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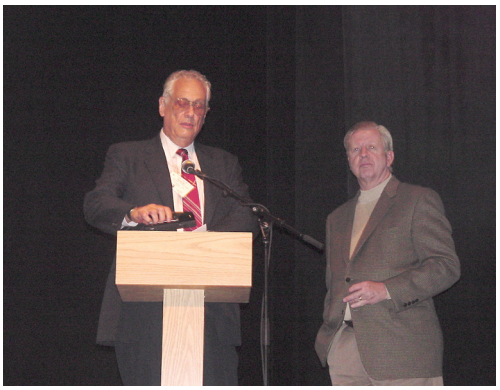

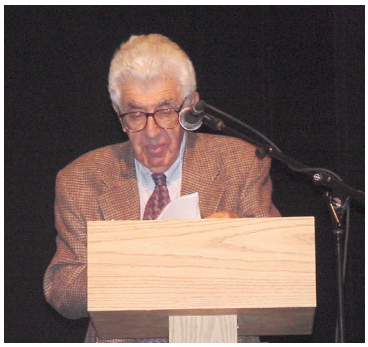

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In This Issue:

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An exciting adventure is being planned

Glutathione: Free Radical Scavenger That Protects Against Cell Damage

By Ann C. Brown
Department of Biology, Medgar Evers College, Brooklyn, NY 11225

A free radical (FR) is a chemical species capable of independent existence that contains one or more unpaired electrons that occupies an atomic or molecular orbital by itself[1-3]. Such unpaired electrons cause a chemical species to be paramagnetic (attracted slightly to a magnetic field) and thus highly reactive. Radicals form quite frequently during metabolism, as covalent bonds break and one of the paired electrons goes to each fission species. FRs are unstable due to the existence of at least one unpaired electron. It is the pairing of the electrons that renders them stable. Unpaired electrons have a tendency to form a chemical reaction with another chemical species and creates a potential danger which can cause harm to the cellular mechanisms. They are short-lived and can cause damage. This is especially true for oxygen-related species often formed during metabolism.

A general *theory of oxygen toxicity* was first formulated by Gerschman in 1959[5]. The theory proposed that oxygen induced damage is caused by free radical intermediates generated in excess such as superoxide anion. The enzyme, superoxide dismutase, was discovered by McCord and Fridovich in 1969[6] and its scavenging of superoxide anion gave support to the FR *theory of oxygen toxicity*[7-9]. Since then, numerous research papers and conferences have been held presenting research data in support of this theory.

The oxygen-free radicals or ROS (reactive oxygen species) include: superoxide anion, hydroxyl radical, lipid peroxyl radical, singlet oxygen, hydrogen peroxide and hypochlorous acid. Oxygen is a good oxidizing agent. If a single electron is added to O_2, the reduction product is O_2^- (superoxide radical) with one unpaired electron. If two electrons are added to O_2, the reduction product is H_2O_2 (hydrogen peroxide) or the protonated form of O_2^{2-}. If four electrons are added to O_2, the reduction product is water ($2H_2O$) or protonated form of O_2^{2-}. Since H_2O_2 (O-O) has relatively weak bonds, it decomposes easily to give hydrogen radical (4).

$$H_2O_2 \text{ ----------> } 2\,OH^- \quad \text{(Energy)}$$

If the pH is alkaline, H_2O_2 decomposes to give a peroxide radical (O_2^{2-}). With the exception of Zn, all transition metals contain unpaired electrons and can qualify as radicals. This is especially true with iron (Fe). Iron (FeII) and hydrogen peroxide can react with many organic molecules. This was first discovered by Fenton in 1894[4]. The reaction involving hydrogen peroxide, a quasi-radical, has become known as the *Fenton reaction*:

1. Fe^{2+} (Reduced) + H_2O_2 (Hydrogen peroxide) ——-> Fe^{3+} (Oxidized) + OH* (Hydroxyl radical) + OH^- (Hydroxyl anion)

2. Fe^{3+} (Oxidized) + H_2O_2 (Hydrogen peroxide) ——-> Fe^{2+} (Reduced) + O_2^- (Superoxide anion)

When equations 1 and 2 are combined:

$$2H_2O_2 \xrightarrow[\text{catalyst}]{\text{Fe-salt}} O_2 + 2H_2O$$

With the combined equations above both the superoxide anion and hydrogen peroxide can be scavenged with the transition metal, Fe, acting as a catalyst, decreasing the FRs in two steps. A different approach was later proposed called the *iron-catalyzed Haber-Weiss Reaction*. This was first postulated by F. Haber and J. Weiss in 1934, and uses traces of transition-metal ions to scavenge the two reactants. The reaction is summarized as:

$$O^{2-} \text{ (Superoxide anion)} + H_2O_2 \text{ (Hydrogen peroxide)} \xrightarrow{\text{Fe-salt catalyst}} O_2 \text{ (Oxygen)} + OH^* \text{ (Hydroxyl radical)} + OH^- \text{ (Hydroxyl anion)}$$

