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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.

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Use of Laboratory Microcosms for Undergraduate Research: Studies of Eelgrass (*Zostera marina* L.) Growth in Jamaica Bay, New York

by

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Abstract

Various approaches exist for preparing undergraduate students for careers in the biological sciences. One strategy is to teach biology in a research context and encourage students to participate with the faculty in their ongoing research projects. In this paper we describe how we were able to initiate an eelgrass (*Zostera marina* L.) remediation research project, which enabled us to perform experiments compatible with our teaching/campus responsibilities at Kingsborough Community College of the City University of New York (CUNY), and use various laboratory microcosms to involve undergraduate students in scientific research projects. This experience enriched not only our research and collaborations, but also enhanced student understanding and growth in the sciences.

Introduction

Zostera marina L., [family Zosteraceae; order Potamogetonales], or common eelgrass, is a submerged coastal marine seagrass found in temperate waters of the North Atlantic and Eastern Pacific Oceans. It is a perennial rhizomatous aquatic angiosperm having a single short stem and 4-6 ribbon shaped leaves that range from 1-6 ft (30.5-182.9 cm) in length. *Z. marina* uses a large proportion of its resources for maintenance of roots and rhizomes. Both vegetative propagation (rhizome elongation) and sexual propagation (seeds) maintain beds and allow colonization of new areas[1]. It inhabits sandy and muddy bottoms in tidal and subtidal bays and estuaries[2], and is considered an indicator of a healthy coastal marine environment. Its primary productivity contributes to the food web and estuarine ecosystem as a whole, and serves as attachment for numerous epiphytes and many species of associated microfauna[3]. Eelgrass communities are species-rich, second only to coral reefs in richness and productivity. It is a direct food source for Canada geese and other aquatic birds and various protozoans, and microbes feed on dead and decaying leaves. Dried eelgrass was once commercially used as mattress filling. Eelgrass communities provide shelter and nursery ground for juvenile fish and many marine invertebrates including the soft shell clam (*Mya arenaria*), the Atlantic bay scallop (*Argyropecten irradians*) and blue mussel (*Mytilus edulis*), and serve as substrate for epiphytic attachment of organisms such as algae (*Enteromorpha*), trumpet-stalked jellyfish (*Haliclystus*) and colonial sea squirts (*Ciona)*. In addition, eelgrass helps to attenuate wave action[2,3,5], protect coastlines from erosion by stabilizing bottom sediments, and improve water clarity by trapping nutrient–rich silt from marine water and surface sediments. Many benefits can be gained both locally and globally by supporting eelgrass remediation projects to damaged coastal ecosystems.

Worldwide, this past century, eelgrass meadows have dramatically declined in many areas including the eastern North American seaboard. Suspect factors include a fungal wasting disease, eutrophication, and/or physical environmental disturbances[4,6,7]. Habitats of these plants along the New York Long Island coast, including the Jamaica Bay area, have been altered by channeling, storm erosion and development. Eelgrass no longer exists in Jamaica Bay, which is adjacent to the Kingsborough Community College (KBCC) campus. Jamaica Bay consists of 10,000 acres of the southern coast and shoreline of Brooklyn and Queens. Gateway National Recreation Area (National Parks Services) is located within the bay, and provides shelter and food to numerous avian and aquatic species, as well as a migration and breeding area for several birds. Jamaica Bay's history has included agriculture utilization, both sports and commercial fishing, and industrial development and shipping. Concomitant with this growth, in the twentieth century significant topographical changes occurred. Many channels were filled and marshes and meadows within the bay were eliminated. In 2001, *The New York Times* reported Jamaica Bay as "a region experiencing accelerated deterioration, in need of urgent attention"[7]. In 1997, with the support of grants received from PSC-CUNY and the Eppley Foundation we initiated an eelgrass remediation project with the long-term goal of restoring of *Z. marina* to an inlet within the Gateway National Recreation Area called "Dead Horse Bay." Prior to actual transplantation, several questions needed to be addressed that could influence successful reintroduction of this plant to the Jamaica Bay ecosystem. To determine the feasibility of transplanting *Z. marina* to Jamaica Bay we first designed laboratory microcosms to evaluate whether existing conditions in Jamaica Bay would support eelgrass growth in the field. In Spring 2000 three identical sets of aquarium microenvironments were established in which transplanted eelgrass plants could be studied under various conditions. Concomitant with the initiation of

this project, Medgar Evers College/CUNY in conjunction with the Biological Sciences Department at KBCC, received a NIH Bridges to the Baccalaureate grant that provided additional funds to involve undergraduates in the research project.

Undergraduate Research

Biology professors have the opportunity to interact with students in both the lecture and laboratory components of their courses. Especially in the laboratory, students benefit when professors convey their own personal research interests and experiences in the context of scientific inquiry and methodology used by scientists in general. Most undergraduate biology majors, especially those in a community college setting, are unaware of the many different career opportunities available in the biological sciences, or how research experiences could enrich their science understanding in general, or improve their chances of becoming successful applicants for medical and other allied health programs. With this in mind, we set out to involve interested students in our ongoing eelgrass remediation research by designing short-term projects they could complete either during the semester or summer sessions. When the opportunity to work on a research project involving a plant, much less a marine plant, was first presented many students were leery, and wonder, "How does this apply to my becoming a physician or a dentist?" When it was explained to them how each eelgrass research project can be related to a biomedical application, it became clear how studying a plant's growth, metabolism and microbial associations can enhance their educational pursuits.

Since 1999, six students (three male, three female) have worked under our mentorship on eight research projects involving eelgrass. These summer research projects were of a short duration and focused on various areas of study, including eelgrass growth under varying conditions, plant chlorophyll content, microorganisms associated with eelgrass sediment, and plant DNA content. All have been presented in poster or oral sessions at regional and national scientific conferences.

In 1999, our first student worked on a project studying the microbial content of sediment in areas where eelgrass is growing compared to our target remediation site. The project, funded by the Alliance for Minority Students at The City College of New York, compared microbial composition of sediment from a number of locations on eastern Long Island where eelgrass grew, to various sediment sites in Jamaica Bay[8]. Winogradsky columns were set up to represent Smith Point Park, Long Island, where eelgrass growth is luxuriant, and Jamaica Bay environments, and observed over time. Her results suggested that these sites in Jamaica Bay may not be suitable for eelgrass remediation. This project demonstrated to her the importance of microorganisms in the ecosystem, regardless of the biological field one was interested in.

During the summer of 2001, a Bridges to the Baccalaureate student did a project over a six-week period in July and August studying whether growth environs differentially influenced eelgrass growth rates[9]. Eelgrass plants were selected from Smith Point Park and plant weight, rhizome length, number of nodes, number of shoots, number and length of leaves were measured. Plants were hole-punched, and growth rate was determined by measuring the distance the punch mark traveled up the shoot over time. The student was able to relate how the growth rate of a plant, just like the growth rate of a human can be influenced by environmental factors. Her work generated two published abstracts and a poster presentation in 2001 at the Annual Conference of the Metropolitan Association of College and University Biologists (MACUB). She was also selected as one of 50 students from approximately 1200 to give an oral presentation of her work at the 2001 Annual Biomedical Research Conference for Minority Students (ABRCMS) in Orlando, FL. In 2002, the same Bridges to the Baccalaureate student did another project that advanced our original study on the effect of microbial environment of the sediment and eelgrass growth[10]. Fresh sediment and one-year old laboratory microcosm sediment were collected and Winogradsky columns set up representing both environments. Results showed that there was greater microbial growth in the Jamaica Bay sediment, which, again, could affect eelgrass survivability in this environment. This work generated two more published abstracts and two more poster presentations, one at the 2002 ABRCMS in New Orleans, LA and the other at the 2002 Annual MACUB Conference.

Another Bridges to the Baccalaureate student, who was pursuing a career in the health sciences, worked with us in the summer of 2002 studying the effect of water turbulence on eelgrass growth[11]. Previously, it had been reported that water turbulence had an adverse affect on eelgrass growth[12, 13]. Our experiences and measurements in the field confirmed stronger water turbulence in Jamaica Bay compared to Smith Point Park. The student hypothesized this could be a factor in successful eelgrass remediation to Jamaica Bay and we assisted him in setting up aquaria with eelgrass, each having a different water flow rate. When it was explained to him that that blood flow turbulence can have a detrimental effect on the human cardiovascular system, and that water turbulence could have a detrimental effect on a non-human organism (eelgrass), the project's relevance took on a whole new light. At the end of the study his work supported his hypothesis that water turbulence had a negative effect on eelgrass growth. His project generated two published abstracts and two poster presentations that he gave at the 2002 ABRCMS and the 2002 MACUB Conference.

Our fourth student, was also part of the Bridges to the Baccalaureate program, and worked on a project studying the effect of environment on changes in DNA content and meristem morphology in the hopes of learning whether differences existed between Smith Point Park eelgrass and eelgrass transplanted to our Jamaica Bay laboratory microcosm[14]. Differential mitotic activities between these two environments could be an indication of varying fitness and survivability of eelgrass in the proposed remediation location. His results showed a difference in genomic DNA content between field collections and laboratory microcosm specimens suggesting that Jamaica Bay conditions may be inhibitory to eelgrass growth. The student, who is interested in a career the biomedical field, gained the experience of how to conduct a genetics study regardless of the organism being used. His work generated a published abstract and he presented his work at a poster session of the 2002 ABRCMS conference in New Orleans.

In the summer of 2003, another Bridges to the Baccalaureate student examined eelgrass growth rate under varying conditions of light attenuation[15]. Light attenuation was examined by several seagrass researchers, and found to be detrimental to eelgrass beds[16, 17, 18, 19, 20]. The student hypothesized that diminished light availability would have a negative effect on eelgrass growth rate. Eelgrass plants were set up in our laboratory microcosms to simulated Jamaica Bay conditions with water and sediment to quantify and/or correlate the effects. Each plant was hole-punched and exposed to various simulated daylight hours. Her results indicated that attenuated light had a detrimental effect on eelgrass growth. The impact of pollution on the clarity of Jamaica Bay waters, how this affects the amount of light plants receive each day, and the possible effects on the fishing and human recreational industries made it clear to her how relevant it was from a biomedical standpoint. Her work generated a published abstract and an oral presentation at the 2003 ABRCMS conference held in San Diego, CA.

Our sixth student was also funded by the Bridges to the Baccalaureate program and worked with us during the summers of 2002 and 2003 [21, 22] on a project to determine if differences detected in chlorophyll levels could relate to eelgrass photosynthetic activity (rate) and productivity. Numerous studies of eelgrass have included chlorophyll content analyses[17, 23]. Chlorophyll is an important pigment in plants, essential for photosynthesis, and further knowledge of this pigment may be of value for eelgrass remediation efforts. Two experiments were designed: one to compare chlorophyll content of plants grown in eastern Long Island conditions to eastern Long Island plants that were transplanted to our Jamaica Bay laboratory microcosms, and the other to determine the effect of varying light conditions on chlorophyll content on eastern Long Island plants transplanted to our Jamaica Bay laboratory microcosms. His results indicated a difference in chlorophyll content between plants grown under the different light cycles over the experimental period. This work generated three published abstracts and the student presented his work at the 2002 ABRCMS conference in New Orleans, the 2002 MACUB conference, and the 2003 ABRCMS conference in San Diego.

Discussion

The eelgrass microcosm studies demonstrated how meaningful scientific research could be conducted in an urban community college setting. Through laboratory experimentation, the studies provide preliminary transplantation feasibility data supporting the ability of eelgrass clones to survive the Jamaica Bay environment. Even though contributing factors responsible for the decline of *Z. marina* in this area and worldwide have not been fully identified, it is clear that a number of factors challenge its re-establishment and survival. A multi-pronged approach may best address the restoration of this ecosystem, which has experienced a great many environmental stresses. The laboratory microcosm set up will be of value in future experiments involving cultivation of additional eelgrass plants for propagation potential studies, evaluation of photosynthetic capacity, and genotypic analyses of these populations. Continued studies that include field transplantation as well as laboratory aquaculture experimentation will hopefully provide additional insight and strategies to successfully enhance eelgrass fitness for survival.

A significant component of our student-driven grant programs requires that each participating student become involved in a faculty mentored research project, related to the biomedical sciences. The eelgrass research work we had underway provided many opportunities for these students, many of who are of backgrounds historically underrepresented in the sciences, to become actively engaged in ongoing scientific research projects. Not only did these projects give them hands-on experience with scientific research, they also provided us with valuable information applicable to future eelgrass remediation endeavors. Our microcosm eelgrass studies clearly promoted a deeper understanding of science for these students, as well as encouraged them to remain biology majors, with many of them now speaking of graduate degrees. Four of the six students involved in the various research projects described have graduated from KBCC with Associate degrees in Biology and have transferred to four-year colleges to pursue Bachelor's degrees, and we expect the remaining two students to graduate within the coming year. The students who have graduated continue to stay in touch to let us know how they are doing at their respective four-year institutions and each has commented on how their research experience has

enhanced their educational experience and has given them "an edge" over their classmates who have not had this opportunity. Not only do they feel better prepared, they have gained a confidence that cannot be quantified. For us, as educators and mentors, this is the greatest reward. We hope to continue mentoring students, and in the process, pursue our own research toward the goal of eelgrass remediation in Jamaica Bay, NY.

Acknowledgements

This research was supported in part by the Medgar Evers/Kingsborough Community College Bridges to the Baccalaureate program grant #1R25GM62003 of NIGMS, the NSF funded Alliance for Minority Participation Grant, the Eppley Foundation grant #74251-00-01 and PSC-CUNY grants # 61240-00-30 and # 62244-00-31. The authors gratefully acknowledge Dr. Arthur Zeitlin, Chair of the Department of Biological Sciences at KBCC for his support and help in establishing a renovated laboratory facility to set up the experimental laboratory microcosms; Drs. Peter Lanzetta and Peter Pilchman for their contributions to the project; Dr. John Tanacredi, formerly of Gateway National Recreation Area (National Parks Services) for his input and assistance; Dr. Dennis Thoney (former curator, New York Aquarium for Conservation) for his input with microcosm design; and all the students who contributed to this ongoing research.

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The Fall 2004 Conference Poster Abstracts

Poster Presentation Award Winners

First Place - Undergraduate

Investigating the Function of an Element that is Necessary for Autonomous Plasid Maintenance in Trypanosoma Brucel. Charleen Hunt, Amin Espinal and Mario Sampson, William Paterson University, Faculty Mentor: Dr. Pradeep Patnaik

The aim of this project is to define an element that is critical for plasmid maintenance in *Trypanosoma brucei*. To do this we will exploit a model system (plasmid pEV-Luc and its derivatives) that can replicate autonomously in this parasite. Prior analysis has indicated two regions within pEV-Luc that are essential for this process. We are working to define these regions in greater detail and to determine their precise role(s). One of the essential elements (promoter proximal element) co-localizes with a region harboring a RNA polymerase I (GPEET) promoter that drives the polycistronic transcription of a reporter gene (luciferase) and a selectable marker (neo^R). It is important to note that any RNA polymerase can support mRNA transcription in *T. brucei* and that pEV-luc has no known transcriptional terminator. My interest is in the second essential region called the plasmid maintenance sequence (PMS). Sequence analysis of the PMS indicates that it consists of three unlinked segments from the *T. brucei* genome that were juxtaposed during the initial construction of the library from which pEV-Luc is derived (see drawing below). Early experiments suggested that the PMS may function by impeding a transcriptional complex originating at the GPEET promoter from going around the circular plasmid and interfering with a replicational complex assembled (or assembling) at the promoter proximal element. We tested this hypothesis by replacing the PMS with a previously defined *T. brucei* RNA polymerase I (pol I) transcriptional terminator which was inserted in either orientation. Neither of these plasmids replicated suggesting that a terminator cannot substitute for the PMS on this plasmid. In fact, our data suggests that the pol I terminator exerts a dominant effect and may act as a replication barrier in the manner reminiscent of the pol I terminator from yeast (Gerber et al 1997 Cell v90 559-567).

