashley, Brandone Roberts, Eddy Santos, Joshua Schoch, Vincent Scuttaro, Jacqueline Simeon, Michael Traylor, Kimberly T. Valle, Teyanna Weekes, Mitchell Woodford, Lanese Henry, Peter J. Park, and Jacqueline M. Washington, Nyack College, Dept. Natural Sciences, Nyack, NY.

During 2013-14, the second year of the SEA-PHAGES program at Nyack College, phage hunters isolated and characterized 18 mycobacteriophages which infect the strain *Mycobacterium smegmatis* mc<sup>2</sup>155, from the New York/New Jersey area. Six of these phages were sequenced and classified into clusters A, E, or F. BeesKnees and Dynamix are A1 phages, BabyRay and DaHudson are A3 phages, SuperGrey is an F1 phage, and Tuco belongs to Cluster E. Phages were isolated from independent soil samples, with the exception of BeesKnees and Tuco, found in the same soil sample. Bioinformatic analysis revealed that DaHudson has 23 stoperators that match the published A3 stoperator consensus sequence GTTCTCTGTCAAG, which is typical of A3 phages. BabyRay is different, having only two matches to this A3 consensus, but it has 24 matches to the A4 stoperator consensus sequence GTGCGATGTCAAG. Comparative analysis of repressors show that the A3 phages with the A4-like stoperator consensus are more similar to each other and other A4 phages such as Peaches and Eagle than to the other A3's. Immunity assays were performed using lysogens made from 16 phages, including all six that were sequenced. DaHudson was unable to superinfect A3 lysogens as expected, but surprisingly, unable to superinfect the E, F1, and some putative

Cluster A lysogens. Interestingly, a SuperGrey lysogen of *M. smegmatis* was homoimmune to DaHudson, several unsequenced putative A3 phages and Tuco (E) but not to BabyRay. In addition, a MichelleMyBell lysogen was homoimmune to A3 phages, with the exception of BabyRay. We thank the Howard Hughes Medical Institute, University of Pittsburgh, and Queens College for their assistance on this project.

**Construction of Rhomboid SCO3855-*S.coelicolor* Knock-out Mutant.** Brandon Ackerman, Naydu Carmona, Peter Novick and Monica Trujillo, Queensborough Community College, CiUNY, Bayside NY.

Rhomboid proteins are intramembrane proteases originally discovered through genetic analysis of *Drosophila* embryogenesis that are now known to have animal, plant, protozoan, and bacterial homologues. Their role in bacteria is mostly unknown. This project aims to elucidate the role of these proteases in *Streptomyces*. These bacteria have a complex developmental cycle, a signaling system not fully characterized, and produce the majority of antibiotics used in medicine and agriculture, as well as pharmacologically active metabolites with anti-tumor, anti-parasitic, and/or herbicidal properties. *Streptomyces coelicolor* is the model species for the study of *Streptomyces* biology, as genetic tools to manipulate the strain have been developed, and its genome has been fully sequenced. Our preliminary genomic analysis has identified four putative rhomboid homologues in *S. coelicolor*. For the current project, we propose to characterize the biological function of one of these genes (SCO3855) by constructing a knockout mutant and comparing its properties with the wild type counterpart.

**Effect of Black Tea Extract on Herpes Virus Type-2 Infection of A549 cells.** Anum Aftab, Lee H. Lee and Sandra D. Adams, College of Science and Mathematics, Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ.

One of the leading causes of sexually transmitted diseases, STD's is Herpes Simplex Virus type-2 (HSV-2). This enveloped virus belongs to  *$\alpha$ -Herpesviridae* subfamily and consists of a double stranded DNA enclosed in a

capsid in the inner core. The outer core contains tegument proteins that are covered by glycoproteins. HSV-2 virus initiates infection by infecting epithelial cells through lytic infection following a latent infection supported by the neurons. Currently, there is no cure for HSV-2 infections. *Camellia sinensis* produces Black Tea Extract (BTE) that contains theaflavins, the main type of flavanol in BTE. Theaflavin is a dimer of different catechins and its fermentation causes the catechins to polymerize producing theaflavins and thearubigens. Cells are protected against damage due its high antioxidative properties and a high number of hydroxyl (OH) groups that surround the theaflavins. Previous studies reported that theaflavins are capable of inhibiting certain types of viruses. Similarly, the purpose of this study was to determine if BTE with concentrated amounts of theaflavins can inhibit HSV-2 infection in A549 cells. A cell viability assay and cell proliferation assay were used to observe the effect of BTE concentration, ranging from 14mM to 0.014nM, on A549 cell morphology, proliferation, and toxicity. Cell treated extracts and virus treated extracts were collected and viral titer was determined through TCID<sub>50</sub> or tissue infective dose. An antiviral cell proliferation assay and plaque assay were used to determine the effect of BTE concentrations and virus on A549 cells and viral titer. Major findings showed inhibition of HSV-2 is achieved at 1.4mM concentrations of BTE.

**A Comparison of Summer Macroinvertebrate Communities and Selected Environmental Factors in Two Locations of Muddy Branch Tributary, Montgomery County, Maryland. Chantal Agnew and Donald Stearns, Wagner College, One Campus Road, Staten Island NY.**

The issue of understanding and preserving healthy water quality in our ecosystems is of enormous importance. The purpose of this research was to compare the overall stream water quality of two different sites along the Muddy Branch Tributary of the Potomac River in Montgomery County, Maryland: West Side Drive (near the head of the tributary in an urban area) and Blockhouse Conservation Point Park (in the conservation park region of the same tributary). To determine water quality, the sites were compared for physicochemical parameters (pH, chloride, phosphate, nitrate, dissolved oxygen, stream flow rate), as well as macroinvertebrate biodiversity. While free phosphate levels were low at both sites, and nitrate levels were consistent with healthy streams at both sites, Blockhouse Conservation Point Park showed generally higher water quality

indicators than West Side Drive for pH ( $p < 0.05$ ), dissolved oxygen, chloride ( $p < 0.05$ ) and biodiversity. The better health of Blockhouse Conservation Point Park could be attributed to its location in a conservation park where it is directly exposed to much less runoff and pollution from roads, factories, and other impervious surfaces, compared with the West Side Drive site.

**The Effects of Lipophilic Green Tea Polyphenols in Controlling Endospore Germination in *Bacillus cereus*. Bushra Ali, Hassan Tahir, and Lee H. Lee, Department of Biology and Molecular Biology, Montclair State University, NJ.**

Endospores pose high concern when found in various environments due to their highly resistant characteristics. To investigate a method in controlling endospore germination, particularly outgrowth, purified endospores were treated with two types of lipophilic green tea polyphenols on *Bacillus cereus*: cLTP (crude lipophilic green tea polyphenols) and pLTP (purified lipophilic green tea polyphenols). The aim of this experiment is to test the minimal treatment time needed to kill off *Bacillus cereus* endospores with a range of 95%-100% of inhibition. The American Society for Testing and Materials (ASTM) method-purified 10-day grown spore crops were boiled at 100°C for 20 minutes to kill any remaining vegetative cells. Heated samples were treated with 1% and 5% of cLTP and pLTP for 5-, 10-, 15-, and 30 minutes, diluted and plated onto nutrient agar plates, and subsequently incubated at 37°C for 24 hours. Non-starved cells and starved cells without treatment were designated as controls. Transmission electron microscopy (TEM) photographs with pLTP treatment display complete spore surface disruption. cLTP (1%) treatment at 15 minutes resulted in an average inhibition of 98.7% and pLTP (1%) treatment at 15 minutes resulted in an average inhibition of 99.6%. In comparison, cLTP (5%) treatment at 15 minutes resulted in an average inhibition of 99.9% and pLTP (5%) treatment at 15 minutes resulted in an average inhibition of 100.0%. Results obtained suggest that these lipophilic green tea polyphenol compounds play a role in inhibiting endospore germination best at a 5% concentration and at a 15-minute treatment time. This experiment proposes that natural antimicrobial compounds may aid in preventing food and beverage spoilage caused by spore-forming bacteria, prevent contamination of devices in the medical industry, and overall help control the germination of *Bacillus cereus* endospores.

**ATP Modulates Hypothalamic Oxytocin Exocytosis via Mitochondrial Calcium. Michael Altamari<sup>1</sup> and Jaya Halder<sup>2</sup>, <sup>1</sup>Queensborough Community College/CUNY and <sup>2</sup>St John's University, Queens, NY.**

Previous investigators in our laboratory have demonstrated oxytocin (OT) release from the posterior pituitary, midbrain, and spinal cord. The current work extends this observation to hypothalamic synapses. Synaptosomes were prepared from the hypothalamus of 30-day-old Sprague Dawley rats. Data suggest that ATP has a stimulatory effect on the release of oxytocin from hypothalamic synaptosomes. A minimum increase of 200% in release of OT over control was observed. Data obtained with pyridoxal phosphate 6-azophenyl-2',4' disulfonic tetrasodium salt (PPADS), a selective P2X<sub>1</sub>, 2 or 3 receptor antagonist, demonstrate that ATP mediated release of OT may not be associated with stimulation of a P2X purinergic receptor. Data from ATPγS, a selective agonist of P2X<sub>4/6</sub> receptors suggests that P2X<sub>4</sub> or X<sub>6</sub> receptors are not active. ADP, agonists of P2Y receptors, did not stimulate release. GTP did not stimulate OT to the same extent as ATP arguing against a simple metabolic effect for ATP. These data suggest an alternative mechanism in hypothalamic synaptosomes that is not directly mediated by a known receptor. Experiments with CGP37157, a mitochondrial Ca<sup>++</sup> efflux channel antagonist, inhibited OT release from hypothalamic synaptosomes. These data suggest that calcium sequestration and release by mitochondria play an important role in the control of OT release from hypothalamic synaptosomes.

**Putative Transition Proteins in 12 Sequenced Drosophila Species. Zain A. Alvi, Tin-Chun Chu and Angela V. Klaus. Department of Biological Sciences, Seton Hall University, South Orange, NJ.**

The current study is aimed at identifying and analyzing the conserved domains that are found in transition proteins in the original 12 sequenced species of *Drosophila*. These proteins facilitate the process of nuclear transformation during spermiogenesis. The transition proteins (TPL94D in *Drosophila melanogaster*) aid in transitioning the histone bound sperm DNA to a protamine (protamine-like in *D. melanogaster*) bound sperm DNA. We have putatively identified sequences for transition proteins in *D. simulans*, *D. sechellia*, *D. yakuba*, *D. erecta*, and *D. pseudoobscura* by using the reference sequences found in *D.*

*melanogaster*. Our current work indicates that TPL94D is conserved among the *Drosophila* species in the melanogaster group and in *D. pseudoobscura*, but not in the subgenus *Drosophila*. All TPL94D matches have a putative conserved DNA binding domain. RNA-Seq differential expression analysis on the testes revealed that the identified sequences for TPL94D are highly expressed in *D. melanogaster*, *D. simulans*, *D. yakuba*, and *D. pseudoobscura*.

**Establishing the Embryonic Zebrafish as a Model of Neuronal Development Under Environmental Stressors. Amith, M.<sup>1</sup>, Sherine, F.<sup>1</sup>, Chan, K.<sup>1</sup>, Hernandez, A.<sup>1</sup>, Arumov A.<sup>1</sup>, Ciprian, A., Agosto A.<sup>1</sup>, Aspiazu, K.<sup>1</sup>, Demaria, A.<sup>1</sup>, Feratovic, E.<sup>1</sup>, Fletcher, D.<sup>1</sup>, Nolan, K.<sup>1</sup> and Dell A. L.<sup>1,2</sup>. <sup>1</sup>Department of Biology St. Francis College, Brooklyn, NY and <sup>2</sup>Department of Neuroscience, University of Pennsylvania, Philadelphia, PA.**

Neuronal and cardiac birth defects are correlated with pesticide application and water quality. Human exposure to these pollutants may occur through drinking water, or during contact with water in recreational areas, but the molecular pathways that cause these defects are not well defined. In order to investigate the roles of common environmental pollutants on neuronal development, we collected and analyzed samples from recreational freshwater sources in the New York Metropolitan Area. Sample sites included Alison Pond (Queens), Clove Lake (Staten Island), Flushing Meadows Park (Queens), Lakes Mahopac and Cassie (Putnam County), The New Croton Reservoir (Westchester County), Snug Harbor Botanical Garden (SI), Spuyten Duyvil Pond (Bronx), and Willowbrook Park Pond (Staten Island). Two types of spring water (Poland Spring and Gerolsteiner) served as our controls. For each location we measured pH, Ammonia Nitrogen, Free Chlorine, Dissolved Oxygen, Nitrate and Phosphate. pH levels ranged between pH 6 and pH8 for all samples tested. We observed high phosphate levels (0.5ppm) in Willowbrook Park and elevated nitrate levels in Lake Mahopac, Spuyten Duyvil Pond, and Allison Pond. Low dissolved oxygen levels were observed in Flushing Meadows Park and Allison Pond. Our next step is to examine the morphology and neuronal development of zebrafish embryos raised in water from sample sites, and correlate observed developmental changes with alterations in gene expression. This work was supported by a St. Francis College Faculty Research Grant.

**Causes of *Bromelia pinguin* Dominance in Lowland Wet Forests and its Effects on Plant Diversity in Costa Rica.** Katherine Andrade<sup>1</sup>, Martha Jane Peters<sup>2</sup>, Alessa Vindas-Cruz<sup>1</sup> and Daniela Shebitz<sup>1</sup>, <sup>1</sup>Kean University, Union, New Jersey, USA and <sup>2</sup>Northwestern University, Evanston, Illinois.

*Bromelia pinguin* is a plant species found in the northern area of Costa Rica at the Maquenque National Wildlife Refuge (MNWLR). An estimated 200 km<sup>2</sup> of primary forest are being lost per day. Since this is a threatened ecosystem, this study was characterized by focusing on one of the plants that has a huge influence in transforming an understory. *B. pinguin* grows in dense patches in the primary forest of the Maquenque National Wildlife Refuge. This study was designed to determine what environmental variables contribute to *B. pinguin* forming dense monocultures and how its dominance influences other plants. A survey was conducted to measure the dimensions of each *B. pinguin* patch found within the total area of approximately 1 km<sup>2</sup> of the primary forest. The recorded *B. Pinguin* patches ranged from 6.7 m x 1 m to 93.8 m x 22.2 m. Ten randomly selected *B. pinguin* dominant patches (BDP) were set. Each plot consisted of a designated area that represented the center, edge, and outer area of each BDP. Data indicates the most significant differences were seen in the center plots which had less species diversity and greater total % understory. Interestingly, the trends were pronounced at center plots but diversity recovered immediately at the edge and outer plots. The biggest differences seen were plant diversity though abiotic variables such as soil characteristics and light, tended to remain consistent with no significant relationships. Abiotic variables and plant data suggests that BDP are most pronounced on South facing slopes. This work was supported and funded by the National Science Foundation Research Experience for Undergraduates and Kean University.

**Using Ethnobotanical Indicators for *in vitro* Antimicrobial Screening of Medicinal Plant Leaves from the Lowland Wet Forests of Costa Rica.** Sana Baig and Daniela Shebitz, Kean University, Union, NJ.

Traditional medicine remains the primary drug treatment for 80% of people in developing countries (WHO 2011). Globally, most communities do not have access to conventional medicines and their health is inextricably linked to the availability of plant resources. The tropical wet

lowland forests of Maquenque National Wildlife Refuge (MNWLR) in the Northern Zone of Costa Rica provide habitat to numerous medicinal plants, yet few have been documented. By virtue of its proximity to the border, this biologically diverse area has a blending of Nicaraguan and Costa Rican cultures. The objectives of this research were: (1) to document the commonly used medicinal plant species in the MNWLR based on local knowledge and (2) to determine if extracts from these medicinal plants used to treat infection would show antifungal and antibacterial properties in laboratory assays. Semi-structured, open-ended interviews were conducted with seven people who were locally recognized for their knowledge of medicinal plant use. Uses and preparations were discussed for 60 species. Fifteen of the most commonly cited plants were gathered with the local informants from the forests or home gardens. Alcohol and aqueous extractions were made of plant parts that were specified. Extracts were screened against gram-negative bacterium *Escherichia coli*, gram-positive bacterium *Bacillus subtilis*, and fungus *Candida albicans* using triplicate disc diffusion assays. Preliminary results indicate that many of the plants used locally for medicine do indeed have efficacy in-vitro. This work also includes contributions from Katherine Andrade, Betsy DeLa Cruz, Elvin Demereckas, Diego Morales, and Alessa Vindas-Cruz.

**Molecular Characterization and Antimicrobial Susceptibility of *Staphylococcus aureus* isolates from a Healthy Student Population.** Elyssa Baron, Elizabeth Kulko and Luis Jimenez, Biology and Horticulture Department, Bergen Community College, Paramus, NJ.

Phenotypic tests, PCR analysis, and DNA sequencing were used to determine the frequency of *S. aureus* in a healthy student population. Sterile swabs from the nostrils were streaked on mannitol salt and blood agar. All isolates exhibiting beta hemolysis and mannitol fermentation were analyzed by using the coagulase test and Gram stain. PCR amplification of the isolates DNA detected a 273 bp DNA fragment encoding for a 16S rRNA gene. DNA sequencing and BLAST analysis of the amplified ribosomal genes demonstrated a 98% homology with *S. aureus* 16S rRNA genes. Six percent of the subjects were confirmed to carry *S. aureus* in the nares. Antimicrobial testing showed that the *S. aureus* isolated from a healthy population were susceptible to several antibiotics, peppermint oil, and lavender oil.

**Dioxin Exacerbates Prostatic Disease by Increasing Collagen Deposition in Mice Prostates.** Isaac Beaubrun<sup>1</sup>, Jalissa Wynder<sup>2</sup>, Tyler Bauman<sup>2</sup>, Jonathan Ewald<sup>2</sup>, Kimberly Keil<sup>2</sup>, Chad M. Vezina<sup>2</sup> and William A. Ricke<sup>2</sup>,  
<sup>1</sup>Medgar Evers College, Brooklyn, NY and <sup>2</sup>University of Wisconsin-Madison, Madison, WI.

2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) is a persistent environmental toxin capable of causing increased incidents of prostatic diseases such as benign prostatic hyperplasia (BPH) and prostate cancer (PRCA). BPH is a disease causing prostate enlargement leading to obstruction of the prostatic urethra impeding urine flow. PRCA is a disease described as overexpression of carcinoma cells that can metastasize to neighboring organs. Physiological levels of hormones are also associated with prostate disease in older males. We hypothesized that dioxin and adult hormone exposure will increase collagen deposition in the prostate. Here we investigated the effects on in utero dioxin exposure on collagen content in the prostate of genetically modified mice (GEM). GEM were administered TCDD while mice received oil as a vehicle. When male pups reached sexual maturity were surgically implanted with subcutaneous pellets containing Testosterone (T) and Estradiol (E<sub>2</sub>). We examined the histology of the bladders, prostates, seminal vesicles and urethras stained using picosirius red (PSR) to assess collagen fiber content of treated and untreated mice. As a result an increase in red birefringence was seen in the ventral prostate lobe, and no indication of increased birefringence distribution was seen in the anterior and dorsolateral prostate lobes. In conclusion, TCDD induces collagen deposition in the ventral prostate lobes indicating bladder outlet obstruction and lower urinary tract symptoms in mice.

**Genetic Engineering of a Novel *Streptomyces* Strain.** Linsy Benjamin and Monica Trujillo, Queensborough Community College, CUNY, Bayside, NY.

MTE4a is a *Streptomyces* strain isolated from New York soil. MTE4a is a prolific producer of secondary products and recently we have sequenced part of its genome. A diterpene, 17 hydroxy cyclooctatin has been isolated and characterized from this strain. We are interested in elucidation of the metabolic pathway for the

synthesis of this compound. The first step is to develop the protocols to introduce DNA into this new strain. The current project is the development of protocols for conjugation with *E. coli* to modify the MTE4a strain.

***In Vitro* Synergistic Antiviral Activity of Black Tea Theaflavins and Acyclovir on Herpes Simplex Virus Types 1 and 2 in A549 Cells.** Cody Berkefeld, Dr. Sandra D. Adams, and Lee H. Lee, Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ.

Herpes simplex virus (HSV) is responsible for one of the most common infections within the population. The primary antiviral used against HSV infections are nucleoside analog drugs such as acyclovir. However, in recent years the number of cases of drug resistant HSV has increased, resulting in interest for new novel treatments. Promising antiviral agents are theaflavins found within black tea derived from *Camellia sinensis*. These theaflavins include theaflavin (TF1), theaflavin-3-monogallate (TF2A), theaflavin-3'-monogallate (TF2B), and theaflavin-3-3'-digallate (TF3). Previous studies have supported that theaflavins from black tea, specifically TF3, interact with viral surface proteins thus interfering with the process of absorption. Due to this mode of action, black tea theaflavins show potential for synergistic antiviral activity when combined with drugs such as Acyclovir. This study examined the antiviral activity of black tea extract and TF3 with acyclovir on HSV-1 and HSV-2 infections in A549 cells. Cytotoxic analysis was performed with a cell viability and proliferation assay supporting that concentration of 100 µM of TF3 or 100 µM BTE in combination with 5 µM of acyclovir showed no cytotoxicity. Antiviral activity was measured using a WST-1 based antiviral assay. In each case theaflavins showed higher antiviral activity when combined with acyclovir. Moreover, the mixture showed higher antiviral activity than acyclovir alone. Furthermore, isolated TF3 with acyclovir showed higher levels of viral inhibition than the combination of theaflavins with acyclovir. In conclusion, acyclovir and black tea theaflavins have shown synergistic activity and may provide an alternative regimen to decrease prevalence of resistant strands of HSV types 1 and 2.

**Presence of Octopamine Receptors in Heart of the Bivalve *Crassostrea virginica*. Fiana Bess, Ave Harris, Christopher Welsh, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College, Brooklyn, NY.**

Octopamine, a biogenic amine first identified in octopus, is well studied in arthropods and gastropods where it functions as a neurotransmitter and hormone. The presence or function of octopamine has rarely been reported in bivalves. Previously, using HPLC we found octopamine in cerebral ganglia, visceral ganglia, gill, heart, palps and hemolymph of the oyster *Crassostrea virginica* and using immunohistofluorescence we visualized octopamine in cerebral ganglia, visceral ganglia, gill and heart. Our physiological studies also found that octopamine was cardio-active when applied to *C. virginica* and *Mytilus edulis* hearts. We hypothesize that octopamine receptors are present in the heart of *C. virginica*. To test this we did Western Blot analysis using an pan TAAR (trace amine-associated receptor) primary antibodies, which are reactive with octopamine, beta-phenylethylamine (b-PEA), p-tyramine (p-TYR) and tryptamine receptors, but unresponsive to classical biogenic amines and histamine receptors. For Western Blot analysis, heart tissue lysate was prepared by polytron disruption in ice-cold NP-40 detergent buffer containing protease inhibitor, followed by centrifugation to obtain supernatant with solubilized membrane proteins. Up to 30 µg of solubilized protein was subjected to SDS-PAGE with 10% acrylamide gels and electroblotted onto nitrocellulose. Pan TAAR receptor immunoreactivity was revealed after incubation with primary antibodies followed by incubation with HRP-conjugated secondary antibodies. The Western Blot studies showed a strong band at 85 kD corresponding to octopamine receptors in heart. The present project, coupled with our immunohistofluorescence and cardio-physiology studies, confirms the presence of octopamine receptors and furthers the understanding of a physiological role for octopamine in *C. virginica*. This work was supported by grant 0516041071 of NYSDOE.

**Prevalence of *Escherichia coli* Among Ruminants in Public Animal Settings in Both Cold and Warm Temperatures. Judith Betz<sup>1</sup>, Marc Valitutto<sup>2</sup>, Kathleen A. Bobbitt<sup>1</sup> and Christopher P. Corbo<sup>1</sup>, <sup>1</sup>Department of Biological Sciences, Wagner College, Staten Island, NY and <sup>2</sup>Staten Island Zoo, Staten Island, NY.**

Public settings that have animal interaction exhibits, such as petting zoos are popular attractions but can be associated with zoonotic disease outbreaks in humans. A common zoonotic bacteria is *Escherichia coli* which is part of the natural intestinal bacterial flora in ruminants such as cattle, sheep, and goats. When interacting with these species in a petting zoo setting, hand washing is strongly advised as the most important defense against bacterial disease. In this study, animals were sampled to see if *E. coli* was present and if the difference in seasons made an impact on the prevalence of the bacterium. A test of sensitivity was done on positive samples with common antiseptic solutions to see if *E. coli* is inhibited. Samples were collected from the oral cavity, pelage, and anus of the small ruminants of an immersion exhibit in a local petting zoo. In the winter, the percentage of positive *E. coli* found from the anus was approximately 79% and 21% found from the pelage. In the summer *E. coli* was detected in 40% of samples from the anus, 20% found from the pelage, and approximately 36% found from the oral cavity. There were seven animals total that accounted for positive *E. coli* samples in both the winter and the summer; five of which were ruminants. For the total collection of samples from this study which took place from March to August of 2014, approximately 74% came from ruminants. Roughly 54% of all positive *E. coli* samples were collected from the anus of the animals, 23% were found from the pelage and 23% from the oral cavity. Disk sensitivity tests concluded that 87% of *E. coli* was inhibited by the use of GOJO Hand Soap.

**Characterization of *Leishmania major* Phosphatidylethanolamine Methyltransferases *LmjPEM1* and *LmjPEM2* and Their Inhibition by Choline Analogs.** Stergios S. Bibis<sup>1,2</sup>, Kelly Dahlstromc, Tongtong Zhua and Rachel Zufferey<sup>1,3</sup>, <sup>1</sup>Department of Biological Sciences, St John's University, Jamaica, NY, <sup>2</sup>Biology Department, University of Bridgeport, Bridgeport, CT and <sup>3</sup>Department of Biochemistry, Kansas State University, Manhattan, KS.

Phosphatidylcholine (PC) is the most abundant phospholipid in the membranes of the human parasite *Leishmania*. It is synthesized via two metabolic routes, the *de novo* pathway that starts with the uptake of choline, and the threefold methylation of phosphatidylethanolamine. Choline was shown to be dispensable for *Leishmania*; thus, the methylation pathway likely represents the primary route for PC production. Here, we have identified and characterized two phosphatidylethanolamine methyltransferases, *LmjPEM1* and *LmjPEM2*. Both enzymes are expressed in promastigotes as well as in the vertebrate form amastigotes, suggesting that these methyltransferases are important for the development of the parasite throughout its life cycle. These enzymes are maximally expressed during the log phase of growth which correlates with the demand of PC synthesis during cell multiplication. Immunofluorescence studies combined with cell fractionation have shown that both methyltransferases are localized at the endoplasmic reticulum membrane. Heterologous expression in yeast has demonstrated that *LmjPEM1* and *LmjPEM2* complement the choline auxotrophy phenotype of a yeast double null mutant lacking phosphatidylethanolamine methyltransferase activity. *LmjPEM1* catalyzes the first, and to a lesser extent, the second methylation reaction. In contrast, *LmjPEM2* has the capacity to add the second and third methyl group onto phosphatidylethanolamine to yield (lyso)PC; it can also add the first methyl group, albeit with very low efficiency. Finally, we have demonstrated using inhibition studies with choline analogs that miltefosine and octadecyltrimethylammonium bromide are potent inhibitors of this metabolic pathway.