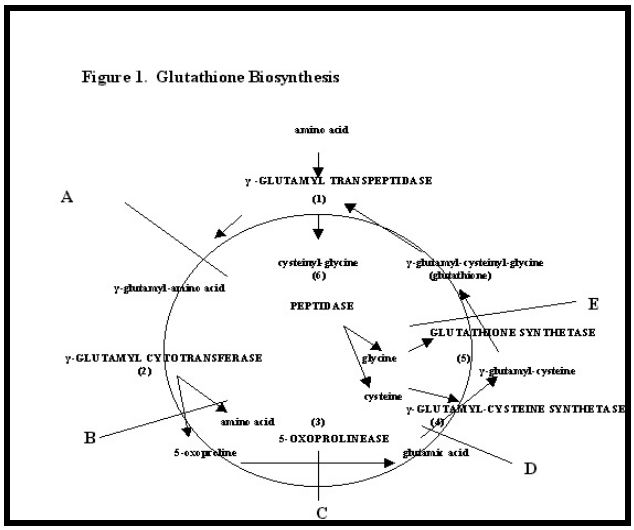
It has been shown that the iron chelator, desferrioxamine, binds Fe^{3+} tightly so it cannot be reduced by O^{2-}, inhibiting the formation of OH*[1]. In recent years, FRs have been implicated to play roles in a variety of biological processes that occur during cellular transformations and neoplasia[1-4]. The generation of neoplastic cells by some chemical agents are thought to involve a series of stages which generate FRs, particularly those of molecular oxygen. Furthermore, normal cellular functions may become disturbed or altered when an abnormal balance of FRs or free radical scavengers (FRS) are present in the cellular environment[10-12]. Free radical generators such as phorbol esters or 12-O-tetradecanoylphorbol-12-acetate (TPA), have been shown to influence a series of chemical changes that in some cases may lead to DNA damage by FR[13-16].

Cells have multiple indigenous protective

mechanisms against certain FR damage in the form of FRS. Many of these protective molecules are classified as antioxidant. Examples include: vitamin C (ascorbic acid), beta-carotene, vitamin E (tocopherols), glutathione, and enzymes such as superoxide dismutase (SOD), catalase, and peroxidases. This minireview will focus on one of the most well-studied antioxidant, antitoxin, FRS present in all mammalian cells - Glutathione.

Glutathione Biosynthesis

The synthesis of glutathione was described in detail by Alton Meister in 1981, 1983[17,18] (see Fig. 1). In this system, α-glutamyl transpeptidase, a membrane-bound enzyme, transports glutamic acid across the cell membrane (reaction A). A second enzyme, α-glutamyl cyclotransferase (reaction B), catalyzes the conversion of α-glutamyl amino acids to 5-oxoproline. In reaction C, 5-oxoprolinase reacts with its substrate, 5-oxoproline to form glutamic acid. α-Glutamylcysteine synthetase (reaction D) is a critical in the glutathione cycle and can be inhibited by sulfoximines such as buthionine sulfoximine (BSO), depleting the cell of glutathione. Glutathione is essential for this resistance and certain levels need to be maintained for cellular homeostasis. Glutathione synthetase (reaction E), adds the final amino acid, glycine, to the dipeptide α-glutamylcysteine to form the tripeptide, glutathione. A decrease in the plasma or cellular levels of glutathione with BSO reflects not only its biosynthesis, but its transport. Since plasma glutathione is derived mainly from the liver, inhibition of glutathione synthesis in the liver decreases the plasma level[19]. It is clear that glutathione levels are important for certain cellular functions. The L1210/PAM cell line derived from L1210 mouse, which is resistant to cisplatin toxicity, was found to reverse its resistance when depleted of glutathione by BSO[20].