Second Place Tie - Undergraduate

Down-Regulated Expression of Lipocalin mRNA Following *E. coli* Infection of the Murine Epididymis. Rachel Truhan[1], University of Delaware. Collaborators: Dr. Otto Fröhlich and Dr. Leona G. Young, Emory Univ. Faculty Mentor: Dr. Michael A. Palladino, Monmouth University. [1]Summer 2004 research student at Monmouth Univ.

Maturation, storage, and protection of spermatozoa against various insults including microbes, occurs in the epididymis. Bacterial, yeast, and viral infections can cause epididymal inflammation and reduced fertility yet relatively little is known about antimicrobial properties of this organ. The purpose of this project was to use differential display PCR (ddPCR) analysis to identify microbial response genes in a murine model of epididymal infection. Vasa deferentia of Black 6 mice were microinjected with ~5 x 10^4 *E. coli* to allow for retrograde movement of bacteria into the epididymis. Contralateral organs served as sham controls. Three days post-injection, epididymides were excised, examined for inflammation, and whole tissues used for RNA isolation. Inflammation was indicated by a 1.2-fold increase in epididymal weight and recovery of bacteria. For ddPCR analysis, total RNA was reverse transcribed to synthesize complementary DNA (cDNA), and ddPCR carried out with the GeneFishing™ system of oligo$(dT)_{15}$ primers and 60 arbitrary primers. Amplified products were separated by agarose gel electrophoresis and differentially displayed cDNAs identified by a minimum 1.5-fold change in expression and reproducibility in two samples (n=2). Differential cDNAs were cloned, sequenced, and evaluated by BLAST analysis of GenBank. One differential cDNA, which showed a 5.6-fold decrease in expression, was identified as the mouse lipocalin gene. Lipocalins encode small secreted proteins that bind and transport hydrophobic ligands such as fatty acids and steroids, and they have been implicated in antimicrobial, immune, and inflammatory responses in other tissues. In conclusion, down-regulation of lipocalin mRNA expression in the *E. coli* infected murine epididymis suggests that lipocalins play a role in the response to microbial challenge of the epididymis.

Regulation of the JNK pathway upon Contact Inhibition in Human Fibroblasts. Ahmed Rizvi, Jennifer Sielski, Joshua Wayne, Ketleine Georges, Monmouth University, Faculty Mentor: Dr. Dorothy Hutter.

The c-Jun N-terminal kinase (JNK) pathway is a mitogen-activated protein (MAP) kinase pathway known to have a role in growth control and apoptosis in normal mammalian cells. However, little is known about the role of negative regulation of JNK by MAP Kinase Phosphatases (MKPs). To investigate the role of MKPs in the regulation of JNK during the transition to a contact inhibited state, cultures of normal fibroblast cells (BJ) and fibrosarcoma cells (HT-1080) were grown to different stages of confluency. The levels of MKP-1 expression and the amount of active JNK in the fibroblast cultures were assessed through Western blot analysis and compared to those of the fibrosarcoma cultures. In normal fibroblasts, the amount of both total JNK and phosphorylated (active) JNK is higher in subconfluent cells than in confluent cells, while density-dependent regulation of JNK is not seen in fibrosarcoma cultures. Further experimentation will delineate the causal relationship between MKP activity and growth control.

Third Place Tie - Undergraduate

Selection of Eelgrass Transplantation Site in Dead Horse Bay, NY Based on Current Flow Adella Atwell, Kesha Martin, Mary T. Ortiz, Ph.D., Anthea M. Stavroulakis, Ph.D., Arthur Zeitlin, Ed.D., Department of Biological Sciences, Kingsborough Community College, Brooklyn, NY.

In coastal ecosystems, various factors hinder the growth of seagrasses. One of these factors is excessive current flow. This parameter can be harmful to one type of seagrass, *Zostera marina*, also known as eelgrass. Eelgrass is a marine angiosperm found in temperate waters along the east and west coasts of the United States. Its presence indicates a healthy ecosystem in that is stabilizes sediment, provides food for migrant birds, and is a haven for juvenile aquatic species. The purpose of this study was to identify an optimal site for eelgrass transplantation in Dead Horse Bay, NY, based on current flow measurements. Tidal flushing is important for eelgrass survival. However, if currents are too strong, eelgrass cannot take hold in the sediment, and will not survive. Based on this information, we set out to locate the best site for transplantation on the east coast of Dead Horse Bay, part of Jamaica Bay, NY. Three sites were identified, and current flow was measured at various tide levels with a Global Flow Probe between the hours of 3-6 pm over a six-week period in July and August 2004. Our results indicate that Site #1, located furthest inland, had the lowest flow rates, and that higher flow rates existed during high tide versus low tide. Based on these findings we recommend that Site # 1 would be most suited for future transplantation of eelgrass in order to help restore Dead Horse Bay to a healthier coastal ecosystem.

The Incidence of *Wolbachia* in Lepidoptera from Costa Rica. Dieshia Rosa, Carolle Bolnet, Medgar Evers College and Rob Desalle and Elsie Burbano, American Museum of Natural History. Faculty Mentor: Carolle Bolnet.

Wolbachia is a cytoplasmic inherited bacterium that causes reproduction alterations in many invertebrates including insects. These alterations are parthenogenesis, cytoplasmic incompatibility and feminization of genetic males. In parthenogenesis (virgin birth) an unfertilized egg in a female insect suddenly develops as a healthy female offspring. Cytoplasmic incompatibility is the process *of Wolbachia*, residing in a female egg cells and passing on to forthcoming generations. The feminization process is the ability to transform a male embryo into a female. Not only does *Wolbachia* disrupt the insects reproduction, it also increases the number of female offspring as well as suppresses or eliminates males. Our goal was to determine the presence of *Wolbachia* from several species of the order Lepidoptera that were collected in Costa Rica. Abdominal dissection of each moth and butterfly in order to obtain its reproductive system and perform a DNA extraction. A Polymerase Chain Reaction (PCR) was performed successfully using eukaryotic (28s) forward and reverse primers. The PCR product was analyzed on a 1.5% agarose gel that revealed bands without contamination. Once all of the bands showed positive results for the eukaryotic primers, a PCR was done using *Wolbachia* Specific (wspec) primers for each sample. This particular primer determines the presence or absence of *Wolbachia*. Our results showed that 5 out of the 17 butterflies and 7 out of the 20 moths that were tested were infected with the *Wolbachia* bacterium. In addition, 3 out of the 5 butterflies were found to be of the same genus Adelpha, but not of the same species. As for the moths, they were all of a different genus and different species. Work supported by grant DEB/0203466 UMEB/NSF program.

First Place - Graduate

Bioinformatic Analysis of Metal-Binding Protein Families and Heavy Metal Resistance among Cyanobacteria. Tin-Chun Chu, Patricia Platner and Doris Lui. UMDNJ-SHRP and Montclair State University, Faculty Mentors: Dr. Lee H. Lee, Dr. Shankar Srinivasan, Dr. Quinn Vega, Dr. Bonnie Lustigman and Dr. Jack Gaynor.

Cyanobacteria are often used as an indicator of the presence and level of pollutants in the environment. They have been especially recognized for their ability to identify contamination of heavy metals. Class II metallothioneins (MTs), usually found in cyanobacteria, are low molecular weight metal-binding proteins and may be required for heavy metal tolerance. In this study, the phylogenetic pattern as well as prokaryotic evolution of metal-binding protein families among cyanobacteria have been examined. All the available protein sequences of cyanobacteria MTs from GenBank, PDB and Pfam have been aligned and the phylogenetic tree was constructed by utilizing four multiple sequence alignment software ClustalW, T-Coffee, POA and GCG-PileUp. Eight cyanobacteria included in this study were *Synechococcus* sp. PCC 7942*, Synechococcus* sp. WH 8102*, T. vulcanus, T. elongates* BP-1*, Nostoc* sp. PCC 7120*, G. violaceus* PCC 7421*, O. brevis,* and *M. magnetotacticum.* 22 reported heavy metal resistant sequences from these 8 species of cyanobacteria were aligned. A phyletic pattern search tool provided by Cluster of Orthologous Groups (COGs) database was also used to select a desired pattern of presence-absence of species. Cn3D 4.1 program was used for structural alignment. The results indicated that the tree was composed by five clusters. Most *Synechococcus* and *Thermosynechococcus* were clustered into 2 clades while others had relatively far genetic distance with *Synechococcus* but closely linked to each other. Structure alignment of metallothionein among cyanobacteria indicated that a major portion of their structure are not identical but with similar properties such as polarity. The results clearly showed several conserved C-X-C motifs near N- and C-terminus of Class II metallothioneins.

Second Place - Graduate

Activity of CART peptides in hippocampal neurons. Rezaul Alam and Elizabeth Helmer, Long Island University, Brooklyn, and Yemiliya Berman, New York University Medical Center.

CART (Cocaine and Amphetamine Regulated Transcript) mRNA was isolated as a transcript whose expression in striatum is up-regulated by psychostimulant drugs, such as cocaine and amphetamine. There are several forms of biologically active CART peptides, including CART 55-102 and 62-102. CART peptides exert a variety of physiological effects in experimental animals. They increase locomotor activity, affect feeding behavior, and mediate stress responses. Little is known about a putative CART receptor and intracellular signaling activated by CART ligands. We used hippocampal neurons to study the ability of CART to modify the activity of several key protein kinases involved in mediating the action of various extracellular ligands, including the activity of Calmodulin kinase II (CAM-KII) and mitogen activated protein kinase (MAPK). Both CART 55-102 and 62-102 increase the activity of CaM-KII and MAPK in hippocampal neurons and CART 62-102 is more potent than CART 55-102. Treatment of hippocampal neurons with the Ca^{2+} chelator, EGTA, abolishes this activation, which suggests that the function of both CaMKII and MAPK pathways in hippocampal neurons is dependent on extracellular Ca^{2+}. The L-type Ca^{2+} channels may be involved in CART action because in the presence of nimodipine, the L-type Ca^{2+} channel-specific inhibitor, the activation of CAM-KII by CART peptides is significantly reduced. Also, the effects of CART on the activity of CAM-KII are specific to this enzyme because presence of KN-62, a specific CAM-KII inhibitor attenuates the activation of this enzyme by CART peptides. Lastly, our preliminary study demonstrates that CART 62-102 increases the amount of phosphorylated cAMP-response element binding protein (CREB) in hippocampal neurons.

Third Place - Graduate

Water transport and root-to-shoot ratio in partially defoliated tobacco. Sally Cohen, Montclair State University, Faculty Mentor: Dr. Dirk Vanderklein.

Previous research has suggested that plants have increased stomatal conductance following partial defoliation due to increased root-to-shoot ratio. An increased root-to-shoot ratio following partial defoliation is believed to increase leaf specific hydraulic conductance in the plant, which then leads to increased stomatal conductance. We tested whether two variants of tobacco (*Nicotiana tabacum*) would respond similarly to partial defoliation. One variant was genetically modified to produce more roots than the other variant (wild type). We found that despite having greater root mass, the modified plants also had greater shoot mass, which resulted in root-to-shoot ratios similar to that of the wild type. Variation in root-to-shoot ratio *per se* prior to defoliation had no influence on leaf specific conductance or stomatal conductance. However, increasing root-to-shoot ratio by removing half of each leaf resulted in an increase in leaf specific and stomatal conductance in both variants.

Bioin1formatics analysis of the *CG12134* gene in *Drosophila melanogaster*. Alvin Acerbo*, Iona College, Faculty Mentor: Dr. Charles Sackerson.

The *Drosophila* genome project has reported a previously unknown gene, *CG12134*, adjacent to *even-skipped (eve*), based on computational analysis. The presence of this gene within a previously characterized enhancer for *eve* prompted us to explore it further. Six gene prediction tools were used to analyze the genomic region; considerable variation in structure was predicted, although all predicted an exon we call exon 2. A BLAST search through NCBI revealed that exon 2 is highly conserved, from yeast to mice; however, in none of these organisms has the gene or its protein been functionally characterized. Since the region has been sequenced from 5 Drosophila species, we subjected exon 2 to an evolutionary analysis. The K_a/K_s ratio is similar to that of known genes, including *eve* and *Adh*, indicating the sequence is under selective pressure. A search of the Conserved Domain Database at NCBI predicted seven WD40 repeats, a widely distributed protein-protein interaction motif.

Selection and characterization of soil bacteria using 16s rDNA. May R. Antoine, Carolle Bolnet Medgar Evers College, Rob deSalle, Ph.D., American Museum of Natural History. Faculty Mentor: Dr. Carolle Bolnet.

In continuance with our previous research project which was designed to select and identify the antibiotic producing soil bacteria *Streptomyces*, this study attempts to typify the variety of soil bacteria growing in the same soil samples as our *Streptomyces* colonies. As done before soil samples were taken from three diverse terrestrial regions in Prospect Park located in Brooklyn, New York. We were interested in making a comparison of the diversity of bacterial colonies grown as a result of a single procedural variant. The soil samples were dried for time intervals of 1 week, 2 weeks, and 4 weeks at 37 degrees C. These dried samples were then diluted in water, plated onto agar media selective for spore forming bacteria and incubated for 15 days at 37ºC. Our results showed that as the drying time increased, the variety of colonies found decreased. Ultimately, it was discovered that the same type of colony proliferated in the soil dried for 4 weeks. To identify this bacterium, DNA was extracted from pure cultures using MoBio Ultra Clean DNA extracting kit and Polymerase Chain reaction was performed using the 16S rDNA forward and reverse primers. The cleaned PCR product was then sequenced using Big-Dye chemistry and the ABI 3730 automated sequencer. The sequences obtained were compared with GenBank bacterial 16S r DNA sequences. The resulting search revealed a 100% nucleotide similarity to the 16S r DNA sequence of the genus *Bacillus*. Species identity remains to be investigated. Work supported by grant DEB/0203466 UMEB/NSF program.

Increased Phosphate Levels Alter the Effects of Non-Genotoxic Xenobiotics in *Candida albicans*. Jonathan Blaize and Maureen Downey, The College of Staten Island. Faculty Mentors: Dr. Elana McCoy and Dr. William L'Amoreaux

In an accompanying study, we show that *Candida albicans* can be used to assay the effects of non–genotoxic xenobiotics. In yeast, phosphate acts as a nutrient signal and may affect membrane potential of mitochondria. To determine the role(s) of increased phosphate levels on cellular changes associated with treatment of yeast cells with dibutylphthalate, Tween 80, or the combination, we supplemented minimal media with 100 mM phosphate. Addition of high phosphate resulted in increased vacuole content, as well as polyvacuolar bodies. DBP had no effect on cell wall shedding in minimal medium containing 100 mM phosphate, but an increase in vacuole content was observed. Addition of Tween 80 in the presence of high phosphate reserved the increase in cell wall thickness normally observed and decreased vacuole number. Combining the two chemical agents resulted in an increase number of vacuoles as was observed with either phosphate or DBP addition. We conclude that addition of phosphate alters the response of yeast cells to xenobiotics.