**Uncontrolled Non-Production Materials Have Led to a High Audit and Injury Risk at 18 Chrysler Facilities.** Tiffany Bobb-Semple, Amy Humphries and Shelly Nault, Medgar Evers College, Brooklyn, NY and Chrysler Group LLC, Auburn Hills, MI.

Over the past six (6) years, 18 Chrysler Facilities has been cited with similar audit conditions of Uncontrolled Non-Production Materials. The intensity of this issue promoted the risk of injury, undetected losses, inaccurate inventory records, difficulty in locating required materials, excessive aging material on the plant floor, and continued unnecessary purchases for parts that were already available. It was estimated to be costing the company millions of dollars. After fully analyzing the issue from a World Class Manufacturing standpoint, we hypothesized that the audit and injury risk would be reduced if an effective tagging solution was set in place and materials were 5S (Sift, Sort, Sweep, Sustain, and Sanitized). We led a Major Kaizen across every Chrysler facility, in which we communicated the issue with every plant staff, assisted with the identification of the non-production materials and provided a checklist to all plants for them to perform regular audits and provide a status update to their plan. During the processes of the Major Kaizen, we completed a Full Advanced 5W1H as well as a Relations and Affinity diagram, and found that there were no proper tagging solutions set in place to locate the Uncontrolled Non-Production Materials. To further complete the Project, we created several tagging solutions that will be read across all Chrysler Facilities in order to reduce the high audit risk, and created One Point Lessons on how to store certain materials that were left in the open to reduce injury. The study showed that an effective tagging/inventory solution can be used to locate the Uncontrolled Non-production Materials, as well as minimizing materials left in the open with an effective storage, which will then reduce a high audit risk and injury.

**Histamine and Histamine Receptor Involvement in Sensory-Motor Integration of Gill Lateral Cell Cilia Activity in the Bivalve *Crassostrea virginica*.** Beatrix Boissette, Ave Harris, Patrick Akande, Edward J. Catapane and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.

*Crassostrea virginica* gill lateral cells are innervated by serotonin and dopamine nerves. While motor aspects have been well studied, the sensory side has not. Histamine is a neurotransmitter and ligand for sensory receptors in invertebrates, but studies in bivalves have rarely been reported. We used HPLC to quantify histamine in ganglia and tissues of *C. virginica*. We also found *C. virginica* can adjust lateral cell cilia beating in response to chemical cues, including histamine applied to mantle. Histamine does not alter cilia beating when applied to gill. Applying histamine to mantle decreased cilia beating. Our studies show the mechanism involves sensory tentacles of mantle rim and visceral ganglia, indicating histamine is a sensory neurotransmitter in mantle receptor cells synapsing with afferents going to visceral ganglia. We hypothesize histamine receptors are present in mantle. To test this we used histamine H1, H2 and H3 receptor agonists and antagonist at the mantle rim. Dose responses were conducted and cilia beating observed. H2 agonists and antagonists had the strongest effects. For Western Blot analysis, mantle body and mantle rim lysates were prepared by polytron disruption in NP-40 detergent buffer containing protease inhibitor, followed by centrifugation to obtain supernatant with solubilized mantle body and mantle rim membrane proteins. Up to 30 Fg of protein was subjected to SDS-PAGE with 10% acrylamide gels and electroblotted onto nitrocellulose. H2 receptor immunoreactivity was revealed after incubation with primary antibodies followed by HRP-conjugated secondary antibodies, then resolved via colorimetric development using CN/DAB substrate kit. Western Blot showed a band at 70 kD corresponding to H2 receptors in mantle body and mantle rim. The study shows mantle body and rim contain H2 receptors and demonstrates a role of histamine in sensory-motor integration of gill lateral cell cilia activity. Supported by 2R25GM0600309 of NIGMS and 0516041071 of NYSDOE.

**Optimization of Biofuel Production in *Chlamydomonas Reinhardtii* by Introduction of a Synthetic *FATB2* Gene.** Elizabeth Calvente<sup>1</sup>, Maritza Galeas<sup>1</sup>, Kamai Silber<sup>1</sup>, Natasha Tsay<sup>1</sup>, Joseph Saccente<sup>1</sup>, Dimitrios Papamichail<sup>2</sup> J. Robert Coleman<sup>1</sup> and Kerry A. Lutz<sup>1</sup>, <sup>1</sup>Bioscience Department, Farmingdale State College, Farmingdale, NY and <sup>2</sup>Department of Computer Science, The College of New Jersey, Ewing, NJ.

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

**A Comparison of the Effectiveness of Traditional and Nontraditional Antifungal Agents. Sashane A. Campbell, Mary T. Ortiz and Loretta Brancaccio-Taras, Kingsborough Community College, Brooklyn, NY.**

Traditional agents are available to treat fungal infections. These treatments have become less useful due to development of microbial resistance and toxic effects these agents cause to humans. Therefore, new agents and probiotics are being studied due to their less toxic nature and potential as economical alternatives to traditional drugs. This study examined the effectiveness of alternative agents in comparison to traditional antifungal treatments. The hypothesis is: Nontraditional agents (tea tree oil, burdock root, garlic, echinacea, probiotic 10, probiotic *Acidophilus*) will be at least as effective as nystatin in killing the fungi *Saccharomyces cerevisiae* and *Candida albicans*. The procedure was a standard agar diffusion assay. Tryptic soy agar plates were inoculated with the test fungi; disks of nystatin and the nontraditional agents were placed on the surface of the inoculated plates. Plates were incubated (24h, 37°C) and zones of inhibition measured. Fourteen trials were conducted; zone sizes were averaged and compared statistically using the Mann-Whitney U-test. Based on the statistical analysis probiotic 10, probiotic *Acidophilus*, burdock root, garlic and echinacea were not as effective as the traditional antibiotics in killing *S.cerevisiae* and *C.albicans* ( $p < 0.05$ , two-tailed). However, tea tree oil was statistically more effective than nystatin. The mean zone size  $\pm$ SEM for nystatin against *C. albicans* was  $22.10 \pm 0.53$ mm; for *S. cerevisiae*, the mean zone size was  $28.10 \pm 0.42$ mm. In comparison, zones sizes produced when using tea tree oil were  $28.79 \pm 0.42$ mm for *C. albicans* and  $43.64 \pm 4.03$ mm for *S. cerevisiae*. Based on these results, the hypothesis is rejected for probiotic 10, probiotic *Acidophilus*, burdock root, garlic, and echinacea. However, the hypothesis is accepted for tea tree oil. Studies are required to confirm the effectiveness of tea tree oil and determine minimum concentrations at which is it most effective to treat fungal infections. This work was supported by grants NIH 2R25GM06003 (Bridge Program) and CSTEP 0537121091 (NYSED).

**Cloning and Sequencing of 16S rRNA Genes Isolated from Soil DNA to Detect the Predominant Bacterial Species in New Jersey Soils. Isabella Canals, Elyssa Baron and Luis Jimenez, Biology and Horticulture Department, Bergen Community College, Paramus, NJ.**

Microbial DNA was extracted from soil samples using the ZR Soil Microbe DNA MiniPrep protocol. Eubacteria ribosomal genes from soils were amplified by PCR using universal 16S rRNA primers. A 1.5 kb eubacteria fragment was detected in all samples. The amplified DNA fragments were cloned using plasmid pCR®4-TOPO. Transformations were performed using Mix and Go Competent *E. coli* strains. White colonies grown on Luria Bertani (LB) Agar with ampicillin (50 ug/ml) were transferred to LB broth containing ampicillin (50 ug/ml). Samples were incubated overnight at 37°C. Plasmids were isolated from each clone using the Zyppy Plasmid Miniprep Kit. Cloned plasmid DNA was reamplified using the eubacteria DNA primers to verify the presence of the 1.5 kb inserts. DNA sequencing of clone libraries of eubacteria 16S rRNA genes showed the predominant presence of the phyla Acidobacteria, Cyanobacteria, and Proteobacteria. Some of the bacterial species detected were *Candidatus Solibacter usitatus*, *Oscillatoria nigro-viridis*, *Thiobacillus denitrificans*, and *Microcoleus* sp.

**Use of qPCR to Map the Distribution and Seasonal Changes in Early Developmental Forms of the Atlantic Sea Nettle (*Chrysaora quinquecirrha*) in Barnegat Bay, New Jersey. Maria Carvalho, Dena Restaino, Nashali Ferrara, Zachary Fetske, Isabella Pastore, Paul A.X. Bologna, and John J. Gaynor. Dept. of Biology & Molecular Biology, Montclair State University, Montclair, NJ.**

Real-time quantitative PCR (qPCR) is rapidly becoming the method of choice for identifying species-specific DNA in environmental samples (eDNA). We have developed a real-time qPCR assay to detect the presence of sea nettle DNA in water samples from Barnegat Bay, NJ. The sea nettle, *Chrysaora quinquecirrha*, is abundant in estuaries of Mid-Atlantic States and frequently blooms in warm summer months. Various factors may be contributing to the increasing rise of sea nettles and other jellyfish including eutrophication, overfishing, global warming, construction and species introduction. Despite its abundance and frequent distribution within estuarine systems, very little work has been

done to detect and quantify the early developmental stages of this organism. Ephyra and planula larval stages of *C. quinquecirrha* can now be detected and quantified using a qPCR assay specific for the 16S rDNA locus of the mtDNA genome. This assay is species-specific, is linear over a 9-log range, and can detect as few as 10 copies of 16S rDNA. 20-liter field samples were filtered through 500  $\mu$ M and 100  $\mu$ M mesh to separate ephyra from planula larvae and gametes, respectively. Quantifiable levels of *C. quinquecirrha* 16S rDNA were detected at all 16 baywide locations and 8 lagoonal sites in Barnegat Bay, with levels varying on both spatial and temporal scales. Identifying and quantifying early stage *C. quinquecirrha* using molecular techniques may allow us to develop predictive models regarding the onset and intensity of sea nettle blooms.

**Three-dimensional Reconstruction of Planarian Micrographs in Search of Human Proto-oncogene Orthologs.** †Michael Cataldo, James Ducey and Jonathan Blaize, Wagner College, Department of Biological Sciences, Staten Island NY.

The mechanisms controlling morphallactic regeneration are among the most complex and well studied of all biological processes. Since the 18<sup>th</sup> century planaria have served as a model organism for the study of regeneration due to their immense developmental plasticity, simple body plan and relative abundance. In our investigation, fresh water brown planaria supplied by Carolina Biological Sciences (*Dugesia dorotocephala* or *tigrin*) were employed to determine whether a variant of human mesenchymal epithelial transition factor (MET), a key contributor to liver regeneration, could be detected through the use of established immunohistochemical protocols. Our initial data suggests that a MET ortholog is expressed by these species, though results from subsequent experimentation have been inconsistent. We conclude that while a MET variant is likely absent from the planarian genome, proteins that contribute to tissue repair in a similar fashion are undoubtedly present. In a concurrent study, light and electron micrographs were augmented by image analysis software to create novel, three-dimensional depictions of the aforementioned flatworms. Inclusion of this open-source program revealed ultrastructural information that would remain hidden otherwise and provides a reliable method for quantitation of immunological markers.

**Study the Effect of Different Tea Polyphenols on the Biofilm formation in *Pseudomonas aeruginosa*.** Christopher Chen, Hassan Tahir and Lee H. Lee, Montclair State University, Montclair, NJ.

Green tea has been studied for decades because of their reported anti-bacterial, anti-cancerous, anti-carcinogenic, anti-inflammatory, and antioxidant properties. Although they display numerous beneficial properties, attention has been aimed towards using these polyphenols as a means of moving away from antibiotics to treat biofilm-forming bacteria. Biofilm forming bacteria pose a health risk because patients that undergo joint replacements, catheter insertions, or arthroscopic surgeries are at a higher risk of getting post-invasive infections with bacteria such as *Pseudomonas aeruginosa*. We examined the effects of tea polyphenols as a novel approach to prevent biofilm formation. Crude and purified green tea polyphenols (cGTP & pGTP) and crude and purified modified lipophilic tea polyphenols (cLTP & pLTP) were used to study their effect on the formation of biofilm from *P. aeruginosa*. Three different methods were used to analyze the effect of these tea polyphenols on biofilm formation. The morphological changes in the process of biofilm formations was also observed using SEM. When cells were viewed with SEM there was a noticeable change in cell morphology under treatment concentrations. Crystal violet assays indicated that with 50 – 100 ug/ml of cGTP. pGTP. cLTP, and pLTP bacterial biofilm formation decreased over the treatment period from 45% up till 93% using tea polyphenols. Additionally, when performing a Congo red assay, we viewed biofilm formation over time and how treatments affected biofilm growth. Overall tea polyphenols were proven to work as a novel approach to preventing biofilm formation from *P. aeruginosa* under various treatment concentrations. These results will be used to further analyze the mechanism of how polyphenols work on inhibiting biofilm formation.

**Some Don't Like it Hot: the Ability of the Juice from Different Varieties of *Capsicum annuum* to Inhibit the Growth of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Salmonella typhimurium*, and *Enterobacter aerogenes*.** Yikie Creighton and Elizabeth Mulligan. Kingsborough Community College, Brooklyn, NY.

Capsaicin is an irritant that causes a burning sensation when it comes in contact with mucus membranes, and is known to have antimicrobial properties. It is found naturally in the wide variety

of plants comprising the species *Capsicum annuum*. This single species includes peppers ranging from the mild Bell pepper, to the extremely hot Habanero pepper. We wanted to investigate different peppers' ability to inhibit bacterial growth. The Scoville scale, which is measured in Scoville Heat Units (SHU) is an indirect measure of the average capsaicin concentration in pepper varieties. Using this scale, we selected peppers with a range of capsaicin concentrations (Bell, Jalapeño, Serrano, and Habanero), and investigated their ability to inhibit the growth of *Escherichia coli*, *Enterococcus faecalis*, *Salmonella typhimurium*, and *Enterobacter aerogenes*. We hypothesized that peppers with higher concentrations of capsaicin would inhibit the growth of these bacteria more than peppers with low concentrations of capsaicin. We extracted pepper juice, and incubated bacteria in a mix of pepper juice, and Tryptic Soy Broth. After incubation, the liquid cultures were serially diluted, a viable plate count using Mueller-Hinton agar was conducted. Our preliminary results indicated that for *E. faecalis* and *E. aerogenes* there was a marked decrease in the number of viable cells when incubated with Serrano or Habanero peppers. Therefore, we concluded that at least for *E. faecalis* and *E. aerogenes* our hypothesis was supported. This work was supported by grant 0537141091 of the CSTEP program of NYSED.

**Jazz flies: Can Adult *Drosophila Melanogaster* Discriminate Consonant from Dissonant Tones.** Brianna D'Elia, Claudia Ko, Ramona Nadres, Nelson Casanova, Alexa Decker, Emily Whitney and Julian Paul Keenan, Montclair State University, Montclair, NY.

It is speculated that perceiving or differentiating combined tones (i.e., an interval) is not an evolutionarily evolved trait in *Drosophila melanogaster*. However, in humans and other advanced mammals, recognizing two simultaneously presented auditory stimuli is often thought to be a critical component of verbal linguistic communication. It is not known when tone interval differentiation evolved or if genes exist in insects that might translate into complex interval recognition abilities. Here, we examined *Drosophila melanogaster* to determine if they could discriminate between a consonant and dissonant tone pairing. The consonant tone pairing was a 440Hz Sine Tone paired with a major 5th. The dissonant tone was a 440Hz paired with a major 7th. To determine if the adults could discriminate the tones we set up a classical

conditioning paradigm. Previous research has indicated that sucrose is an unconditioned stimulus that elicits a positive (e.g., approach) response. Conversely, caffeine elicits a negative response. Following 2 conditioning trials of 5 minutes each, the organisms were tested for conditioning. White noise was included as a control. Differences were found between the consonant and dissonant categories. Furthermore, these differences indicate that evolutionary mechanisms may play a significant role in auditory discrimination. Further research should focus on molecular genetic mechanisms and the role of individual differences in genomics

**Antiviral Activity of Black Tea Theaflavins against Herpes Simplex Virus 1.** Aline de Oliveira and Tin-Chun Chu, Seton Hall University, South Orange, NJ.

Black tea originates from the leaves of *Camellia sinensis* plant and it contains theaflavin (TF1), theaflavin-3-monogallate (TF2A), theaflavin-3'-monogallate (TF2B), and theaflavin-3,3'-digallate (TF3). A549 and Vero cells were used to evaluate the effect of purified individual black tea theaflavins as anti-herpes simplex virus 1 agents. The results demonstrate that TF3 is a more potent inhibitor of HSV-1 than TF2 and TF1 and is not toxic to Vero or A549 cells in culture. Viral titers, flow cytometric assays, and fluorescence microscopy were used to demonstrate that TF3 concentrations of 50 mM and above completely block the production of virulent HSV-1 particles. Thus, TF3 may provide a novel treatment for HSV-1 infections suggesting that further studies should be conducted in appropriate models.

**Induction of Osteogenesis in Mesenchymal Cells Isolated from Limb Buds of Early Chicken Embryos,** Nicole DellaPorta, Danielle Jarvis, Taylor Kenney, Matthew McLeod, Meghan Orlando and Anthony Tolvo, Molloy College, Rockville Centre, NY.

Chicken embryo mesenchymal cells have been used to study developmental aspects of multipotent and pluripotent stem cell populations. One of our goals was to establish and characterize a chick embryo derived mesenchymal cell line for use in future studies. We report the ability of chick mesenchymal cells to undergo osteogenic induction *in vitro*. Limb buds from early embryos (stages 25 – 28) were dissected under aseptic conditions and the tissue explants were teased apart to free the mesenchymal cells. Cells were cultured for several passages, assessed for viability and used

directly for osteogenic induction. For induction, cells were initially plated in 100 mm dishes (experimental and control) at  $1 \times 10^5$  cells/ml in  $\alpha$ -MEM with 10% FBS, high glucose and 1% antibiotic-antimycotic solution. For differentiation, 10mM  $\beta$ -glycerophosphate, 50  $\mu$ g/ml ascorbic acid and  $10^{-8}$  M dexamethasone were added to the experimental culture medium and all cells were cultured for at least 7 additional days. After removing the medium, cells were fixed with 4% paraformaldehyde and stained for mineral deposits with 5% silver nitrate (Von Kossa stain) for 30 – 60 minutes while exposed to ultraviolet light. The cells were photographed using bright field phase 1 microscopy. Results revealed that treatment of the mesenchymal cells with the induction medium caused a dramatic increase in the deposition of mineralized matrix in the cell monolayer over controls. The results show that chick embryonic limb bud mesenchymal cells can undergo rapid differentiation into osteogenic cells at this stage of development and validate the avian embryonic model for such differentiation studies. Future studies examining the potential of these cells for chondrogenic differentiation will complete their characterization as mesenchymal stem cells.

**Preliminary Characterization of a Streptomyces Strain Collection. Paula Delos-Reyes, Kimberly Deleon, Kanchanpreet Kaur, Chung Tse, Monica Trujillo and Mangala Tawde, Biology Department, Queensborough Community College, CUNY.**

Streptomyces are Gram-positive G+C rich filamentous soil. They are the largest and best-known genus of Actinobacteria and are characterized by their unique secondary metabolism. The mechanisms to elicit the production of secondary metabolites are very diverse and not completely understood. The standard laboratory procedures to grow bacteria as pure cultures are not ideal to study their interactions with other species since bacterial species exist in communities in natural environments. We have characterized a Streptomyces collection isolated from New York State soil by studying the interactions between ten isolates among themselves and with the model organism *Streptomyces coelicolor*. We identified several interesting interactions amongst various isolates such as inhibition of growth, inhibition or augmentation of pigment production among others. We identified strains that produced antimicrobial compounds only when they are growing next to certain other strains. Here we have characterized some of these interactions.

**A DNA Superstructure Study: Bioinformatics Applied to Mapping a *Drosophila biarmipes* Gene. Sherley Demetrius and Cindy Jo Arrigo, Department of Biology, William J. Maxwell College of Arts and Sciences, New Jersey City University, Jersey City, NJ.**

To better understand the role that DNA packing has on the dynamics of gene expression our group uses comparative genomics to trace the evolution of the tightly packed but functioning distal arm of the fourth chromosome in *Drosophila*. Here, 55,020 base pairs of sequence found in contig 8 from *Drosophila biarmipes* August 2013 release was analyzed by computation, respecting the basic rules of biology; for example, a complete coding region starts with methionine and ends with a stop codon. As our ultimate goal was to create a gene model, we worked sequentially by first looking for evidence that there were any reference species (*D. melanogaster*) orthologs. We then determined the gene structure of the identified ortholog and mapped all exons using BLASTX to identify millions of years of conserved regions. To construct our final gene model, we located the exact start and stop base positions for each coding DNA sequence (CDS). Some of the bioinformatics tools that were used included the ab initio gene predictor *GenScan*, evidence-based gene finders, gene record finder, genome browser, and BLAST. We identified the CD32000 gene for *D. biarmipes* in the positive frame within the 55,020 base-pair contig 8 sequence of chromosome 4 and created a custom gene model for the 9 isoforms identified. This work was supported by an HHMI grant to S.C.R. Elgin, and by the NIH-GMS IRACDA award to C.J. Arrigo.

**Antibacterial Effect of *Polygonum multiflora*. Andy S. Demianicz and Tin-Chun Chu. Seton Hall University, South Orange, NJ.**

*Polygonum multiflora* (Chinese Knotweed) is a tonic herb that is used predominately to enhance bodily function, but previous reports suggest that Chinese Knotweed expresses antioxidant effect and antiviral activity. Chinese Knotweed is of interest due to the large shift from modern medicine to more traditional and natural remedies. It has also been noted that eastern medicine, the mixture and interaction of compounds may result in better medication than purified and/or synthetic compound. In this study, the antibacterial effect of the Chinese Knotweed was assessed with various concentrations at 2.5%, 1.25% and 0.625%. Four Gram positive bacteria *Bacillus cereus*, *Bacillus megaterium*, *Staphylococcus epidermidis* and *Streptococcus pyogenes* and four Gram negative

bacteria *Enterobacter aerogenes*, *Escherichia coli*, *Proteus vulgaris* and *Pseudomonas aeruginosa* were included in this study. Minimum Inhibitory Concentration (MIC) and antibacterial activity for each bacteria has been determined. The synergistic antibacterial activity of various antibiotic and the compound has been investigated. *Streptococcus mutans* has been used to evaluate the biofilm inhibition activity of Chinese Knotweed. The results demonstrate that Chinese Knotweed has strong antibacterial and biofilm inhibition activity, as well as synergism with antibiotics. Thus, Chinese knotweed may become a novel antibacterial agent.

**Protein Interaction Networks and Novel Isoforms in Schizophrenia and Concordance in a Murine Model. Brittiny Dhital, Elizabeth Kolmus and Jeremy Seto, New York City College of Technology, CUNY, Brooklyn, NY.**

Schizophrenia is a psychiatric disorder characterized by hallucinations, delusions, and irregular body movements. While researchers have identified several genes associated with the disease, environmental influences contribute to the onset of symptomology. To better understand these interactions, Maternal Immune Activation (MIA) model in mice was compared to an existing clinical data-set. Offspring of MIA mice demonstrate a normal phenotype until being challenged in adulthood when they display a schizophrenic-like disorder and hyper-susceptibility to hallucinogens. A meta-analysis of existing data can reveal possible clusters of importance within protein interaction networks. Additionally, RNA-Seq data can demonstrate the shared alternative transcriptional start sites in genes of significance. Identification of these unique isoforms can lead the way to verification by qPCR and provide insights into precise pharmacologic therapeutic interventions. This work was supported by NSF DUE-1323522 and PSC-CUNY 43 Research Award # 65127-00 43.

**Computational Study of the Cerebellar Function: a Model of Cerebellar Circuit for Motor Error Detection and Correction. Abraham Dickey III and Shao-Ying Hua, York College of CUNY.**

The cerebellum, one of the major structures of the central nervous system, functions as a rapid, corrective feedback loop, smoothing and coordinating movement. Furthermore, there has also been evidence indicating that this “little brain” modulates cognitive-emotional processing as well. Motor learning, which is predicated upon integrative neuroplasticity within and between neurons, is the capacity to acquire new repertoires of movement and skills that emerge from the detection and adjustment of “motor error.” Since their pioneering 1967 monograph “The Cerebellum as a Neuronal Machine”, John Eccles, Masao Ito and Janos Szentágothai paved the way for the thorough construction of network models representing information processing within the cerebellum. Surprisingly, up until this very moment, despite an enormous body of research mapping out cerebellar connectivity and performance, the exact understanding of how this distinct area of the brain operates remains a mystery. By employing firmly established neurobiological insights, modified Hodgkin-Huxley equations, MatLab<sup>®</sup>, and NEURON<sup>®</sup> software, we modeled a functionally and biologically realistic neuronal system that simulates the abstract physiology and network dynamics of information processing within the cerebellum. Thus far, our formula generates mathematical portrayals of individuated action potentials and systematically introduces motor disturbance and correction via change in synaptic conductance. In addition, by calculating the average spike frequency of neurons over time, it also provides an opportunity to predict and evaluate the incorporation of firing differentials, signaling delay, synaptic summation, and neuronal population dynamics within cerebellar neurocircuitry. Hence, overall, our research suggests that the neurons of the deep cerebellar nuclei (DCN) play a critical role in detecting and correcting motor error. The DCN receives inhibitory projections from Purkinje cells as well as excitatory input from the pontine/granule nuclei; therefore, it may serve as a “robust neural integrator of sensorimotor calibration” as proposed by Gauck & Jaeger (2000) and Koulakov *et al.* (2002).

**Manganese Accumulation in Leaves and Radishes Grown in Manganese Supplemented Soils.** Hasani Douglas, Kortni Garcia, Shellyann Clarke-Lambert, Karl Ruddock and Dereck Skeete, Medgar Evers College, Brooklyn, NY.