Glutathione a tripeptide(α-glutamylcysteinylglycine) is found in most mammalian cells. It was first detected in yeast in 1888[17]. Its composition is derived from three amino acids: glutamic acid, cysteine, and glycine synthesized within the cytosol of the cell. Because of its cysteine moiety, glutathione acts as a storage and transport form of sulfur. It facilitates the destruction of quasi-stable hydrogen peroxide and other organic peroxides, which can generate toxic FR species[21]. Glutathione exists in two forms: reduced glutathione (GSH) and oxidized glutathione (GSSG). Its scavenging effect is determined by the ratio of GSH/ GSSG within the cell. This ratio may be a good indicator of oxidative stress within the cell and the concentration of glutathione is controlled both inside and outside, homeostatically. The concentration of glutathione in mammalian liver (4 - 12 mM) is highest in the intracellular compartment and lowest in the extracellular fluids such blood plasma[17]. It plays many roles along with various other anabolic and catabolic enzymes in cellular expression. In particular, levels of glutathione and the proper balance of GSH/GSSG, along with the activation of certain protein kinases, may act as key regulators of cell cycle events[22].

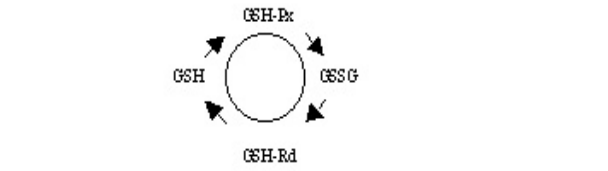
Many functions of glutathione are related to its electron-donating sulfhydryl (-SH) functional group, which is capable of donating $-H^+$ that acts as an antioxidant, antitoxin and enzyme cofactor that participates in many cellular processes. It is this function that protects cell components against oxidative damage. In the abnormal chronic hereditary condition sickle cell anemia, the life span of the red blood cell decreases from an average to 120 days to 17 days. The sickling has been shown to be associated with oxygen $p0_2$ levels and increased oxidative stress due to a decrease in cellular glutathione[23-26].

The mitochondria is the metabolite machinery of the cell that uses oxygen to extract energy from glucose. During this process, hydrogen peroxide, superoxide anions and lipid peroxides build-up can cause necrotic cell damage followed by cell death. Within the mitochondria are antioxidants in the form of FRS that assist in decreasing such damage. These oxidant defenses include manganese superoxide dismutase (MnSOD) and glutathione peroxidase (GSH-Px). The mitochondrial MnSOD catalyzes the conversion of superoxide anion radical to hydrogen peroxide, while GSH-Px uses the substrate GSH to reduce hydrogen peroxide to water[4, 27]. MnSOD is the major antioxidant in the mitochondria where it catalyzes the dismutation of 0^{2-} species.

Fig. 2, shows that there is a relationship between the glutathione cycle, FR levels, SOD and catalase. The conversion of reduced and oxidized glutathione in

the glutathione cycle plays a critical role in the detoxification of oxygen-related species. This conversion is initiated by the level FRs in the cell. The selenium-dependent glutathione peroxidase is necessary for the oxidation of GSH to GSSG. Glutathione reductase is required for the reduction of GSSG to GSH, as illustrated below:

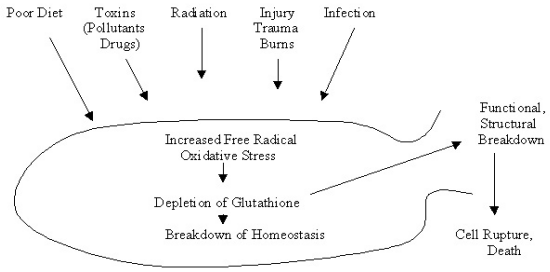
Figure 2. The Glutathione Cycle



Glutathione *in vivo* and *in vitro*: FRS, including glutathione, have been shown to down regulate the effects of tumor promoters on epithelial cells[16]. Because of the importance of glutathione in normal and abnormal cells, Brown and Lutton determined glutathione levels *in vivo* and *in vitro* in L1210 murine leukemia cells[10]. These studies showed highest GSH/GSSG ratios in subcellular fractions in the mitochondrial and cytosolic compartments, which remained high after 3 days in culture, indicating a predominance of glutathione reductase activity. Our results indicate that high levels of superoxide can inactivate SOD and stimulate GSSG formation, and stimulate GSH reductase and NADPH in an attempt to maintain a balance in the glutathione cycle within the cell.

Ninety-eight percent of all intracellular glutathione is in the form of GSH, whereas the remainder is extracellular glutathione[22]. This suggest that GSH oxidation is of physiological importance as a regulator of cell function. Studies on human lymphoid cells grown in tissue culture showed that inhibition of glutathione synthesis by BSO led to a gradual decrease in intracellular glutathione. A similar BSO inhibition of GSH was shown in erythrocytes[28] and macrophages[29] synthesis of leukotriene C, in which glutathione is a precursor in the arachidonic acid pathway. A number of endogenous and exogenous factors can contribute to the depletion of glutathione from the cell leading to cell death (Fig. 3). Some factors include poor diet, drugs/toxins, radiation, tissue trauma, and infections. All of these factors may increase free radicals, deplete the cell of glutathione, and terminate in cell death[30 - 32].