Unequal Reinforcement Values From Equally Warm And Cool Temperatures In *Drosophila*. Giselle Carmichael[1], Melissa Zars[2] and Troy Zars[2], [1]Kingsborough Community College and [2]University of Missouri-Columbia.

Insects inhabit extreme temperature environments and evolved mechanisms to survive there, altering their behavior to avoid freezing or high temperature induced death. *Drosophila* has a preferred temperature for of 24^o over 18^o suggesting low temperature may have reinforcing qualities. A heat-box was used to test effectiveness of warm and cool temperatures as reinforcers. Flies were allowed to run freely in chambers are heated or cooled depending on their behavior. Temperatures either nine degrees above or below 24^o, were effective reinforcers. The 24/15^o pair induced a place preference for the cool associated half of the chamber. Tests varying training duration and reinforcement temperature showed the 15^o reinforcer reaches asymptotic memory levels of 0.2 while 33^o reinforcement plateaus at 0.4 on a 0 to I scale. To test for the conservation of molecular mechanisms of warm and cool induced memories, wild-type CS, rut-AC and white mutant flies were tested. Rut-AC and white mutants are defective in place memory formation. To determine whether warm and cool reinforcers serve equally well in reversal learning, flies were trained to avoid half of a chamber then trained to avoid the other half. Using a 33^o reinforcer, place memories increased with each training session. The effectiveness of the 15^o reinforcer was lost after the first reversal session which may indicate the additional experience with only limited temperature extremes allows flies to conclude temperature changes in the chambers are sub-lethal, and can be ignored. The evidence indicates flies can use cool temperatures as reinforcement in forming place memories. The effectiveness as reinforcers are not equal. This work was funded by: NSF-REU Biology & Biochemistry.

Effects of Various Doses of Methylene Blue on Radial Maze Acquisition in Rats. Natalia Castrillon[1], Johanna Fiorucci[1], I. Rodriguez[2], S. Khan[2], M. Rodriguez[2], A. Antonakopoulos[2] and Dr. Francisco Villegas[2]. [1]Dept. of Biology, Queensborough Community College, Bayside, N.Y., [2]York College, N.Y.

Methylene Blue (MB) has been shown to enhance memory of inhibitory avoidance (Martinez *et al*., 1978) and improves reference memory and reversal in a Hole Board Maze test in rats (Callaway *et al*.,2001,2004). The aim of this study is to evaluate the effects of various dosages of MB on spatial memory test. Methods: Thirty-two male Long-Evans rats were used in this study. After five days of HT animals were randomly assigned to one of eight experimental groups (with four animals per group): saline, 0.5, 1.0, 3.0, 4.0, 5.0, 6.0, and 8.0 mg/kg. Following the HT the animals were tested using a delayed non-matching-to-sample (DNMTS) procedure for 20 consecutive days. During the pre-delay session, four of the eight radial arms were blocked with removable doors and the remaining four were baited with food reward pellets. After entering all four open arms the rat was returned to its home cage for a five-minute delay. During the post-delay session, the rats were returned to the maze and all eight arms were open. However, only those arms that were blocked during the pre-delay session were baited with food pellets. After the completion of every trial (Pre-delay and Post-delay), rats were injected intraperitoneally with their corresponding dose. Results and Conclusion: The results of our study show that all dosage groups had increases in total number of mean errors, retroactive and proactive, in a dose dependent manner when compared to saline. Natalia Castrillon and Johanna Fiorucci are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (grant 1 R25 GM65096-01).

Bioaccumulation and Tissue Distribution of Copper and Cadmium in *Crassostrea virginica* Grown in Jamaica Bay, New York. Alisa N. Crawford, Juan Luxama, Edward J. Catapane and Margaret A. Carroll, Medgar Evers College.

New York harbor area, including Jamaica Bay (JB), contains metals and other pollutants in levels higher than NYS Water Quality Standards. JB was abundant with oysters until the 1920's when growing industrialization and urbanization contributed to a decline in water quality. We showed that *Crassostrea virginica* seed transplanted to JB accumulated copper and other metal pollutants despite excellent survival and growth. We also showed *in vitro* additions of copper had deleterious effects on gill mitochondrial 0_2 utilization, and copper pretreatments reduced the activity and prevented induction of glutathione S-transferase, an Phase II enzyme involved in detoxification of electrophilic xenobiotics. We now compare the distribution of two metal pollutants, copper and cadmium, in tissues of *C. virginica* transplanted to JB and grown 1 year either in floats at the surface or in cages at the sediment. The NYC Dept of Environmental Protection reports cadmium is present in biosolids from JB sludge at about 7 mg/kg dw, while copper is about 1 mg/kg. We sort to determine whether there was a difference in amounts and tissue distributions of copper and cadmium in oysters grown near the surface compared to those grown near the sediment. The distributions were not homogeneous with shell having very low amounts, and paradoxically oysters grown near the sediment accumulated less cadmium and copper than those grown at the surface.

The work was supported by grants 1R25GM62003 of NIGMS, 0516041071 of NYSDOE, the CUNY Groundworks Program and 66288-0035 of PSC-CUNY. We thank Frank M. Flower & Sons, Inc., Oyster Bay, NY for supplying oysters.

Genotype and Phenotype of *Nicotiana alata* X *Nicotina rastroensis.* Marie P. Descorbeth[1] and Bruce McClure[2], [1]Kingsborough Community College and [2]University of Missouri-Columbia, Columbia, MO.

Gametophytic self-incompability (SI) is a process which enables plants to prevent inbreeding depression by rejecting self-pollen and pollen from closely related individuals. S-specific pollen rejection is controlled on a multi-allelic locus, the S-locus. If the S-allele of the haploid pollen matches either of the diploid pistil S-alleles, pollen tube growth is inhibited. The product of the S-locus is the active ribonuclease, S-RNase. We set out to test whether putative S_{c10} S-RNase growth from *Nicationa rostroensis* truly segregates as an allele of the S-locus. We used a hybrid of *Nicotiana alata* and *N. rastroensis* for our study. The *N. alata* parent was homozygous for the S_{105} S-allele and the *N. rostroensis* parent had an S_{c10} and another unknown S-allele (Sx). Our experiment was to find out the genotype of the hybrids, and test the plants for rejection of S_{c10} pollen. We emasculated and pollinated flowers with S_{A2}, S_{105}, and S_{c10} pollen from *N. alata*. S-RNase expression leading to a pollen rejection phenotype was determined by fruit set. SDS-PAGE and western blot analysis with specific S-RNase antibodies was used to determine the genotype of the hybrids. The result expected was 50% of the plants have S_{105}/S_{c10}, and 50% have S_{105} and the unknown Sx, but we found that 75% contained S_{105} + 25% had S_x. We saw that *N. rastroensis* S_{c10} S-RNose rejects S_{c10} pollen and accepts S_{105} pollen. Thus, we observed allele specific pollen rejection from the S_{c10} allele.

This work was funded by the UMC Molecular Biology Program.

Some Blood Characteristics Of Poeciliid Fishes. Dorfman, D. Monmouth University, West Long Branch, NJ.

Hemoglobin and serum patterns of blood from *Poecilia reticulata, Gambusia affinis,* and *G. holbrookii* were determined by agarose gel electrophoresis (Titan Gel High Resolution Protein System, Helena Laboratories, Beaumont, Texas). Blood was collected from female fishes by severing the caudal peduncle. Blood was collected in 10 ul capillary tubes, centrifuged, and the serum separated from the red blood cells (rbcs). The rbcs were then centrifuged in a microcentrifuge tube (Dorfman, MACUB, 2004). Patterns were Coomassie stained. The bands were density traced and the percent of the total of each band determined. For serum 10 bands were obtained for P. *reticulata,* and nine each for *G. affinis* and *G. holbrookii.* For each species, no band exceeded 20% of the total. Greater similarity between *Gambusia* patterns was observed. P. *reticulata* has one cathodal (seven% of the total) and three anodal hemoglobin bands. *G. affinis* has two cathodal (30% of the total) and two anodal hemoglobin bands. *G. holbrookii* has two cathodal (23% of the total) and three anodal bands. Future work includes analysis of other Poeciliid species to determine what affinities, if any, exist between species.

Obtaining Adequate Blood Samples From Small Fishes. Donald Dorfman, Ph.D., Department of Biology, Monmouth University, W. Long Branch, NJ.

It is difficult to obtain an adequate sample of blood from small fishes (e.g. fishes weighing approximately one gram) for electrophoresis. To obtain adequate blood from Poeciliidae, for a study involving both Poecilia and Gambusia, the tail was severed at the caudal peduncle. Blood was collected in 10 μl plain capillary tubes (non-heparinized). The blood was centrifuged and the serum and the red blood cells (rbcs) separated. To obtain the hemoglobin from the approximately two μl of the rbcs packed at the bottom of the capillary tube, the clay end of the tube was removed. It is difficult to extract the rbcs from the remainder of the capillary tube, so several of these small tubes were then placed into a 1.7 ml microcentrifuge tube containing approximately 3 μl of deionized water. This was centrifuged for five minutes. The resulting mix of water and rbcs provides an adequate amount of sample for application to several lanes for analysis of hemoglobin by agarose electrophoresis. Adequate quantities of serum are also available for electrophoresis by this method.

Dibutylphthalate and Tween 80 Induce Morphological and Biochemical Changes in the Yeast *Candida albicans.* Maureen Downey and Jonathan Blaize, The College of Staten Island. Faculty Mentors: Dr. Elena McCoy and Dr. William L'Amoreaux.

Candida species can be used to assay the effects of environmental contaminants on induction of peroxisome proliferation. In our assays, we used dibutylphthalate (a known inducer of peroxisome proliferation in rats), Tween 80 (an oleate that can induce esterase or peroxidase activity) or a combination of the two to determine their effects on peroxisome number and catalase activity in *C. albicans.* Cultures treated with dibutylphthalate alone increased the presence of vacuoles and peroxisomes. This treatment also had the effect of the outer cell wall being peeled into the medium. In the Tween 80 treated cells, there was both an increase in cell wall thickness and peroxisomes. Cultures treated with both dibutylphthalate and Tween 80 had an increase in the size and number of vacuoles plus increased peroxisomes, but did not show cell wall peeling. Our results demonstrate that these chemicals can induce peroxisome proliferation and that *C. albicans* can be effectively used to test environmental contaminants.

Sugar Maple (*Acer sacharum* Marsh.) Seedling Growth and Resprouting Potential Under a Vessicular Arbuscular Mycorrhizal (VAM) Modified Rhizosphere. Emmanuel Duran, Melisa Pellicer, Marneece Williams and Kristen Dolberry, Caldwell College, Faculty Mentor: Dr. Eduardo A. Zappi.

The forest rhizosphere is a complex environment often containing VAM fungi mutualistic with plants, as well as several bacterial species that interact with the fungi in various ways. This research attempted to shed light on the interaction between sugar maple seedlings and VAM, as well as the relationship between VAM and species of the two most common soil bacterial genera *Pseudomonas* and *Bacillus*. VAM innoculated sugar maple seedlings grown in one-half gallon pots containing a sterilized 4:1 sand: peat mixture, received weekly watering with a minimal nutrient solution during 8 weeks. There was no observed yield increase in plant height, number of leaves or total leaf area per plant relative to the uninnoculated plants. Plants were subsequently cut back to the soil line in order to simulate browsing by wild herbivorous animals, then allowed to resprout over an additional 8 weeks. Plants innoculated with VAM showed improved performance over the control in terms of a larger number of sprouts per plant, larger sprouts, greater leaf area, as well as greater root and shoot fresh weight. It was hypothesized that although VAM does not increase yield of sugar maple outright, it may be beneficial in its native environment where strong resprouting is necessary as a response to animal browsing. Additional *in vitro* rhizosphere trials were conducted in which VAM was grown separately with the two common soil bacterial species *Pseudomonas fluorescens* and *Bacillus subtilis* on nutrient agar. VAM inhibited growth of the former but did not affect the growth the latter species, suggesting that it may be responsible for altering the forest rhizosphere composition.

Creating Case Study Presentations: A Survey of Senior Seminar Students. Dr. Patrick R. Field, Kean University.

A survey, regarding the opinions of senior seminar students (n = 56) towards a course that required them to create an original formal case study presentation, resulted in an accumulation of quantitative and qualitative data that were supportive of the case study method. The survey also revealed statistically significant correlations between the numerical data from responses that were also supportive of the case study method as an important pedagogical tool for learning scientific information.

Cloning of Acetoacetyl CoA Thiolase from Sunflower Cotyledon and Construction of Expression Vector. Mario E. Giron, Ronald B. Realubit, Rojita Sharma and Jaroslaw Slusarczyk. Montclair State University. Faculty Mentor: Dr. James Dyer.

The glyoxysomal beta-oxidation system in sunflower (*Helianthus annuus* L.) cotyledons is distinguished by the coexistence of two different thiolase isoforms, thiolase I and II. So far, this phenomenon has only been described for glyoxysomes from sunflower cotyledons.Thiolase I (acetoacetyl-CoA thiolase, EC 2.3.1.9) recognizes acetoacetyl-CoA only, while Thiolase II (3-oxoacyl-CoA thiolase, EC 2.3.1.16) exhibits a more broad substrate specificity towards 3-oxoacyl-CoA esters of different chain length. Here we report on the cloning of thiolase I from sunflower cotyledons. The known DNA sequence of *Arabidopsis thalianus* thiolase I was used to generate primers for cloning the corresponding thiolase from sunflower cotyledons. A 3'-RACE strategy was used to generate a 3' fragment of sunflower thiolase I, and based on this sequence, 5'-RACE was used to obtain the 5'-end. Full-length cDNA was generated using RT-PCR with sunflower thiolase specific primers flanking the coding region. The resultant gene encodes a thiolase with at least 80% identity to plant thiolases at the amino acid level.

Orientation by Magnetic Compass in the Eastern Red-Spotted Newt, *Notopthalmus viridescens*: A Field Study. Shawn Goring, Montclair State University. Faculty Mentor: Dr. Scott L. Kight.

A number of studies have examined the magnetic compass orientation of Eastern Red-Spotted Newts (*Notopthalmus viridescens*) in laboratory conditions, but we are aware of no rigorous studies conducted in the field. Newts were collected from shoreline sampling sites from a lake at the New Jersey School of Conservation in Stokes State Forest. In Experiment One, newts were placed into circular arenas graduated by 20^{o} compass labels ($0\text{-}360^{o}$) located either (a) directly perpendicular to the collection site, to the (b) left or (c) right of the collection site, or (d) on the opposite shore from the collection site. Each newt was observed in each arena for 10 minutes and compass direction noted at the end of each period. To control for celestial cues, some experiments were run at 10:00, some at 12:00, and some at 14:00. Regardless of arena position, newts were significantly more likely to be located in the compass quadrant facing the collection site than the three other quadrants. In Experiment Two, newts were placed in the previously described arenas located in the center of the lake. Again newts were significantly more likely to be located in the compass quadrant facing the collection site. To our knowledge this is the first quantitative field study of magnetic compass orientation in this species.

Fiddler Crabs as Bioindicators of Recovery from an Oil Spill in Staten Island Salt Marshes. Matthew Gray, Wagner College, Faculty Mentor: Brian Palestis.