Manganese is a naturally occurring element, essential in trace amounts for living organisms, but is potentially toxic in high concentrations. Certain occupations including mining, welding and steel manufacturing can expose workers to chronically high levels of airborne manganese, leading to a clinical condition known as Manganism, which has Parkinson like symptoms. Recent studies report that excess dietary manganese can impair immune and reproductive functions in birds. Previously we showed that manganese is present in some commercially available fertilizers. We hypothesize that plants grown in soils high in manganese or supplemented with fertilizers containing manganese will accumulate manganese in their leaves and fruits. To test this we grew radishes in soils supplemented with fertilizers containing manganese, as well as in soil without added manganese. Samples (0.5 g) of each of the fertilizers as well as radish leaves were digested with nitric acid in a CEM Discovery Microwave Digester. Digested samples were analyzed for manganese levels using electrothermal vaporization with deuterium lamp background correction in a Perkin Elmer AA800 Atomic Absorption spectrophotometer with a THGA graphite furnace. We found that leaves accumulated manganese up to about 129.7  $\mu\text{g/gm}$  tissue. The Control leaves contained 66.50  $\mu\text{g/gm}$  of manganese, which was significantly less than all the experimental groups. Soil that were supplemented with fertilizers containing manganese had a significantly higher concentration of manganese than the plant tissue. The highest concentration of manganese recorded in the soil was 371.8  $\mu\text{g/gm}$ , while the lowest concentration was 61.6  $\mu\text{g/gm}$ . The study shows that plants will accumulate manganese from the soil and that use of fertilizers with high concentrations of manganese will increase the accumulations, possible creating a situation where animals and people ingesting the fruits and vegetables might be subjected to elevated manganese levels. This work was supported by grant 0516041071 of NYSDOE.

**Diagnosing KRAS Gene Mutations Using Molecular Beacons and SuperSelective Primers.** Alix Duarte<sup>1</sup> and Salvatore A.E. Marras<sup>2</sup>, <sup>1</sup>New Jersey City University, Jersey City, New Jersey and <sup>2</sup>Rutgers, The State University of New Jersey, Newark, NJ.

Single nucleotide polymorphisms (SNPs) in the KRAS gene are common factors in colorectal, pancreatic and lung cancer development. Different SNPs have different effect on tumor malignancy and treatment responsiveness, therefore knowing the SNP present on each case, would help choosing the most convenient treatment for each patient. Two RT-PCR assays were designed and tested to best detect the most common KRAS mutations. Four molecular beacon probes were successfully used to find specific SNPs while differentiating from the others. Multiplex assays were also possible and results were improved doing asymmetric RT-PCR. A second assay utilized SuperSelective primers, which were able to detect and amplify one KRAS mutant cell in the background of at least 10,000 wild-type KRAS cells. This work was supported by the National Science Foundation(NSF) and New Jersey City University GS-LSAMP. Special thanks to PHRI-Newark and Drs. Salvatore Marras, Diana Vargas, Sanjay Tyagi and Fred Kramer for their willingness to teach and help me in every aspect of this research experience.

**p-Aminosalicylic Acid (PAS) Reverses the Neurotoxic Effects of Manganese on Dopamine Post-Synaptic Receptors.** Loren Dubose<sup>1</sup>, Kurt Loney-Walsh<sup>1</sup>, Edward J. Catapano<sup>2</sup> and Margaret A. Carroll<sup>2</sup>, <sup>1</sup>Kingsborough Community College, Brooklyn, NY and <sup>2</sup>Medgar Evers College, Brooklyn, NY.

Manganese, a neurotoxin causing Manganism a Parkinsons-like disease, disrupts dopamine neurotransmission, but the mechanism is not fully resolved. Reports postulate manganese toxicity is related to dysfunction of dopamine D2 receptors (D2DR). Lack of effective treatments is an obstacle in managing Manganism. Lateral gill cell cilia of *Crassostrea virginica* are innervated by dopamine neurons from their ganglia, causing cilio-inhibition. Our lab showed manganese treatment blocks dopamine's inhibitory effects and the post-synaptic dopamine receptors in the cells are D2DR type. We also showed treating animals with manganese in the presence of p-aminosalicylic acid (PAS) prevented the toxic effects. We hypothesize PAS would effectively reverse

manganese neurotoxicity on D2DR when applied after manganese treatments. To test this we treated *C. virginica* with manganese (500  $\mu$ M) followed by PAS (500  $\mu$ M). Three sets of controls were similarly treated: manganese alone, PAS alone, or neither. Gills were excised, fixed, exposed to 1<sup>o</sup> antibodies against D2DR and FITC-linked 2<sup>o</sup> antibodies, paraffin embedded and sectioned. We visualized D2DR in gill cells with a fluorescence microscope with FITC excitation and emission filters. Gill treated with antibodies showed bright FITC fluorescence in lateral cells and other cells, including cells lining the blood channels. Fluorescence intensity of lateral cells was quantified using ImageJ software from NSF. Results showed fluorescence intensity from animals treated with manganese had a progressive decrease in fluorescence of up to 40% less than non-manganese treated controls. Animals treated with PAS after manganese exposure did not show reduced fluorescence, indicating PAS was able to reverse manganese induced loss of post-synaptic D2DR fluorescence. This immunohistological study shows a positive correlation between the loss of D2DR fluorescence in gill lateral cells in manganese treated animals vs controls and that PAS can effectively reverse the toxic effects of manganese on D2DR. Supported by 2R25GM06003 of NIGMS and 0516041071 of NYSDOE.

**Molecular Characterization of Microbial Community Composition as a Function of Depth in Estuary Sediments. A. Espinosa, D. Jadev and J. Coombs, Adelphi University, Garden City, NY.**

Estuary ecosystems are diverse and dynamic. Although the major flora and fauna of most estuarine systems is well characterized, the microbial diversity in estuary sediments remains a “black box”, and microbial contributions to organic matter turnover and nutrient cycling, particularly in the salt marsh rhizosphere, are poorly understood. In this study, an 8-foot long estuary sediment core was obtained from the Lido Beach Nature Area, Long Island, NY using a vibracoring technique. The core was aseptically sampled, and environmental DNA at three depths was extracted, cloned and sequenced. Sequence analysis revealed that many of the organisms detected through this culture-independent method resembled other documented uncultured clone sequences, and had lower similarity to cultured, biochemically-characterized organisms. Furthermore, the environmental clones obtained

from the estuary core formed phylogenetic clusters with specific anaerobic or candidate division taxonomic groups. Although some of these bacterial groups appear to be cosmopolitan in the sediments, for example *Chloroflexus*-like organisms appear at all three depths sampled, other organisms appear to have a very specific depth distribution. This is particularly true at the surface within the rhizosphere of the salt meadow cordgrass *Spartina patens*, where *Spirochete*-like and *Actinomycece*-like organisms were found. This study provides preliminary information about the relationship of microbial communities to depth in estuary sediments, and serves as a foundation for future high-throughput diversity studies in this environment.

**Egg Densities of the Atlantic Horseshoe Crabs (*Limulus polyphemus*) on the East ends of Plumb Beach (Brooklyn NY). Ernest Fatoke-Osobukola and Christina Colon, Kingsborough Community College, Brooklyn, NY.**

Horseshoe Crabs date back over 450 million years. Of the four species that exists today, only one is found in North America. The Atlantic horseshoe crab (*Limulus Polyphemus*) comes ashore every spring, at the night high tide during the new and full moon to spawn, a team of researchers went to Plumb Beach a pivotal Horseshoe crab breeding beach, and collected egg samples from the Eastern section of the Beach in order to see if there is a change in eggs density. It was hypothesized that more eggs would be laid in 2014 in comparison to the decline observed from 2011 to 2013. Despite a late spring, it was hypothesized that the crab population would rebound since there had not been a major storm in 2014. Sand cores were collected at new and full moons and sieved through a bucket of water. Eggs were counted and classified as live, dead, embryo or hatchling then returned to the beach. Data were compared with counts from previous years; my hypothesis was supported. Egg data collected in 2014 was higher than the numbers collected in the 2012 and 2013 breeding seasons but did not reach levels observed in 2011. It can be inferred that the reason for the rebound in the egg numbers was that there were no major storms as had occurred in the previous year. Based on these data, the numbers of eggs has yet to reach previous level therefore, research should continue. This work was supported by grant 2R25GM0600309 of the Bridge Program of NIGMS and grant 0537121091 of the CSTEP Program of NYS&ED.

**Bioinformatics Couples *D. biarmipes* RNA Editing of Calcium Activated Protein for Secretion (CAPS) mRNA to Potential Involvement in Developmental Expression Levels.** Jasmine Fenner and Cindy Jo Arrigo, Department of Biology, William J. Maxwell College of Arts and Sciences, New Jersey City University, Jersey City, NJ.

Bioinformatics tools can be used effectively to analyze large biological data sets. Robust tools allow investigators to, for example, compare nucleic acid sequence and expression patterns across a spectrum of differences and make inferences. As part of a multi-institutional DNA superstructure study, we analyzed 55,020 bases of *D. biarmipes* genome from the Aug. 2013 version 2 assembly. Here we show that *D. biarmipes* has the Calcium Activated Protein for Secretion (CAPS) gene on its dot chromosome as is seen in the *D. melanogaster* reference organism. We mapped all 5 isoforms of the ortholog to the base-pair and identified an alternative (GC) donor sequence in CAPS isoforms A, E. Custom gene models were created for the five isoforms identified. Some modENCODE RNA-sequence data support the notion that the CAPS gene is preferentially expressed in mixed embryos over adult females and males. Recently, CAPS messenger RNAs have been shown by others to be edited before translation. Taken together, we propose that RNA editing of CAPS might be involved in the observed expression level differences. This work was supported by an HHMI grant to S.C.R. Elgin, and by the NIH-GMS IRACDA award to C.J. Arrigo. We thank Dr. David Swope for his general counsel and advice.

**A North-South Analysis of Estuarine Water Quality in the New York Metropolitan Area.** Fletcher D.<sup>1</sup>, Feratovic, E.<sup>1</sup>, Ciprian, A.<sup>1</sup>, Hernandez, A.<sup>1</sup>, DeMaria, A.<sup>1</sup>, Batchu, M.<sup>1</sup>, Dell, A.L.<sup>1,2</sup> and Nolan, K.<sup>1</sup>, <sup>1</sup>Department of Biology St. Francis College, Brooklyn, NY and <sup>2</sup>Department of Neuroscience, University of Pennsylvania, Philadelphia PA.

The Hudson River encompasses many microclimates in New York City. In order to determine how water quality changes over time and space we collected water samples from New York Harbor, Brooklyn Bridge Park, East River Ferry Park, Newtown Creek, and Spuyten Duyvil in May and June of 2014. Our assessment included pH, Ammonia-Nitrogen, Nitrate,

Orthophosphate, Dissolved Oxygen, and Free Chlorine. We compared our measurements to control samples from the U.S. Virgin Islands and the Maritime Aquarium (Norwalk, CT). A microanalysis of Brooklyn Bridge Park compares Dissolved Oxygen, Temperature and pH measurements determined manually vs. those measured using a Vernier system. We observed high nitrate levels in Newtown Creek and Grand Ferry Park, which could stress aquatic organisms.

**Transcriptional Changes that Occur in Response to the Activation of Receptor Tyrosine Kinase RET.** Elizabeth Y. Flores and Quinn C. Vega, Department of Biology and Molecular Biology, Montclair State University, NJ.

The receptor tyrosine kinase RET is expressed in neural crest cell lineages and has a key role in regulating cell proliferation, migration, differentiation and survival during embryogenesis. Mutations in RET cause constitutive activation or inactivation of the receptor, resulting in the cancer syndrome Multiple Endocrine Neoplasia or Hirschsprung's disease, respectively. Although the importance of RET in these disease states has been well established, it is less clear how the receptor is involved. While it is expected that RET activates transcription of specific genes, it is not clear which specific genes are activated and it is not clear what role these genes play in either the wild type or RET induced disease state. This project is designed to study the changes in transcription of specific genes that occur in response to the activation of RET. Etv4, Etv5, Shp2, Sprouty1, Sprouty2 and Gif are components of a gene network downstream of RET. Some of these genes promote and control branching in kidney morphology while others, when mutated, are associated with several human diseases. Analyzing the expression levels of each gene in response to the activation of RET will aid in understanding the role of RET on downstream signaling.

**Sand Fiddler Crabs (*Uca pugilator*) Appear Not to be a Vector for Dermo (*Perkinsus marinus*) infection of Eastern Oysters (*Crassostrea virginica*). Victor Flores, Craig Hinkley, and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.**

Eastern Oysters (*Crassostrea virginica*), which are economically and environmentally valuable, grew in great numbers in Jamaica Bay, NY, before the 1920's. For decades these molluscs declined because of over-fishing, pollution, habitat destruction, and disease. One of these diseases, dermo, is caused by the protozoan *Perkinsus marinus*. One known pathway of transmission occurs "oyster to oyster" as the infected oyster's body decomposes, releasing ready-to-infect *P. marinus* parasites into the water. Our laboratory has been growing oysters from spats in Jamaica Bay and some of the mature oysters have tested positive for *P. marinus*. However, since there are no known oysters in the bay, how are these oysters becoming infected with dermo? We suggest that a vector could have transmitted *P. marinus* into eastern oysters. We hypothesize that since sand fiddler crabs coexist with oysters in the bay, they serve as a vector for *P. marinus* disease. Ten sand fiddler crabs, *Uca pugilator*, were the subject of our study. We isolated DNA from either the major claw or part of the body using the DNeasy Blood and Tissue kit. We ran a polymerase chain reaction (PCR) to amplify a 700-bp region of the mitochondria cytochrome-oxidase -1 (CO1) gene with the isolated DNA using the Folmer primer set. The amplified DNA was subjected to agarose gel electrophoresis to verify the correct size of the PCR product. The CO1 gene was amplified in six out of the ten samples and these six DNA samples were then tested for *P. marinus* DNA by PCR. None of the samples tested positive for *P. marinus* DNA. In conclusion, this finding does not support our hypothesis. Even though none of our six samples tested positive for *P. marinus* DNA, we believe that further studies need to be performed with more sand fiddler crabs since our sample size was small. This work was supported by grant 0537141091 of the CSTEP Program of NYSED.

**Comparison of Chromosome Four Protein-Coding Regions between *D. melanogaster* and *D. biarmipes*. Najee Ford and Cindy Jo Arrigo, Department of Biology, William J. Maxwell College of Arts and Sciences, New Jersey City University, Jersey City, NJ.**

The heterochromatic fourth chromosome of *D. melanogaster* houses active genes and shows some distinct organization, making it useful for studying the relationship between DNA structure and function. The evolutionary history of this arrangement can be assessed by comparing the DNA sequences of various *Drosophila* species. Here we show the 30,003 base pairs of sequence found in contig 49 from *D. biarmipes* Aug. 2013 version 2 assembly departs in some ways from analogous sequence in the reference species *D. melanogaster*. While the ab initio gene predictor, Genscan Genes, suggests that this *D. biarmipes* assembly region contains the unc-13 ortholog, our human-curated analysis reveals challenges to that. Using conservation data between just the coding sequences for *D. biarmipes* compared to *D. melanogaster*, and additional algorithm data we note the absence of strong evidence for some exons in the would-be unc-13 isoforms. We describe here challenges to annotating this stretch of DNA sequence and provide a putative gene model for the *D. biarmipes* unc-13 protein-coding sequence. This work was supported by an HHMI grant to S.C.R. Elgin, and by the NIH-GMS IRACDA award to C.J. Arrigo.

**A Bioinformatics Method for *Cis*-Regulatory G-quadruplex Motif Density Calculations in the 5'-Untranslated Regions of Mammalian Exomes. Melissa Mayberry, Scott Frees and Paramjeet Bagga, Ramapo College of New Jersey, Mahwah, NJ.**

G-quadruplexes are non-canonical structures formed by guanine rich nucleic acids. They are composed of stacks of four-guanine layers called tetrads, each held together by Hoogsteen hydrogen bonding. These make the structure very stable. *Cis*-regulatory G-quadruplexes help to regulate transcription and may help facilitate RNA processing by identifying splice sites and polyadenylation. Automated computational methods can be employed for genome wide analysis to determine the significance of G-quadruplexes in regulating human biological processes. The goal of the current investigation is to develop a method for calculating the density of G-quadruplex occurrence in the 5'-untranslated

regions (UTR) of the human exome. Density calculations are used to assign a numeric value the amount of G-quadruplexes in the 5'-UTR of each gene. The density is calculated by dividing the number of nucleotides in the 5'-UTR involved in a G-quadruplex by the total number of nucleotides in the 5'-UTR. Unlike other methods of calculating the amount of G-quadruplexes in a sequence, using density inherently normalizes the data by using the length of the section in the calculation. Using density also reduces the complications of dealing with overlapping G-quadruplex motifs in a sequence, as they can be included in the calculation without causing bias from "double counting". To calculate the G-quadruplex density of a large quantity of genes, we constructed a MongoDB database pre-populated with mRNA data from NCBI's databases, mapped all G-quadruplex motifs in the human transcriptome, and stored them in our database. Additional scripts filtered the motifs based on various parameters and calculated each transcript's G-quadruplex density in the 5'-UTR. The goal of future projects is to find genes with high G-quadruplex densities in their 5'-UTR and investigate any correlation between this and their gene functions. Studying the unique similarities between the functions of these genes may help in better understanding G-quadruplex functions.

**Genetic Differences in the Northern and Southern Populations of *Crassostrea virginica* on Either Side of the Gulf Stream in North Carolina. Joanna Fung, Craig Hinkley, and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.**

*Crassostrea virginica*, eastern oysters, are a keystone organism in bays along the Eastern seaboard. In previous experiments, comparisons of the cytochrome-c-oxidase I (COXI) gene from oysters collected along the eastern coast of the United States showed there was a single polymorphism found in oysters from southern populations (T→A) that was not present in northern populations. This suggests that there might be a geographic barrier that prevents mixing of oysters from the two regions. One possible barrier could be the intersection between the Gulf Stream and the Labrador Current around Cape Hatteras (CH), North Carolina. If this were true, then oysters collected north of CH would not be expected to have the polymorphism. Our hypothesis was that oysters north of Cape Hatteras would not have the polymorphism and

oysters south would. To test this hypothesis, DNA was extracted from the gill and mantle tissue of six oysters each collected north and south of CH using the DNeasy kit and the DNA was used to amplify a 700-bp region of the COXI gene. Agarose gel electrophoresis was performed to make sure that the amplified DNA was the correct size and the DNA was sent to ELIM Biopharmaceuticals for sequencing. A BLAST search was performed to ensure each sequence was from the COXI gene. A multiple sequence alliance showed that 17% of northern oysters contained the "A" polymorphism, whereas 100% of the southern oysters had the "A" polymorphism. Our hypothesis was not completely supported since the "A" polymorphism was found in the northern oysters. This suggests that the northern oysters we tested may be within a geographic barrier rather than north of a barrier. In the future we would like to test oysters further north of Cape Hatteras. This work was supported by grant 0537141091 of the CSTEP Program of NYSED.

**Development of a Mini-Reporter System to Test Gene Transfer of RNA Therapeutics. Kerianne Fuoco, Ashmi A. Patel and Martin J. Hicks, Monmouth University, West Long Branch, NJ.**

Glioblastoma multiforme (GBM), the most common central nervous system (CNS) malignancy, has a median survival of only 14 months. Although a great deal is known about the aberrant biology and up-regulation of growth, proliferation and migration pathways exhibited by GBM, the application of therapies against these biologic processes is limited by the blood-brain barrier which restricts systemically administered therapies from reaching the brain. We are creating novel strategies to bypass these barriers by developing gene transfer vectors to deliver the genetic sequences of RNA therapy molecules to alter the splicing pattern and expression of tyrosine kinase receptors (TKR), creating soluble TKR decoys. In this approach, we expect to modify GBM and CNS cells to deliver the therapeutic anti-cancer molecule into the local milieu. To test this approach, we are creating an *in vivo* tissue culture model. We have designed mini-reporter gene constructs that contain the targeted regulatory elements, including the 5' and 3' splice sites as well as the intronic region of interest of the TKR, vascular endothelial growth receptor 2, VEGFR2 (KDR). In this strategy, we will deliver anti-sense RNA molecules complementary to the

5' and 3' splice sites upstream of the transmembrane domain and test the efficacy to block splicing inclusion of exons 13 to 14 and retention of intron 13 which includes an alternative intronic polyadenylation signal thereby creating a short soluble peptide decoy TKR. We expect to use this mini-reporter gene for other TKRs that are up-regulated in cancer as well as other RNA therapeutics.

**Development of a Gene Transfer Strategy to Deliver an anti-EGFR RNA Therapeutic Aptamer to the Glioblastoma Microenvironment. Andrew R. Gilson, Sachin Parikh and Martin J. Hicks, Monmouth University, West Long Branch, NJ.**

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

**The Effects of Dipentyl Phthalate on *Drosophila melanogaster* Development. Amy Gimpel and Heather Cook, Wagner College, Staten Island, NY.**

In recent years, much attention has been given to endocrine disrupting chemicals (EDCs) and the many adverse effects they are suspected to have on humans and wildlife. EDCs are found in countless products and environments to which humans are daily exposed. In order to further investigate EDCs and their effects on animal development, recently laid wild type *Drosophila melanogaster* eggs were allowed to develop in the presence of di-n-pentyl phthalate (DnPP), a putative endocrine disruptor frequently used as a plasticizer in many common products. After eleven days chronic exposure, fewer adult flies eclosed when exposed to 100,000 ppm DnPP compared to the control vials and vials containing 1,000 ppm DnPP. In addition, the adult flies that did eclose died sooner and more frequently when exposed to high concentrations of DnPP. The data therefore suggests that exposure to high concentrations of DnPP is toxic to fruit flies and may adversely affect their development.

**Characterization of an eLLRon Like Protein in *Caenorhabditis elegans* Embryo Development. Katherine A. Rivera Gómez<sup>1</sup>, Andrew Singson<sup>2</sup> and Matthew Marcello<sup>1</sup>, <sup>1</sup>Department of Biology, Pace University, New York, New York, and <sup>2</sup>Waksman Institute of Microbiology, Rutgers University, Piscataway, NJ.**

Mammal epithelial cells secrete the extracellular matrix (ECM), a collection of extracellular molecules, composed of an interlocking mesh of fibrous proteins including collagen, elastin, fibronectin and laminin. One of the functions of the ECM is to provide a protective barrier. The epithelial junction stimulates ECM's remodeling and disintegration necessary for regrowth and healing of tissue. The molecular function of ECM is not completely understood. Extracellular leucine-rich repeat only (eLLRon) proteins are responsible for the organization of the ECM. *Caenorhabditis elegans* EGG-6 protein shares the characteristics mammalian eLLRon proteins. The purpose of the study is to be able to identify the role of *egg-6* in nematode embryo development. We are using embryo development as a model to study ECM function. To study the function of *egg-6*, we used RNA interference. RNA interference (RNAi) works by introducing double stranded RNA (dsRNA) to the organism causing

an interruption in the synthesis of a specific protein. Variable concentrations of dsRNA were used. In every RNAi experiment conducted there was a significant decrease in the percent progeny produced between ~20-30% compared to wild type. Future goals include the characterization and localization of EGG-6 in *C. elegans* through antibody staining. This work was supported by the Summer Research Program at Pace University, New York City, New York, and the collaboration of The Waksman Institute of Microbiology, Rutgers, Piscataway, NJ.

**Proteomic Investigation of Style Development in *Petunia hybrida*: An SDS-PAGE Study of Total Proteins in Styles of Buds and Mature Flowers. Artem Gordon and Farshad Tamari, Kingsborough Community College, Brooklyn, NY.**

The molecular aspects of pistil development has not been well studied in the angiosperm genus *Petunia*. The mechanisms involved in the morphological development of *Petunia* flowers are also understudied. The goal of our research was to study how proteins change through time in the female reproductive organs of the flowering plant *P. hybrida*. We hypothesized that: 1. The total number of proteins will increase in pistils throughout development; and 2. Protein abundance (quantity of each protein) will increase in quantity for some proteins, while for others it will remain the same or even decrease depending their roles in development. Flower pistils from buds at -4, -3, -2, -1 days before anthesis, and that from mature flowers, were extracted. Total protein separation was obtained using SDS-PAGE. Coomassie staining was used to achieve visualization of proteins. Supporting our hypothesis, the number of proteins and their quantities sometimes vary during development while remaining roughly the same (20-21) at other times. Some protein quantities remain the same throughout development, while others increase or decrease depending on the stage of development. In the future, we would like to extend this study to other reproductive organs such as anthers, and would like to identify some of the interesting proteins that show significant accumulation throughout development. This work was supported by grants grant 0537141091 of the CSTEP Program of the NYS Department of Education, and the President's Faculty Innovation Award to FT.

**Macrophage LC3 Expression Correlates with M-CSF Mediated Monocyte to Macrophage Differentiation and Survival. Janelle Grizzle, Shana Kay Henry-Grant, Bradley Miller and Carla A. Martin, Dept. of Biology, Farmingdale State College, Farmingdale, NY.**

The long-lived tissue macrophage population requires macrophage colony stimulating factor (M-CSF) for maturation, local proliferation and survival. Autophagy is an evolutionarily conserved survival mechanism that degrades stressed or damaged organelles and proteins and recycles the byproducts as nutrients. Autophagy is required for M-CSF mediated transition of monocytes into macrophages. We hypothesized that M-CSF could also up-regulate expression of an autophagy mediator, LC3, and that expression would correlate with macrophage maturation and survival. Human mononuclear cells were isolated from blood by density centrifugation and enriched for macrophages by adherence to tissue culture plates. Adherent cells were harvested and assayed for intracellular LC3 levels by indirect immunofluorescence staining and flow cytometry data analysis. We found that maturation during monocytes to macrophages transition correlated with increases in LC3 expression and that M-CSF induced LC3 expression was significantly higher than that in cells incubated with media alone by day three of culture ( $p=0.029$ ). Preliminary data also suggests that M-CSF induced LC3 expression is not adhesion dependent but might be further regulated by macrophage integrin-dependent adhesion. This work is supported in part by a FSC Title III Grant from the US Department of Education and funds from the FSC CSTEP program.

**A Practical Response to the Antibiotic Crisis: Student-led Research in the Isolation and Characterization of Antibiotic Producing Bacteria. Julia Halbersma, Rebecca Przywara and Jacqueline Washington, Nyack College, Nyack, NY.**

In 2014, Nyack College was selected as a Partner Instructor School to join The Center of Scientific Teaching at Yale University's Small World Initiative: Crowdsourcing the Discovery of Antibiotics. This inquiry-based lab discovery course introduces lower-level undergraduate students to authentic scientific research and, in doing so, exposes them to the looming antibiotic crisis, raises awareness, and potentially contributes to the discovery of new antibiotics. In

this study, antibiotic producing bacteria were isolated from soil on the Nyack College campus in Nyack, New York. The samples were serially diluted and plated on Luria Agar and Potato Dextrose Agar and incubated at 30°C. Bacterial counts ranged from  $3.9 \times 10^8$  to  $6.5 \times 10^8$  CFU/g. A total of 48 isolates were screened for antibiotic production against five safe relatives of ESKAPE pathogens. Four of the isolates exhibited antimicrobial activity against *Staphylococcus epidermidis*, *Bacillus subtilis*, and *Enterobacter aerogenes*. These isolates were characterized morphologically, as well as through biochemical tests, and in addition, the 16S rRNA gene sequenced to aid in identification. In the second half of the course, the chemical extracts of the isolates will be performed and assayed for antibiotic activity.