Figure 3. Cell breakdown related to depletion of GSH



Glutathione in Aging

In 1956 Harman proposed the *free radical theory of aging*[33]. Numerous observations and clinical research have given support to this theory. Some support is based on protective effects observed in animals in which their diet was high in antioxidants[34-36]. In this respect, many times the glutathione levels are low in the elderly and sick[37]. A series of accumulative changes involving FRs have been implicated in the aging process and progressive increases in the chance of disease and death[38, 39]. The *free radical theory of aging* postulates that some aging changes are caused in part by FR reactions[33,40].

Studies on Down's Syndrome indicate that increased SOD levels have damaging effects on the mitochondrial functions, with decreased ATP production and increased H_2O_2 and O^{2-}, associated with aging changes and death[41-43]. When glutathione concentration was measured in people over 60 years of age, those with chronic conditions such as heart disease, arthritis and diabetes had lower levels of glutathione than those without the diseases. It was not discussed whether glutathione is a predictor of aging or a cause of it. The former would identify those at risk related to aging and the latter would seek to understand the biology of aging for preventive interventions. The answer was not definitive but rather suggested a slight correlation[43,44].

In yet another study, GSH concentrations were determined in mice throughout their life-span. At all ages, total glutathione and GSH concentrations in the liver was three times that in the kidney and ten times that in the heart. In the old (31 months) mice the GSH contents were lower by 30% in the liver, 34% in the kidney, and 20% in the heart than in the mature (17 - 23 months) animals[45]. These findings were consistent with the hypothesis that the reducing potential of tissue decreases in senescence. Further research concluded

that oxidative stress is able to promote the process of aging that might play a role in the development of stochastic disorders which increase the probability of those age-specific diseases where free radicals are implicated[46-48].

Pigments associated with aging (lipofuscin and ceroid) are thought to be products of FR tissue damage. These pigments have been observed in the liver, heart, skeletal muscle and brain of the elderly[39]. The fluorescent yellow material derived from melanin catabolism is thought to be a by-product of oxygen derived FR reactions and is suggestive of inadequate body defenses against oxidative stress[49]. It is believed that senescence is the most powerful risk factor of old age. Studies have shown a reduction in SOD, GSH peroxidase and catalase FRS can result in neuronal degeneration[49].

Mitochondrial glutathione also plays a key role in the protection against FR damage associated with aging[50]. In Parkinson's disease, a disorder of brain cell nuclei using dopamine as a neurotransmitter, defects in mitochondria of the nuclei in the substantia nigra pars compacta of the midbrain have been observed[51-53]. It was proposed than an increase in FR and the accumulative effects during aging contribute to this condition. A similar neuronal degeneration is seen in Alzheimer's patients[54-55]. One of the characteristics of Alzheimer's disease is the accumulation of beta-amyloid plaques[54]. Scientists have described the creation of antioxidant-containing thiols (-sulfur) that target the mitochondria[49]. Ames[56-58] summarized the importance of the mitochondria in aging as follows: "Aging appears to be due, in good part, to the oxidants produced by mitochondria as by-products of normal metabolism."

Glutathione and Lipid Peroxidation

Levels of lipid peroxidation have been attributed directly and indirectly to many abnormal states of cells and tissues. Lipid peroxidation involves reactions that are influenced by a wide variety of factors. Those chemical systems that have the ability to reduce iron such as ascorbic acid (vitamin C) and glutathione, as already shown in Fig. 2, function as antioxidants by reducing organic peroxide damages[4]. In the membrane the FR process consists of several chemical processes in sequential steps of initiation, propagation, and termination. Several steps of the biological effects involved in the oxidation of unsaturated fatty acids, linoleic acid, represent the kinetic stages in the propagation of lipid peroxidation[30, 58]. Molecular oxygen adds across the double bond of unsaturated fatty acids, forming lipid peroxides. This process can be inhibited by vitamin E, which suppresses the formation of hydroperoxides[59]. Selenium-dependent glutathione peroxidases converts the lipid hydroperoxides to nonreactive lipid alcohols[59]. *In vitro* lipid peroxidation is determined by the thiobarbituric acid (TBA) assay for malondialdehyde (MDA) where MDA is one of the products of lipid peroxidation and used as a consistent indicator of the rate of lipid peroxidation[59, 60].