Organisms are frequently used to study the effects of environmental contamination. Burger and colleagues conducted a behavioral study of mud fiddler crabs (*Uca pugnax*) after the January, 1990 Exxon spill of No. 2 oil in the Arthur Kill. This data was compared to control data of the same species of crab found in the same area before the spill. Fourteen years later we performed several of the same tests to see if there was any improvement in behavior. Other studies have shown long term effects of oil spills on fiddler crabs and other salt marsh organisms. We collected crabs from two of the three original test sites of the 1990 study. The sample sizes from the two sites were 15 crabs. We tested three behavioral traits. The first was the ability of the crab to right itself when placed on its back. The second test was a locomotion test. This was to see how far the crab would move when placed on a flat surface. Lastly, we performed a test of the crabs' ability to move up an incline. In addition, we also recorded the size of all the crabs that were tested. After all the tests were performed, the data revealed that the crabs' behavior resembled that of the control crabs that were tested before the 1990 spill, suggesting recovery from the oil spill.

Growth and Survival of the American Oyster *Crassostrea virginica* in Jamaica Bay, New York. Alexis. Greene[1], Wendy Barreiro[2], Gary Sarinsky, Margaret A. Carroll, Ebere Nduka, and Edward J. Catapane, [1]Kingsborough Community College and [2]Medgar Evers College.

Jamaica Bay (JB) is a major inlet opening to the Atlantic Ocean. It was abundant with oysters until early 1900's. Over-harvesting, pressure from predators, parasitic invasion and declining water quality often are cited as causes. Despite actions to arrest and reverse the pollution, oysters are not reestablished. We are studying factors relating to the rehabitation of *Crassostrea virginica* in JB to determine if the water quality and environmental conditions are suitable for their survival. We found oysters placed in JB grew well when housed in protective containers and growth was influenced by placement near the sediment as compared to the surface. Oysters placed 1 foot above the sediment grew larger that those suspended 1 foot below the surface. Water temperature, pH, turbidity, salinity, conductivity, chlorophyll-a and dissolved O_2 were taken to compare water quality at each site. To study growth and survival in a more natural condition, oyster seed and adults were placed just off the bottom in unprotective containers and photographed. After 8 weeks they are growing and surviving well. Thus far there are no serious signs of predation by crabs or starfish. The study continues to show that JB water quality is suitable for oyster growth under the various conditions of our experiments.

The work was supported by grants 1R25GM62003 of NIGMS, 0516041071 of NYSDOE, the CUNY Groundworks Program, and 66273-0035 and 66288-0035 of PSC-CUNY. We thank Frank M. Flower & Sons, Inc., Oyster Bay, NY for supplying oysters.

Cretaceous Dinosaurs Of Central New Jersey. Habrour, G., and D. Dorfman, Department of Biology, Monmouth University, W. Long Branch, New Jersey.

Fossils have been collected from Big Brook, Marlboro, and from Ramanesson Creek, Holmdel, New Jersey. The collection includes dinosaur fossils from the Upper Cretaceous (Maaestrichtian) period. Monmouth County was once a marine and estuarine environment. A shallow ocean, part of a coastal region which marked the northeastern terminus of the Cretaceous Interior Seaway, covered most of modern New Jersey. Dinosaur remains had to wash out and fossilize, making them more difficult to find then marine types. Herbivorous dinosaurs outnumbered carnivores, and included Hadrosaurs, plant eating species. At least 95% of all dinosaurs found in New Jersey Cretaceous creeks are Hadrosaurs. Fossilized remains of various Theropod species less frequently encountered. The productive duckbills (Hadrosaurs), and mid-ranged Theropods must have inhabited the coastal margins of modern northern New Jersey and eastern Pennsylvania since most of central and southern New Jersey were under water during the late Cretaceous. Hadrosaur fossils found include non-diagnostic bone fragments, femur sections, a toe bone, tooth fragments, a vertebra, and a section of a right clavicle. Theropod fossils include a section of the upper humerus, the ostrich dinosaur (*Ornithomimus antiquus*), and a lateral tooth, and a coprolite from *Dryptosaurus aquilunguis.*

Symbiotic Marine Bacteria Isolated From the Surface of Seaweeds of the New Jersey/New York Coast and Their Production of Antimicrobial Substances. Vanessa Heba and Michael Ganger, Montclair State University, Faculty Mentor: Dr. Bonnie Lustigman.

Marine seaweeds represent a favorable substrate for symbiosis with epiphytic bacteria, and many marine bacteria are thought to exist associated with seaweeds or invertebrates as epiphytes. Competition among microorganisms for food and space in this environment is strong, which has led to the development of various strategies for survival. In this study, marine epiphytic bacteria associated with seaweeds of the New Jersey/New York coast were cultured, isolated and screened for production of antimicrobial substances. Marine bacteria were isolated from common seaweeds (*Fucus vesiculosis, Polysiphonia, Enteromorpha intestinalis)* and cultured on minimal marine agar. This agar, in contrast to commercial marine agar, used only filtered seawater and agar as nutrient sources. Isolates were gram stained and identification through fatty acid analysis was performed. Scanning electron micrographs of the seaweed samples were prepared. These showed colonization by the bacteria and the presence of many diatoms. Screening for antimicrobial substances was undertaken using human pathogens such as *Escherichia coli* and *Staphylococcus epidermidis* with several strains producing antibiotic substances that were active against gram positive and/or gram negative bacteria. These results suggest that seaweed-associated bacteria may be useful for further development in the production of antimicrobial or antifouling substances.

Distribution of Periodontal Pathogens in Families Adult Periodontal Patients. Vanessa Hernandez, Dr. Raji Subramaniam, Dr. Patricia Schneider, and Dr. Regina Sullivan. Department of Biology, Queensborough Community College, Bayside, NY 11364.

Severe forms of adult periodontal disease are associated with anaerobic gram-negative bacteria, in particular *Prophyromonas gingivalis, Treponema denticola*, and *Bacteroides forsythus.* While there is evidence that these bacteria can be spread from person to person through saliva, the impact of demographic variables and household pets on familial infection is largely unknown. This study examined the distribution and routes of transmission of periodontal bacteria among family members. Two patients, an Asian Indian male and a Caucasian female, with severe periodontitis were recruited from a private dental practice. Subgingival plaque samples from these patients, their spouses, children and household dogs were tested for pathogens by enzyme assay and DNA analysis. The BANA (N-benzoyl-DL-arginine-2napthyamide) test detected arginine hydrolase, an enzyme produced by all three periodontal pathogens. The polymerase chain reaction (PCR) detected specific pathogens based on the amplification of signature sequences of the small subunit16S rRNA genes. We examined the relationship between bacterial distribution, BANA score, clinical parameters (pocket depth, dental history and bleeding on probing) and demographic variables (ethnicity, gender and age). Vanessa Hernandez is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (grant 1 R25 GM65096-01).

Characterization of the Active Site of tRNase Z by Site-Specific Mutagenesis. Angela Hopkinson, Munmun Zareen and Hua Yan, York College/CUNY, Faculty Mentor: Dr. Louis Levinger.

tRNase is the enzyme which endonucleolytically removes the 3' end trailer from pre-tRNAs. The PDE (phosphodiesterase II) domain of tRNase Z in the carboxyl half of the enzyme, including the signature sequence HxHxDH, is an essential part of the active site. Mutations in this region would therefore be expected to affect the tRNase Z activity. We introduced single amino acid substitutions into the PDE (consensus sequence xxøøø(S/T) HxHxDHxxGxx) to further elucidate its function. Substitutions were made by overlap extension PCR and each mutant tRNase Z was expressed using the baculovirus system. Mutant tRNase Zs were affinity purified using the N-terminal His tag and nickel chelate chormoatography and the tag was cleaved with rTEV protease. Efficiency experiments with a limiting concentration of radioactively labeled substrate pre-tRNA were performed to determine a suitable concentration of each mutant enzyme for Michaelis-Menten kinetics, which generally give more reliable values for catalytic efficiency. Residues in and around the PDE can be categorized into three classes based on the effects of the substitutions on reaction efficiency. The first class can process substrate with efficiency similar to that of wild type. The second class are mutants with moderately reduced processing capabilities. The third class is comprised of mutants with strongly reduced processing capabilities. The Michaelis-Menten kinetics indicates that reduced processing efficiency is due to a reduced V_{max} and therefore a reduced k_{cat} compared to the wild type with practically no effect on k_M. Gel shifts were used to determine a K_d, which was on the same order as k_M. Binding of the mutants was unlinked from catalysis of substrate in the absence of Mg^{2+} and presence of EDTA and by binding at 4^{o}C. The dissociation constant (k_D) of all mutants and wild type obtained from electrophoretic gel mobility shift assay and Scatchard analyses suggest that the PDE domain of tRNase Z is not responsible for substrate recognition and binding. The residues essential for substrate recognition must therefore reside elsewhere in the protein. Funding by the MORE division of NIH is gratefully acknowledged.

Antibiotic Resistance in Thermotolerant Fecal Indicator Organisms Isolated from Resident Canada Geese. Lydia Horvath and Travis Gehringer, Fairleigh Dickinson University, Faculty mentor: Dr. June Middleton.

Thermotolerant fecal indicator organisms carried by resident Canada geese may serve as reservoirs of antibiotic resistance. As part of an ongoing survey, we examined the patterns of antibiotic resistance in *Enterococcus spp.* and *Escherichia coli* isolated from goose feces. Fresh fecal samples were collected from the Loantaka Brook Reservation in Morris County, New Jersey during June, July, and August of 2004. Thermotolerant *Enterococcus spp*. and *E. coli* were isolated by standard techniques. Twenty-four primary isolates of each indicator organism were selected from each sample and screened against a panel of antibiotics. *E. coli* isolates were evaluated to determine resistance to tetracycline, chlorotetracycline, penicillin G, ampicillin, cephalothin, streptomycin, gentamycin, ciprofloxacin, nitrofurantoin, sulfamethoxazole and chloramphenicol. Enterococcal isolates were also screened against erythromycin and vancomycin. All geese carried *E.coli* resistant to ampicillin, penicillin G, cephalothin, and sulfathiozole; no *E.coli* isolates were resistant to ciprofloxacin or nitrofurantoin. All birds carried enterococcal isolates resistant to cephalothin, chlorotetracycline, streptomycin, gentamycin, and sulfathiozole; no enterococci were resistant to ampicillin or chloramphenicol. Multiple antibiotic resistance (MAR) profiles were calculated for each sampling (June, July, August, respectively: *E. coli* = .440, .464, .437; *Enterococcus spp.* = .299, .340, .329).

Effects of Copper on Mitochondrial O_2 Consumption and Cytochrome c Oxidase of the American Oyster, *Crassostea virginica.* Turkesha Huggins, Johanna Espinoza, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College.

The ongoing oyster rehabitation study we have been conducting shows that *Crassostrea virginica* transplanted to Jamaica Bay (JB), NY readily accumulate copper. Copper, a required trace metal, has prooxidant effects when present in excess. Mitochondria are sensitive to increased oxidative stress caused by metal toxicity. We studied the effects of copper on 0_2 utilization in *C. virginica* gill mitochondria from animals incubated 1-2 days with 0 to 100 ppb copper and grown for 3 years in the waters of JB. In control animals, adding 5 or 50 mg of $CuSO_4$ decreased respiratory rates by 12 and 32%, respectively. Oysters grown in JB or exposed to copper pretreatments were significantly more sensitive to copper additions with 5 mg $CuSO_4$ decreasing O_2 utilization in excess of 34% and 50 mg additions causing complete inhibition. The results indicate exposure of oysters to copper in the lab or field heighten copper's deleterious effect. Other experiments examined *in vitro* effect of copper on cytochrome c oxidase (COX)in the presence and absence of added copper in mitochondrial samples prepared from oysters from clean and copper polluted sites. We found an over 90% drop in COX activity with as little as 25 ug of Cu^{+2}. The toxic effects of copper on oyster mitochondrial respiration could be of significance to the growth and health of oysters and other marine animals living in a copper polluted environment.

This work was supported by grants 1R25GM62003 of NIGMS, 0516041071 of NYSDOE, the CUNY Groundworks Program, and 66288-0035 of PSC-CUNY. We thank Frank M. Flower & Sons, Inc., Oyster Bay, NY for supplying oysters.

Involvement of TolC protein in the export of siderophore enterobactin in *Escherichia coli.* Jason Hunter[1], J. L. Furrer[2] ,Mark A. McIntosh[2]. [1]Long Island University, Brooklyn NY and [2]University of Missouri, Columbia MU

To acquire the necessary iron against harsh competition in the environment, iron starved bacteria synthesize, excrete and retrieve iron scavenging molecules termed siderophores, one of which is enterobactin. TolC protein may play a vital role in the secretion of enterobactin. Enterobactin molecules destined for secretion must cross both the inner (cytoplasmic) and outer membranes and the intervening periplasmic space, believed to be a distance of at least 130Å across. The structure of TolC resembles a trans-periplasmic tunnel embedded in the outer membrane of the cell. TolC is open to the external environment but is closed at its periplasmic entrance. In order for the cell to export enterobactin, TolC is recruited by substrate specific membrane complexes (translocases) in the periplasmic space and inner membrane. When TolC is recruited, the entrance is opened to allow substrate passage through a continuous machinery spanning the entire cell envelope, from the cytosol to the external environment. PCR primers specific for TolC were designed to amplify the TolC gene. The quality of the PCR product was confirmed using agarose gel electrophoresis. The TolC gene was cloned into a pBAD directional TOPO vector containing an N-terminal His-tag and a gene for kanamycin resistance. The recombinant vector was then transformed into One Shot TOP10 competent *Escherichia coli* cells. Transformants were selected for by plating on LB medium supplemented with kanamycin. Transformed colonies were analyzed using PCR and restriction digestion. Positive transformants were selected and expression was induced with arabinose. SDS-PAGE assay with His-tag In-gel stain revealed TolC expression. Furthermore, analysis of TolC-null mutations using high performance liquid chromatography (HPLC) reveals that the TolC mutant secretes little, if any, enterobactin. However, some levels of breakdown products 2,3-dihydroxybenzoylserine (DHBS) monomer, dimer, and trimer are observed. These data establish that TolC may be a critical component of the *E. coli* enterobactin secretion machinery and may represent a type of siderophore export mechanism previously undescribed. TolC family proteins are ubiquitous among gram-negative bacteria, and the conserved apertures present a possible chemotherapeutic target in multidrug-resistant pathogens.

Daily patterns in DRP loads in Loantaka Brook above and below Kitchell Pond. Daniela Italo. Fairleigh Dickinson University. Faculty Mentor: Dr. Paul Benzing.

The purpose of our research was to determine daily patterns in input and output of P concentrations and loads in Loantaka Brook. Loantaka Brook, one of the five contributors to the Great Swamp, is responsible for its biggest P load. Loantaka Brook is the only contributor that meets none of the Great Swamp Watershed Water Quality Standards. Although Phosphorus is essential for life, an excess can cause eutrophication, ultimately leading to imbalance in the aquatic community. We selected one sampling location above Kitchell Pond (AK) and one below Kitchell Pond (BK). Data was obtained on three separate dates, the first of which was a twelve hour, hourly collection. On the remaining two days collections were made four times within a twelve hour time period. Phosphorus samples were taken and stream discharge transects performed at each site. Spectrophotometric analysis for Dissolved Reactive Phosphorus was performed using the Molybdate-Ascorbate Method on the stream samples to determine absorbencies; and mean concentrations were calculated. Using data collected from the transects, discharges were calculated. Ultimately, discharges were multiplied by DRP concentrations to determine DRP loads. Our research shows that Kitchell pond appears to have an effect on the patterns of DRP concentrations and loads over the course of the day. Early morning DRP concentrations AK began high and gradually decreased throughout the day. However, BK DRP concentrations were lower and more stable than AK. DRP loads followed a similar pattern.