**Histamine Receptors in Gill of the Bivalve *Crassostrea virginica* and the Actions of Histamine at the Gill Interfilamental Junctions. Ave Harris, Jarreau Harrison, Fabienne Mondelus, Edward J. Catapane Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.**

Ganglia and innervated organs of the bivalve *Crassostrea virginica* contain serotonin and dopamine, which mediate physiologic functions. Histamine is a neurotransmitter in nervous systems and ligand for sensory receptors in invertebrates, but information on it in bivalves has rarely been reported. We showed in *C. virginica* histamine is involved in sensory reception in the sensory-motor integration of gill lateral cell cilia activity. We also used HPLC to quantify histamine in ganglia and tissues, and immunohistofluorescence to detect histamine and histamine H2 receptors in various tissue locations including gill interfilamental junctions. We hypothesize histamine H2 receptors in gill could be confirmed by Western Blot and histamine has a physiological action on gill interfilamental junctions. For Western Blot, gill cell lysate was prepared by polytron disruption in NP-40 detergent buffer containing protease inhibitor, followed by centrifugation to obtain supernatant with solubilized membrane proteins. Up to 30 µg of solubilized protein was subjected to SDS-PAGE with 10% acrylamide gels and electroblotted onto nitrocellulose. H2 receptor immunoreactivity was revealed after incubation with primary antibodies followed by HRP-conjugated secondary antibodies. Receptor proteins were resolved via colorimetric development using CN/DAB substrate

kit. To determine if histamine has a physiological effect of at interfilamental junctions we observed gill sections with a microscope, and photographed responses of interfilamental junctions to histamine and the histamine antagonist famotidine. Western Blot showed a strong band at approximately 70 kD in gill corresponding to H2 receptors. The physiology study showed histamine ( $10^{-3}$  -  $10^{-5}$  M) caused dose-dependent contractions of interfilamental junctions which were blocked by famotidine ( $10^{-3}$  -  $10^{-5}$  M). The study confirms previous immunohistofluorescence findings of the presence of H2 receptors in gill of *C. virginica* and further identifies a specific physiological role of histamine in the animal's gill. Supported by 2R25GM0600309 of NIGMS and 0516041071 of NYSDOE.

**Characterizing a Novel Protein Interaction Involving Acetyl-CoA Carboxylase. \*Jarreau Harrison<sup>1</sup>, Jay J Thelen<sup>2</sup> and Matthew Salie<sup>2</sup>, <sup>1</sup>Medgar Evers College, Brooklyn, NY and <sup>2</sup>University of Missouri-Columbia, MO.**

The demand for oils for agricultural and industrial use is increasing due to increasing population. Crop plants used to produce these oils, such as soybean, are not able to provide enough oil to meet the growing global demand. The *de novo* fatty acid synthesis (FAS) pathway in the chloroplast is responsible for producing the oil that is stored in the seed. The first and committed step of this pathway is catalyzed by acetyl-CoA carboxylase (ACCase), where acetyl-CoA is carboxylated to malonyl-CoA. ACCase is known to be highly regulated, but the specific regulatory mechanisms are still unknown. In dicots and non-graminaceous monocots, chloroplast ACCase is made up of four subunits: biotin carboxylase, biotin carboxyl carrier protein (BCCP1 and BCCP2), and  $\alpha$ - and  $\beta$ - carboxyltransferase. The BCCP subunit is biotinylated, which allows for the carboxylation of acetyl-CoA. In previous work, we precipitated ACCase from isolated *Arabidopsis thaliana* chloroplasts using a BCCP2-specific antibody and observed co-precipitation of a chloroplast-localized protein termed 'Protein X'. We hypothesize that protein X has a regulatory role in FAS by acting as another BCCP subunit. Since BCCP is biotinylated and able to dimerize, Protein X must also have these qualities. To test this hypothesis, we analyzed recombinant Protein X using western blotting and mass spectrometry. To determine if Protein X can dimerize with the

BCCP isoforms, we performed *in vitro* dimerization assays and then resolved the resulting dimers with Blue Native PAGE. Western blotting and mass spectrometry analysis showed that recombinant Protein X can dimerize but is not biotinylated in *E. coli*. Amino acid sequence alignment shows evidence of a biotinylation site at Lys253 in Arabidopsis. This study confirms the homo dimerization of Protein X and the absence of biotinylation of Protein X expressed in *E. coli*.

#### **Modeling Enzyme Activity. Jordan Hay, Suffolk County Community College, Selden, NY.**

Quantitative models provide a way for systems-level integration of metabolism. As an alternative to extreme reductionism, model building puts together parts provided by reductionist analysis and shows how they work together. This systems biology paradigm is being explored in the context of an introductory enzyme activity laboratory. Catecholase activity in a crude extract of potato (*Solanum tuberosum*) was characterized using standard spectrophotometric methods. Based on measured time courses of product accumulation, enzyme kinetic parameters were estimated using the software application COPASI (COmplex PATHway Simulator). Simulated kinetics were in reasonably good agreement with measurements. Quantitative analysis, mathematical modeling, and software application proficiency are discussed in relation to technology-enhanced learning.

#### **Subcellular Localization of Akt Protein in Unaffected and Bloom's Syndrome SV40-Transformed Fibroblasts Stimulated with Insulin-like Growth Factor. Britni Hinderhofer, Anthony Mangelli and Maureen Sanz. Molloy College, Rockville Centre, NY.**

Inheritance of two mutations in the gene *BLM*, that encodes the protein BLM, a RecQ DNA helicase, results in Bloom's syndrome (BSyn). BSyn is a very rare genetically-determined growth disorder characterized by proportional dwarfism, insulin resistance, non-insulin dependent diabetes mellitus (NIDDM), and a predisposition to cancer. Absence of functional BLM protein results in genomic instability featured in BSyn cells as hypermutability and hyperrecombinability, quite possibly the explanation for the predisposition to cancer. An explanation for the short stature and disturbed glucose metabolism observed in individuals with BSyn has not been elucidated. Endocrinological evaluations of a small number of persons with BSyn have shown that

individuals with BSyn produce normal amounts of growth hormone but, from infancy on, they exhibit insulin resistance that in two cases progressed to impaired glucose tolerance and NIDDM in early adulthood. The Akt signaling pathway is common to regulation of cellular growth and carbohydrate metabolism, both of which are affected in persons with BSyn. Mice deficient in Akt1 exhibit growth defects at all stages of development. Mice deficient in Akt2 exhibit insulin resistance and impaired glucose tolerance. A defect in the IGF-1/insulin signaling cascade to growth factors and glucose transport may explain the dwarfism and glucose metabolism abnormalities in BSyn. Subcellular localization of Akt in unaffected and BSyn SV-40 transformed fibroblast cell lines activated by IGF-1 was compared by *in situ* immunofluorescence. Akt was present in nuclei of normal and BSyn cells. Western blotting analysis confirmed the presence of Akt protein in stimulated and unstimulated cells. Following confirmation of these preliminary results, a comparison of phosphorylated Akt activated by IGF-1 in unaffected and BSyn fibroblast cell lines will be made to determine if a defect in the post receptor Akt pathway exists in BSyn cells. This work was supported by a Molloy College Faculty Research Scholarship Award.

#### **Modifying the Surface Chemistry of Two Types of Electrodes: Boron-Doped Diamond (BDD) and Glassy Carbon (GC). Azeez Ibrahim<sup>1</sup> and Greg M. Swain<sup>2</sup>, <sup>1</sup>Medgar Evers College, Brooklyn, NY and <sup>2</sup>Michigan State University, East Lansing, MI.**

This research project investigated whether the surface of carbon electrodes can be chemically modified and, if so, what effect does the changes in surface chemistry have on basic electrochemical properties of a soluble redox system. Three surface terminations were studied: hydrogen-terminated, oxygen-terminated and amine-terminated. Hydrogen-terminated surfaces were introduced via microwave plasma in the presence of hydrogen, while the oxygen and amine-terminated surfaces were produced in radio frequency plasma using oxygen and ammonia, respectively. Once the surface chemistry was changed, the question of the effect the change some basic electrical chemical properties of the electrode were studied. Cyclic voltammetry (CV) was used to investigate the background current and Faradaic current response for two soluble redox systems:  $\text{Fe}(\text{CN})_6^{-3/-4}$  and  $\text{Ru}(\text{NH}_3)_6^{+3/+2}$ . I hypothesize that for both electrodes, the hydrogen-terminated surfaces should exhibit high activity for both redox systems. For the oxygen-terminated surfaces, we expected high activity for  $\text{Ru}(\text{NH}_3)_6^{+3/+2}$  and more inhibitory effects on Fe

(CN)<sub>6</sub><sup>-3/4</sup>. The activity of the amine-terminated surfaces is dependent on the solution pH. With the amine groups protonated (positive surface charge), high activity was expected for Fe(CN)<sub>6</sub><sup>-3/4</sup> while more inhibited electron transfer was expected for Ru(NH<sub>3</sub>)<sub>6</sub><sup>+3/+2</sup>. To prepare the surface of the electrodes, they were purged with argon gas to remove contaminants. Surface of the carbon electrodes were then purged with their respective organic compounds (hydrogen, oxygen and nitrogen) and then analyzed through the use of an electrochemical cell. Our results showed distinctions between the two-carbon electrodes, proving to us that certain surface terminations cause changes to the surface chemistry of the respective carbon electrode, as well as affects certain electrochemical properties of the carbon electrodes. The significance of this research is that it will provide a greater understanding of modified electrodes. Such modification could serve as a foundation for electrochemical detection schemes of enzymes, proteins, and DNA.

**The Effectiveness of Nontraditional Agents in the Treatment of Mycobacterial Infections. Hadiya James, Mary T. Ortiz and Loretta Brancaccio-Taras, Kingsborough Community College, Brooklyn, NY.**

*Mycobacterium* infections are a global health issue. Multi-drug resistant strains are prevalent. Better agents are necessary to treat mycobacterial infections. This study compared the effectiveness of alternative to traditional agents on nonpathogenic strains of *Mycobacterium*. The hypothesis is: Nontraditional agents (Vitamins C and D, garlic, burdock root, echinacea, goldenseal, marshmallow) will be at least as effective as rifampin against *Mycobacterium smegmatis* and *Mycobacterium phlei*. The procedure was a standard agar diffusion assay. Tryptic soy agar plates were inoculated with the test organisms; disks of rifampin and the nontraditional agents were placed on the surface of the inoculated plates and incubated for 24h at 37° C. Zones of inhibition were measured. Five to sixteen trials were conducted and zone sizes averaged and compared statistically using the Mann-Whitney U-test ( $p \geq 0.05$ , 2-tailed). Based on the statistical analysis there was no significant difference between the effect of rifampin and echinacea on *M. smegmatis* and *M. phlei*. The mean zone size  $\pm$  SEM for rifampin against *M. smegmatis* was 24.10 $\pm$ 0.73mm; for *M. phlei*,

24.90 $\pm$ 0.7mm. However, zone sizes against *M. smegmatis* for echinacea at 120mg/ml were 25.15 $\pm$ 0.88mm and for echinacea at 240mg/ml, 22.80 $\pm$ 0.92mm. Zone sizes produced against *M. phlei* with echinacea at 120mg/ml dH<sub>2</sub>O were 22.20 $\pm$ 2.03mm and for echinacea at 240mg/ml, 23.40 $\pm$ 1.03mm. The lower echinacea dose was as effective as the higher. The former should be investigated as an alternative to rifampin. Rifampin was statistically more effective than Vitamins C and D, garlic, burdock root, goldenseal and marshmallow. Based on these results, the hypothesis of this study is accepted for echinacea, but rejected for Vitamins C and D, garlic, burdock root, goldenseal and marshmallow. Further studies may confirm the effectiveness of echinacea and determine minimum concentrations at most effective for treating *Mycobacterium* infections. This work was supported by grants NIH 2R25GM06003 (Bridge Program) and 0537121091 CSTEP Program (NYSED).

**Analysis of Genes Coding for tRNA in the Genome of Mycobacteriophage Littleton. Yi Jiang and Urszula Golebiewska, Department of Biological Sciences, Queensborough Community College, Bayside, NY.**

Mycobacteriophages ("Phages") are viruses that infect mycobacterial hosts, such as *Mycobacterium tuberculosis* and *Mycobacterium smegmatis*. Thousands of phages have been isolated using a single host strain, *M. smegmatis* mc2155, over 500 of which have been completely sequenced. The complete genome sequences reveal the phages to be highly diverse. Currently they are classified into clusters from A to S including subclusters. Particularly, phages display a remarkable genetic diversity with respect to the genes coding for tRNAs (the "tRNA genes"). The amount of tRNA genes that a phage has varies from 0 to over 40 among all the phages sequenced so far. Most of the phages do not carry tRNA genes because they generally use the translation mechanism of their hosts, so tRNAs genes are not necessary. However, several phages do have a considerable amount of tRNA genes, mainly the viruses belonging to clusters C and M. We studied in detailed a C-cluster phage Littleton and identified 34 genes coding for tRNAs. Our analysis revealed that Littleton carries tRNA for every amino acid. Next, we compared the codon usage of Littleton with these specific tRNAs and with the codon usage of its host *M. smegmatis*. There was very little correlation

between the codon preference and the presence of corresponding tRNA gene. We also compared the codon usage of other phages from C and M clusters and compared it to their host. There was no correlation. There was also no significant sequence similarity between the tRNA genes of different phages. Our results indicate that the tRNA genes modulate the optimal expression of the phage's proteins during development, but the difference in codon preference between the phages and their host may not explain why a phage carries particular tRNA genes.

**Plant Polyphenols Reduce Invasive Potential of Human Melanoma Cells. Correy R. Jones<sup>1</sup>, Carleta A. Joseph<sup>1</sup>, Virinder S. Parmar<sup>2</sup> and Anthony L. DePass<sup>1</sup>, <sup>1</sup>Long Island University, Brooklyn, NY, Department of Biology and <sup>2</sup>University of Delhi, New Delhi, India, Department of Chemistry.**

Melanoma is the most serious type of malignant skin cancer due to its ability to metastasize, and appears highly resistant to many forms of cancer treatments. Plant polyphenols have a number of beneficial health effects, and are well noted for their anti-cancer properties. To develop more effective treatments for melanoma, we assessed the chemotherapeutic potential of various plant polyphenol derivatives on the migration ability of A375 human melanoma cells as an *in vitro* model. Treatment of A375 cells with polyphenols MLN-1249, MLN-1337, and MLN-2287 resulted in inhibition of cell migration. Employing cell viability assays, the compounds resulted in dose-dependent cytotoxicity at concentrations ranging from 0 to 100  $\mu$ M. Using cell invasion assays, we found that the polyphenols inhibited activity on cell migration at concentrations of 1  $\mu$ M over a 72 h time period. The inhibition of cell migration correlates to the expression of genes involved in the apoptosis, NF $\kappa$ B, and epithelial-to-mesenchymal transition pathways. Together, these results show that the polyphenols have the ability to inhibit cell migration, a crucial step of metastasis. This work is supported by the Access to Research Comprehension and Careers (ARCC) grant through the MPBI (Master's Degree Program at Predominantly Black Institutions) program funded by the U.S. Department of Education.

**Effects of Ultraviolet Light on *Serratia marcescens*' Prodigiosin Production. Alyssa Joyce Bacalan<sup>1</sup>, <sup>1</sup>Hunter College, New York, NY (Research was done previously while attending Kingsborough Community College, Brooklyn, NY).**

The effect of four different time exposures (0, 30, 60, 90 seconds, respectively) to ultraviolet (UV) light on *Serratia marcescens*' prodigiosin production were observed. Results showed that as exposure time increased, the intensity of red pigmentation decreased, and the growth of white-colored colonies increased. The hypothesis that an increased exposure time to ultraviolet light will inhibit *Serratia marcescens* from producing prodigiosin, was supported. Further work will verify these results. Huge thanks to Mr. Philip Joseph for preparing the media used in this experiment. Most importantly, thanks to Professor Mary Ortiz for supervising and assisting; without her dedicated involvement and guidance, this lab report would have never been accomplished.

**Self-assembled Monolayer Formation of Alkyl Phosphate on Tooth Enamel for Tooth Decay Prevention. Bumjung Kim<sup>1</sup>, Shrushti Patel<sup>1</sup>, Marcos Castillo<sup>2</sup> and Thomas Howard<sup>3</sup>, <sup>1</sup>Department of Chemistry, New Jersey City University, Jersey City, NJ, <sup>2</sup>North Bergen High School, North Bergen and <sup>3</sup>St.Peters Preparatory School, Jersey City, NJ.**

Tooth enamel is mainly composed (96%) of hydroxyapatite (HA), which makes enamel the hardest tissue in human body. However, enamel is susceptible to acids and it decalcifies under exposure of acids. Decalcification, loss of calcium ions, of tooth enamel is mainly attributed by acids that are generated by bacteria through fermenting carbohydrates. Enamel is non-regenerative tissue and successive decalcification of enamel results in permanent dental caries through the exposure of dentin layer. Filling dental caries with artificial materials, such as composite resins, amalgam, or metal alloys, has been widely used to stop further aggravation of dental caries growth, but they only guarantee good adhesion on dentin layer and they are not suitable for early stage dental caries enamel layer. In this context, we suggest a way to prevent enamel decalcification by chemically modifying enamel surface with self-assembled monolayer (SAM) of alkyl phosphonic acid. Self-assembled monolayer technique, widely used in surface chemistry and nanotechnology, modifies surface properties of metal, metal oxide or other

inorganic surfaces by chemically attaching a single layer of self-assembly molecules. Not limited by nanotechnology but also in osteology and dentistry SAM technique is used for dissolution surfactant of HA nanoparticles or adhesive of filling materials on dentin layer. Using this technique, we form hydrophobic SAM on tooth enamel which will not only cover and protect the surface of enamel mechanically, but also chemically prevent enamel from acid decalcification.

**C-Peptide Secretions and Diffusion from Rat Insulinoma Cells using a 3-D Printed Fluidic Plate Device. Azel King<sup>1</sup>, Chengpeng Chen<sup>2</sup>, Yueli Liu<sup>2</sup> and Dana Spence<sup>2</sup>, <sup>1</sup>Medgar Evers College and <sup>2</sup>Michigan State University.**

C-peptide is a 31 amino acid peptide that is co-secreted with insulin by the beta cells in the pancreas. It was found that its main role was to facilitate folding of the pro-insulin molecule. Recently, research has shown that C-peptide has beneficial effects *in vivo* and may be a valuable source in diabetes therapy. Research has shown that C-peptide has an effect on erythrocytes (red blood cells, RBCs) by stimulating ATP release from the cells, which stimulates nitric oxide (NO) production in endothelial cells, which further relaxes smooth muscle cells on vessel walls. In this study, a cell line known as INS-1 was used to produce endogenous C-peptide that would be used on a 3D-printed circulation mimic fluidic device. We hypothesize that C-peptide should increase linearly upon stimulation over time before it plateaus. The secretion pattern of C-peptide as a function of time was first studied, by measuring C-peptide in the solution above cultured cells at different time points. Then the cultured INS-1 cells were integrated onto the circulation device to mimic the endocrine process of C-peptide existing pancreatic islet and entering circulation. Specifically, the amount of C-peptide that diffused from INS-1 cell culture inserts into the circulation was quantified against time with enzyme linked immunosorbent assays (ELISA). Results showed that 25nM c-peptide was produced by the cells and approximately 2nM diffused into the device channel. The 3-D printed fluidic device can be a good mimic for real time beta cell secretion and can be used for looking at the downstream bio-effect of RBCs and endothelial cells.

**Cloning and Sequencing of 16S rRNA and ITS Genes Isolated from Compost DNA to Describe the Microbial Community of a Composting System. Elizabeth Kulko, Elyssa Baron, and Luis Jimenez, Biology and Horticulture Department, Bergen Community College, Paramus, NJ.**

Food compost was produced by the Rocket<sup>®</sup> Composter System (RCS) after 2 weeks. 16S rRNA and ITS gene sequencing of clone libraries derived from compost DNA ascertained the composition of the microbial community. Eubacteria and Actinobacteria 16S rRNA genes were PCR amplified and cloned using plasmids pJet1.2 blunted vector and pCR<sup>®</sup>4-TOPO. The amplified products from the PCR analysis of ITS genes were cloned using plasmid pCR<sup>®</sup>4-TOPO. Transformations were performed using Mix and Go Competent *E. coli* strains. Cloned libraries of eubacteria 16S rRNA genes showed that the phylum Firmicutes comprised 86% of clone sequences while Proteobacterial sequences accounted for 14%. The dominant family and genus within the Firmicutes were Bacillaceae and *Bacillus*, respectively. *Geobacillus* was the second most common genus. *Geobacillus sp.* was the most common species detected. Within the Proteobacteria the genus *Bordetella* was the predominant type. Molds were not culturable from the samples neither any mold ITS sequences were detected in clone libraries. Actinobacteria 16S rRNA sequences were found in compost DNA using Actinobacteria-specific 16S rRNA primers. Clone libraries of Actinobacteria 16S rRNA sequences indicated the predominant presence of *Corynebacterium halotolerans* and *Thermobifida fusca*.

**Antioxidants Boost Male Fertility: the Role of Reactive Oxygen Species in Modulating Fertility and Sperm Viability in *D. melanogaster*. Weily Lang, Min Shin and Preethi Radhakrishnan, LaGuardia Community College, Long Island City, NY.**

Reactive oxygen species (ROS) are by-products of REDOX reactions which are produced during times of cellular stress and immune insult. In large amounts ROS have been known to cause lipid peroxidation of sperm. Our research is the first of its kind to show the effects of ROS on reproductive effort pre-and post-copulation in *D. melanogaster*. Our findings indicate that dietary antioxidant supplementation (Melatonin and Lipoic Acid) can protect gametes from ROS attack thereby resulting in more viable healthy offspring.

Our results draw strong implications on the effects of dietary antioxidant consumption on maintaining and boosting fertility at a molecular level (though sperm viability). We also analyze the effects of toxic herbicides such as Paraquat on elevating ROS levels and in reducing sperm viability. Our research is supported by the PSC-CUNY grant (Cycle 44) and the Elsevier Foundation grant for Women in S.T.E.M.

**The Male Reproductive System and Testis Stem Cell Niche in *Drosophila ananassae* and *Drosophila persimilis*. Cassandra Lawson, Crystal Calise and Angela V. Klaus, Department of Biological Sciences, Seton Hall University, South Orange, NJ.**

The goal of this project was to characterize the morphology of the male reproductive system and the testis stem cell niche in two species of *Drosophila* flies. The stem cell niche is a micro-environment within the testes that generates spermatogenic stem cells. This structure has already been well-characterized in *Drosophila melanogaster* and partially characterized in *D. simulans* and *D. pseudoobscura*, but has not been visualized in any other *Drosophila* species. This project will analyze the testes of two species of interest because of their evolutionary relationship to previously characterized species. These species are: *D. ananassae*, and *D. persimilis*. *D. persimilis* is in the obscura group and shares an unusual ellipsoid testis morphology with *D. pseudoobscura*. *D. ananassae* shares a testis morphology (coiled tubule) that is similar to *D. melanogaster*. Recent work in our lab demonstrated that the stem niche in the ellipsoid *D. pseudoobscura* testis is significantly different in structure from the more common tubular testis morphology found in *D. melanogaster*. We hypothesize that *D. persimilis* will follow the ellipsoid niche structure. *D. ananassae*, given its phylogenetic placement, may exhibit a hybrid niche morphology.

**Identifying Candidate Reproductive Genes from Apomictic Pistils of *Cenchrus ciliaris* (Buffelgrass) Using Genomic Methods. Victor Leon, Jermin Adrawy and Terry L Kamps, Biology Department, New Jersey City University, Jersey City, NJ.**

Apomixis is a mechanism of clonal reproduction through seeds which occurs in a wide variety of plant species. From a practical perspective, researchers are interested in

apomixis to utilize it to rapidly fix desirable genetic characters in cultivated plants. Apomixis is of interest from an evolutionary biology perspective because it is an unusual mode of reproduction considered by some to be an evolutionary dead end, despite the fact that it is a not uncommon process in several species of plants. Buffelgrass is valuable as a forage grass and the existence of sexual and apomictic genotypes makes this species an important resource for investigating the genetics and mechanisms determining modes of reproduction. Apomictic reproduction in buffelgrass is through aposporous apomeiosis. BLASTx to the Uniprot database was performed using 10318 sequences derived from a previously assembled expressed sequence tag (EST) library constructed from young ovaries of obligate apomictic buffelgrass plants. A total of 32 candidate genes involved in general reproduction and apomixes were identified by Gene Ontology (GO) results in combination with a syntenic cross species *in silico* mapping strategy. Among these were genes involved in auxin signaling pathways, methionine biosynthesis, endoreduplication, and programmed cell death. Additional candidates were identified by significant BLASTn hits to a *Panicum maximum* apomictic pistil cDNA library. Future studies will include comparative expression assays of the identified candidate genes and tBLASTx analysis of ESTs that failed to match known proteins in the Uniprot database.

**Conservation of Mammalian U-Rich Elements Involved in Polyadenylation. Mingzhao Liu, Scott Frees and Paramjeet Bagga, Ramapo College of New Jersey, Mahwah, NJ.**

Polyadenylation is an essential process in the formation of the 3'-end of eukaryotic mRNAs. Polyadenylation determines the site of cleavage in the 3' untranslated region (UTR) and can regulate gene expression. Cleavage is achieved through the formation of a multi-component protein complex that binds to specific *cis*-regulatory elements in the 3' UTR. U-rich sequence elements (URS) are located downstream of the polyadenylation/cleavage site. The Cleavage Stimulation Factor (CstF) protein of the cleavage complex, required for efficient cleavage of the polyA site, binds to URS. The strength of the U-rich element affects how readily CstF binds to it. As such, URS are considered important regulatory elements in polyadenylation. Alterations of known URS have been known to cause adverse effects on the process of polyadenylation, and can change the cleavage site's positioning. In order to

understand the biological importance of URS, there is a need to identify them on a genomic scale. Computational approaches are useful for wide scale analysis of sequence motifs. However, the challenge is to filter out false positives from the ones that are likely to be biologically relevant. Identifying evolutionarily conserved U-rich sequence motifs can help filter out these false positives. The aim of this specific project is to devise a computational method for determining the conservation of URS by comparing their distance from the polyadenylation site and their relative strengths. We are using these two characteristics to assign an overall conservation score to a U-rich motif. We are studying the distribution and conservation of U-rich elements in human mRNA compared to homologous mouse mRNA to help determine which U-rich sequence motifs are likely to be involved in regulating polyadenylation.