An increase in free radical species associated with lipid peroxidation may affect membrane fluidity and functions. High levels of peroxides were measured for thiobarbituric acid reactive species (TBARS), reactive oxygen species, and glutathione in 20 week-old and 100 week-old adult rats. Hepatic TBARS levels correlated negatively with other membrane molecules such as arachidonic acid. In addition to a correlation with TBARS levels, the annular fluidity of the bile canalicular plasma membrane decreased in old rats as compared with young adult rats, which suggests an age-related deterioration of membrane fluidity[60].

Metals such as Fe have been shown to act as catalysts in reducing oxygen toxicity. Metals also have been shown to reduce heme oxygenase levels, which provides protection[61]. The effects of mercuric chloride on lipid peroxidation, glutathione reductase, and SOD was studied in various organs of mice[62]. Glutathione reductase levels were high in kidney with a single dose of mercuric chloride, whereas glutathione peroxidase levels in kidneys and the epididymis required a larger dose. SOD levels were high in kidneys at all doses of mercuric chloride used. These data indicated that mercury treatment enhanced lipid peroxidation in all tissues.

Caffeine (1,3,7-trimethyl xanthine), an ingredient in coffee was examined for its FRS effects in rat liver microsomes. Reactive oxygen species such as, hydroxyl radical, peroxyl radical and singlet oxygen were determined. It was demonstrated that caffeine inhibited lipid peroxidation in microsomal membranes and this was similar to that of GSH and greater than that for ascorbic acid[63]. This may also suggest that glutathione and caffeine may decrease lipid peroxidation in some membranes, which would reduce membrane damage.

Conclusion

Glutathione, a tripeptide, is present in all cells, and has numerous functions. Its major function is to protect the cell against endogenous free radicals and other oxidative stressors. The biosynthetic enzymes of glutathione, namely, glutathione peroxidase (GSH-Px, glutathione S-transferase, and glutathione reductase (GSSG-Rd) activities have been determined in numerous normal and abnormal neoplastic cells[10].

Under normal conditions, cells continuously generate free radical species. Cells contain mechanisms of FRS as protection from these species. This scavenging effect is determined by the ratio of GSH/GSSG within the cell. This ratio is a good indicator of the level of oxidative stress within the cell. Cells which are experimentally depleted of glutathione and its synthetic enzymes by BSO are more sensitive to cell death, indicating that the glutathione cycle plays a major protective role against cell death.

Certain FRS and scavenger-like systems are demonstrable in subcellular fraction from murine L1210 leukemia[10]. In L1210 bone marrow microsomes, a predominance of GSH-Rd activity has been observed. In all cases, GSH levels were always greater than GSSG levels, indicating a greater activity of the steady state enzyme, GSH-Rd. In contrast, L1210 leukemic livers showed an equal balance between GSH-Rd and GSG-Px (ratio - 1.0). Peroxidase is necessary for the oxidation of GSH to GSSG; reductase is required for the reduction of GSSG to GSH. The L1210 leukemic cells may be contributing to the FR/FRS imbalance in this condition, and have adverse effects on the normal hematopoietic microenvironment In non-leukemic cells peroxidase is a critical enzyme to regenerate GSSG in response to levels of hydrogen peroxide quenching. However, other factors such as the presence of other antioxidants (vitamin C) may also play a part in determining a normal glutathione balance in normal cells.

After decades of research dealing with lipid peroxidation, it is presently thought that lipid peroxidation plays a casual role in cell injury due to oxidative stress that occurs in the cell. Oxidative stress is an imbalance between prooxidants and antioxidants and this result in peroxidation-induced changes in membrane fluidity and cell permeability. The final resolution of the role of lipid peroxidation in oxidative stress lies in the methodology, interpretation and application of the research results. Studies have shown that lipid peroxidation can amplify a number of free radical initiations and increase the number of chain reactions of the membrane, especially in challenging conditions of the elderly[64]. One reaction involves metal ions and metalloproteins that generate lipid peroxides that can participate in the initiation of free radical chain reactions.

Since GSH-Px catalyzes the detoxication of lipid peroxides in mammalian cells, in a tissue such as the liver, when NADPH (an electron carrier) is in limited concentration during oxidative stress, GSSG (oxidized) concentrations can increase and leave the cell at risk because the lack of the protective effect of GSH, antioxidant protectors of free radical damage.

In the elderly with chronic conditions such as heart diseases, arthritis, diabetes, and other health-related problems, glutathione levels have been observed to be consistently low. In progressive neurodegenerative conditions clinically observed in the elderly such as Alzheimer's disease, where neurofibrillary tangles and amyloid proteins have been observed, and in Parkinson's disease, where there are deficiences in the neurotransmitter dopamine, samples of brain cell mitochondria show low levels of glutathione leaving brain tissue at risk for cell damage and cell death.