Genetic characterization of a critically endangered population of North Atlantic Right whales (*Eubalaena glacialis*) using historical samples. Ballington Kinlock, Carolle Bolnet, Medgar Evers College, Corky Gaines, Rob deSalle, Howard Rosenbaum, American Museum of Natural History. Faculty Mentor: Dr. Carolle Bolnet.

Northern Atlantic Right Whales (*Eubalanea glacialis*) are comprised of an eastern and western stock. Mitchell and Reeves (1986) hypothesized that: (a) these two stocks of whales are from the same population with no genetic distinction, (b) these two populations are isolated populations. To test these hypotheses we investigated the genetic diversity of both critically endangered stocks using the mitochondrial DNA control region. While haplotype diversity of the western stock has been well studied, little is known of the eastern stock. Due to the nearly depleted status of the eastern stock, we used 38 historical samples collected from museums across Europe. Mitochondrial DNA was extracted from tissue samples that were believed to be Right whales using a modified Quiagen Dneasy kit protocol. We ran several PCR's with whale specific primers. Sequencing was accomplished by utilization of Big-Dye chemistry and the ABI 3730 automated sequencer. Of the 38 samples, 17 of them were in fact right whales. Preliminary analysis of these historical samples reveals that the most common haplotype found in the western stock is also the most common haplotype found in the eastern stock with slight variations. Three of the five haplotypes known from the western stock are yet to be found among the eastern samples. In addition, two new haplotypes not previously seen in the western stock have been discovered in the eastern samples. Our discovery of 2 new haplotypes suggests that these two stocks of whales are separate populations with very little gene flow between them. Work supported by grant DEB/0203466 UMEB/NSF program.

Immunological Analysis of a Putative Virulence Protein of *Haemophilus influenzae*. Kawasi Lett[1], Thomas Phillips[2], Arnold Smith[2] and Miriam Golomb[2]. Medgar Evers College[2] and Univ. of Missouri-Columbia, Columbia.

Haemophilus influenzae, a gram negative bacterium, is part of the normal flora of the human upper respiratory tract. They are also known to be pathogenic. Nonencapsulated *H. influenzae* (NTHi) are responsible for respiratory illnesses. Before widespread vaccination, encapsulated *H. influenzae* of serotype b (Hib) was a major cause of childhood meningitis. Although Hib meningitis has nearly disappeared from the developed world, invasive disease (meningitis and septicemia) occasionally are associated with NTHi, which are vaccine-resistant. We are studying strain R2866 isolated from a child with meningitis. R2866 has several genes that are absent in nonpathogenic *H. influenzae*, some of which may account for its increased virulence. A probable virulence gene, *lav*, is found in many pathogenic NTHi, including invasive strains, but not in commensal isolates. A phase-variable gene, *lav* has multiple copies of a GCAA repeat within the coding sequence. A close homologue exists in *Neisseria meningitidis* and it is acquired by horizontal passage from *H. influenzae*. Lav belongs to the AIDA-1/ VirG/PerT family of autotransporters, bacterial virulence proteins, which facilitate their own secretion. Subsequent to transport into the periplasm, the beta-domain forms a pore in the outer membrane through which the passenger domain is exported. We employed anti-peptide antibodies to visualize the cellular location, processing, and phase variation of lav, by Western blotting, fluorescence microscopy and TEM. Unlike most autotransporters, the lav passenger protein is not cleaved, but remains covalently bound at the surface. This project was funded by NSF-REU Biology & Biochemistry grant.

Effects of gyrase inhibitors and betaine on expression of heat-labile enterotoxin by *E. coli.* Jennie Liu, Milana Velikovich, Leah Roth and Julie Trachman, Dept. of Biology, Long Island University-Brooklyn. Faculty Mentor: Julie Trachman# (# Present address: CUNY - Hostos Community College).

Enterotoxinogenic *E. coli* (ETEC) strains producing heat-labile enterotoxin (LT) are among the leading causes of diarrhea in man and agricultural animals. A clearer understanding of the genetic and environmental parameters involved in LT regulation will lead to the development of improved chemotherapeutics. Our laboratory has determined that the histone-nucleoid structuring protein, H-NS, is involved in the LT thermoregulation. H-NS seems to do this by binding to a downstream regulatory element (DRE) located in the LT-A open reading frame. Recently, we have shown that LT expression is thermo-osmotically regulated; however, the DRE and H-NS are not involved in the osmotic induction of LT. LT expression is also sensitive to pH conditions. H-NS and related proteins mediate regulation of a considerable array of genes in E.coli in response to a wide variety of environmental signals including temperature, osmotic stress, and changes in pH. These effects are influenced often by DNA topology changes presumably occurring near the promoters of sensitive genes. Supercoiling effects on LT expression were investigated by growing E.coli in the presence of the gyrase inhibitors, novobiocin or nalidixic acid. The osmoprotectant, betaine, was also tested. Like the gyrase inhibitors, betaine has been shown to influence DNA topology.

Induction of a Temperate Cyanophage AS-1 by Heavy Metals. Doris Lui, Patricia Platner, Tin- Chun Chu and Shi-Fang Hsu. Montclair State University. Faculty Mentors: Dr. Lee H. Lee, Dr. Quinn Vega, Dr. Bonnie Lustigman and Dr. Jack Gaynor.

It is reported that many marine cyanophage are temperate and they can be induced from lysogenic to lytic by different agents such as UV, Mitomycin C, temperature, and heavy metals. In our study, the activity of a temperate cyanophage, AS-1 was induced by different concentrations of different heavy metals. Two heavy metals were used, $CuSO_4$ with concentrations of 3.1×10^{-3}M, 3.1×10^{-4}M, 3.1×10^{-5}M and 3.1×10^{-6}M and $ZnCl_2$ with concentrations of 1.7×10^{-2}M, 1.7×10^{-3}M, 1.7×10^{-4}M, and 1.7×10^{-5}M. The population of the host, unicellular cyanobacteria, *Anacystis nidulans* was monitored by direct count using hemacytometer and turbidity study with spectrometer 20 at wavelength of 750 nm. The number of virus is derived from plaque forming unit (PFU) by direct plating method and viral titer. The results suggested that with $CuSO_4$, the concentrations of 3.1×10^{-5}M and 3.1×10^{-6}M are both able to cause induction of virus; 3.1×10^{-6}M induced approximately 1.5 times (526/372 plaques) than the control and 3.1×10^{-5}M induced approximately 1.2 times (416/353 plaques) than the control. The concentrations of 3.1×10^{-3}M and 3.1×10^{-4}M may be too high to be significant inducers for temperate cyanophage. $ZnCl_2$ induced best with the concentrations of 1.7×10^{-5}M and 1.7×10^{-6}M; 1.7×10^{-5}M induced approximately 1.32 times (196/148 plaques) than the control and 1.7×10^{-6}M induced approximately 1 times (146/148 plaques) than the control. These results suggested that Cu^{2+} and Zn^{2+} are significant inducers for lysogenic bacterial cells and consequently will be a potential trigger in the cyanobacteria population in fresh aquatic environment.

Analysis of the Ability of Pine Extracts to Inhibit the Replication and Infection of Fort Morgan Virus in Cultured Vero Cells. Almetra Lundy, Montclair State University,Dr. Dirk Vanderklein and Dr. Sandra Adams - Faculty Mentors.

The objectives of this research were to determine if: (1) Pine extracts will have some effect on Fort Morgan virus (FMV replication and infection of Vero cells; (2) There will be a difference in the effects of two species of pine on the inhibition of FMV infection; and (3) there are differential effects on viral inhibition dependent upon the tissue source of the extract. Pine extracts were prepared from *Pinus strobus,* White pine, and *Pinus nigra*, Austrian pine. Vero cells were treated with varying volumes of each of the pine extracts and monitored microscopically to determine the effects of the extracts on cultured cells. Treated cells, at volumes that did not lead to cellular distortions, were infected with FMV and monitored for the appearance of cytopathic effects (CPE). Results indicated that the pine extracts were effective in preventing the appearance of CPE. White pine extracts appeared to be more effective in inhibiting FMV infection of Vero cells. White pine xylem samples and Austrian pine leaf samples consistently resulted in cellular distortion, regardless of volume.

Characterization of bacteria in sediments of a planned *Zostera marina* (eelgrass) remediation location in Jamaica Bay, New York using the Winogradsky column. K. Martin, A. Atwell, A. Stavroulakis, M. Ortiz and A. Zeitlin. Kingsborough Community College, Brooklyn, NY.

As a primary producer, *Zostera marina* (eelgrass), a marine angiosperm, is vital in coastal ecosystems. It provides food for waterfowl and several aquatic species, provides shelter, improves water quality, and is a shoreline stabilizer. Eelgrass once inhabited Jamaica Bay (JB), which surrounds our campus, but has disappeared due to many factors. To restore eelgrass to this area, researchers at Kingsborough Community College are conducting remediation studies of areas in these waters. My project's goal was to supplement and expand the laboratory microcosm data previously conducted, which suggests that Dead Horse Bay (DHB), an area of Jamaica Bay, would be a suitable transplantation site. Winogradsky columns were observed over an eight-week period to characterize the types of microorganisms that oxidize and reduce sulfur compounds. Succession changes were consistent with previous studies in JB. The aerobic zone of the DHB column indicated presence of sulfide-oxidizing bacteria, possibly *Thiobaccillus*. Where at the beginning of this experiment sediments were the same color, by the fourth week the DHB columns were darker and had developed an unpleasant odor. This color change and accompanying odor most probably was due to sulfate-reducing bacteria such as *Desulfovibrio*. Biofilms were also prepared for the sites, and showed both Gram positive and negative bacilli and cocci, as well as protozoans, diatoms and algae. These data were observed in prior biofilm and microbiological studies in JB and Smith Point Park, NY, an area where eelgrass growth is abundant. Although laboratory microcosm studies demonstrated eelgrass growth and propagation potential in JB in short-term experimentation, this study indicates that the JB sediment may, in general, be harmful for eelgrass rhizome and root growth, in the absence of adequate sediment flushing.

Effect of a Novel Anti Cancer Agent on Angiogenesis in Human Prostate Cancer Cell Line DU145. Niccolo Moretti[1], J.I. Wilson[1], T. Hawke[1], D. Argibay[1], J. Pena[1], D. E. Johnson[2], K. Parker-Johnson[2] and A. L. DePass[1], [1]Long Island University, Brooklyn, NY and [2]Dillard University, New Orleans, LA.

Studies have shown that angiogenesis inhibitors can be effective therapeutic agents for cancer treatment. The Vascular Endothelial Growth Factor (VEGF) and its receptors can contribute to tumor-associated angiogenesis, which brings about tumor growth and metastasis. In addition, VEGF has been directly implicated in the inhibition of apoptosis within cancer cells. DJ52, a novel anti-cancer agent, has shown in previous experiments to inhibit the proliferation of human prostate cancer cell line DU145 in a concentration dependent manner with an IC_{50} of 1 micromolar. This study investigates the effects of this agent on angiogenesis by measuring its effect on the expression of VEGF. We report a concentration dependent inhibition of VEGF expression in DU145 cells treated with DJ52. Based on these results, we believe that DJ52 could be a potential angiogenesis inhibitor.

Phytochrome A Mediated Photomorphogenesis in *Arabidopsis.* Lesley-ann Nelson[1], Dr. Patricia Schneider[1], Dr. Timothy Short[2]. [1]Department of Biology, Queensborough Community College, Bayside, New York; [2] Department of Biology, Queens College, Flushing, New York.

Many of the biochemical reactions responsible for plant growth and differentiation are light-induced. In higher terrestrial plants, these photomorphisms are usually dependent on long light (red) wavelengths. Phytochrome A is produced in darkness as P_R (P_{660}) which is biologically inactive. Exposure to light of 660 nm wavelength transforms this allosteric protein into P_{FR} (FR=far-red) which is biologically active. P_{FR} is converted back to P_R when exposed to light of a wavelength of 730 nm. P_{FR} has been shown to be responsible for many physiological responses in *Arabidopsis.* This study investigated the role of phytochrome A in the synthesis of the *Arabidopsis* pigments, chlorophyll and anthocyanin. Wild type (ws) *Arabidopsis* and a mutant deficient in phytochrome A (PhyA) were exposed to different wavelengths of light. At the end of the 3 to 5 day incubation period, high levels of anthocyanin and low levels of chlorophyll were detected in the wild type. Results indicate that phytochrome A pathway is not functioning in mutant 37 and that it is suppressed in mutant 23. There are ongoing experiments to discover if there is a genetic basis for the physiological responses. Lesley-Ann Nelson is a participant in the QCC-NIH Bridges to the Baccalaureate Program (grant 1 R25 GM65096-01).

Identification and Distribution of Dopamine and Serotonin in *Crassostrea virginica* by HPLC and ELISA. Kizzy Phillip[1], Terry-Ann Hudson[1], Kenesha Brown[2], Margaret A. Carroll[1], Ebere Nduka[1] and Edward J. Catapane[1], [1]Medgar Evers College and [2] Kingsborough Community College.

Biogenic amines are neurotransmitters and hormones in animals. They are well studied in the bivalve mollusc *Mytilus edulis*, but not as well in oysters, particularly *Crassostrea virginica*. We studied their presence in *C. virginica* using an isocratic, ion-pairing HPLC analysis with fluorescence detection to resolved norepinephrine, epinephrine, dopamine, 3,4-dihydroxyphenylacetic acid, 3,4- dihydroxyphenylalanine, tryptophan, tyrosine, serotonin, 5-hydroxytryptophan, N-acetyl serotonin, tyramine and octopamine. Tissues were dissected, weighed, homogenized, centrifuged, filtered and injected into the HPLC system fitted with a BDS Hypersil C18 column and a Hitachi F-1050 Spectrofluorometer with a 12 µL flow cell. We quantified norepinephrine, epinephrine, dopamine and serotonin in mantle, gill, heart, palps, posterior adductor muscle and visceral ganglia in low amounts (100s of ng/g) which correlates well with published reports of related bivalves. We then employed an ELISA method to corroborate the HPLC results and possibly improve the sensitivity of the assay. ELISA tests for dopamine and serotonin confirmed their presence and the distribution we determined with the HPLC. We believe the study will be an important step in elucidating neurobiological and neuroendocrine functions in *C. virginica* and of these biogenic amines in general.

The work was supported by 1R25GM62003 of NIGMS, 0516041071 of NYSDOE, CUNY Groundworks Program & 66273-0035 & 66288-0035 of PSC-CUNY. We thank Frank M. Flower & Sons, Oyster Bay, NY for supplying oysters.

Induction of Temperate Cyanophage AS-1 by UV Irradiation and Mitomycin C. Patricia Platner, Doris Lui, Tin-Chun Chu and Shi-Fang Hsu. Montclair State University, Faculty Mentors: Dr. Lee H. Lee, Dr. Quinn Vega, Dr. Bonnie Lustigman and Dr. Jack Gaynor.