**Linking an Increase in Inflammation in LADMAC Cells Exposed to a Genetic Variant Beta-casomorphin-7 with Cerebral Inflammation in Autistic Individuals. Katia Macklin, Ritchell Goldman, Tisha Paul, Suzan Benitez, Joyce Mangalathu, Arun Rambarran and Mary Kusenda. Molloy College, Rockville Centre, NY.**

Beta-casomorphin-7 (BCM-7) and Beta-casomorphin-9 (BCM-9) are proteins derived from casein that affect individuals with a heightened sensitivity to casein. Both are genetic variants found in milk, created through chemical digestion within the intestine and absorbed into the blood stream. Out of the two, BCM-7 is absorbed as an opioid which causes inflammation and crosses the blood-brain barrier. Ingesting milk that breaks down into BCM-7 has possible links to the neuropathogenesis of Autism Spectrum Disorders (ASD), as a casein-free diet has been shown to decrease autistic symptoms. In our study we utilized LADMAC cells (ATCC-CRL2420), a lymphocyte cell line with monocyte morphology to determine if BCM-7 produces more inflammation than BCM-9, whether it did so in a dosage dependent fashion, and whether naloxone can block the inflammation produced by BCM-7. LADMAC cells exposed to the additives for 24hours release Chemoattractants as an inflammatory response, which were used in a colorimetric chemotaxis assay. Our results show that LADMAC cells exposed to BCM-7 showed increased inflammation than those cells exposed

to BCM-9. This increase in inflammation of cells exposed to BCM-7 was dosage dependent. Further we demonstrate that the inflammation caused by BCM-7 is reduced by exposure of cells to Nalaxone. Our results also postulate a possible explanation as to why Autism cases on a casein-free diet exhibit mitigated symptoms and may open up the discussion of using Nalaxone as a treatment for certain autism cases.

**Green Tea Polyphenols Inhibit Biofilm Formation in *Staphylococcus aureus*. Kevin Marques, Christopher Chen, Hassan Tahir and Lee H. Lee, Montclair State University, Montclair, NJ.**

With the challenge of biofilm resistance to current antimicrobial treatments, natural compounds are necessary as a novel alternative to modern antibiotic therapies that have shown a pattern of ineffectiveness. *Staphylococcus aureus* (*S. aureus*) is an infectious bacterium common in medical settings and known for forming resilient biofilm that is able to survive a various range environments, which are the cause for complications amongst those treated within these surroundings. Biofilm is a mass of extracellular polymeric substance, which is produced by select microorganisms as a mechanism to bind the cells together to increase durability in their local environment while also increasing intercellular communication. These properties can initiate acute infections by eluding host's defense and due to the resilience of growth inhibition and conventional treatments; chronic infections can result, especially in those patients with an impaired immune system. In our study, we confirm the production of biofilm matrices from *Staphylococcus aureus* and used green tea polyphenols from plant *Camellia sinensis* to tackle this riddle of biofilm pliability to current solutions. Hydrophilic and lipophilic green tea polyphenols at different concentrations, along with three different experimental approaches were tested for the biofilm inhibition of this organism. Our data indicated that a direct correlation between the different concentrations of the tea polyphenol treatments and the degree of biofilm growth when being compared to the control. The lipophilic molecules worked better than the hydrophilic molecules. By using this novel approach with an organic non-toxic compound with no known side effects, this study shows evidence of potential usage as therapeutic agents to inhibited biofilm production.

**Spatial Learning and Memory in a Rat Model of Sporadic Alzheimer's Disease.** Shanique Martin<sup>1</sup>, Juan Mosquera<sup>1</sup>, Jamel Travis<sup>2</sup> and Francisco Villegas<sup>2</sup>, <sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>York College, Jamaica, NY.

Alzheimer's disease (AD) affects 1 in 8 individuals ages 65 and older in the United States. Studies in sporadic Alzheimer's, also known as "type 3 diabetes", have shown impairments in insulin signaling, cerebral glucose utilization and energy metabolism as preliminary abnormalities that may precede or accompany the initial stages of cognitive impairment (Steen *et al.*, 2005). This study examined the effects of Exendin-4 (Ex-4) on spatial learning and memory in a rat model of sporadic Alzheimer's disease. Ex-4 was used as a treatment against hippocampal neurodegeneration after intracerebroventricular injections of streptozotocin (STZ). STZ produces high oxidative stress, insulin resistance, cognitive deficits and behavioral abnormalities. The Morris Water Maze (MWM) was employed in order to assess spatial learning and memory. We hypothesized that Ex-4 would reduce deficits in spatial learning and memory, death of neurons as well as the dysregulation of tau and glycogen synthase kinase 3 $\beta$  (GSK-3 $\beta$ ) protein in STZ+EX-4 subjects. In regards to the MWM, our preliminary results suggest that there were no differences in performance between STZ+Ex-4 subjects and STZ+PBS subjects, whom also performed similarly to the aCSF+PBS and aCSF+Ex-4 groups. There were no significant differences between groups, both in distance traveled and escape latency. Our findings suggest that the dosage of STZ administered may not have been sufficient in producing deficits in spatial memory and learning. Afterward, in order to investigate the efficacy of Ex-4 within the hippocampus, we will use flouro-jade C, which is a marker of neuronal death. Finally, Western blot analysis will be used to detect and quantify the presence of GSK-3 $\beta$  and tau protein between groups. Shanique Martin and Juan Mosquera are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

**The Impact of Beach Renourishment on Spawning Habitat of the Atlantic Horseshoe Crabs (*Limulus polyphemus*) on Plumb Beach (Brooklyn NY).** Safinaz Mashali and Christina P. Colon, Department of Biological Sciences, Kingsborough Community College, CUNY, Brooklyn, NY.

A Study was conducted in summer 2014 to investigate the impact of beach renourishment on spawning habitats of the Atlantic Horseshoe Crabs (*Limulus polyphemus*) on Plumb Beach (Brooklyn NY) after Superstorm Sandy. The Army Corps of Engineers added 127,000 cubic yards of sand in 2012 to the west side of Plumb Beach which had suffered long term erosion. This process yielded two possible outcomes; either could have aided the crabs by creating new habitat for better spawning activity or it could have prevented spawning due to sudden dramatic alteration of their habitat. A study in 2013 revealed that at first beach renourishment did not increase spawning success. It was hypothesized that the observed difference in egg densities for the west and east ends of Plumb Beach will persist in the second breeding season. Sampling occurred biweekly on the east and west ends of the beach from May through July. Ten 5cm deep and ten 20cm deep of sand samples were collected randomly. A total of 24,371 eggs, embryos and hatchlings were observed. Egg densities on the eastern sector were higher compared to the renourished western sector by 99.7%. The 2,469 embryos represented a 92% survival rate. These data strongly supported the research hypothesis; however surveys of spawning activities by NYC Audubon and juvenile number by other researchers indicated that abundance spawning activity occurred on the western beach. It is possible that the observed low egg counts could be a sampling anomaly due to highly aggregated densities and distribution of eggs depositions on the western beach. Eventually, the renourished beach on Plumb Beach was a success transition for the crabs to begin their spawning habitat.

**Richness and Abundance of Beneficial Insects on Native and Horticultural Plantings at Bergen Community College's Paramus Campus. Jackie Mateo, Katelyn Nunberg, Marie Manzan and Elena S. Tartaglia, Bergen Community College, Paramus, NJ.**

Many insects provide beneficial services to both ecosystems and humans. Included among these services is pollination which is essential to human life as well as being a critical function in ecosystems. Pollination provides food for humans and reproductive services for plants. Pollination services are provided mainly by bees (F. Apidae) but are also carried out by wasps (O. Hymenoptera) and some species of hover fly (F. Syrphidae). Our first question examined whether these pollinating insects are more attracted to native or horticultural plantings. Native plants have co-evolved with insects, however horticultural plantings do still provide nectar and pollen resources. We sampled populations of bees, wasps and hover flies at native plantings and horticultural plantings around Bergen Community College's Paramus Campus in Paramus NJ with bowl traps. We found that native plantings attracted more pollinating insects than horticultural plantings. We also assessed color preferences for blue vs. yellow bowls in bees, wasps and hover flies and found that yellow was a more attractive color for these insects. This work was supported by Bergen Community College's STEM-GPS program.

**p-Aminosalicylic Acid (PAS) Reverses Neurotoxic Effects of Manganese on a Dopaminergic System. Cassandra Mezalón, Toshanna McBean, Edward J. Catapane and Margaret A. Carroll, Medgar Evers College, Brooklyn, NY.**

Manganese (Mn) is a neurotoxin causing Manganism, a Parkinsons-like disease in humans. Mn neurotoxicity involves disruption of dopaminergic neurotransmission. The mechanism by which Mn produces dopaminergic dysfunction is not fully resolved and reports postulate the underlying mechanism to be more related to downstream neuronal pathways than deficits in nigrostriatal function. Lack of effective treatment for Mn toxicity has been a major obstacle in the clinical management of Manganism. Recently, p-aminosalicylic acid (PAS) was reported to be an effective treatment of Manganism; however its mechanism of action is unclear. Lateral cilia of gill of *Crassostrea virginica* are controlled by

serotonergic-dopaminergic innervations from their ganglia. Dopamine (DA) is the neurotransmitter causing cilio-inhibition, serotonin cilio-excitation. Previous work of our lab showed Mn blocks cilio-inhibitory effects of DA and this is prevented by co-treatments with PAS. We hypothesize that PAS would effectively reverse the neurotoxic actions of Mn when applied after Mn. We treated *C. virginica* for up to 3 days with 500  $\mu$ M Mn, then for up to 5 more days with 500  $\mu$ M PAS. Control animals were similarly treated without PAS. Ciliary activity of gill lateral cells was measured by stroboscopic microscopy. We found in congruence with our earlier studies that Mn treatments disrupted the DA induced response of the ciliated cells. The PAS treatments after Mn treatments effectively reversed the neurotoxicity and the ciliated cells responded to DA ( $10^{-6}$  -  $10^{-4}$  M) by decreasing their beating rates. The study shows that PAS can effectively reverse the neurotoxicity effects of Mn and these findings are helpful to understand causes and potential therapeutic treatments of Manganism, particularly concerning the therapeutic use of PAS for the treatment of Manganism. This work was supported by 2R25GM06003 of the Bridge Program of NIGMS, 0516041071 of NYSDOE, and 0622197 of the DUE Program of NSF.

**Western Blot Identification of Dopamine and GABA Receptors in Gill of the Bivalve *Crassostrea virginica*. Fabienne Mondelus, Beatrix Boissette, Fiana Bess, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College, Brooklyn, NY.**

It is well established that ganglia and innervated organs of the bivalve mollusc *Crassostrea virginica* contain serotonin and dopamine, which mediate physiologic functions in their gill and other organs. Gill lateral cells of *C. virginica* are controlled by serotonergic-dopaminergic innervations from their ganglia and regulate cilia beating rates. Dopamine slows down cilia beating rates and serotonin speeds up cilia beating. GABA is a neurotransmitter in the nervous system of vertebrates and many invertebrates, but studies in bivalves have rarely been reported. Recently we used HPLC to show that GABA also is present in ganglia and tissues of *C. virginica* and that GABA acts as a ganglionic neurotransmitter modulating gill lateral cell cilia activity. We also used immunohistofluorescence to localize GABA receptors in ganglia and gill, and identify the dopamine receptors in gill lateral cells

that slow down cilia beating rates as D2-like (D2DR). We hypothesize that Western Blot analysis would verify the presence of D2DR and GABA receptors in gill of *C. virginica*. For Western Blot analysis, gill cell lysate was prepared by polytron disruption in ice-cold NP-40 detergent buffer containing protease inhibitor, followed by centrifugation to obtain supernatant with solubilized membrane proteins. Up to 30 µg of solubilized protein was subjected to SDS-PAGE with 10% acrylamide gels and electroblotted onto nitrocellulose. D2DR and GABA receptor immunoreactivity was revealed after incubation with primary antibodies followed by incubation with HRP-conjugated secondary antibodies. The Western Blot studies showed strong bands between 70 - 75 kD corresponding to dopamine D2DR and GABA RA1 $\alpha$ 6 receptors in gill. The present project allows us to confirm our previous and immunohistofluorescence studies showing the presence of dopamine and GABA and furthers the understanding of their physiological roles in *C. virginica*. Supported by 2R25GM0600309 of NIGMS and 0516041071 of NYSDOE.

**Restoration of Sustained Attention in a Rat Model of Sporadic Alzheimer's Disease. Juan Mosquera<sup>1</sup>, Shanique Martin<sup>1</sup>, Jamel Travis<sup>2</sup> and Francisco Villegas<sup>2</sup>, <sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>York College, Jamaica, NY.**

Alzheimer's disease (AD) affects 1 in 8 individuals ages 65 and older in the United States. Studies in sporadic Alzheimer's, also known as "type 3 diabetes", have shown impairments in insulin signaling, cerebral glucose utilization and energy metabolism as preliminary abnormalities that may precede or accompany the initial stages of cognitive impairment. This study examined the effects of Exendin-4 (Ex-4) on spatial learning and memory in a rat model of sporadic Alzheimer's disease. Ex-4 was used as a treatment against hippocampal neurodegeneration after intracerebroventricular injections of streptozotocin (STZ). STZ produces high oxidative stress, insulin resistance, cognitive deficits and behavioral abnormalities. The 5-Choice Serial Reaction Time Task (5-CSRTT) was employed as a measurement of sustained attention. We hypothesized that Ex-4 would reduce deficits in the capacity for sustained attention, death of neurons as well as the dysregulation of tau and GSK-3 $\beta$  protein. For the 5-CSRTT, our preliminary results suggest that subjects treated with Ex-4 performed better than STZ+PBS subjects by making fewer omissions and shorter latency in correct responses. Our findings suggest that Ex-4

may be a viable treatment for the recovery of sustained attention in sporadic Alzheimer's disease. Subsequently, by using fluoro-jade C, a marker of neuronal death, we will examine the feasibility of Ex-4 treatment in the hippocampus. Lastly, Western blot analysis will be used to detect and quantify the presence of GSK-3 $\beta$  and tau protein. Juan Mosquera and Shanique Martin are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

**Building a Rat Model of Benign Essential Blepharospasm. Ellen Mutter<sup>1</sup> and Craig Evinger<sup>2</sup>, <sup>1</sup>Rockland Community College, Suffern, NY and <sup>2</sup>Department of Neurobiology and Behavior, Stony Brook University, Stony Brook, NY.**

The dystonias are a complex group of neurological disorders characterized by involuntary muscle contractions. While not life threatening, focal dystonias significantly impact the quality of life of those affected. Benign essential blepharospasm (dystonia of the eyelid) causes spasms of lid closure that cause functional blindness. The current treatments for dystonia are repetitive injections of botulinum toxin or brain surgery to implant stimulating electrodes. Thus, there is a pressing need for an animal model of dystonia with which to test new treatment options. Focal dystonia is believed to arise from the confluence of a predisposing and a triggering condition. In our model, theta frequency subthalamic nucleus deep brain stimulation (STN DBS) acted as the focal dystonia predisposing factor and mild corneal irritation induced by removal of the exorbital gland provided the triggering event. We predicted that combining the two conditions would cause rats to develop spasms of lid closure characteristic of blepharospasm. We analyzed different aspects of blinking before and after exorbital gland removal while the rats underwent continuous 7 Hz STN DBS. Measuring spontaneous and reflex blinking with electromyographic activity of the lid closing orbicularis oculi muscle, we found that 7 Hz STN DBS increased reflex blink amplitude but did not enable spasms of lid closure. Exorbital gland removal exaggerated reflex blink amplitude and led to spasms of lid closure. Thus, by combining 7Hz STN DBS and the removal of the exorbital gland we were able to create a rat exhibiting the characteristics of benign essential blepharospasm. Supported by EY07391, Thomas Hartman Parkinson's Disease Research Center at Stony Brook to CE, HHMI, CSME, and the Chancellor's Education Pipeline Biomedical Research Award.

**Physiological and Molecular Analyses of ZnCl<sub>2</sub> Stress Response in Cyanobacterium *Synechococcus* sp. IU 625. Robert Newby Jr. and Tin-Chun Chu, Seton Hall University, South Orange, NJ.**

Cyanobacterial harmful algal blooms (CHABs) are becoming a pressing issue globally. Zinc is a consistent contaminant in water bodies. Zinc is an essential trace element but can cause toxic effects in excess. Due to the increasing risk of CHABs, physiological and molecular analyses of ZnCl<sub>2</sub> stress response have been carried out by using a cyanobacterium *Synechococcus* sp. IU 625, lab strain RMTc over the course of 29 days. When culturing in medium containing ZnCl<sub>2</sub> at levels of 0, 10 mg/L, 25 mg/L and 50 mg/L, RMTc is able to grow up to 25 mg/L with no signs of inhibition. Significant elongation of the cells in concentrations of ZnCl<sub>2</sub> of 50 mg/L has been demonstrated to be occurring microscopically after growth in ZnCl<sub>2</sub> for 10 days. Viability staining and imaging using SYTOX® via confocal microscopy has determined that viable populations of cells exist in all concentrations. Expression of *smtA*, a metal binding protein, is shown to increase in response to ZnCl<sub>2</sub> by qPCR analysis. Flow cytometry was used to show the change in population composition as measured by FSC, SSC, Phycoerythrin, Allophycocyanin, and Chlorophyll-A composition. These methods will allow an insight into what physiological changes are occurring during a long-term exposure to zinc; which will allow for better probes and assays for predicting and responding to algal blooms in metal contaminated waters.

**Exploring Relationships Among Different Melons in Cucurbitaceae Family. Aisha Noor and Nidhi Gadura, Queensborough Community College, Bayside, NY.**

DNA Barcoding is a method for identifying species using their genomic DNA. Specifically, this technique is based upon using a small section of mitochondrial DNA (*COI* gene) and chloroplast DNA (*rbcL* gene) that have been preserved over many generations and are used as an identification tool in species. In this project we used 4 species of Cucurbitaceae family (water melon, bitter melon, yellow melon and cantaloupe) to identify evolutionary relationship among these and how they differ from each other in their genetic makeup. Genomic DNA was extracted from each sample. Specific primers were used to target *rbcL* region and polymerase chain reaction

(PCR) as performed in order to amplify this region, which was analyzed by Gel Electrophoresis. PCR products were sent for sequencing in order to create phylogenetic tree and the results were analyzed using Bioinformatics tools created by Cold Spring Harbor DNA Subway. Evolutionary relationships between different melon species will be discussed at the presentation.

**Horseshoe Crabs (*Limulus polyphemus*) from Shell Bar and Davis Park in New York are from the Same Population. Michael K. Nyarko, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.**

Horseshoe crabs (*Limulus polyphemus*) are arthropods that live primarily in shallow ocean waters on soft sandy bottoms. They are very old—the earliest fossils were found in strata roughly 450 million years old. One important feature is that their blood can be processed and used for detection of bacterial endotoxins in medical solutions. Horseshoe crabs have become endangered from over-hunting for use as bait and from destruction of their habitat. Survival of horseshoe crabs will depend on better methods of preservation including determination of the genetic structure of their populations. In order to determine the genetic structure of their populations, we compared crabs from Shell Bar (SB) and Davis Park (DP) in New York. Our hypothesis was that horseshoe crabs from SB and DP are of the same genetic population. To test our hypothesis, we isolated DNA from horseshoe crabs using the DNeasy Blood and Tissue Kit. We then used the polymerase chain reaction to amplify a 700-bp region of the cytochrome c oxidase I (COXI) gene with the Folmer primer set, which is specific to DNA of invertebrates. We used an agarose gel to verify the size of the amplified DNA. The DNA was sent to ELIM Biopharmaceuticals for sequencing and each sequence was subjected to a BLAST search to confirm they were from the COXI gene of *Limulus polyphemus*. A multiple sequence alignment showed the DNAs were identical over the entire range we sequenced. This supports our hypothesis that horseshoe crabs from Shell Bar and Davis Park are from the same genetic population. These two regions are fairly close and thus in the future we would like to compare horseshoe crabs from a wider region. This work was supported by grant 2R25GM06003 of the Bridge Program of NIGMS and grant 0537141091 of the CSTEP Program of NYSED.

**Investigating the Roles of *EGR1* and *ANGPTL4* in the Protection of Rat Testis Following Lipopolysaccharide-induced Inflammation. Mitchell I. Parker, Rekha Penmetcha and Michael A. Palladino, Monmouth University, West Long Branch, NJ.**

Until recently, reproductive biologists believed that foreign infectious agents were incapable of infiltrating the male reproductive organs and inducing inflammation. Studies, however, have demonstrated that the male reproductive tract is in fact vulnerable to invading microbes and viruses, and contains unique antimicrobial properties. Research into the defense mechanisms that occur in the environment of these tissues is of interest to reproductive biologists because bacterial and viral infections are known to cause infertility, cancers of the male reproductive tract, and erectile dysfunction, among other pathologies. Yet, relatively little is known about the gene and protein pathways involved in the detection and clearance of microbes that enter the male reproductive tract. Previous studies in our laboratory on gene expression following lipopolysaccharide (LPS)-induced inflammation of the male rat testis have demonstrated a distinctive crosstalk between inflammatory and hypoxic genes. We hypothesize that two hypoxic genes, *Egr1* and *Angptl4*, play a significant role in the antimicrobial defense of the rat testis because mRNA expression of these genes was significantly up-regulated following LPS treatment. The overall goal of our research is to determine what proteins are most essential to safeguarding the male reproductive tract from inflammation and to discover the functional significance of these proteins. The objective of our investigation was to determine if the proteins *EGR1* and *ANGPTL4* are important contributors to the cellular responses of the testis to inflammation. Inflammation was induced in previous studies by injecting Sprague-Dawley rats intraperitoneally with LPS from *P. aeruginosa* at a dosage of 5 mg/kg body weight. The rats were then sacrificed at 3 and 6 hours (n=3-5 animals/times point). Proteins were extracted from rat testes samples and examined using western blot analysis. Results are currently being analyzed and will be discussed at the conference. Funding Source: Bristol-Myers Squibb and the School of Science at Monmouth University.

**The Effects of EGCG-stearate and DMSO on the Cellular Processes of HSV-1 Infected Vero cells. Valerie Paschalis and Quinn Vega, Montclair State University, Montclair, NJ.**

The Herpes Simplex Virus (HSV) is the cause of oral and genital herpes and infects one in six individuals globally (CDC). Epigallocatechin-3-gallate (EGCG) is the most common polyphenol derived from green tea, and has been shown to exhibit antioxidant, anticancer, and antiviral properties. Since antiviral medication can only reduce the number of outbreaks but cannot cure herpes, EGCG-stearate, a lipid-soluble derivative of EGCG, is of interest as a novel treatment due to the fact that it has been shown to reduce HSV infection in cultured cells. While EGCG-stearate as an antiviral is promising, the cell signaling effects of EGCG stearate on cells undergoing viral infection are not fully known. Additionally, in these studies, dimethyl sulfoxide (DMSO) was used as a solvent of EGCG-stearate at a concentration of 1.5%. This is potentially concerning; although DMSO is commonly used as a cryoprotectant, high concentrations of DMSO are known to have adverse effects on cells. The purpose of this research is to determine how EGCG stearate affects the cell surface receptors of African Green Monkey Cells (Vero cells) that have been infected with HSV-1, and to explore the effects of DMSO on Vero cells. In this project, Vero cells were treated with different concentrations of DMSO ranging from 0.5% to 2%, and protein activation was measured by probing for phosphotyrosine through SDS-PAGE and Western blots.

**In Vitro Artificial RNA Selection of an Aptamer against the Oncometabolite 2-Hydroxyglutarate. Krima Patel and Jonathan Ouellet, Monmouth University, West Long Branch, NJ.**

Current treatments for cancer include chemotherapy which is a painful ordeal for any. Chemotherapy is beneficial even though it does produce numerous side-effects. With this project, one of my goals is to develop an aptamer against 2-HG, 2-hydroxyglutarate. The short term aim for my project is to have a working cycle and establishing a pool of molecules from which to develop a single strand of RNA, called an aptamer, that will ultimately act as a biosensor for the oncometabolite 2-hydroxyglutarate. 2-HG is a metabolite that is produced due to a mutation caused by an IDH1 mutation in the citric acid cycle. For this project, DNA strands have been designed by randomizing forty nucleotides labeled

as N in the strands The aptamer being developed should have enough specificity that it can bind 2-HG and induce the self-cleavage of the annexed hammerhead ribozyme (an RNA with catalytic cleavage capacity). To develop this aptamer, the technique that will be used is called SELEX (Systematic Evolution of Ligands by EXponential enrichment). SELEX includes various steps such as PCR (Polymerase Chain Reaction), Transcription, Reverse Transcription, etc. In the end, doing many cycles will help to obtain the best aptamer while reducing the percentage of background (non-binders). This project may be a new platform in cancer detection and treatment which just needs further development. This way of treatment would be less harmful for patients as well. Ultimately, the hope for this project is to develop a cell-targeted therapy for cancer cells. This work was supported by Monmouth University School of Science, the Department of Chemistry & Physics as well as the Benjamin Cummings/ MACUB Research Grant 2014.

**Development of a Gene Transfer Strategy of Antisense RNA Therapeutic to Alter HGFR Expression. Priyal Patel, Sarah C. Falotico, and Martin J. Hicks. Monmouth University, West Long Branch, NJ.**

Glioblastoma multiforme (GBM) is the most aggressive form of glioma. The current standard of care, surgical resection, radiation and chemotherapy only extend survival by 8 months to 1 year. Tyrosine kinase receptors (TKR) are targets for therapy, specifically the hepatocyte growth factor receptor (HGFR) of the c-MET pathway. Radiation and chemotherapy induce hypoxia which has been shown to increase activation of c-MET. In addition, up-regulated of c-MET leads to increased levels of vascular endothelial growth factor (VEGF) and epidermal growth factor receptor (EGFR) as well as other oncogenes involved in GBM. The application of therapies against these c-MET processes in GBM is limited by the blood-brain barrier which restricts systemically administered therapies from reaching the brain. We are creating novel strategy to bypass these barriers by developing a gene transfer vector to deliver the genetic sequences of RNA therapy molecules to alter the splicing pattern and expression of HGFR, creating a soluble HGFR isoform which will serve as an HGFR decoy. In this approach, we modify GBM and CNS cells to deliver the therapeutic anti-cancer molecule into the local milieu. In this

strategy, we will deliver anti-sense RNA molecules complementary to the 5' and 3' splice sites upstream of the transmembrane domain of HGFR and test the efficacy to block splicing inclusion of exons 12 to 13 and retention of intron 12 which includes an alternative intronic polyadenylation signal (AAUAAA) thereby creating a short soluble peptide decoy HGFR. In this system, we will be testing the efficacy of the spliceosomal localization element, U7snRNA and other secondary structure elements to stabilize the RNA therapeutic molecule. In the future, we hope to extend this approach to additional TKRs.