In conclusion, abnormal free radical levels lead to progressive changes in metabolic and cellular properties that promote the aging process and cell death. This may be due, in part, to inadequate levels of scavenge-related vitamins (E and C), glutathione and other critical nutrients.

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The Fall 2002 Conference Poster Presentation Abstracts

Poster Presentation Award Winners

Dimerization of Mu-opioid Receptor Splice Variants with KOR-3 Opioid Receptor. [1]Dusan Bogunovic, [2]Arumugam Premkumar, and [2]Gavril Pasternak, [2]Laboratory of Molecular Neuropharmacology, Department of Neurology, Memorial Sloan Kettering Cancer Center, New York, NY and [1]Biology Department, University of Bridgeport, Bridgeport, CT. Advisor: [1]Spiros Katsifis.

Mu opioid receptor (and its splice variants) along with KOR-3 opioid receptor were coexpressed in the same cell line. Competitive inhibition studies have shown that endogenously found OFQ is competed by morphine and some other drugs in KOR-3/MOR-1 cell membranes. In this study HEK and CHO cell lines were transfected with the FRT vector so the uniform expression level of MOR-1 and splice variants could be achieved in the background of the already expressed KOR-3. At this stage we observed that KOR-3 and tagged HA KOR-3 were expressed in CHO, using binding assay with OFQ ligand. Different clones have shown different levels of receptor expression. Based on receptor level expression in mouse brain certain clones have been selected. Further studies are currently being conducted.

A 'G'rich Element Conserved In Human Pre-mRNA's May be Involved In RNA Processing Site Selection. Harshani Pieris, Sophia Weise-Riccardi and Rajintha Bandaranayake, Bioinformatics Group, Ramapo College of New Jersey, Mahwah, NJ 07430. Faculty Mentor: Paramjeet Bagga.

RNA binding proteins of the nucleus play vital roles during RNA-processing, an essential component of eukaryotic gene expression. Previously in our lab, one such protein, DSEF1, belonging to the hnRNPH family of proteins was found to enhance polyadenylation of mammalian pre-mRNAs by interacting with a conserved 'G'-Rich Sequence (GRS). The presented Bioinformatics research was conducted to map 'G' rich sequences near human RNA processing sites and to investigate a possible role of GRS in site selection. More than 400 genes were analyzed during these studies. Over 90% of the genes were found to contain an identifiable GRS suggesting an important role for this element in cellular activities. A high percentage of GRS occurrences were detected in the introns. Moreover, this conserved sequence was more likely to be found near the 5' splice sites rather than the 3' splice sites. These findings suggest possible involvement of GRS in the splicing events, especially near 5' sites. GRS was also found in more than 40% of the analyzed poly (A) regions, thereby suggesting a significant role of such sequences in cleavage-polyadenylation. This finding also corroborates our earlier results. Nearly 35% of the analyzed 5' cap regions exhibited presence of a 'G'-Rich sequence, indicating its possible role in cellular activities at this site. Distribution analysis of GRS among alternatively spliced genes revealed its association with selective gene products only. Similarly, this element was found to be present only near one of the alternative poly(A) signals in many genes. These findings suggest a role of GRS in RNA-processing site selection.

Employing the Genbank and TIGR Databases for Modeling Plant Molecular Evolution and Phylogeny. Daniel Larko, Montclair State University. Faculty Mentors: James J. Campanella and John Smalley.

Genbank is the repository of all published DNA sequences available to the scientific community, while the Institute for Genomic Research (TIGR) is a major center of genomic sequencing and functional gene annotation. We have found that we can take advantage of these two sites to obtain DNA and cDNA sequence data for use in model studies in phylogenetics and molecular evolution. Our laboratory researches the ILR1-like family of hydrolase genes originally isolated in the model plant *Arabidopsis*; these gene products are involved in controlling active levels of the plant hormone indole-acetic-acid. We are interested in how this family of genes has evolved in more evolutionarily distant dicot and monocot species. We have employed the Genbank and TIGR databases to retrieve putative homologs for the ILR1 hydrolase gene in barley, tomato, potato, maize, sorghum, wheat and rice. Our present studies indicate that there are clear evolutionary differences at the DNA level between monocots and dicots for this family of enzymes. We are also examining other homologs of the ILR1-like family to determine if they have diverged in a similar fashion.

Role of Subunit C Mitochondrial ATP Sythetase in CLN6-late Infantile Form in NCL Diseases. Sherise Warner and Jaana Tyynela[1], Medgar Evers College and [1]Univ. of Helsinki, Finland. Faculty Mentor: Charles desBordes.