Most ecological investigations of viral/bacteria interactions have focused on the process of cyanobacteria mortality resulting from lytic infection and induction of lysogenic infection. We have investigated the process of lysogeny, whereby a virus establishes a stable genetic symbiosis with its host. In this study, UV irradiation and Mitomycin C were used as agents to study induction of the temperate cyanophage, AS-1. The temperate phage was exposed to UV irradiation for 1.0, 2.5, 5.0, 10 and 20 minutes respectively. Induction was assayed as an increase in viral direct count (plaque forming units) relative to those obtained in the control. With 1 minute UV exposure the viral plaques were 1.9 times greater than the control, with 2.5 minutes UV exposure plaque formation was 2.4 times greater than the control, for 5.0, 10, and 20 minute UV exposure time the plaque formation was 0.76, 0.71 and 0.46 times greater respectively when compared to the control. These results suggest that low UV dosages such as 1.0 and 2.5 minutes induce the production of lytic virus. Various concentrations of Mitomycin C (0.1, 0.5, 1.0 and 5.0 mg/ml) were also added to induce prophage. Our results show that 0.5 and 1.0 mg/ml can induce the production of lytic virus. Concentration of 0.5 mg/ml Mitocmycin C induced 1.87 times that of the control and 1.0 mg/ml induced 2.2 times greater as compared to the control. For Mitomycin C concentrations of 0.1 and 5.0 mg/ml induction of prophage was insignificant with 1.0 and 1.16 times that of the control. These results indicate that prophage induction may be triggered by UV irradiation at certain exposures and by the antibiotic, Mitomycin C.

A 10 base pair sequence within Domain III of the GPEET promoter is essential for autonomous DNA replication in *Trypanosoma brucei*. Jedidiah Quijano, Robert Lorenzo, Amin Espinal, Mario Sampson, and Christopher Mulligan , William Paterson University, Faculty Mentor: Dr. Pradeep Patnaik.

he aim of this project is to define an element controlling DNA replication in *Trypanosoma brucei*. To do this we will exploit a model system that consists of a small circular DNA element (plasmid pEV-Luc and its derivative pCJRP) that can replicate autonomously in this parasite. Prior analysis has indicated two regions within pEV-Luc that are necessary for this process. We are working to define these regions in greater detail. One of the essential regions co-localizes with the *T. brucei* GPEET promoter, that drives the expression of a reporter gene (luciferase) and a selectable marker (Neo^R). Replacement of the GPEET-promoter with a rRNA promoter (plasmid pEV-Rluc) abolishes replication. We are using deletion and linker substitutions analysis to precisely delineate the replication control elements located in this region. Previous experiments indicate that the GPEET promoter has 4 domains (I, II, III, & IV) that are important for transcription. Linker substitution analysis demonstrates that a 10 base pair region within domain III is critical for replication. A Domain II mutant with an impaired promoter (~ 50 fold lower rate of transcription) replicates but only after a considerable (5 day) lag period. On the other hand, linker insertion into Domain I has a significant effect on transcription (~700 fold lower) but no effect on replication. None of the inter-domain mutants analyzed thus far show any significant effect on either transcription or replication. These results allow us to conclude that the replication and transcription functions that co-localize within the GPEET promoter are not identical although they may share some common element(s). We have generated 9 additional linker-substitution mutants to begin an analysis of Domain IV and to better define the boundaries of the critical replication control element in Domain III. These will be assayed for replication in the near future.

Examination of Yeast Cell Size Using Optical Diffusion. Janie Quizhpi, Troy Minott, Dr. Tak Cheung, Dr. Alex Flamholz, Dr. David Lieberman, Dr. Peter Wong, and Dr. Patricia Schneider. Departments of Physics, Chemistry, and Biology, Queensborough Community College, Bayside, New York 11364.

Optical technology is being explored as a non-invasive method to diagnose various cellular abnormalities. The purpose of this study was to develop an optical diffusion technique to detect cell parameters in solid tissue using a He-Ne 633nm laser as a light source and packed yeast cells. *Saccharomyces cerevisiae* and *Schizoaccharomyces pombe* were cultured and separated into density fractions by centrifuging. The top and bottom layers of packed cell volume (PCV) displayed a density variation of 15 %. Cells were digitally photographed under 100X oil immersion lens and measured using Mitotic Imaging Plus 2.0 software. The low density fraction of *S. cervisiae* contained large cells with a long tailed distribution. In contrast, the high density fraction contained smaller cells with a Gaussian-like distribution. Both fractions produced similar light diffusion profiles, but specking was more intense in the low density sample. *S. pombe* showed similar results suggesting that cell size distribution is independent of yeast type. Cell morphology affects PCV when centrifuged resulting in observable differences in optical diffusion. These results suggest that density is a viable parameter to characterize yeast.

Effect of Copper on Glutathione S-Transferase Activity in the American Oyster, *Crassostrea virginica.* Inefta Reid, Margaret A. Carroll and Edward J. Catapane, Medgar Evers College.

Copper is a common aquatic pollutant. The NY harbor area including Jamaica Bay (JB) contains metal and organic pollutants in levels higher than NYS Water Quality Standards. Bivalve mollusks are often utilized for metal monitoring and bioaccumulation kinetics studies but little is known about the biochemical responses to metal accumulations. We showed *Crassostrea virginica* transplanted to JB accumulated copper and other metals. Metal accumulations increase oxidative stress by various means including depletion of important cellular antioxidants such as the thiol reduced glutathione (GSH). Glutathione S-transferases (GSTs) are a ubiquitous group of Phase II detoxification enzymes that utilize GSH in the conjugation of electrophilic substrates such as organic xenobiotics. In this study GST activity of the post-mitochondrial fraction of gill from clean and copper polluted sites was measured using CDNB and GSH as substrates. We showed oysters from copper polluted areas have lower GST activity than those from unpolluted areas and oysters from clean sites have decreased GST activity when exposed to a 2 day incubation in copper polluted water. We also showed an *in vitro* inhibitory effect of three metal pollutants, Cu^{+2}, Fe^{+3} and Hg^{+2} on GST activity. We showed added GSH has a protective effect against the inhibition caused by Cu^{+2} but not Fe^{+3} or Hg^{+2} and that the mechanism of Cu^{+2} inhibition is different from that of Fe^{+3} or Hg^{+2}.

This work was supported by grants 1R25GM62003 of NIGMS, 0516041071 of NYSDOE, the CUNY Groundworks Program, and 66288-0035 of PSC-CUNY. We thank Frank M. Flower & Sons, Inc., Oyster Bay, NY for supplying oysters.

Habitat Preference is Associated With Morphology, but not Phototaxis, in Eastern Red-Spotted Newts, *Notopthalmus viridescens*, Anthony Richardson and Christine Connoly, Montclair State University. Faculty Mentor: Dr. Scott L. Kight.

Eastern Red-Spotted Newts (*Notopthalmus viridescens*) were collected from shoreline sampling sites with differing shade conditions from a lake at the New Jersey School of Conservation in Stokes State Forest. Immediately following capture, newts were placed in circular arenas in which one half was shaded from sunlight and the other half exposed. After a five-minute acclimation period, newts were observed for a ten-minute period in which the orientation of shade in the arena was moved to the opposite side after five minutes to control for magnetic compass bias. Time was noted when a newt moved from shaded to unshaded side of the arena (or vice versa). Hence total time spent in shaded or unshaded habitat was known for each subject. Each individual was observed in this manner twice: once at 10:00 and once at 14:00. Before release, each newt was photographed under standard lighting conditions in the laboratory. We found that all newts, whether collected in shaded or unshaded habitats, significantly preferred the shady half of the arena. We also found that both larval and adult newts were significantly darker when collected from shaded habitats.

Probing the Interaction Between Proteins and Some Small Molecules Using Fluorescence Spectroscopy
Rosa Patricia Rosales[1], Saida Bibi[2] and Dr. Ruel Z. B. Desamero[2]. [1]Dept. of Biology, Queensborough Community College, Bayside, N.Y.; [2] Department of Chemistry, York College, Jamaica, N.Y.

The overall objective of the study is to understand the interplay between protein structure and mechanism, for some biologically important macromolecules. As a model system the enzyme dihydropteridine reductase (DHPR) was studied. DHPR catalyses the NADH-mediated reduction of quinonoid dihydrobiopterin to give tetrahydrobiopterin, which functions as an essential cofactor in the biosynthetic reactions that convert phenylalanine to tyrosine, tyrosine to dihydroxyphenylalanine, and tryptophan to dihydroxytrptophan. In this study the fluorescence signature of tyrosine, tryptophan, NADH, NAD^+, some pteridines and the enzyme dihydropteridine reductase (DHPR) was determined. The presence of DHPR quenches the fluorescence of the cofactor, NADH, and the inhibitors folic acid, methotrexate and trimethoprim. One intriguing result was that for one inhibitor, 6,7-dimethyl 5,6,7,8 tetrahydropterin, the presence DHPR results in an enhancement of fluorescence. We also measured the fluorescence spectra of the ternary complexes involving DHPR/NADH/ inhibitor. It is clear from our results that small molecules interact with DHPR and it appears that the inhibitors interact with DHPR even in the absence of the cofactor, NADH. We also conclude that fluorescence spectroscopy is an effective tool to study DHPR and we will extend this work to do fluorescence based transient measurements. Rosa Rosales is a participant in the QCC-NIH Bridges to the Baccalaureate Program (grant 1 R25 GM65096-01).

SMA, TSA & R2A for Environmental Sampling. Stacy Rosales, Montclair State University & Robert Wojtowicz, Stevens Institute of Technology, Faculty Mentor: Dr. Quinn Vega.

In the pharmaceutical industry, environmental water sampling is important for the regulation of purity in product. In order to provide for adequate water sampling, effective and efficient methods of testing must be in place. Standard Methods Agar (SMA), a high-level nutrient agar, Tryptic Soy Agar (TSA), a mid-level nutrient agar, and R2A, a low-level nutrient agar, are all adequate for the testing of microbes typically found in environmental water samples. However, the nutrient level has a great impact on how well the microbes respond. If microbes are present in water samples and are then transferred to nutrient-rich media, they may undergo shock and thus perish in the media. In this case, the water sampling technique would be inadequate for its purpose. In this study, five microbes were challenged against SMA, TSA & R2A to determine which is the most promising for growth. In terms of average number and size of colonies, both SMA and R2A were found to be suitable for environmental water sampling, with SMA showing to be the most versatile among the media.

Mitochondrial Phylogenomics of Selected Mammalian Orders With Emphasis on Scandentia and Primata. Reji Roy, Bergen Community College. Faculty Mentor: John V. Smalley

The phylogenetic placement of the tree shrews has historically been a controversial issue. Originally a member of the Order Insectivora, they were reclassified as primates and finally placed in their own Order Scandentia. The phylogenetic relationship of Scandentia to other mammalian orders has itself been a matter of debate. Morphological and molecular data have suggested sister group status with either the primates or the lagomorphs. The current explosion of genomic information available in publicly accessible databases has made a variety of phylogenetic and phylogenomic analyses possible. We have compared the complete mitochondrial genomic sequences of tree shrews, primates, lagomorphs, and rodents, using all sequences currently available. The results of our analysis support the currently accepted phylogenetic relationships within and among the orders under investigation. The placement of Scandentia as a sister group of the lagomorphs is clearly supported.

Correlating genetics, molecular biology, and genomics in the *even-skipped* region of *Drosophila* chromosome 2. Dr. Charles Sackerson, Iona College.

The *even-skipped (eve*) region of *Drosophila melanogaster* has been intensively studied since the gene was discovered in the classic screen of Wieschaus and Nusslein-Volhard. The recent release of the complete sequence of the Drosphila genome provides an opportunity to revisit data on this region collected over the years through genetic and biochemical studies. A summary of the mutants, transcripts, enhancers, and Dnase I hypersensitive sites in the 50 kb around *eve* will be presented.

Azetidine-2-carboxylic acid is toxic to various crop pests. Ryan Scally[1], Kristin Vazzana[1], Jessica Chapman[1], Dawn Gurigan[2], David O'Gurek[2] and Jamie Nolan[2] . [1]Monmouth University, [2] Saint Joseph's University. Faculty Mentors: [1]Dr. Mirjana Seskar and [2]Dr. Paul Tefft.

Lily of the valley (*Convallaria majalis)* contains high concentrations of Azetidine-2-Carboxylic acid (A-2-C). It is believed that A-2-C works as a proline analogue and may aid in the protection by interfering with the pests' protein synthesis. To test this hypothesis, we conducted experiments with three agriculturally important host/pest systems: the potato plant/ Colorado Potato Beatle (CPB), the kidney bean plant/ Mexican Bean Beatle (MBB) and soybean/ soybean cyst nematode. Feeding study experiments showed significant effect of A-2-C on weight reduction in neonate stages of insects. Similarly, A-2-C affected both juvenile viability and egg hatching rates in soybean cyst nematodes. These results validate our hypothesis for role of A-2-C in plant defense mechanisms against grazers and pests, and support further research in cloning of enzymes involved in biosynthesis of this compound.

Biology Enrichment Workshops. Dr. Patricia Schneider and Dr. Dwight Meyer. Department of Biology, Queensborough Community College, Bayside, NY 11364.

The highest attrition of science/health majors at the College occurs in freshman year, after they fail to perform in General Biology. On average, only 23% of students who enroll each semester receive C or better. A Treisman-style "Enrichment Workshop" program was established to increase academic achievement in General Biology I. Participants meet once a week to work in groups on challenging problems that go beyond the basics. The curriculum also includes animations, hands-on-activities and attendance at a research seminar. The two-hour sessions are run by full-time faculty who offer suggestions and encourage discussion, but do not teach. Students who successfully complete the program are awarded Honors transcript recognition. Each semester, approximately 22% or 40 of the 180 students enrolled in General Biology I participate in the program. Almost half (20) complete the Workshop series; of these 80% (16) receive grades of A, B or C. In contrast, only 22% (35 out of 160) of those who do not complete the Workshops achieve C or better. When surveyed using a scale of 1 (strongly disagree) to 5 (strongly agree), students reported that the sessions increased their understanding of course content ($\underline{M}$ = 4.3), and that they would recommend the program to others ($\underline{M}$ = 4.8). In this the second year, five Workshop students have been recruited to conduct laboratory research with faculty advisors.

Correlations Between Aquatic Biota and Water Properties and the Uneven Distribution of *Chrysemys picta* In Seven Ponds Located in Black Rock Forest. Nadine Sicard, Carolle Bolnet, Medgar Evers College, Dave Karrmann American Museum of Natural History. Faculty Mentor: Dr. Carolle Bolnet.

A population of painted turtles (*Chrysemys picta)* is found in Black Rock Forest, a natural preserved area. This forest of 3700 acres consists of seven ponds, one is a natural "glacial" pond (Sutherland Pond approximately 14,000 years old) and the other six are man made (Upper Reservoir, Aleck Meadows, Auther's Pond, Tamarack, Sphagnum and Jim's Pond approximately 75-150 years old). In comparison to the other ponds in Black Rock Forest, records have shown that Aleck Meadow Pond has the greatest painted turtle's population than all the other ponds together. Our goal is to study the various ecological factors that may have an impact on each population. This was accomplished by using several methods such as: estimating the population size of each pond (baited nets, basking traps, PIT tag) studying of biota, and assessing levels of acidity. As for the biota, each pond was found to be rich in nutrients plants and invertebrate that are good food sources for the turtle's Our results showed that the total number of turtles that was found within all the ponds, was approximately 188(113 females, 75 males) and 55 percent were from Aleck Meadow. Furthermore, we found that Aleck Meadow was the closest to the neutral range in pH, and all other ponds were highly acidic. In conclusion, our preliminary results showed a correlation between the increased acidity of the ponds and a lesser number of the painted turtle's population. Work supported by grant DEB/0203466 UMEB/NSF program.

Use of antisense oligonucleotides to enhance exon 7 incorporation in the pre-mRNA splicing of SMN2. Cyntra Singh[1], T. Baughan[2] and C. L. Lorson[2], [1]Long Island University, Brooklyn NY and [2]University of Missouri, Columbia MU.