**Green Tea Polyphenols, EGCG and EGCG-Stearate as Potential Inhibitors of Herpes simplex virus-1 in Human Epithelial A549 Cells. Shivani N. Patel, Lee H. Lee and Sandra Adams, Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ.**

Epigallocatechin gallate (EGCG), a green tea polyphenol possesses antioxidant, antibacterial, anticancer and antiviral properties. EGCG-Stearate (EGCG-S) is of interest for this study because of its stability and lipophilic properties. Herpes simplex virus-1 (HSV-1), a member of *Alphaherpesviridae* subfamily is a leading cause of human viral diseases in the United States. In this study, 25  $\mu$ M, 50  $\mu$ M and 75  $\mu$ M of EGCG and EGCG-S were used to carry out cytotoxicity, cell viability and cell proliferation assays to determine the maximum non-cytotoxic concentrations on A549. The results suggested that 75  $\mu$ M of EGCG and EGCG-S is the appropriate concentration to further study their effect on the infection of HSV-1 in A549 cells. Infectivity, antiviral and plaque assays were performed to study the effects of EGCG and EGCG-S on HSV-1 infection. Infectivity assays demonstrated no cytopathic effect at the tested concentrations on EGCG and EGCG-S treated HSV-1 and suggested that the treated HSV-1 did not affect the cells. An antiviral assay indicated that the polyphenols treated HSV-1 inhibit the HSV-1 by 80%. Plaque forming units were significantly reduced in the EGCG and EGCG-S treated HSV-1. Confocal microscopy images further supported the inhibitory effects of 75  $\mu$ M EGCG and EGCG-S on HSV-1 infection in A549 cells. The long-term goal of this research is to use EGCG-S as a possible novel therapeutic treatment to limit the spread of HSV-1 infections.

**Examination of Household Chemicals on the Growth of Normal Flora. Blondine Paul and Kevin Bonney Kingsborough Community College, Brooklyn, NY.**

Humans release many household chemicals into the environment as waste and some of these compounds may have unknown effects on the growth of microorganisms. To investigate whether different common household compounds inhibit or promote the growth of microorganisms, we isolated normal flora from the palm of a human hand and screened a number of compounds to determine if they affected microbial growth. The compounds tested were soda, cough syrup, baby oil, olive oil, hot sauce, Clorox, and ammonia. By comparing the turbidity of test cultures with the turbidity of control cultures at different time points, we were able to assess whether growth was being promoted or inhibited. Our hypothesis was that ammonia and Clorox would inhibit bacterial survival and soda and olive oil would promote bacterial growth and replication. Our experimental results demonstrated that hot sauce was the strongest inhibitor of microbial growth, because it inhibited microbial growth at a lower concentration than any other compound tested. We found that olive oil was the strongest promoter of microbial growth since it caused a greater increase in observable growth than any other compound tested. Our findings suggested that hot sauce could be further investigated as a potential antibacterial agent, and that bacteria can actually use olive oil as a source of food. Our hypothesis was partially supported because certain concentrations of ammonia also inhibited the growth of the bacteria, while the olive oil promoted the growth of bacteria in our experiment, but the finding that hot sauce was the strongest inhibitor of growth was unexpected. This work provides the basis for studying the effect of household chemicals on other microorganisms that may encounter wastewater, such as those that are important in river and bay ecosystems.

**Extraction and Antibacterial Activity Evaluation of Freshwater Cyanobacterial exopolysaccharide. Jose L. Perez and Tin-Chun Chu, Seton Hall University, South Orange, NJ.**

Natural polysaccharides have been used for miscellaneous, mass-produced industrial products. Previous reports suggest the polysaccharides remain stable under extreme conditions and they possess possible rheological

characteristics and antimicrobial properties. In this study, we successfully extracted exopolysaccharide (EPS) from a freshwater cyanobacterium *Synechococcus* sp. IU 625 - ATCC 27344 (SIU 625) with modified Watcharamusik's method. We further investigated the antibacterial activity of extracted EPS on *Escherichia coli* and *Bacillus megaterium*. The results showed SIU 625 EPS was able to inhibit the growth of both *E. coli* and *B. megaterium* with 4 hours treatment. The inhibition of sporulation and germination of *B. megaterium* were also being observed.

**Role of Glutamate Receptor Interacting Protein 1 (GRIP1) in Pseudophosphorylated CaMKII Targeting Inhibitory Synapses. Giancarlo Perez, Reed C. Carroll and Anthony Torres, Biology Department, New Jersey City University, Jersey City, NJ.**

The activity of neurons is controlled by a balance of signals from other neurons at excitatory and inhibitory synapses. This balance of excitatory and inhibitory signaling is highly important for information processing and in neuroplasticity. Ca<sup>2+</sup>/calmodulin dependent protein kinase II $\alpha$  (CaMKII $\alpha$ ) can play a critical role in regulating the strength of both neuronal excitability and inhibition in response to different synaptic stimuli. Following strong glutamatergic stimulation, activated NMDA-type receptors strengthen excitatory synapses through CaMKII activation. With moderate NMDA activation, however, CaMKII strengthens inhibitory synapses. While the functions of CaMKII at excitatory synapses are well studied, it is not understood how CaMKII localizes to and regulates inhibitory synapses. This study first investigated whether Glutamate Receptor Interacting Protein (GRIP), found at inhibitory synapses strengthened by CaMKII, may act as a target to which activated CaMKII binds. HEK cell lines showed high levels of co-localization of transfected CaMKII/GRIP1 as did NMDA-treated neurons. Coimmunoprecipitation studies in HEK cells provide evidence for a direct interaction of active CaMKII and GRIP1. Additionally, knockdown of GRIP1 using si-RNA, reduced the ability of CaMKII to localize to inhibitory synapses. Further studies examined whether the phosphorylation of CaMKII could influence its localization at inhibitory synapses. Calcineurin reduces CaMKII phosphorylation. Cyclosporin A, an inhibitor of calcineurin, increased CaMKII co-localization at inhibitory synapses. A co-IP using wildtype and mutant

forms of CaMKII suggests that a pseudophosphorylated mutant (T286D/T305D) interacted more strongly with GRIP. This indicates the phosphorylated state of CaMKII may have a critical role in the synaptic localization of CaMKII. This research was done under the support of the Closing the Gap – Title V Grant from the Department of Education and an LSAMP-NSF grant. Thank you to Summer High School Research interns Declan Wollard and Armando Jimenez.

**Src Kinase is Required for the Interruption of Cholera Toxin Uptake in Cells Overexpressing Ack1.** Devina Persaud<sup>1</sup>, Victoria Prieto-Echagüe<sup>2</sup>, Deborah A. Brown<sup>3</sup>, W. Todd Miller<sup>4</sup> and Azad L. Gucwa<sup>1</sup>, <sup>1</sup>Department of Biomedical Sciences, Long Island University, Brookville, NY., <sup>2</sup>Institut Pasteur de Montevideo, Montevideo, Uruguay, <sup>3</sup>Department of Biochemistry and Cell Biology and <sup>4</sup>Department of Physiology and Biophysics, School of Medicine, Stony Brook University, Stony Brook, NY.

Ack1 (activated Cdc42-associated kinase 1), a 1038 amino acid protein, is a non-receptor tyrosine kinase and a direct effector molecule of Cdc42. Ack1 is overexpressed in various cancers, including breast, lung, and pancreatic cancer. The overexpression of Ack1 is correlated with poor prognosis of cancer, and has been associated with increased cell migration. Ack1 is activated in response to several different ligands as well as cell adhesion, and plays a role in clathrin-mediated internalization of EGFR. Our lab has found that overexpression of Ack1 results in the inhibition of several endocytic pathways, including the caveolar pathway. The aim of this study was to identify a region of interest within Ack1 that is responsible for inhibiting caveolar endocytosis by mutational analysis. Uptake of cholera toxin, a marker of caveolin-dependent internalization, was tested in cells overexpressing wild-type or truncated mutant constructs. Cholera toxin uptake was blocked in COS-7 cells expressing wild-type Ack1, but not in cells expressing a construct with a termination codon at amino acid 577. Moreover, inhibition of its uptake was restored with expression of a construct truncated at position 732. This suggested a portion of the proline-rich region that is required for interaction with Src kinase may be required for this inhibitory effect. We next tested the overexpression of wild-type Ack1 in the SYF mouse embryo fibroblast cell line,

a cell line deficient for Src family members Src, Yes and Fyn to determine the importance of Src. Interestingly, overexpression of full-length Ack1 resulted in what seemed to be normal cholera toxin uptake. This further suggested the interaction between Ack1 and the Src kinase family may play a role in caveolin-dependent endocytosis. Future work will focus on studying this interaction further, and to determine whether Src is essential for the inhibition of other endocytic pathways.

**MYST1 is the New Co-activator that Regulates the Proliferation of PCa Cells** Marc Philzaire<sup>1</sup>, Shiraz Mujtaba<sup>1</sup>, Kerry Burnstein<sup>2</sup> and Alice Levine<sup>3</sup>. <sup>1</sup>Department of Biology, Medgar Evers College, CUNY, Brooklyn, NY, <sup>2</sup>Department of Molecular and Cellular Pharmacology, Miller School of Medicine, University of Miami, Miami, FL and, <sup>3</sup>Department of Medicine, Mount Sinai School of Medicine, NY, NY.

Prostate cancer (PCa) is one of the most common malignancies in men and the second most prevalent cause of death in the United States. In New York alone, African-American males are reported to have a higher incidence of PCa as compared to other ethnic groups. Signaling mediated by the transcription factor Androgen Receptor (AR) is crucial to the growth of normal prostate gland as well as PCa. Despite early success of androgen ablation therapy, reactivation of AR signaling either due to a mutation or amplification of the AR gene leads to the development of a castration-resistant and malignant PCa. Previous studies have speculated that a functional synergy between reactivated AR and its co-activator supports the metastatic growth of castrate-resistant PCa. In parallel, PCa growth is further complicated by the activation of Nuclear Factor-Kappa B (NF-κB) which causes metastasis and blocks apoptotic promoting mechanisms. However, mechanism(s) supporting this pathological synergy between AR and NF-κB is not fully understood. Since transcriptional coactivators regulate the functions of a transcription factor, we hypothesize that transcription factors AR and NF-κB are regulated by a common coactivator, which could synergize functions of these two transcription factors. The luciferase data revealed that besides CBP, which is a known co-activator of AR and NF-κB transcription functions, MYST1 activates AR and NF-κB transcriptional activities after treatments with DHT and TNF. The immunohistochemical data verified that MYST1 is

overexpressed in the PCa cells *in contrast* to the cells from the benign region of the prostate tissue. The siRNA data revealed that while PC3-AR cells showed growth arrest in G2M phase of the cell cycle; PC3 and LNCaP cells exhibited apoptosis. Our investigations not only identified a *new* coactivator, MYST1, of AR and NF- $\kappa$ B transcriptional functions, but also demonstrated its biological role in controlling the PCa proliferation.

**Antiviral Activity of *Polygonum multiflorum*. Derek Prince and Tin-Chun Chu, Seton Hall University, South Orange, NJ.**

*Polygonum multiflorum* (Chinese Knotweed) is an herbaceous vine native to the south central regions of China. The herb has long been praised as an effective natural remedy, swiftly garnering attention from researchers. Recently, purified extracts of *Polygonum* species have been studied and results indicate impressive antioxidant, antibacterial and antiviral properties. In the present study, the antiviral activity of Chinese Knotweed is evaluated against herpes simplex virus-1 (HSV-1). HSV-1 is of increasing medical importance due to its impressive ability to infect cells, evading the host immune system and conveniently alternating between lysogenic and lytic states. To determine Chinese Knotweed's antiviral effectiveness, cytopathic effect (CPE) monitoring studies and plaque assays were performed. Results from CPE monitoring assays indicate that at concentrations as low as 0.1%, HSV-1 viral infection was completely inhibited over a seven-day period. Plaque assay results mimicked those of the CPE monitoring study. Furthermore, cell viability and cell proliferation tests show Vero cells to be unaffected at Chinese Knotweed concentrations as high as 1%. The results suggest that Chinese Knotweed could be a novel antiviral agent.

**Determination of Phylogenetic Relationship between Potato Family by DNA Barcoding. Daysi Proano, Weiwu Li, Eunjung Shin and Nidhi Gadura. Queensborough Community College, Bayside, NY.**

Potatoes, sweet potatoes, and yams are main carbohydrates sources in many parts of the world. They have high starch content, vitamins, and minerals that can be part of a healthy diet. There are a large variety of potatoes and most consumers are not sure about difference between sweet potatoes and yams. In this project several samples of potatoes and yams were chosen to explore their phylogenetic relationships by using DNA barcoding protocol developed by Cold Spring

Harbor Lab. We hypothesized that potatoes and yams diverged long time ago while white, purple and red potatoes evolved most recently. First we extracted genomic DNA from each sample. Then PCR primers were used to amplify a specific region of *rbcL* gene, a short DNA sequence from chloroplast this has been identified as the barcode region to identify species. Then, it was analyzed by Gel Electrophoresis. PCR sample was sent out for sequencing. Bioinformatics tools were used to BLAST the sequences. To our surprise, the results showed different phylogenetic relationships to what we expected. Funding for Daysi Proano to attend this conference is supported by US DOE Queensborough MSEIP grant to Dr. Gadura.

**The Effects of Atypical PKC on the Differentiation of Kidney Cells. Fatime Qosaj, Alana Doonachar and Alan Schoenfeld, Adelphi University, Garden City, NY.**

Mutations of the Von Hippel-Lindau (VHL) tumor suppressor gene have been correlated to abnormal tumor growths, including hemangioblastomas of the central nervous system, pheochromocytomas, and most important to this study, renal cell carcinoma. The gene product of VHL, pVHL, functions in a multi-protein complex, the ubiquitin E3 ligase complex. Here, pVHL signals the degradation of specific substrates in the proteasome, via polyubiquitination, in order to suppress tumor growth. One such target of the complex is the transcription factor, hypoxia inducible factor- $\alpha$  (HIF- $\alpha$ ), which under oxygenic conditions is signaled for proteasomal degradation. pVHL has also been shown to bind atypical PKC (aPKC). However, because VHL and aPKC have similar cellular roles, such as integrin level regulation and the proper maintenance of intercellular junctions, it is hypothesized that aPKC plays a cooperative role with VHL as opposed to the antagonistic role apparent in the target protein, HIF- $\alpha$ . In this ongoing study, an RNA interference technique was conducted on the different kidney cells lines. In this study, we have attempted to silence endogenous atypical PKC in these renal cell lines by infection with retroviruses coding for short hairpin RNA targeting PKC zeta (one of the isoforms of atypical PKC). This procedure was done in 786-O renal cells that either lack VHL or have VHL reintroduced. Using these cells, it will be possible to understand if lowering the levels of atypical PKC would hinder or help VHL with regards to phenotypic changes in kidney cell differentiation.

**Elucidating the Effects of Dopamine On Pharyngeal Pumping in *Caenorhabditis elegans*.** Madeeha Rahat, University of Southampton, Southampton, United Kingdom and SUNY College at Old Westbury, Old Westbury, NY, Faculty Mentor: Dr. Fernando Nieto, SUNY College at Old Westbury.

The study investigated the role of dopamine on the feeding behavior of the wild type and mutant worms *C. elegans*. Dopamine is a neurotransmitter known to be released in presence of food. Since food is taken in through the mouth and passed down to the intestine using the pharynx, activity of the pharynx was observed to see if it changed in presence and absence of food and dopamine. The pharyngeal pumping rate was hypothesized to be higher in presence of food. The wild type worms showed a higher pharyngeal pumping rate in presence of food and dopamine as compared to just food. The wild type worms' pharyngeal activity was seen to increase significantly in presence of dopamine and absence of food as compared to absence of both dopamine and food. The Dop-4 mutant worms showed parallel results as the wild type worms. The dop-4 mutants lack the only dopamine neurotransmitter (dop-4) found in the pharynx still responded to the presence of dopamine, concluding that it is unlikely for the response caused by dopamine to be directly from this receptor. In other words, it suggests that the system of response is more complicated, and the feeding behavior may be regulated by extra-pharyngeal neurons rather than just the dop-4. It is also possible that other dopamine neurons present elsewhere in the whole worm are acting to modulate feeding behavior. These experiments provide a basis for further studies to characterize dopamine's role in feeding

**Examination of Social Foraging in *Bufo americanus*.** Elizabeth Ramirez and Charles Sontag, Bergen Community College, Paramus, NY.

Tadpoles of *Bufo americanus*, the American toad, may be a model species to study social foraging. In prior research, Sontag *et al.* (2006) found conclusive evidence that *B. americanus* employed group living to locate and determine food quality and broadcast this information using pressure waves. This summer we studied the ability of *B. americanus* to make fine scale discriminations of food quality. We presented tadpoles with food patches of different quality and noted the feeding choices of three tadpoles, and see how one foraging tadpole fared in comparison. We were then able to correlate this newfound information with prior research that demonstrated simple choice and association.

**Comparison of Selected *Enterococcus* and *E. coli* Detection Methods in Recreational Waters.** Myla Ramirez<sup>1</sup>, Alessandra Rossi<sup>1</sup>, Edward Wong<sup>2</sup>, Meiyin Wu<sup>1</sup> and Lee H. Lee<sup>1</sup>, <sup>1</sup>Montclair State University, Montclair, NJ and <sup>2</sup>Livingston High School, Livingston, NJ.

The detection and enumeration of microorganisms in recreation waters are an essential part of water quality and public health monitoring. Currently, there are more than fifty detection methods for pathogen indicators. In this study, five detection methods for two commonly used pathogen indicators, *Enterococcus* and *E. coli*, were evaluated. Fluorogenic Substrate Enterococcus Test (SM9223D) and Enterococci in Water by Membrane Filtration Using membrane-Enterococcus Indoxyl- $\beta$ -D-Glucoside Agar (mEI) (EPA 1600) were used to test *Enterococcus*, and Enzyme Substrate Coliform Test (SM9223B), Total Coliforms and *Escherichia coli* in Water by Membrane Filtration Using a Simultaneous Detection Technique (MI Medium) (EPA 1604), and m-ColiBlue24<sup>®</sup> Hach Company Test (Method No. 10029) for *E. coli*. The results of this study showed a significant difference between the colony counts of *Enterococcus* between the two selected methods with a difference of two-fold. Similar findings were observed on colony counts of *E. coli* using the three selected methods and ranged between 4856 CFU/100mL and 6156 CFU/100mL. The results suggest that the method used might impact results of pathogen levels. Special attention should be paid while selecting methods for pathogen indicators.

**Determining the Structure of Citrate, Glycine and Zinc Complex in Aqueous Solution Using Vibrational Spectroscopy.** Washington Ramirez<sup>1</sup>, Jinnette Tolentino<sup>2</sup>, Ruel Z. Desamero<sup>2</sup>, <sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>York College, Jamaica, NY.

Zinc is an important element that is found in every cell of the body and it has been shown to be effective in treating the common cold, and cold sores. Researchers have suggested that amino acids enhance the biological availability or efficacy of the zinc since amino acids can increase the solubility of zinc salts such as, zinc citrate, succinate and oxalate. Therefore, the aim of this project was to characterize the Zn<sup>2+</sup>-citrate interaction as a function of amino acid concentration. For this experiment, Vibrational Spectroscopy was employed to identify which functional groups are involved in Zn<sup>2+</sup>-citrate interaction in the presence of glycine. Different ratio of citrate to glycine, 1:1, 1:3, 1:5 and 1:10,

were titrated with various concentration of Zinc. Our results indicate that at lower ratio of citrate to glycine, both molecules are interacting with the metal. According to the FTIR spectra, there are two complexes formed in solution. Complex 1 is citrate interacting with Zn (II) and complex 2 is glycine and Zn (II). However, the FTIR data do not show that there is formation of a new glycine-Zn<sup>2+</sup>-citrate complex at the ratio of 1:1 and 1:3. At the ratio of 1:5 and 1:10 citrate to glycine, the FTIR spectra depicts a new interaction between citrate, glycine and Zn (II). Understanding the nature of this interaction could be the key to possible implementation of such an amino acid-zinc delivery system. Washington Rammirez is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

**Nuclear Tip60 Overexpression Exacerbates Chemotherapeutic Drug Treatment in Breast, Lung and Pancreatic Cancer Cell Lines. Priyadarshini Ravichandran and Daniel S. Ginsburg, LIU Post, Brookville, NY.**

The Tip60 lysine acetyltransferase acetylates histones, the p53 tumor suppressor, the ATM kinase DNA repair enzyme, and the androgen receptor transcription factor. Tip60 plays a vital role in transcription, DNA repair, and apoptosis. There is conflicting evidence that Tip60 may function as both a tumor suppressor and an oncogene. We are interested in analyzing Tip60's role in breast, pancreatic, and lung carcinomas. We would also like to gauge Tip60's potential as a therapeutic agent in these cancers. We hypothesize that due to Tip60's role in DNA repair and apoptosis, it serves as a tumor suppressor in breast, pancreatic and lung cancers. Therefore, overexpression of Tip60 should decrease proliferation in tumor cells and enhance the effects of chemotherapeutic agents. We have shown that Tip60 levels in six different breast, pancreatic and lung cancer cell lines were significantly lower as compared to non-tumorigenic cells. While Tip60 overexpression itself was found to reduce cancer cell proliferation in only one cell line, Tip60 overexpression when accompanied with paclitaxel treatment, decreased proliferation 30-60% more than administration of paclitaxel alone amongst the cancer cell lines. In addition, we discovered that the subcellular localization of Tip60 varied amongst the cell lines, with cytoplasmic localization in cancer cells and nuclear localization in non-cancer cells. Overexpression of Tip60

containing an N-terminal nuclear localization signal (NLS) decreased cancer cell proliferation more than Tip60 lacking the extra NLS. These results suggest that Tip60 serves as a tumor suppressor in breast, lung, and pancreatic cancers, consistent with previous data, and that the proper localization of Tip60 may be more important for its tumor suppressor activity than overall Tip60 levels. Our work provides evidence that Tip60 may be useful as part of a cancer therapy in combination with currently used drugs. This work was supported by the LIU Post Research Committee.

**Vascular Tissue-resident Mesenchymal Stem Cells; Friend or Foe? Heather Renna, Lauren McHugh, Eddie Bochynski, Victoria Flemm and Jodi F. Evans, Molloy College, Rockville Centre, NY**

Mesenchymal stem cells (MSC) are ideal candidates for stem cell-based therapies of vascular inflammation. They are progenitor cells that can replace damaged cells and they can modulate immune response cells. MSC from bone marrow and adipose tissue regulate inflammation by promoting the switch of macrophage cell from an inflammatory to an anti-inflammatory phenotype. Much less is known about the tissue resident MSC's and their interaction with macrophage cells. We hypothesized that aorta-derived mesenchymal stem cells (mAo MSC) would also promote the expression of the anti-inflammatory phenotype among macrophage cells. The interaction of mAo MSC with the macrophage was examined by co-culturing the cells and exposing them to the inflammatory mediator, lipopolysaccharide (LPS). A bone marrow derived MSC cell line was used as a control. Nitric oxide (NO) and the tumor necrosis factor- $\alpha$  (TNF $\alpha$ ) and interleukin-12 (IL-12) cytokines were measured using Griess reaction and ELISA assay respectively. The impact of the interaction on phagocytosis was measured using zymosan-A. We found that bone marrow derived MSC, when in co-culture with macrophage cells, performed as expected and suppressed NO, TNF $\alpha$ , and IL-12 production. Unexpectedly, the mAo MSC enhanced NO and TNF $\alpha$  production by the macrophage cells, which is indicative of the inflammatory phenotype; IL-12 production by macrophage remained unchanged. Macrophage cell phagocytic activity was significantly increased by contact with mAo MSC, which represents enhancement of the anti-inflammatory phenotype.

The potential for the tissue-resident stem cell to participate in vascular inflammatory diseases should be considered when designing stem-cell based therapies. Continued research would further define the role of the tissue-resident stem cell, making it possible to improve current treatments of diseases such as coronary artery disease and peripheral artery disease. This work was supported by a Benjamin Cummings/MACUB student research grant.

**The Northern Rock Barnacle (*Balanus balanoides*) Does Not Appear to Be an Intermediate Host for MSX (*Haplosporidium nelsoni*).** Andrea Saavedra, Craig Hinkley and Gary Sarinsky. Kingsborough Community College, Brooklyn, NY.

Our lab recently found that some Eastern Oysters (*Crassostrea virginica*) grown from spats in Jamaica Bay, N.Y tested positive for MSX (*Haplosporidium nelsoni*). The disease was first documented in 1957 in Chesapeake Bay where it caused massive oyster mortalities. The transmission of MSX is not understood. There is some research to suggest that there might be an unknown intermediate host involved in its life cycle. The ecosystem in Jamaica Bay is similar to Chesapeake Bay and many of the same organisms are present. The Northern Rock Barnacle (*Balanus balanoides*) is found permanently attached to rocks, pilings, or any hard substrate in intertidal and subtidal habitats. Since barnacles are observed throughout Jamaica Bay it is hypothesized that the barnacles serve as an intermediate host in the life cycle of MSX. DNA was isolated from barnacle tissues using a DNeasy Blood and Tissue kit. PCR amplifications were carried out using the MSXA and MSXB small subunit rRNA and the mitochondrial cytochrome c oxidase 1 (CO1) gene primer sets respectively. The MSX amplified products and a positive control for MSX were then subjected to agarose gel electrophoresis to determine correct size (564-bp.) All of the 13 barnacles were negative but we demonstrated that MSX under the conditions used with the positive control was amplified. To verify that DNA was obtained from all of the oysters, the CO1 amplified products were subjected to agarose gel electrophoresis to determine correct size (702 bp) and were found to be present in all 13 samples. The MSX amplified control and CO1 amplified products were sequenced by Elim Biopharmaceuticals and were subjected to NCBI blast searches which further verified that the CO1 gene from was from *Crassostrea virginica*. The results of these experiments did not support our hypothesis that barnacles are an intermediate host in the life cycle of MSX.

**Immunohistofluorescence Localization of Histamine and Histamine Receptors in Ganglia and Tissues of the Bivalve Mollusc, *Crassostrea virginica*.** Danellie Semple<sup>1</sup>, Ayana McLeod<sup>2</sup>, Margaret A. Carroll<sup>2</sup> and Edward J. Catapane<sup>2</sup>, <sup>1</sup>Kingsborough Community College and <sup>2</sup>Medgar Evers College, Brooklyn, NY.