Neuronal Ceroid Lipofuscinosis (NCL), also known as Battens disease, is a neurodegenerative disorder leading to severe psychomotor retardation and early death in children. All forms of NCL are inherited in an autosomal recessive fashion and the accumulation of autofluorescent proteinous storage material found in the neurons of the brain causes neuronal death. CLN6 is a late infantile/early juvenile variant of NCL, with an onset age of 4-8 years of age. Clinically, it is characterized by vision failure, epilepsy and psychomotor decline with death occurring between 5-12 years. ClN6 is also detected in the well studied South Hampshire ovine model. The accumulation of subunit c of mitochondrial ATP synthetase (subunit c) was initially discovered in NCL diseases, using the sheep model. By a series of bioassay methods, the proteinous storage material found in the nerve cells of the brain of the CLN6 human and sheep models were tested by electrophoresis, western blot, silver stain and immunohistochemistry. These assays were done to detect if the histochemical levels were similar between the human and sheep model. After testing, it was shown that this proteinous material stored in CLN6 patients was similar to the well studied ovine model. However, the storage material is more pronounced in the human model than the ovine model, as indicated by fluorescence analysis. In conclusion, the type of storage material is comparable between the human and sheep model, but the degree of accumulation is greater in the human patients than the sheep model.

S. Warner is a participant in the Biology-CSTEP of MEC, grant 051601105 of CSTEP of NYS Dept. of Education, and a Fogarty Fellow of the MIRT Program of NIH.

Analysis of Floatables in Recreational vs. Non-recreational Sandy Beach Environments. Shawlorna Morris[1], Peter Lanzetta, Ph.D.[1], Mary E. Dawson, Ph.D.[1], Arthur N. Zeitlin, Ed.D.[1], Kawasi Lett[1], Turkesha Huggins[1], Aleta Abel [2]and Dara McEwen[2]. [1]Kingsborough Community College, Brooklyn, NY, USA and [2]Medgar Evers College, Brooklyn, NY,USA.

Recently, the incidence of debris, *i.e*. floatables, washing up on public and protected beachfronts has become an environmental concern in New York City. The following study was started to examine the pattern and amount of spread of floatable and non-floatable debris on a recreational as compared to a limited access sandy beach environment. Also, we attempted to determine whether different environmental factors, such as heavy rainfall, would change the amount of floatable debris washing onshore from sewage overflow. Approximately one and one-half hours following high tide, a 200 x 25 foot rectangular plot was surveyed for floatable and non-floatable debris as defined by the New York City Department of Environmental Protection. It was determined that regular public beach maintenance, such as raking and trash removal, dramatically reduced the amount of floatable debris recorded. In comparison, the limited access beachfront consistently accumulated more debris in every category, especially floatables. These observations were made at four locations along the north shore of Jamaica Bay in New York City. We hope to determine the source(s) of the debris found on the beaches, for example sewage overflow, illegal beach use, boating refuse, or illegal dumping. Future studies will try to determine if a relationship exists between the type of debris washed up and potential beach closings due to bacterial or medical waste contamination.

Application of HPLC with Fluorescence Detection to Analyze Biogenic Amines in the American Oyster, *Crassostrea virginica*. Candice King, Ayodeji Nicholson, Ebere Nduka[1] and Edward J. Catapane[1], Kingsborough Community College, and [1]Medgar Evers College. Faculty Mentor: Ebere Nduka.

Biogenic amines including the catecholamines, dopamine, norepinephrine and epinephrine, and the indoleamine, serotonin and related chemicals are neurotransmitters and hormones in invertebrates and vertebrates. These chemicals have been well studied in the bivalve mollusc, *Mytilus edulis*, but not in oysters. We began a study of the presence and functions of these biogenic amines, their precursors and metabolites in *C. virginica* to elucidate their roles in this animal and to expand knowledge about these chemicals in general. As a first step we set up an HPLC based analysis utilizing a simple isocratic, ion-pairing separation with fluorescence detection. It can resolve norepinephrine, epinephrine, dopamine, 3,4-dihydroxyphenylacetic acid, 3,4-dihydroxyphenylalanine, tryptophan, tyrosine, serotonin, 5-hydroxytryptophan, N-acetyl serotonin, tyramine and octopamine in a twenty minute run. Thus far we have identified norepinephrine in oyster gill tissue. The identity of several other peaks is not yet confirmed. We believe this study will be an important step in elucidating neuroendocrine functions in *C. virginica* and of these biogenic amines in general.

Candice King is an undergraduate research participant. Ayodeji Nicholson is a student participant in the MEC/ KBCC Bridges to the BA Program of MEC. This work was supported by grants 1R25GM62003 of the Bridges to the BA Program of NIGMS and the Groundworks Program of the CUNY. We thank Frank M. Flower and Sons, Inc., Oyster Bay, NY for supplying oysters.