Spinal muscular atrophy (SMA) is a neurodegenerative disorder that is relatively common in humans and is caused by loss of the survival motor neuron 1 (SMN1) gene. SMA is the leading cause of hereditary infant mortality by causing anterior horn cell degeneration in the spinal cord resulting in trunk and limb paralysis. The survival motor neuron 2 (SMN2) gene is located proximally to the SMN1 gene on chromosome 5q and the two genes are almost identical. Interestingly, only mutations in SMN1 cause SMA, whereas mutations in SMN2 have no clinical consequence. A differential pre-mRNA splicing event results in SMN2s failure to compensate fully for SMN1 mutations. Exon 7 is excised during SMN2 RNA splicing and this causes expression of a non-functional gene product. SMN2 produces the SMN protein at low levels (~10% compared to SMN1) but not enough to compensate for the loss of SMN1. Previous studies have shown that the use of antisense oligonucleotides can significantly decrease recognition of the 3' splice site of exon 8, resulting in an increase in increased levels exon 7 inclusion in SMN2-derived transcripts. Here, we have developed in vivo expression vectors that generate antisense oligonucleotides spanning two regions of the SMN2 transcript: a repressor exon 7 splicing "repressor" region and the exon 8 splice acceptor site. We are adding a pol III terminating sequence downstream of the antisense sequences to ensure that the clones are only making short oligos. If successful, these vectors could be used to increase SMN protein expression in an SMA context and may open a new area of SMA therapeutics, as well as providing a fundamental basis for treating other genetic disorders where splicing events are the main cause of disease.

Modeling and simulation of carbohydrate metabolism, Sirajee, M. Faculty Mentor: Isaac Barjis. New York City College of Technology, Brooklyn, N.Y. 11201.

In this paper modeling technique is used to model, simulate and analyze biological processes. In particular, we study application of Petri nets to model the processes of glycolysis and capture dynamic behavior of reactions that occur during this process. Glycolysis is the beginning of generation of metabolic energy from carbohydrate metabolism, where in this process one molecule of glucose is converted into two molecules of pyruvate, with concomitant generation of two molecules of ATP. During this process some of the potential energy stored in the hexose structure is released and used to derive the synthesis of ATP from ADP. There will be give an overview of the carbohydrate metabolism and a Petri net model would be constructed for the carbohydrate metabolism, which will show all the involved pathways in carbohydrate metabolism. However the paper would concentrate on glycolysis, which is the initial pathway in the catabolism of carbohydrates. The main goals and purpose of modeling biological entities at a system (holistic) level are: analysis, simulation, prediction, etc. Thus, while analysis does not necessarily require complete models of the systems involved, simulation and especially prediction are not feasible without complete knowledge of the biological system. Therefore first the paper will explain the process of glycolysis and than based on biological information a Petri net model of the glycolysis process will be constructed.

Expression Analysis of the auxin amidohydrolase family in *Medicago truncatula*. Stephanie M. Smith, Shiri Wexler, LaShire J. Hull and Jutta Ludwig-Mueller, Montclair State University, Faculty Mentor: Dr. James Campanella.

We are using molecular genetic approaches to characterize the regulation of auxin conjugate hydrolysis in *Medicago truncatula* (barrel clover). *Medicago* is a major model legume system for host-symbiote interactions, with evidence that mycorrhizal formation may be regulated by auxins. In the *Medicago* genome, we have distinguished seven putative, auxin amidohydrolases that are closely homologous to the IAR3 gene of the ILR1-like family in *Arabidopsis thaliana*. Five of those hydrolases have full-length open reading frames capable of expressing a protein, while two appear to be pseudogenes. We have been able to clone all of the full-length genes (MtIAR31, MtIAR32, MtIAR33, MtIAR34 and MtIAR35). Temporal expression analysis was performed by relative quantitative real-time RT-PCR. It was found that the MtIAR32 transcript is expressed at the highest levels of any gene at days 1-20 after germination, while MtIAR31 was expressed consistently at the second highest level. The MtIAR33 transcript was expressed at the lowest level all the way through day 20. Expression was also analyzed spatially, where MtIAR32 had the highest relative expression in all tissues tested (roots, stems, terminal leaves, and basal leaves). MtIAR33 continued to demonstrate the lowest levels of expression in all tissues. These expression data are consistent with our functional analysis, where MtIAR32 has the highest enzymatic activity against the substrates IAA-Alanine, IAA-Glycine, IAA-Phenylalanine, and IBA-Alanine. These results strongly support the hypothesis that MtIAR32 is the most important member of this gene family.

Affects of GFRα-1 co-receptor Mutations on Association with the RET Signaling Complex. Mai Soliman, Catalina Soto. Montclair State University, Faculty Mentor: Dr Quinn Vega.

RET is a mammalian receptor tyrosine kinase required for both kidney development and neural migration. RET has also been implicated as a possible treatment site for Parkinson's disease. RET can be activated through association with a ligand, Glial cell line-derived Neurotrophic factor (GDNF) and a co-receptor (GFRα-1). In order to determine the critical regions of GFRα-1 required for GDNF dependent RET signaling, site directed mutagenesis was performed on the human clone. Once the mutants were obtained, the affects of these mutations on association with RET was determined. Preliminary experiments suggest that the two mutants created were capable of interacting with RET at levels equivalent to the wild type co-receptor. Additional studies are being performed to determine how well these mutants associate with the ligand GDNF. Further analysis will also determine the ability of these co-receptors to activate RET downstream signaling.

Analysis of Floatable Debris and Coliform Bacterial Levels in Jamaica Bay, New York. Peter Springer, Pedro Herrera, Victoria Sorrisio, Carmen Bermudez, Jacky Rendon, M. Dawson, Peter Lanzetta. Kingsborough Community College, Brooklyn, NY.

The wash-up of floatable debris on public and protected beachfronts is of concern in New York City. Under the auspices of the New York City Department of Environmental Protection (DEP) and the Medgar Evers/Kingsborough Bridge Program research studies were conducted to examine this problem. Studies have been ongoing to examine the type and amount of floatable debris on a recreational versus a limited-access (non-recreational) sandy beach environment in the Jamaica Bay area. Environmental (abiotic) factors such as heavy rain and subsequent sewage outflow were investigated and determined as contributing factors to debris accumulation. Surveys were taken approximately 1-hour past high tide in a 200 x 25 foot area. It was found that regular public beach maintenance, such as raking and trash removal significantly reduced the amount of floatable debris recorded. It was found that the limited-access areas still accumulated significant amounts of floatable debris. Recently, the studies were extended to include water sampling for coliform bacteria, mainly Escherichia (E. coli). Water samples from both areas continually tested positive for E. coli. The current study attempts to establish a relationship between amount and type of floatable debris found, and *e.coli* levels in the water.

Identifying the Genetic Variation in Painted Turtles (*Chrysemys picta*) of a Natural and an Artificial Pond Located at Black Rock Forest. Natalee Stephens, Carolle Bolnet, Medgar Evers College, Dave Karrmann and Rob DeSalle, American Museum of Natural History. Faculty Mentor: Dr. Carolle Bolnet.

The genetic make up of painted turtles (*Chrysemys picta*) at Black Rock Forest, were studied to determine if there are genetic variations between the turtles of a natural pond (Sutherland) and turtles of artificial ponds (Aleck's Meadow and Upper Reservoir). To accomplish this, blood samples and carapace notches were collected from 18 of the painted turtles in the natural pond and 16 in the artificial ponds and stored for microsatellite analyses. Microsatellites, are genetic markers consisting of numerous repeats of short sequences of DNA bases, were identified for painted turtles through the construction of a genomic library. Primer Cp2 of forward and reverse sequence: U(CTCTAAGGGTTGCACTTCTAAA), L (GAGGTGGCATCAAAACATACAT) was utilized to determine the diversity. DNA was extracted from blood and the carapace notches by using DNeasy protocol. DNA was concentrated and a standard Multiplex Polymerase Chain Reaction (PCR) was performed using Cp2 forward and reverse primers with FAM label on the 3' end of the forward primer. The PCR product was then analyzed using the 3700 DNA Analyzer. The results of the Cp2 values were examined and showed that the samples from the natural pond had similar Cp2 values which were different from the Cp2 values obtained from samples taken from the artificial pond, signifying different alleles. However, of all the results obtained, 7 of the 34 samples were inconclusive after DNA analysis. Nevertheless, further tests are being carried out regarding the genetic variation amongst other samples by using additional microsatellite primer sequences. Work supported by grant DEB/0203466 UMEB/NSF.

Mitogenomic Analysis of the Perciformes. Andrew Tanner, Bergen Community College. Faculty Mentor: John V. Smalley.

The class Osteichthyes is large and well represented within Genbank, with the sequences of 180* mitochondrial genomes presently listed. The most speciose order of this class, Perciformes, is a worthy subject for molecular phylogenomic investigation. Phylogenetic relationships among all members of the order are not well established, and the membership of some taxa in the order is disputed. For example, it has been suggested by some taxonomists that the family Elassomatidae (pygmy sunfishes) be moved entirely out of Perciformes and into Atheriniformes. Additionally, the family Caproidae (boarfish) has been alternatively placed within Perciformes or Zeiformes, an order which is itself somewhat controversial. We have compared the mitochondrial genomes of the Perciformes using all sequences currently available. Based upon these analyses, phylogenomic relationships within the order are explored. *179 mitochondrial genomes were used for this study.

Prevalence of Periodontal Bacteria Among Asian Indians With Periodontal Disease. Evelyn Teran, Merlyn Brito, Dr. Raji Subramaniam, Dr. Regina Sullivan, and Dr. Patricia Schneider. Department of Biology, Queensborough Community College, Bayside, NY 11364.

Anaerobic gram-negative bacteria, in particular *Prophyromonas gingivalis, Treponema denticola*, and *Tanneiella forsythensis,* are associated with severe forms of adult periodontal disease. Demographic characteristics, such as age, gender and race, have been shown to influence both the incidence of periodontal disease and the bacterial composition of subgingival plaque. However, the impact of these factors on Asian populations is largely unknown. This study investigated the prevalence of the three pathogens in Asian Indian periodontal patients at a private dental clinic. Periodontal bacteria were detected by enzyme assay (BANA hydrolysis) and PCR using specific 16s rRNA probes. We examined the relationship between bacterial distribution, BANA score, demographic factors (age and gender) and clinical parameters (pocket depth, dental history and bleeding on probing). Strong positive correlations were found between the severity of Periodontitis (pocket depth), BANA intensity and patient age. All three anaerobic pathogens were detected with equal frequency, but mixed infections were only found in patients with moderate to severe Periodontitis. These results indicate that all three bacteria are significant pathogens in the Asian Indian Population, however disease progression appears to be associated with mixed infection. Evelyn Teran and Merlyn Brito are participants in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (grant 1 R25 GM65096-01).

Comparative genomic DNA sequence analysis of *Oryza sativa japonica* and *Oryza sativa indica* genome, Mohamed Anwar Bin Umer. Montclair State University, Mentor: Dr. Chunguang Du

The draft sequences of two sub-species of the Rice Genome, *Oryza sativa japonica* and *Oryza sativa indica*, have recently been completed. As opposed to other genomes such as corn, wheat, and oats the relative small genome size of Rice has made it the model organism for genetic studies in cereals. We are using sequence analysis and comparative genomic studies to investigate the genome structures of japonica and indica which include the tranposons and other repetitive elements that form an important constituent of the Rice Genome. Results from one such comparative analysis using molecular markers from the two genomes will help to functionally characterize this important monocot. These results will lead to gene identification, functional annotation, and an in-depth look into the transposon and its possible role in the evolution of the two species. Results from this study will also be used to investigate and characterize other cereal genomes.

Adult HIV/AIDS Data Analysis. Lourdes Vintimilla[1], and Dr. Cheryl Adams[2]. [1]Dept. of Biology, Queensborough Community College, Bayside, N.Y.; [2]York College, Jamaica, N.Y.

The objective of this study was to characterize the Queens Hospital HIV/AIDS patient population in order to identify the factors that contribute to infection. Statistical software (SAS) was used to analyze the data on 807 HIV/AIDS adults in reference to demographics, ethnicity, mode of HIV exposure, age, gender and sex. The vast majority of patients reside close to the hospital in North/West Queens, New York City. The patient group contained a higher percentage of Hispanics (88%) than Queens County (25%). The primary mode of exposure was heterosexual contact at 46%. Most (76%) were in the age category 31-50 years. Seventy-three percent of the patients were males, 27% were females, with one transgender person (0.1%). We concluded that the Queens Hospital's AIDS prevention and treatment is best directed toward the population most at risk: heterosexual Hispanics. Lourdes Vintimilla is a participant in the NIH Bridges to the Baccalaureate Program at Queensborough Community College (grant 1 R25 GM65096-01).

Determination of the Presence of *Haplosporidium nelsoni*, *Haplosporidium costale* and *Perkensis marinus* in the Eastern Oyster (*Crassostrea virginica*) Grown in Jamaica Bay, N Y, Utilizing a Multiplex Polymerase Chain Reaction Assay. Mechelle Stewart-Walker[1], Gary Sarinsky[1], Michael Palladino[2]. Alexis Greene[1], Lilia Gumenik[1]. [1]Kingsborough Community College, Brooklyn, NY, [2]Monmouth University, West Long Branch, NJ.

Over-harvesting, disease and the decline of water quality due to urbanization and industrialization are causes cited for the decline of the eastern oyster (*Crassostrea virginica)* in Jamaica Bay. Our earlier work has demonstrated that oyster seeds grow very well, under controlled conditions. In this study, we examined oysters grown in Jamaica Bay for the past two and three years to see if they had become infected with *Haplosporidium nelsoni* (MSX), *Haplosporidium costale* (SSO) and *Perkensis marinus* (Dermo) utilizing the multiplex polymerase chain reaction (MPCR). These three pathogens have been known to cause significant oyster mortalities on the east coast of North America. Tissues were excised from three-year-old oysters grown at the surface and from two-year-old oysters grown on the surface and others grown off the sediment. Genomic DNA was isolated from these tissues and subjected to MPCR with pathogen-specific primer sets for MSX, SSO and Dermo. Genomic DNA from the three pathogens was used in positive control reactions. The tissues from all of the specimens did not amplify for SSO or MSX but it appears that the two-year-old oyster grown off the water surface had Dermo.

M. Stewart-Walker and A. Greene are participants in the MEC/KBCC Bridges to the Baccalaureate Program of Medgar Evers College. This work was supported by grant 1R25GM62003, Bridges to the Baccalaureate Program of NIGMS. We thank Nancy Stokes from the Virginia Institute of Marine Science, Gloucester Point, VA for supplying genomic DNA for positive controls, and Frank M. Flowers and Sons, Inc. Oyster Bay, NY for supplying the oysters.

Does Inhibition of PKCzeta Produce Parallel Effects on Hippocampus-Dependent LTP and Memory? Emma Wallace[1] and Andre A. Fenton[2]. [1]Medgar Evers College And [2]SUNY Health Science Center at Brooklyn, Brooklyn, NY.