Histamine (His), a biogenic amine, serves as a neurotransmitter in the CNS and sensory receptors. It has rarely been reported in bivalves. We previously showed it is involved in sensory reception in the sensory-motor integration of gill lateral cell cilia beating in the bivalve Mollusc, *Crassostrea virginica*, and showed by HPLC it is present in ganglia and tissues of *C. virginica*. We hypothesize His neurons and His receptors are present in ganglia and tissues of *C. virginica*. We tested this using immunohistofluorescence techniques with His and His receptor antibodies to visualize them in cells. 1° and 2° antibodies were purchased from Abcam and Santa Cruz Biotechnology. Tissues were dissected, snap frozen, cryostat sectioned, fixed with EDAC (N-Ethyl-N'-(3-dimethylaminopropyl) Carbodiimide Hydrochloride) or paraformaldehyde, treated with blockers, and incubated with 1° and 2° antibodies. Whole mounts of gill and mantle also were prepared. Sections were viewed with a Zeiss epilume fluorescence microscope fitted with a ProgRes C3 Peltier cooled camera, as well as a Leica epilume fluorescence microscope with a Leica DFC400 camera. Both had 100 watt mercury lamps and FITC and Texas Red excitation/emission filters. Results show His and His H2 receptors present in visceral ganglia gill, mantle body and sensory tentacles of the mantle rim. Of particular significance is their presence in sensory tentacles as that correlates well with our previous sensory physiology studies, and their presence in gill interlamellar junctions, which have not been well studied. This study coupled with our other work shows His to be an important endogenous biogenic amine in the bivalve *C. virginica*.

**Somatic Progenitor Cell Differentiation to Myofibroblast Requires an Increase in Integrin beta1/CD29 Expression.** Namita Sen, Mark Weingarten, Matthew Lubin and Yakov Peter, Department of Biology and Pulmonary Medicine, Yeshiva University, New York, NY.

Stromal cells play significant roles in wide spectra of human diseases. Of these, myofibroblasts deposit connective tissue and may serve as an important factor in a prospective stem cell niche. One major source of myofibroblasts in the lung is the pulmonary epithelial cell that can undergo epithelial to mesenchymal transition. However, the presence of a stromal progenitor cell cannot be ruled out. To

understand concepts of stromal development we used a primary culture method which isolates a mixed-progenitor cell population. These cells were cultivated for over two weeks and growth and morphology monitored and molecular phenotype investigated and quantified using real-time polymerase chain reaction (RTPCR), flow cytometry, and immunofluorescence. In culture, directed-differentiated stromal progenitor subsets gave rise to cells displaying distinctive myofibroblastic morphologies and patterns of proliferative growth. At the molecular level, the myofibroblast-like population produced alpha smooth muscle actin and demonstrated over a 60-fold increase in normalized integrin beta-1/*Cd29* transcript expression as compared to the stromal progenitor. Cellular expression of CD29 increased over 20-fold, as demonstrated by flow cytometry, manifested as punctuate cell localization seen by immunofluorescence. Normalized transcript expression levels of fibronectin-1 increased over 3,000-fold over the same period as established by RTPCR. These findings suggest that stromal progenitor cells exist and that they undergo a complex cellular and molecular pattern of differentiation. Insights into the process of stromal cell development may lay the foundation to understanding *de-novo* lung structural regeneration and potential causes of fibrotic disease.

**Network Analysis of Gene Expression Changes in Maternal Immune Activation Models of Schizophrenia. Jeremy Seto<sup>1,2</sup>, Jose Moreno<sup>2</sup>, Brittiny Dhital<sup>1</sup>, James-David Brown<sup>3</sup> and Javier Gonzalez-Maeso<sup>2,1</sup>New York City College of Technology and <sup>2</sup>Icahn School of Medicine of Mount Sinai.**

Maternal Immune Activation (MIA) is an animal model of Schizophrenia where *in utero* rodents are subjected to immunological stressors. MIA animals display a hypersensitivity to psychotropic stimuli that induce hallucinations. Cytokine panels and RNA-Seq analysis illustrate profiles of activation conserved between two models of MIA, influenza and stress. Biomarkers identified in these screens define a distinct alteration resulting in a latent phenotype. Utilizing the known biomarkers as a mechanism underlying neurodevelopmental alterations can be illustrated through the use of network analysis to understand the etiology of the human disease. This work was supported by NSF DUE-1323522 and PSC-CUNY 43 Research Award # 65127-00 43.

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

Copper surface alloys can act as antimicrobial sanitizing agents that kill bacteria, fungi, and some viruses. Studies from our lab showed that cell death in bacteria and yeast that occurred soon after contact with copper alloys, had a correlation with increased levels of lipid peroxidation. However, the specific genetic pathways involved in the cell death of microorganisms through contact with copper alloy surfaces is still unknown. A *Saccharomyces cerevisiae* FLEXgene ORF collection in the BY011 expression vector was obtained from the Harvard Institute of Proteomics (HIP) which contained 5530 clones that showed ampicillin resistance in *Escherichia coli*. The clones differentiated from one another by the intensity of a single expressed gene. A selection strategy was developed for screening the library for survivors on lethal doses of copper. Previous studies from this project indicated that cell death occurs in wild type *Saccharomyces cerevisiae* strain BY4741 at 30mM CuSO<sub>4</sub> concentration between 40-50 minutes. Screening the library from survivors for the lethal dosage should help reveal the genetic pathways involved in the copper induced cell death. A better understanding of the genes involved in this pathway could help develop new medical advancements in fighting harmful microorganisms. This project receives funding from the United States Department of Education MSEIP grant to Dr. Gadura.

**Testing a *Saccharomyces cerevisiae* Genomic Library to Determine Copper Induced Cell Death Pathways. Ricky Shao and Nidhi Gadura Biology Department, Queensborough Community College, Bayside NY.**

Copper has been used for decades as a means of preventing bacteria from gaining a foothold in staples such as food and drinking water. However, the biological mechanisms with which bacteria die are still not fully understood. With the growth of so-called "super bacteria" from the proliferous use of antibiotics such as penicillin, the hospital acquired infection rates are on the rise. Our lab is interested in trying to find out the cellular pathways involved in copper mediated cell death. Published results from our lab indicate that copper induced bacterial cell death happens within

30 minutes and correlates with increased level of lipid peroxidation in the cell membrane. Therefore, we decided to screen the *Saccharomyces cerevisiae* overexpression genomic library acquired from the Harvard Institute of Proteomics for survivors on lethal doses of copper. Yeast wild type strain W303 was transformed with overexpressed ORFs and then incubated for a period of 40 minutes in a 30mM CuSO<sub>4</sub> solution. These cells were then plated on YNB -URA Galactose medium to look for survivors. Preliminary results indicate the involvement of genes in cell membrane formation pathways. Funding for Ricky Shao is supported by CUNY Research Scholars program and attendance to this conference is supported by US DOE Queensborough MSEIP grant to Dr. Gadura.

**The Effect of PKD2 Inhibitors on the Feeding Behavior of Hydra. Hyo Jung Shin, Maryam Khan and Susan McLaughlin, Biology Department, Queensborough Community College, Bayside, NY.**

*Hydra* is a multicellular organism belonging to phylum Cnidaria. One of the most interesting *Hydra* traits is its release of cnidocytes during feeding. Cnidocytes are stinging cells located primarily on the tentacles; they are used for prey capture and defense from predators. Cnidocyte discharge requires the presence of external calcium, but the exact molecular mechanisms regulating cnidocyte discharge are poorly understood. TRP (transient receptor potential) channels are nonselective cation channels that play key roles in many sensory processes and are responsive to multiple types of stimuli. Many TRP channels have been identified in the *Hydra* genome. In this research, we focused on the PKD TRP subfamily, which are Ca<sup>+2</sup> permeable nonselective cation channels. *In situ* hybridizations indicated that a PKD2 homolog is expressed in hydra tentacles and in the basal disc. A related PKD2L1 homolog is expressed in a region around the hydra mouth, as well as in scattered cells in the body. In addition, a PKD1 homolog is also expressed in the tentacles and basal disc. PKD2 and PKD1 proteins are believed to interact in the transduction of chemical and mechanical signals. These localized patterns of expression suggest that PKD ion channels are involved in cnidocyte release and in mouth opening. The non-specific PKD2 inhibitors neomycin and gadolinium were used in a prey capture assay to assess the role of PKD channels in hydra feeding. Both neomycin and gadolinium reduced the ability of hydra to

capture prey organisms. Verapamil, an inhibitor of voltage-gated Ca<sup>+2</sup> channels, showed little effect on prey capture. The PKD expression patterns and the results of the prey capture assays suggest that PKD channels play a role in hydra feeding.

**Synergistic Antibacterial Activity of Turmeric and Garlic with Selected Antibiotics. Kirsten Simmons, Nicolle Segarra, Leslie Landy, Jonathan Valsechi-Diaz and Tin-Chun Chu, Seton Hall University, South Orange, NJ.**

Spices are found in various aspects of life, from cooking to cosmetics and medicinal practices. Recent studies have shown that many spices possess antimicrobial activities. In this study, we focused on evaluating the antibacterial activity of two common spices, garlic and turmeric. Two gram negative bacteria, *Escherichia coli* and *Pseudomonas aeruginosa*; and two gram positive bacteria, *Bacillus megaterium* and *Staphylococcus epidermidis* are included in this project. 5% garlic and 5% turmeric were chosen and the Disc diffusion method was used to evaluate the antibacterial activity of each spice. Kirby-Bauer assays were carried out to determine the synergistic antibacterial effect of the spices and selected antibiotics including Ampicillin, Rifampin, Erythromycin, Penicillin, Bacitracin, Gentamicin, Kanamycin, and Tetracycline. The results indicated that both turmeric and garlic have synergistic antibacterial activity with Penicillin (10 µg) and Rifampin (5 µg). We also investigated the potential sporulation and germination inhibition of *Bacillus megaterium* with turmeric. Preliminary results suggested that turmeric could inhibit sporulation and germination process of the spore-forming bacteria, which makes turmeric a potential alternative therapeutic agent.

**Flow Cytometry Analysis of Cyanobacteria in Barnegat Bay, New Jersey. Anaika Singh, Jillian Cortese, Robert Newby Jr. and Tin-Chun Chu, Seton Hall University, South Orange, NJ.**

Cyanobacterial harmful algal blooms (CHABs) contaminated many water bodies throughout the world. It has detrimental effects on not only aquatic life but also animal and human health. In recent years, Barnegat Bay has been contaminated by CHABs due to the increased pollutants including fertilizer run-off in the water. In this study, water samples from different sites of Barnegat Bay were collected and filtered. Flow cytometry analyses were carried out for all water samples with a reference culture of mixed

cyanobacteria, including Anabaena, Nostoc, Oscillatoria, Gloeotrichia and Synechococcus. Profiling of phycoerythrin and phycocyanin were generated for all water samples. The results indicated ten out of thirteen sites contain 90% and above of one or more cyanobacteria in the reference culture while the other three sites contain at least 80% of that population. Cyanophages were also detected by the plaque assays using the reference mixed cyanobacteria culture.

**Characterization of Iron in *Petroselinum crispum* (Parsley) Using Mossbauer Spectroscopy. Stephan Smith<sup>1</sup>, Sunil Dehipawala<sup>1</sup> and Harry Gafney<sup>2</sup>, <sup>1</sup>Queensborough Community College, Bayside NY and <sup>2</sup>Queens College, Flushing, NY.**

Iron is an essential nutrient not only for humans, but also for plants which use iron for chlorophyll formation, RNA metabolism, and transpiration process regulation. The presence of iron increases the thickness of a leaf and hence the flow of nutrients. Iron is one of the most abundant metals in the soil and occurs in a wide range of chemical forms. Since plants can absorb only certain species, all of the iron in the soil is not available for plants. For example, plants can absorb ferrous ions and not ferric ions. This project investigated the correlation between the iron species presents in soil and in *Petroselinum crispum* (parsley), using the room temperature Mossbauer spectroscopy. Mossbauer spectrum of garden soil consists of two doublets. Based on the established isomer shift and quadrupole splitting values of iron, these doublets can be identified as due to octahedrally coordinated Fe<sup>3+</sup> and tetrahedrally coordinated Fe<sup>2+</sup>. Therefore, clearly at least two forms of iron exists in the soil. The Mossbauer spectrum of parsley also consists of two doublets. Commercially available iron supplement, ferrous sulphate, was used as a standard. The isomer shift value of 1.27 mm/s and quadrupole splitting of 2.67 mm/s of the supplement, is consistent with tetrahedrally coordinated Fe<sup>2+</sup>. A Mossbauer spectrum of parsley differs from the standard iron supplement. Most of the iron present in the parsley has the form Fe<sup>3+</sup> or electron density at the site of the iron nucleus similar to that of Fe<sup>3+</sup>. These findings will help establish soil conditions necessary to increase Fe<sup>2+</sup> intake by plants similar to the form of iron present in most supplements. Stephan Smith is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College.

**Characterization and Comparison of *Helitron* Tandem Repeats in *O. sativa*. Kaitlyn Socha and Raed Atiyat, Montclair State University, Montclair, NJ.**

*Helitrons* are a type of transposable element that are found in numerous species of plants and animals. Many characteristics of *Helitrons* are still unknown due to their only recent discovery and the difficulty of locating and identifying them within genomes. It is believed that *Helitrons* replicate using a rolling circle mechanism. If this is indeed the case, this method should produce multiple tandem repeats throughout the genome where the rolling circle duplication has taken place. The purpose of this study was to identify and confirm likely *Helitron* tandem repeats within the *Oryza sativa* genome. The repeats were examined using the Institute for System Biology's RepeatMasker Server to confirm that the repeats were of *Helitron* origin. Tandem repeats that were confirmed as being of *Helitron* origin were further examined. The sequences between these repeats, their junction sequences, were then analyzed. The junction sequences of each set were compared to each other to look for consistencies between the repeats. The sequences were compared using the National Center for Biotechnology Information's (NCBI) Basic Local Alignment Search Tool (BLAST). The junction sequences among different repeat sets were then compared to see if similarities existed throughout the genome at these repeat locations. Faculty Mentors for this project were Dr. Chunguang Du and Dr. Wenwei Xiong. This work was supported by Montclair State University's Science Honors Innovation Program.

**Temporal and Geographic Variation in a Marine Snails Reproductive Investment. Kristin Spsychalsky and Aaren Freeman, Adelphi University, Garden City, NY.**

The marine snails *Busycon carica* and *Busycon canaliculatus* (aka whelks) have native ranges in the United States, spanning from Cape Cod, Massachusetts to Florida. When they reproduce during winter, both whelks deposit strings of egg cases (called "purses") in sandy, subtidal areas. Juvenile whelks hatch from these egg cases later that spring or summer. Egg string samples that washed up on shore were collected from Massachusetts, New York, Georgia and Florida from 2011 to 2014. Each individual egg casing was measured and all eggs inside unhatched cases were counted, measured and weighed. This study compared the average weight

and number of offspring at the different locations during different years. The analysis of the data collected indicates that *Busycon carica* offspring were smaller in 2014 than in previous years observed. Samples from New York were smaller on average than those from Massachusetts. Those collected in 2012 yielded the highest average offspring weight in both species. The purpose of this study is to identify reproductive characteristics of these marine snails that may be particularly adapted to local winter temperature regimes. We will further investigate possible impacts of climate change and this local adaptation on reproductive investment in these whelks.

**Chromatin and its Role in the Protection of DNA. Joey Stabile and Daniel S. Ginsburg, Biomedical Sciences Department, LIU Post, Brookville, NY.**

The chromosomes in eukaryotic cells are organized into a DNA-protein complex called chromatin. The basic unit of chromatin is the nucleosome, in which ~147 bp of DNA are wrapped around eight histone proteins. Because of its tight association with histones, DNA in a nucleosome is inaccessible to most cellular proteins. Thus, chromatin regulates processes involving DNA including transcription, replication, and repair. We hypothesized that one of the functions of chromatin would also be to protect DNA from damage. To test this hypothesis, we investigated the sensitivity of yeast strains carrying histone mutations to DNA damaging agents and caffeine, a DNA repair inhibitor. We found two separate regions of histone H3 that seemed to be important for resistance to UV light (17-20) and caffeine (13-16). Each of these regions contains an acetylable lysine, which may be important for the ability of the histone to incorporate into chromatin. We also analyzed whether DNA repair proteins are recruited to actively transcribed genes, in which the chromatin has been disassembled. We found that Rad16, a double-strand break repair protein, was recruited to the open reading frame of the *GAL1* gene in a transcription-dependent manner, suggesting that there may be damage taking place as the chromatin is disassembled during transcription. Our results support our hypothesis that chromatin serves to protect DNA from at least some types of damage.

**Inhibition of HSV-2 in Vero Cells by EGCG and EGCG-Stearate. James Stamos, Sandra D. Adams and Lee H. Lee, Department of Biology and Molecular Biology, Montclair State University, Montclair, NJ.**

Herpes simplex virus type 2 (HSV-2) is an enveloped; double stranded DNA virus belonging to the  $\alpha$ -*Herpesviridae* subfamily. It is the etiological agent of genital herpes, one of the most common sexually transmitted diseases. HSV-2 establishes a latent infection in neurons of the sacral ganglia after an initial lytic infection of epithelia. A promising antiviral molecule is the polyphenol epigallocatechin gallate (EGCG), which is derived from the plant *Camellia sinensis*. EGCG exhibits many beneficial activities including antioxidant and anticancer properties. Previous studies suggest that EGCG inhibits HSV-1 infection in Vero cells; however EGCG is an unstable molecule. Esterification of fatty acid molecules to EGCG stabilizes its structure and may enhance antiviral activity. Moreover, lipid-soluble derivatives of EGCG enter the cell and may confer uncharacterized effects on the infection cycle. The purpose of this study was to compare the antiviral effects of EGCG and the lipid-soluble derivative EGCG-stearate (S-EGCG) on HSV-2 infection of cultured Vero cells. Three assays were used to determine the maximum non-cytotoxic concentration of these compounds: cytotoxicity, cell viability, and cell proliferation. The maximum non-cytotoxic concentration of 75  $\mu$ M along with lower concentrations of 50  $\mu$ M and 25  $\mu$ M were used to treat the virus. A standard plaque assay was used to calculate the titer of the treated and untreated virus. The titer of HSV-2 was significantly reduced after treatment with S-EGCG for one hour. Additionally, a PCR-based assay was used to elucidate the potential effect of S-EGCG on viral DNA replication. TEM images also support the previous findings. In conclusion, lipid-soluble derivatives of EGCG may potentially represent a novel therapeutic for HSV-2.

**Correlation of Formaldehyde Emissions from Raw Wood to Wood Moisture Content. Joel Strothers<sup>1</sup>, Raymond Fort<sup>2</sup>, Barbara Cole<sup>2</sup> and Ashley Hellenbrand<sup>2</sup>, <sup>1</sup>Medgar Evers College, Brooklyn, NY and <sup>2</sup>University of Maine FBRI, Orono, MA.**

Formaldehyde (CH<sub>2</sub>O) in recent years has stirred up a lot of debate amongst federal and state agencies, industrial companies, researchers and scientist for its overall use, carcinogenic characteristics and in some cases life-threatening side affects. The national attention of formaldehyde spawned from the events that

generated around the FEMA trailers. FEMA trailers were given to the residents of New Orleans, who had lost their homes in the natural disaster of Hurricane Katrina. Within these trailers, residents were exposed to high levels of formaldehyde emissions. Since the given media attention from this instance, more research has been conducted and scientist have become committed to the study of formaldehyde emission and how they can reduce the emissions from composite wood products. We hypothesize the amount of formaldehyde emitted from wood is correlated to the moisture content of the wood. To test this we analyzed two different species of commonly used raw wood (Southern pine and Aspen) and correlated their formaldehyde emissions to their moisture content. We believe that raw wood with greater moisture content and wood that is exposed to higher temperatures would release more formaldehyde when compared to wood of lower moistures content and a lower temperature exposure. Each wood sample was preconditioned in a controlled temperature environment to obtain the desired moisture content. Thereafter, the raw wood samples were exposed to three different temperature (30°C, 50° C and 75°C) settings for duration of 3 hours. Gas Chromatography Mass Spectroscopy (GC /MS) was used to analyze the samples and determine the µg/formaldehyde emitted/g of wood. Our results determined that wood with higher moisture contents and elevated temperatures release more formaldehyde than did the other samples.

**Biological Assessments of the Ursino Dam Area, John's Cove on the Arthur Kill Blueway, and South Front Street Situated at the Mouth of the Elizabeth River and the Arthur Kill Blueway, New Jersey, (A Citizen Science Effort). Bill Surena and Mariam Katu Binti. New Jersey City University, Jersey City, NJ.**

During the summer of 2014, we conducted comparative biology assessments of the Elizabeth River at John's Cove, South Front Street, and the Ursino Dam area, justifying our goals from a citizen science perspective. The purpose of our research was to gather data on water quality, local plants, and animal inhabitants. In addition to water quality testing for pH, salinity, dissolved oxygen, ammonium, nitrates and phosphates, we also documented these environment with visual assessments, mapping, environmental journaling, videography and photography for the study and to raise awareness within the Elizabeth community.

Although the results and data collected indicated that the quality of the waters located at the study sites fell within healthy parameters, additional monitoring and data gathering are required for a successful, citizen scientist- driven research campaign to promote a sustainable environment. The environment belongs to humans, and local plant and animal species alike, yet humans alone can affect change in these environments. Thus, community education and consistent involvement must be stressed. An example of local stewardship is the effort to clean up local waterways of non-biodegradable materials such as plastic bags. As our citizen-science database increases, yearly comparisons of water quality and flora should be performed to monitor changes in the Elizabeth River environment. Equally important, geographical and ecosystem comparisons should be performed to detect any effects that climate change could have on this environment as time progresses. By taking these actions, we will promote healthy and dynamic ecosystems for all living species, as well as creating cleaner and healthier atmospheres in which communities are actively engaged. This work was supported by grants from the National Science Foundation Louis Stokes Alliance for Minority Participation in Science and US Department of Education Title V HSI-STEM.

**Cytoplasmic Localization of the *XRR1* Gene in *Saccharomyces cerevisiae*. Ramita Suwal and Marci J. Swede, Long Island University, Post, Brookville, NY.**

The *XRR1* (eXhibits Rapamycin Resistance) gene has recently been characterized by our lab. *XRR1* deletion mutants have been shown to exhibit temperature-dependent rapamycin resistance when grown at 37°C. Its product has been implicated to physically interacting with FKBP12 (*FPR1*) protein (Uetz et al, 2000). FKBP12 is a protein involved in rapamycin sensitivity in the *Saccharomyces cerevisiae*. FKBP12 binds to rapamycin and causes cell-cycle arrest via the TOR signaling pathway. The aim of our study is to further characterize the function of the *XRR1* gene and understand its role in rapamycin resistance. In addition, we wish to study this gene in in the common human pathogen *Candida albicans* by creating a homozygous deletion strain of the *XRR1* homolog. We used the *S. cerevisiae* with GFP-tagged *XRR1* gene to look at the distribution of this gene product in the cell by fluorescence microscopy.

Our study showed that the gene product has a cytoplasmic distribution. Approximately 40% of cells exhibited GFP fluorescence uniformly throughout the cytoplasm. However, in 30% of the cells the GFP-tagged protein seems to be excluded by the prominent vacuole in the cell. About 2% of the cells visualized showed a punctated GFP staining which could be indicative of stress granules. Comparison of fluorescence between diploid and haploid strain showed brighter signal in diploids indicating that both copies of genes are simultaneously expressed. However, deletion of *FPR1* gene seems to diminish the intensity of the fluorescence.

**Comparison of Lichens from Long Island versus Manhattan, Brooklyn, and Queens for the Presence of Polyketide Synthase Gene. Vanita Thompson and Ivan Shun Ho. Kingsborough Community College, Brooklyn, NY.**

Lichens consist of a mutualistic symbiosis between a mycobiont, and one or more photosynthetic partner as photobiont, usually alga or cyanobacteria. Because of this relationship between mycobiont and photobiont lichens can occur in a variety of habitats and can survive in extreme conditions. Lichens produce secondary metabolites, which are believed to give lichens the ability to thrive in such harsh conditions. Type I polyketide synthase (PKS) is an essential component for the synthesis of secondary metabolites in the hyphae. The presence of PKS gene may suggest the organism's production of secondary metabolites. We examined lichen species from rural, urban, and suburban areas of New York to determine if the PKS gene was present. Our hypothesis is that lichens in heavily polluted areas (urban and suburban) will contain the PKS gene while those in the less polluted areas (rural) will not. Samples were collected from Cold Spring Harbor and Caleb Smith State Park in Long Island, Central Park in Manhattan, Seaview Park in Canarsie, and Cypress Hills in Queens. DNA from these lichens was extracted using Edward's Buffer methodology. Gradient polymerase chain reaction (PCR) was then performed using degenerate primers specific to the PKS gene sequence to determine optimal annealing temperature for amplification. We then checked for PCR product using gel electrophoresis to determine whether lichen species from different areas NYC and Long Island may have the PKS gene in their genomes. Our results suggest that lichens found in the rural

(Long Island) part of NYC tend to contain the PKS gene in their genomes while those found in urban (Manhattan) and suburban (Brooklyn and Queens) do not. This work is supported by Grant 1R25GM62003 of the Bridges to the Baccalaureate Program of NIGMS and Grant 0516051091 of the CSTEP Program of the New York State Department of Education.

**Population Trends of Juvenile Atlantic Horseshoe Crab (*Limulus polyphemus*) on Plumb Beach, Brooklyn, NY Pursuant to a Beach Renourishment Project. Abraham Tuachi and Christina P. Colon, Department of Biological Sciences, Kingsborough Community College, Brooklyn, NY.**

The Atlantic horseshoe crab has indispensable ecological and biomedical value, both for its blood which serves as an indicator of bacterial contamination, and its eggs which are a critical food source for migratory birds. This study focused on comparing juvenile population size on the restored beach with an unrestored area to detect change in juvenile counts from previous years. Due to erosion and storm damage, the western flats supported few juveniles or spawning adults in previous years. It was hypothesized that juvenile densities would increase in both the control (eastern) and restored (western) beach areas. In 2014, only four juveniles were found on the eastern tidal flats, much fewer than in 2013 and 2012, when 23 and 61 juveniles were counted. This refutes one hypothesis. On the eastern flats, a continued decline in juvenile density is cause for concern, and led to the team to broaden its search of the area. This resulted in 152 juveniles being located in an adjacent tidal creek not previously surveyed. The tidal creek's value to the population cannot be overstated given the apparent decline of juveniles on their traditional feeding ground. While the decline of juveniles on the eastern tidal flat remains unexplained, the large number of shed exoskeletons collected along the wrack line of the eastern beach provided reassuring evidence that larger juveniles remain present albeit undetected on the eastern flats. However, in 2014, one year after the western beach was re-nourished, over 259 young of the year were counted in a single survey, which is dramatically more than the 42 young of the year counted in 2013. Thus the other hypothesis was supported. This increase in juveniles on the western flats indicates that the area is recovering despite damage from Superstorm Sandy. It may take the eastern beach more time to recover.