Memory is thought to be created by long-term potentiation (LTP). LTP is a strengthening of synaptic plasticity between neurons. The enzyme PKCzeta is necessary and sufficient for LTP in the hippocampus *in vitro*. We showed in urethane-anesthetized rats that LTP is depotentiated when ZIP (zeta inhibiting peptide) is administered. We also demonstrated infusing ZIP into the hippocampi of active rats prevented learning a hippocampus-dependent place avoidance task. It is unknown if blocking formation, maintenance or retention of memory causes this but it is known that ZIP specifically blocks maintenance of LTP. The current experiments sought to determine if ZIP has a parallel effect and produces an amnestic condition when administered to rats 1 hour and 22 hr after a learning episode. A hippocampus-dependent place avoidance task was chosen because of the ease with which it is learned and requirement of an intact hippocampus. Rats were taught to avoid a sector of a slowly rotating arena specific to the room that was reinforced by being shocked in this sector. The rats had a learning experience consisting of 8 10-min training sessions with 15 min intervals. ZIP was infused into the hippocampi 1 or 22 hr after learning. Since the peak ZIP-induced depotentiation of LTP was observed at 2 hours in the anesthetized rat, retention of the place avoidance memory was tested 2 hours after learning. If ZIP impairs retention of place avoidance this will be direct evidence of a common biochemical pathway underling maintenance of LTP and memory in the hippocampus. Alternatively, if ZIP fails to impair retention of memory, the relevance of LTP as a model for explicit memory will be questionable.

***In Vitro* Effect of Drug Conjugate on CD74 Antigen Expression in Lymphoma Cell Lines. Janet Wangari. Montclair State University, Faculty Mentor: Dr Quinn Vega. Project Mentors: Dr Roz Blumenthal, Rosanna Michel, Garden State Cancer Center.**

CD74 is a class II major histocompatability molecule and a tumor associated antigen expressed primarily on B lymphocytes and Macrophages and therefore expressed in Lymphomas. Immunotherapy using the murine antibody LL1 is used to selectively destroy lymphomas as it recognizes CD74 as a cell surface marker. The efficacy of the antibody can be increased by conjugating it to the anti-tumor antibiotic Doxorubicin which interferes with the duplication of DNA which is needed for cell division and tumor proliferation and therefore interfering with disease progression. The objective of this study is to investigate the effect of metronomic doses of the mLL1- Dox drug conjugate on CD74 antigen expression with the purpose of finding the next optimal drug administration time as dictated by the expression of the cell surface marker and also the development of multi drug resistance before and after drug administration. Time points for the second dose administration were determined while the development of MDR was found not to be significantly different. The time points however would not be practical in a human model because they are too close together to allow tissue and organ recovery from the toxic effects of the therapy.

Molecular population studies of aquatic lake species at the New Jersey School of Conservation employing a novel method of sample collection. Joseph Wezenter, Joseph Satran, Nicholas Reed, Christopher Sikes Keilp, Andrew Mickens, LaShire Hull, Montclair State University, Faculty Mentor: Dr. James Campanella Bergen Community College, Faculty Mentor: John Smalley.

The acquisition of high quality DNA for use in phylogenetic and molecular population genetic studies is a primary concern for evolutionary and genetic researchers. While such DNA is easily obtained from study organisms, it often requires the sacrifice of the subjects in question. Many non-destructive DNA sampling methods have been developed and are used with a variety of taxa in applications ranging from genetic stock assessment to molecular forensics. We have developed a field sampling method for obtaining high-quality DNA from sunfish (*Lepomis*) and newts (*Notophthalmus*) that employs a variation on the buccal swab method and results in the collection of DNA suitable for PCR amplification and polymorphism analysis. The ease of this method-- coupled with its scalability to include large sample sizes, its ambient temperature of field storage and preservation, and its simplicity of sample transport-- makes it applicable to field-oriented population and conservation genetic studies involving a wide range of aquatic organisms. We have applied our novel method to help study aquatic populations in Lake Wappalanne at the New Jersey School of Conservation.

The Effects of Steroid Mimics on Hormone Mediated Development. Daniel Williams and Nicole Rannazzisi, St. Joseph's College NY. Faculty Mentor: Moira E. Royston Ph.D.

There have been numerous reports of reduction in the number of amphibians, fish, and non-pest insects in the wild. It is proposed here that these reductions may be related to the utilization of petroleum-based products and/ or the synthesis of related chemicals. There are numerous materials in the everyday life of people, as well as the rest of the environment, which are based on this chemistry including plastic products, pesticides, and the waste products of fossil fuel that may act as hormonally disruptive compounds. It has been demonstrated in the St. Joseph's College Biology laboratories that the steroid mimics bisphenol-A and dibutyl phthalate result in skewed sex ratios in fish and interfere with development in the insects *Drosophila* and *Manduca*. Steroid hormones serve as signaling molecules for a myriad of functions related to the development and function of multicellular organisms, and include the vertebrate sex hormones and the insect ecdysteroids. They pass through cell membranes and interact with the Steroid Hormone Receptor Superfamily of transcription factors, which in turn modulate RNA synthesis. It is proposed that changes in polytene chromosome puffing in *Drosophila* may serve as a marker to identify the steroid mimic activity potential of such chemicals.

Effect of a Novel Anti Cancer Agent on Angiogenesis in Human Prostate Cancer Cell Line LNCaP. Joshua I. Wilson[1], N. Moretti[1], Z. Mogul[1], D. E. Johnson[2], K. Parker-Johnson,[2] and A. L. DePass[1]. [1]Long Island University, Brooklyn, NY and [2] Dillard University, New Orleans, LA.

The Vascular Endothelial Growth Factor (VEGF) and its receptors have been shown to contribute to tumor-associated angiogenesis, which brings about tumor growth and consequently metastasis. In addition, VEGF has been directly implicated in the inhibition of apoptosis within cancer cells. Recent data has shown that angiogenesis inhibitors can be effective therapeutic agents for cancer treatment. DJ52, a novel anti-cancer agent, has shown in previous experiments to inhibit the proliferation of human prostate cancer cell line LNCaP in a concentration dependent manner with an IC50 of 1 micromolar. We will try to elucidate the effects of this agent on angiogenesis by measuring its effect on the expression of VEGF. We report a concentration dependent inhibition of VEGF expression in LNCaP cells treated with DJ52. Based on these results, we believe that DJ52 could be a potential angiogenesis inhibitor.

Targeted Protein Degradation in Mammalian Cells. Oladapo Yeku[1], Michael Frohman and Guangwei Du, [1]Medgar Evers College and [2]SUNY at Stony Brook.

Loss of function analysis at the DNA (gene knockout) and RNA (RNA interference) level has been successfully used to analyze gene function in plant and animal cells. Here we describe an attempt to establish a technique to silence expression at the protein level in mammalian cells, based on a recent demonstration that controlled redirection of target proteins to the proteasome is sufficient for their degradation in yeast. A protein subunit known as FRB was fused to a target protein (Green fluorescent protein). The complementary subunit FKBP was fused to a subunit of the proteasome complex. A Rapamycin analogue was then added to trigger dimerization of the FRB and FKBP subunits, thus promoting translocation of the FRB-tagged GFP to the proteasome. In theory, close proximity of the GFP to the proteasome complex should result in its degradation.

Loss of GFP was assessed quantitatively over various time periods using western blotting and immunofluorescence. This method could provide a powerful tool for the study of gene and protein.

Modeling of DNA Transcription and Protein Translation and Protein Translation by means of Data-flows. Joe W. Yeol, Polytechnic University, Faculty Mentors: Dr. Issac Barjis, Dr. Yeong Soon Ryu.

The protein production from DNA to protein via RNA is a very complicated process. In this paper, we modeled three major steps of the protein production process; *replication*, *transcription*, and *translation* by the order of products in each transaction DNA, m-RNA, and protein. Biological information and processes are complex and difficult to understand, and teach. However, modeling tools help researcher, scientists, and engineers, to make the processes systemized and to control them. In addition, feasible and suitable modeling methods for various biological system processes are a key to understand them and a milestone to study a process in details. Data-flow modeling is one of the easiest ways to have and to understand the concept of the process in a dynamical system and the modeling elements in the process DNA to protein are categorized as products, processes, enzymes, and control flows; for example, a by-product with an enzyme (a kind of protein) can be processed only after a certain transaction (control flow). In this research work a using data flow modeling tools a model is constructed in a compact notation and detailed notation based on the available biological information and data. The constructed model captures all the molecular events that occur during DNA transcription and mRNA

MCGRAW-HILL/MACUB RESEARCH AWARD PRESENTATION

translation

The Tight Junction: What Is It, Where Is It, What Does It Do, and What Is Its Relation to Enteric Viruses? Steven M. Lipson. Department of Biology, St. Francis College, Brooklyn Heights, NY.

Tight junctions (TJs) are connections between epithelial and endothelial cells that comprise various tissues of the body. They regulate the passage of ions and molecules across the paracellular pathway. Tight junctions selectively open and close in response to various internal and external signals regulating back diffusion between the paracellular pathway. TJs consist of claudins, occludins, the Ig superfamily molecules, and other associated proteins. Claudins are primarily responsible for intercellular strand assembly and ion selectivity. TJs display “fence” and “barrier” functions. Disturbance of TJ integrity and function has been associated with the disregulation of organ and organ systems (e.g., gastrointestinal, liver, and vascular diseases). Microbial pathogens negatively impact TJ structure and function. Studies were performed to investigate the effects of animal enteric viruses (reovirus and rotavirus; members of the Family Reoviridae) on tight junction morphology and function in epithelial cell culture monolayers. Experiments were performed utilizing single and double labeling immunoflourescense microscopy, ATP measurements and electrical resistance. Reovirus and/or rotavirus, affected reduced levels of ATP, reduced transepithelial resistance, and produced a degradation of the TJ molecule claudin-1 and the scaffold protein zona occludin-1 (ZO-1). Neither bacteriophage T4 nor the aluminosilicate kaolinite (K), imparted any morphologic change to the integrity of the monolayer tight junction. K concentrations $\geq$ 200 ug/0.2 ml however, induced a disintegration of the cell monolayer. Tight junction integrity within MA-104 monolayers was compromised after a 1.5-h incubation with cranberry (*Vaccinium macrocarpon*) juice. Inasmuch as the TJ serves as a receptor site for reovirus attachment to its host cell, these data may explain in part, our findings showing an antiviral effect imparted to reovirus by cranberry juice. The TJ is a critical component in tissue function. More studies are needed to address those interactions which occur between viruses, TJ morphology, and cell function.

Faculty Workshop Presentation

Teaching Botany in the Liberal Arts Curriculum. Kumkum Prabhakar, Biology Department, Nassau Community College, Garden City, New York.

Presently, botany as an organismal science is not a popular option of non-science major students taking laboratory science courses. With greater emphasis on balanced nutrition, use and abuse of herbs, fiber therapy, conservation of natural resources, genetically modified food, global warming, agriculture, horticulture, floriculture, and many other emerging venues, it is difficult to deny the place that plant science deserves in the liberal arts curriculum. This workshop will include a technologically -enhanced presentation of the innovative strategies adopted to develop a student-centered curriculum of Bio 124 Plants & Society course at Nassau Community College. The model of constructivist teaching applied in this course expects students to connect the course content to nutritional, medicinal, and ethnobotanical aspects of commonly used plant products. Information management skills are enhanced by botanical (phytochemical) research to include phytogeography and usage of plant products by early humans based on the Doctrine of Signature. Students participate in an on-going investigation that helps them to comprehend various steps of the scientific method. The projects completed in Bio 124 include topics such as vegetative propagation and auxin, seed germination and gibberellins, flowering and day length, fruit ripening and cytokinins, grafting and secondary meristems, and similar physiological concepts. This workshop session will include discussion on a modular approach for hands-on learning experiences in botany.

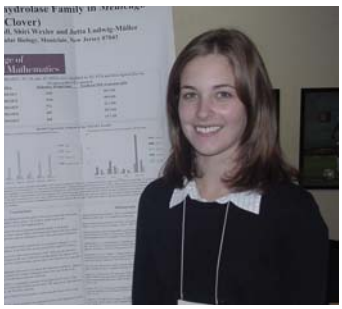
An Innovative Approach Using Writing to Improve Learning In Biology. M. Lakrim, T. Markus, C.A. Biermann, Kingsborough Community College of the City University of New York.

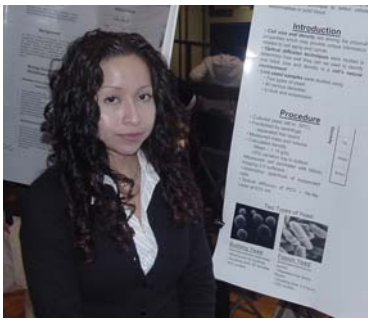
In an attempt to significantly improve the passing rate on the College Preparatory Exam (CPE) at the City University of New York (CUNY) and to simultaneously reinforce and improve reading, writing and critical thinking skills; faculty have initiated the Writing Across the Curriculum (WAC) initiative. The CPE exam is administered to all CUNY students after having reached the 45 credit level. The 3-hour examination is designed to assess reading, writing and analytical; skills. Passing the exam is a requirement to graduate from a CUNY Community College as well as to be able to continue at a Senior College at CUNY. Recognizing that for many students, the sole opportunity to develop and improve these skills is often limited to freshmen English courses, the University has implemented the WAC initiative. This initiative encourages all disciplines to increase the writing components in their course offerings. Writing is to be used as a tool for increasing comprehension and learning. Our presentation will focus on the manner in which the biology courses at Kingsborough Community College (KCC) have been modified to utilize writing and to emphasize how these writing assignments are designed to increase understanding of biological concepts. Through these innovative writing assignments, students obtain numerous benefits. Students are taught to focus on understanding of the course material and to deemphasize rote memorization. Although initially students were apprehensive, they came to appreciate and enjoy the writing assignments and were able to perceive the connection between writing and learning.

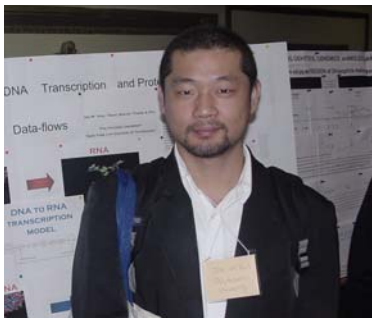
Development of a Macromedia Program. Carla Beeber and Carol Biermann, Kingsborough Community College of the City University of New York.

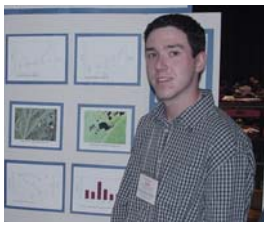
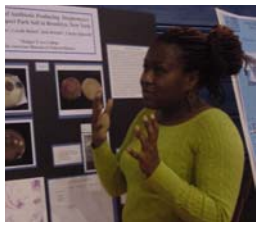
The presentation will consist in the development of a Macromedia program for students on the topic of Osmosis. Osmosis is a difficult concept for students to grasp and this program helps them comprehend the laboratory work on the subject. Comparison of students' performance in laboratory exercises supplemented with program versus students' performance in laboratory exercises conducted with traditional instruction only showed a difference in four classes.



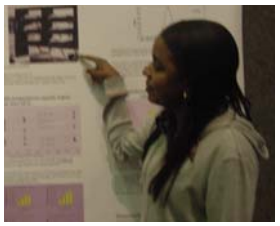





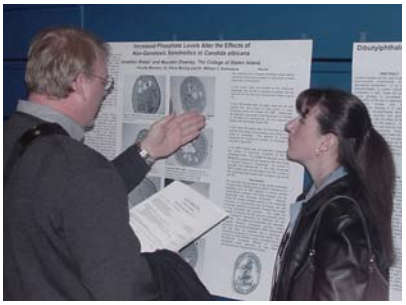
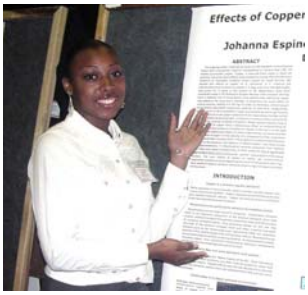


Conference Highlights









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