**Determining Whether Treatment of Depression After Sustaining a Hip Fracture Injury Leads to An Increased Survival Rate Among Geriatric Patients. Victoria Uceda and David Arroyo, Hackensack University Medical Center, Research Associate Program, Hackensack, NJ.**

According to the CDC there were 258,000 hospital admissions for hip fractures among people 65 years and older and by 2030 there is a projected 12% increase. Estimates for one-year mortality range between 20-30%. Studies show that depressed geriatric patients have a significantly increased risk of mortality within two years after a hip fracture. This suggests that decreasing mortality rates among these patients may be possible through the effective diagnosis and treatment of depression. There have not been many studies investigating this in literature. Additionally, the effective treatment of depression in these individuals and its correlation with one year survival rate to our knowledge has not previously been described. This presents the opportunity to fulfill a knowledge gap in literature. Our goal is to see if there is a correlation between the success of a depression treatment and first time hip fracture patients overcoming one year mortality. The research will be two-fold. The first part is a systematic literature review of fifty-eight sources researched through EBSCOHOST. The second part will be a Institutional Review Board (IRB)-certified retrospective cohort study of elderly patients aged 65 and older from August 2011-August 2014. Results of this IRB-certified study are still pending. This work has been made possible through the strong support and contribution of Chinwe Ogedegbe MD, MPH.

**The Horseshoe Crab (*Limulus polyphemus*) Does Not Appear to be a Vector for the Transmission of Dermo (*Perkinsus marinus*) to the Eastern Oyster (*Crassostrea virginica*). Katherine Valdivieso, Craig Hinkley and Gary Sarinsky, Kingsborough Community College, Brooklyn, NY.**

Dermo (*Perkinsus marinus*) is a pathogenic protozoan that was first documented in the 1940's in the Gulf of Mexico where it was associated with extensive Eastern Oyster (*Crassostrea virginica*) mortalities. It is thought that Dermo was a significant factor in the demise of oysters in Jamaica Bay, New York in the 1920's. Dermo is known to be transmitted from oyster to oyster. Recently our labs have been testing two and three year old oysters grown in Taylor floats in Jamaica

Bay and have found that some of them have contracted Dermo. If Dermo is transmitted from oyster to oyster and there are no known oysters in the bay, how did these oysters get infected? Some literature suggests that Dermo might be transmitted by a vector. Horseshoe crabs (*Limulus polyphemus*) are marine arthropods that live in and around shallow waters. Since they inhabit the same environment as the oyster, it is hypothesized that the horseshoe crab acts as a vector for Dermo. DNA was extracted from six horseshoe crabs. PCR amplification was carried out using a Dermo specific primer set and a mitochondrial cytochrome oxidase 1 (CO1) gene set respectfully. The Dermo amplified products that were subjected to agarose gel electrophoresis on the six horseshoe crabs were negative for Dermo and the control was positive. All six samples were also subjected to agarose gel electrophoresis to determine the correct size for CO1. The Dermo amplified control and the CO1 amplified products were sequenced by Elim Biopharmaceuticals and were subjected to NCBI blast searches which further verified that the CO1 gene was from *Crassostrea virginica*. The results for this experiment did not support our hypothesis that the horseshoe crab is a vector for Dermo.

**The Novel Curcumin-Derivative CMC 2.24 Alone or In Combination with Mitotic Inhibitors Reduces Pancreatic Cancer Growth *in Vitro*. Joselin Vargas and Gerardo G. Mackenzie, Stony Brook University, Stony Brook, NY.**

Pancreatic cancer has one of the poorest prognoses among all cancers with a median survival of 6 months and a dismal 5-year survival rate of <5%. The currently limited treatment options for pancreatic cancer underscore the urgent need for novel chemotherapeutic agents. Extensive evidence has shown that curcumin can be a useful agent in the treatment of cancer. However, the anticancer properties of curcumin in humans are limited by its poor bioavailability characterized by decreased oral absorption and the need to use extremely high oral doses of the compound in either animals or humans. In an attempt to improve its bioavailability, our group has synthesized a novel chemically-modified curcumin (CMC2.24), which presents a better pharmacokinetic profile than curcumin. In the current work, we evaluated the anticancer efficacy of CMC2.24 both alone and in combination with other chemotherapeutic drugs in vitro preclinical models of human pancreatic cancer. Vincristine, a

plant alkaloid, and Paclitaxel (taxol), a compound originally derived from the bark of the pacific yew tree, are mitotic inhibitors that are FDA approved chemotherapy drugs used in combination with other anticancer medications. The effect of CMC2.24 alone or in combination with Vincristine or Paclitaxel on pancreatic cancer cell growth in vitro over 24 and 48 hours was examined using Microculture Tetrazolium Assay. CMC2.24 inhibited the growth of human Panc-1 cells in a concentration and time-dependent manner. In addition, CMC2.24 proved to be a strong combination partner with Vincristine and Taxol; displaying synergy in the inhibition of pancreatic cancer growth. CMC 2.24 reduced cell proliferation by up to 50% with an IC50 concentration of 65  $\mu$ M. In combination with Vincristine and Paclitaxel, CMC 2.24 resulted to be effective at a lower concentration. These results suggest that CMC2.24 appears to be a promising compound for the treatment of pancreatic cancer. Future studies are needed to confirm our findings *in vivo*.

**Cellular Suicide in Ovarian Cancer: How DNA Methylation of GSK3 $\beta$  Results in Chemoresistance.** Lauren Vieira<sup>1</sup>, Noelle Cutter<sup>1,2</sup>, Rosivel Flores<sup>1</sup>, Michael O'Sullivan<sup>1</sup>, Rebecca Reinold<sup>1</sup>, Ashley Stumpel and Benjamin Honigsfeld<sup>3</sup>, <sup>1</sup>Molloy College, Rockville Centre, NY, <sup>2</sup>Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and <sup>3</sup>Mepham High School, Merrick, NY.

Epithelial ovarian cancer is the leading cause of death from gynecological malignancies. Currently platinum-based chemotherapy, coupled with a taxane based drug, and debulking surgery are the primary treatment for ovarian cancer. Approximately 25% of patients either present with or rapidly develop resistance to platinum based chemotherapy and all recurrent tumors ultimately become resistant. Epigenetic modifications have been associated with tumor formation and progression and may contribute to therapy response. We performed a methylation screen on a set of tumors and have found a number of genes and family members differentially methylated between resistant patients and sensitive patients. This project looks to examine the functional role that the methylation of GSK3 $\beta$ , a proline-directed serine threonine kinase, plays in increased resistance to platinum chemotherapy drugs. Ovarian cancer cell lines transcriptionally silenced for GSK3 $\beta$  will be evaluated for their invasive properties and apoptosis analysis. Taken together, we hypothesize a role for GSK3 $\beta$  as an

important epigenetic regulator of chemoresistance in ovarian cancer and furthermore suggest that evading apoptosis as one of the underlying mechanisms. Moreover, GSK3 $\beta$  expression might represent a therapy response predictor and could be a future therapeutic target for ovarian cancer.

**Bioinformatic Approach to Investigate a Relationship Between *cis*-regulatory Elements Involved in Mammalian Polyadenylation.** Haley Wight, Scott Frees and Paramjeet Bagga Ramapo College of New Jersey Mahwah, NJ.

*Cis*-regulatory elements control development and physiology by regulating gene expression in both DNA and RNA. For example, *trans*-regulatory protein factors bind to *cis*-regulatory elements on pre-mRNA, creating a multi-component protein cleavage-polyadenylation complex. Polyadenylation determines the site of cleavage in the 3' untranslated region (UTR) and regulates gene expression. The polyA tail protects mRNA from degradation and facilitates its transport into the cytoplasm. Because of the multi component nature of the polyadenylation complex, distinct *cis*-regulatory elements can work cooperatively to regulate this process. The Cleavage Stimulation Factor (CstF) protein is required for efficient cleavage at the polyA site. This protein binds to an important *cis*-regulatory element, U-rich sequence (URS), downstream of the polyA site and forms a cleavage complex. U rich sequences are degenerate; they consist of five base pairs that contain at least 3 U's located typically within 65 nucleotides downstream of the cleavage site. Previous studies have hypothesized URS motifs to work synergistically with other *cis*-regulatory elements such as G-quadruplex structures. A G-quadruplex is a three-dimensional structure formed by guanine rich nucleic acids and plays significant roles in important biological processes, human diseases, and as therapeutic targets. The stability of a G-quadruplex is determined by the number of tetrads and other structural characteristics. The purpose of this study was to computationally establish a relationship between URS and G-quadruplex *cis*-regulatory elements. Our hypothesis is that an inverse relationship exists; a strong G-quadruplex would not require a strong URS and vice versa. This was done by measuring the prevalence of stable G-quadruplex (4 tetrads) that are adjacent to URS of various strengths in the 3' UTR. Our preliminary results provide insight into the prevalence of these two elements categorized by strength.

**Mapping the Ubiquitination Sites of the Transcriptional Repressor ICER. Fanaye Woldeamanuel and Carlos Molina. Montclair State University, Montclair, NJ.**

Inducible cAMP Early Repressor (ICER) is a dominant negative transcriptional repressor that expresses tumor suppressor activity (1-3). In cancer cells, ICER is abnormally expressed and becomes modified by ubiquitination (4,5). Consequentially, ICER is degraded or re-localized from the nucleus to the cytosol where it is nonfunctional. When ICER is reintroduced into cancer cells, it inhibits the transformed phenotype of cancer cells (1-3). The goal of this project is to map the specific ubiquitinated lysines on ICER to define the functional consequences of ICER ubiquitination and cytosolic localization. Eleven mutant forms of ICER were constructed using site-directed mutagenesis and subcloned in a mammalian expression vector. By using these altered forms of ICER, we have found that ICER is ubiquitinated at the N-terminus. This data suggested alternative modes of regulating ICER degradation and subcellular localization. The long-term goal of this project is to identify ways of inhibiting ICER degradation in cancer cells as a new mode for cancer treatment. This work is supported by Novartis Graduate Scholarship

**Fluorinated Protein Block Polymers for Drug Delivery. Cynthia Xu, Joseph Frezzo and Jin Montclare, New York University Polytechnic School of Engineering, Brooklyn, NY.**

Developing cancer therapies that utilize effective drugs are plagued by drug delivery inefficiencies. Use of doxorubicin in treatment of metastatic breast cancer is highly cardiotoxic and use is limited by its poor solubility, tendency to degrade, and reliance on passive targeting. The efficiency of doxorubicin delivery is difficult to track in real time, necessitating invasive measurements of treatment bioavailability. The objective of this project is to develop a magnetic resonance-traceable doxorubicin delivery vehicle that actively targets cancer cells. The CE<sub>2</sub>-RGD block polymer is composed of the cartilage oligomeric matrix protein coiled-coil domain (C) and two elastin-like peptide domains (E) with an N-terminal hexahistidine tag for purification. The pentameric alpha helical C domain bears a hydrophobic core that encapsulates small molecules, such as vitamin D3 and doxorubicin. The E domain permits thermoresponsiveness and stabilizes the block

polymer into a nanoparticle of optimal size for drug delivery. The RGD tripeptide mutated into CE<sub>2</sub> enables targeting to integrins that are over-expressed in some breast cancer cells. Making use of 19F/1H MRI for semi-quantitative delivery measurements, CE<sub>2</sub> was incorporated with either 5,5,5-trifluoroleucine or *para*-fluorophenylalanine. To synthesize these proteins, a plasmid bearing the gene of interest was transformed into strains of phenylalanine or leucine auxotrophic bacteria. Expression of the fluorinated protein was performed by IPTG-induction in the presence of the fluorinated amino acid analogues. CE<sub>2</sub>-RGD expression was confirmed by SDS-PAGE, followed by purification under increasing concentrations of imidazole. Further biophysical characterization experiments using circular dichroism, turbidometry analysis, and <sup>19</sup>F NMR of CE<sub>2</sub>-RGD are currently underway.

**The Role of NMDA Receptors in Cancer. Mina Youssef, Jan Osea, Katrin Llanos and Natalia Coleman, New Jersey City College, Jersey City, NJ.**

Despite intensive research efforts and promising discoveries, cancer still is the leading cause of death in the US. There is growing evidence of the importance of glutamate signal transduction in cancer. N-methyl-D-aspartate (NMDA) receptors are one of the three glutamate receptors found in the mammalian central nervous system. While it is common knowledge that NMDA receptors are essential for spatial learning and memory, little is known about its function in cancer. We previously showed that NMDA receptors are expressed by human prostate, breast and lung cancer cells. The aim of the current study is to evaluate the NMDA receptor antagonist memantine as a potential target for cancer treatment. The cancer cells growth inhibition was determined by using a 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. This work was supported by LSAMP-NSF grant.

**Synergistic Effect of Green Tea Polyphenols with Antibiotics on *Escherichia coli* and *Staphylococcus aureus*. Ayuni Yussof, Syed Samy and Lee H. Lee, Montclair State University, Montclair, NJ.**

Crude lipophilic green tea polyphenol (cLTP) and pure lipophilic green tea polyphenol (pLTP) have been reported to have anti-inflammation, anti-cancerous, antioxidant and antibacterial activities. Currently, the treatment for antibiotic resistance bacteria is a big concern not just among researchers, but also the general public. In this study, *Escherichia coli* and *Staphylococcus aureus* were used to test the effect of the cLTP and pLTP alone and in combination with different antibiotics. Based on previous study, it was reported that *Escherichia coli* works best with erythromycin (E), while *Staphylococcus aureus* works best with tetracycline (TE). Two different concentrations of the antibiotic, cLTP and pLTP were used for this experiment. Both single study using only one antibiotic or compound and combination study with one antibiotic and one of the compound were carried out to test the susceptibility of the bacteria to the compound and the antibiotic itself. Tube dilution methods were used to observe the colony-forming unit (CFU) in different treatments. The samples were treated for an hour before 100  $\mu$ l of the samples were plated and were incubated for 24 hours at 37°C. In the combination study, the cLTP inhibited the growth of *E.coli* with E100 by 95% while with E200 by 91.7%, the pLTP inhibit the growth with E100 by 96% and with E200 by 95%. For *S.aureus*, the cLTP inhibited the growth with T25 by 97% and with T50 by 95%; the pLTP inhibited the growth with T25 by 89.5% and with T50 by 95%. The study suggested that both cLTP and pLTP enhanced the erythromycin effect on *E.coli* and tetracycline on *S.aureus*.

**Engineering Comp Based Fluorinated Coiled-coil Fibers. Kevin Zhang, Haresh T. More, Nikita Srivastava and Jin K. Montclare, New York University Polytechnic School of Engineering Department of Chemical and Biomolecular Engineering, Brooklyn, NY.**

Over the past decade, considerable efforts have been made to develop protein and peptide based self-assembled systems. The  $\alpha$ -helical coiled-coil proteins systems have been successfully engineered to develop structurally defined fibrils with potential application in nanoelectronics and biomedical field. Two rationally designed proteins CC and Q54, derived from the coiled-coil domain of cartilage oligomeric matrix protein (COMPcc), have been designed to self-assemble into fibers. To improve the thermal and chemical stability of proteins and assembly of fibers, we replace leucine from the hydrophobic core with 5,5,5-trifluoroleucine (TFL) by residue-specific incorporation. Successful incorporation of TFL is confirmed by MALDI Spectrometry. Circular dichroism results indicate that the both fluorinated proteins exhibit a stronger  $\alpha$ -helical structure compared to the wild-type protein. To investigate the fibers in solution, fluorescence microscopy is performed. In the presence of the small molecule, curcumin, which exhibits fluorescence upon binding to CCTFL and Q54TFL, fibers of approximately 600 nm in diameter are observed. The proteins are then subjected to BS3 cross-linking to further study their mechanical properties. The results indicate that fluorination is able to impart improved stability on the fibers and investigations on the mechanism of assembly are underway.

## MACUB 2014 Conference Member Presentations

### **Student Perceptions of Anatomical Case Studies in Clinically-based Programs. P. Field, Kean University, Union, NJ.**

Perceptions of anatomical case study practice in Occupational Therapy and Athletic Training Programs was analyzed through surveys involving case studies in the gross anatomy classroom/laboratory. The survey is composed of two distinct parts: ten statements about the case study method that require ranking using a Likert scale (quantitative), and questions that inquire about strengths and weaknesses of the method (qualitative). The results support a positive relationship between case study pedagogy and skills necessary for clinical practice. Specifically, statistical analysis revealed that the majority of students ( $n = 106$ ) perceive anatomically-based case studies as real world applications of clinical concepts, a valuable evaluation tool and an important preparation for clinical reasoning in the profession (critical thinking skills gained through guided learning of information via discussion, feedback and assessment). Although students expressed concern that case studies with typical presentations, in which rote memorization of facts would suffice for a diagnosis, does not apply to the anomalous patient, development of clinical reasoning skills through case study practice increases the ability to approach the anomalous, non-typical case. Case studies that incorporate anomalous structures, that reflect the holistic approach of considering both physical and cognitive symptoms when evaluating subjects, without immediately revealing the diagnosis, can contribute to this preparation.

### **Incorporating Authentic Research Experience in Undergraduate Classroom. Nidhi Gadura, Biology Department, Queensborough Community College, Bayside, NY.**

Over the past five years, the author has noticed that students who take the Biotechnology (lecture/lab) first, do better in the Molecular Genetics course than those who do not. This is especially true for the part that explains the central dogma of biology, Restriction Enzymes, PCR amplification, Gel electrophoresis and DNA sequencing. The author strongly believes that this is because those students who have not conducted hands on experiments cannot fully understand these complex concepts from a textbook alone. To provide her students with a better learning experience, the author changed her pedagogical strategy. She incorporated a DNA Barcoding lab, developed by Cold Spring Harbor (CSHL), in the Genetics course as an honors component. Her Biotechnology students served as mentors to Genetics students while being closely supervised. A detailed curriculum and assessment strategy was developed for the DNA Barcoding. Grades for students were compared before and after the implementation of this project, along with pre- and post-surveys taken by the students. Student gains made will be discussed during this presentation. Queensborough has included undergraduate research as one of its high impact pedagogical tools. This project was developed as part of that program on campus. Authentic undergraduate research experience has shown to be an extremely effective pedagogical tool to engage students in STEM. Author will discuss her experience with the project.

**Assessment of Student Outcomes in Community College Anatomy and Physiology 1. Maureen N. Gannon and Abass Abdullahi, Bronx Community College, Bronx, NY.**

Community college student retention and application of concepts learned in the introductory sequence of Anatomy & Physiology (A&P I) is problematic. Results from a pre- post- test study conducted during the course of the semester were compared to student performance in departmental common final assessment questions addressing the chemical and cellular level of organization. The pre-test and post-tests comprised of 20 questions, equally split between lower and higher level questions, whereas the final consisted of 75 questions on similar concepts as well as other unrelated material covered over the semester. In general, student performance in departmental finals was similar to post-test results assessed in the middle of the semester. Individual question analysis suggested that some basic concepts were mastered and retained, while others were never learned. In addition, student's ability to answer questions designed to be at a higher level of Bloom's taxonomy was poor. Results from our study will be discussed in the context of how community college assessment efforts may be used to improve student advisement and or transition into appropriate allied health fields. Please bring your own observations for an open discussion.

**Ancestors in Our Genome – The New Science of Human Evolution. Eugene E. Harris, City University of New York and the Center for the Study of Human Origins, New York University.**

Two of the biggest scientific breakthroughs in paleoanthropology occurred in 2010. Not only had we determined a draft genome of an extinct Neandertal from bones that lay in the Earth for tens of thousands of years, but the genome from another heretofore unknown ancient human relative, dubbed the Denisovans, was also announced. A one-hundred year old conundrum was finally answered: did we mate with Neandertals? It was now undeniable that modern humans, with all our modern features – our rounded craniums, prominent chins, gracile faces, and long slender skeletons – had met and mated with both these extinct human-like beings. These breakthroughs open a window of fresh air onto the field of anthropology after many decades of speculation. We are also making base-by-base comparisons of our genome with our primate cousins and finding some of the genomic bases of our unique features – our large and complex brains, our complex cognition and spoken language. Simultaneously, we are learning more about the continuum existing between us and other primates. Darwin presciently wrote “the difference in mind between man and the higher animals, great as it is, certainly is one of degree and not of kind.” Today, we are realizing Darwin's dream. Genomes allow us to probe how human populations adapted to hot and cold climates, high altitudes, different diets, and to myriad pathogens we encountered in our world-colonization. Already well-underway, is a large project collecting thousands of genomes of peoples from around the world. By comparing them, we are discovering ancient footprints left by natural selection. Surprisingly, pathogens appear to have left some of the largest footprints in our genome. The genomic highway has an unchecked speed limit; we are experiencing a unique problem where data is pouring in faster than it can be analyzed. We are unlocking fascinating secrets of our ancestry.

**Can Infrared Spectroscopy Have a Place in the Introductory Biology Lab? R. Helburn and K. Nolan, St. Francis College, Brooklyn Heights NY.**

Spectroscopy is one of the most valuable analytical tools that we have for probing biological systems. Accordingly, most 1<sup>st</sup> year biology labs feature an exercise that introduces students to spectrophotometers and absorption measurements. The latter often are made using visible light and for quantitation of a biologically relevant analyte. In the Fall of 2014, the General Biology-1 course at St. Francis College tested a lab in which 'light' as an analytical tool was presented comprehensively, *i.e.* microscopy and spectroscopy were introduced together. The lab was designed around a forensic investigation in which students utilized both a compound microscope *and* attenuated total reflectance Fourier transform infrared spectroscopy (ATR-FTIR) to examine an assortment of materials from a prepared crime scene. Several attributes of ATR-FTIR make it an ideal tool for introducing basic spectroscopy concepts. There is no sample preparation *e.g.* a hair or fiber is laid on the ATR crystal and a spectrum can be acquired and processed in less than a minute. Thus, the focus can be on understanding the nature of a spectrum and the information it can give. The abundance of narrow absorption bands characteristic of IR spectra illustrates more clearly the qualitative fingerprint nature of spectra. Students had no difficulty operating the instrument as modern educational FTIR spectrometers can be used by persons with little theoretical or technical knowledge. A discussion of the lab, written handouts and student responses will be presented.

**The Vascular Flora of Pea Island, Long Island Sound, New York. Richard Stalter, Robert Kerns, Mindita Singh and Kevin Arjune, St. John's University, Queens, NY.**

Pea Island encompassing 0.81 hectares is located in western Long Island Sound at 40.877N, 73.762W. The purpose of this study was to document the island's vascular flora and describe the island's plant communities after the island was inundated by Hurricane Sandy's storm surge, October 30, 2012. The vascular plants species were collected on August 29, 2013 and August 20, 2014. The vascular flora consists of 68 taxa in 57 genera in 30 families. Twenty nine taxa 42.6% of the flora are not native to the region. Non-native taxa are significantly higher on New York's coastal Great Gull, Ellis, Liberty, Hoffman and Swinburne islands, The Asteraceae and Rosaceae were the largest families in the flora with 12 and 4 species respectively. *Rhus* was the largest genus with 3 taxa. Two plant communities, a large ruderal community and smaller salt marsh community were present here. Pea Island was occupied by the Huguenot Yacht Club until the marina was destroyed by the December nor'easter of 1992. The Huguenot Yacht Club has no plans to restore the marina at the present time. Pea Island like its island neighbors Columbia and David's Island flourished in the past; all are devoid of human habitation and influence at the present time. The island's botany, ecology, geology, climate and land use history will be discussed in my presentation.

**A Primate Ecology Flow Chart. Deborah Swartz, University of Maine at Fort Kent, Fort Kent, ME.**

While teaching courses in introductory physical anthropology and primate ecology, it was evident that students needed a flow chart that demonstrated the linkages among environmental food resources, diet, energy levels, maturation and fertility rates, neurological complexity, demographic structure, and social structure. Drawing from reported data in the primate ecology literature, an informal classroom hand-out was formalized as input, throughput, and output. The flow chart was designed for optimal instructional use, rather than inclusion of all possible ecological and biological interactions. The general flow chart was then applied, with comparisons between pairs of related primate taxa: input from the nutritional value of the diet appears to have a causal relationship to the throughput of neurological complexity, fertility, and demographics, and, ultimately, to the output of social associations and organization. This is clear in the comparison between lorises and the galagines, and between the colobines and the cercopithecines. In both sets of comparisons, the consumption of toxic foods (insects for the lorises and leaves for the colobines) apparently relates to the lower activity, lower relative brain size, later onset of maturity and lower reproductive success, and lower rates of social interaction (lorises) or simpler modes of social interaction (colobines) than the more energetically active, more reproductively successful and more socially complex galagines and cercopithecines that ingest non-toxic foods with greater nutritional value. Students were able to use the flow chart to follow the organizational structure of lectures and to comprehend these interactions. They were also able to comprehend that both the ingestion of widely distributed toxic food by lorises and colobines and the ingestion of dispersed high quality food by the galagines and cercopithecines were evolutionary adaptations that permitted the species to survive.

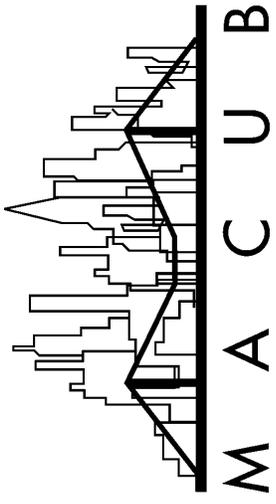
**Dendritic Spine Alterations in Hippocampal CA1 Pyramidal Neurons of Alexander Disease. Rujin Tian<sup>1</sup> and Guomei Tang<sup>2</sup>, <sup>1</sup>Department of Biology, Bronx Community College, CUNY and <sup>2</sup>Department of Neurology, Columbia University, NY.**

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

**The Metropolitan Association of College and  
University Biologists thanks the following  
Affiliate Members for their support**

**AD Instruments  
Anatomy in Clay Systems  
BioPac Systems  
Cengage Learning  
Heyden McNeil Publishing  
I. Miller Microscopes  
John Wiley & Sons  
McGraw Hill Publishing  
Micro-Optics Precision Instruments  
Pasco Scientific  
Pearson Education  
W. H. Freeman and Company**

**Please make every effort to support these affiliate members.  
Their participation help us keep registration fees at a reasonable price.**



Dr. Edward J. Catapane  
Department of Biology  
Medgar Evers College  
1150 Carroll Street  
Brooklyn, New York 11225