Poster Abstracts

The Effect of Polyions on Fort Morgan Virus Infection of Vero Cells. Beatrice Amoakoh and Dr. Sandra D. Adams, Montclair State University.

Fort Morgan virus, FMV, is an alphavirus of the family Togaviridae. Alphaviruses are enveloped, positive-strand RNA viruses, complexed with a capsid protein surrounded by a lipid bilayer in which the spike proteins are inserted. Attachment of virions to specific cell membrane receptors is the primary event of any viral infection. Viral receptors are often involved in defining the host range of a virus. Electrostatic interactions have been found to play a role in the binding of viruses to the cell surface. Specifically, several polyions reduced the replication of Sindbis virus, the alphavirus type species, whereas others had no effect. Therefore, the effect of different polyions on receptor binding of FMV virions was investigated.

The Effect of Cadmium on the Growth of *Chlamydomonas reinhardtii.* Suzen Awad, Darlene Guerrier, and Lucy Ghannoum, Montclair State University. Faculty Mentors: Dr Bonnie Lustigman and Dr. Lee H. Lee.

Chlamydomonas reinhardtii is unicellular green algae found in fresh water areas. It is a good indicator of contamination because it is a simple, sensitive, and ubiquitous organism. Cadmium is a toxic, heavy metal, which, in high concentrations, can inhibit the growth of *C. reinhardtii*. For this study, 100mL solutions of algal 3M media, with vitamix, and the organism, had different concentrations of $CdCl_2$ added to them. These concentrations were 0, 10, 25, 50, 75, and 100 mg/L. Measurement was done using a spectrophotometer at 3 different wavelengths. The cultures were measured at 750 nm in order to check for optical density as an indicator of growth rate. As a result, the 0 mg/L concentration of Cadmium had a regular growth curve, as did the 10 mg/L. The growth rate for the concentration of 25 mg/L $CdCl_2$ dropped somewhat, but the extreme drop in optical density was actually observed for the concentration of 50 mg/L. The concentrations 75 and 100 mg/L observed little growth with time, and also did not experience a decline either. The other two wavelengths used to measure growth were 645 nm and 663 nm. These wavelengths were used to measure the amount of Chlorophyll a and Chlorophyll b, respectively. The results of the Total Chlorophyll for the concentrations of 0, and 10 mg/L $CdCl_2$ were close; they practically had the same rate of growth. 25 and 50 mg/L $CdCl_2$ became less. Although, unlike the measurement at 750 nm, the lowest rate of growth was observed for 75 mg/L $CdCl_2$. The concentration of 100 mg/L of Cadmium was slightly higher than the lowest rate. This study was done for a two-week period, and 5 readings were taken. At the end of the experiment, pH levels were measured. The lowest concentrations of Cadmium had pH levels between 9 and 9.2 and the highest concentrations of Cadmium had pH levels between 6.6 and 6.8. Thus, 50-75 mg/L $CdCl_2$ is algacidal for *Chlamydomonas reinhardtii.*

***Arabidopsis suecica* IAA amidohydrolase has altered enzymatic expression from its *Arabidopsis thaliana* Homolog, Vinela Bakllamaja & Ania Cartier, Montclair State University, Faculty Mentors: Drs. James J. Campanella and Jutta Ludwig-Mueller**.

We have isolated a homolog of the *Arabidopsis thaliana* IAA amidohydrolase ILR1 from the related species *Arabidopsis suecica*. Using PCR, *A. suecica* produced an amplified, genomic product (sILR1) of 2027 bp which was then sequenced. The DNA homology between sILR1 and ILR1is 98%. The cDNA of sILR1 was subsequently cloned and sequenced. The sILR1 cDNA has 98% homology to its homolog ILR1. The predicted identity between the expressed sILR1 and ILR1 proteins is also 98%. Additionally, we have been able to express and isolate the sILR1 protein which is 50 kD in size. Enzymatically, sILR1 protein can use IAA-Alanine and IAA-Glycine as substrates while ILR1 can not hydrolyze IAA-Gly. Additionally, sILR1 can not cleave IAA-Phe or IAA-Leu while ILR1 is able to hydrolyze these substrates. The ILR1and sILR1 pH optima are identical in a Tris buffer at pH 8.0. Four sequence alterations occur in the putative activity site of the sILR1 protein [aa 103 (Cys>Gly), aa 132 (Asp>His), aa 143(Tyr>His) and aa 227 (His>Tyr)]. One or more of these alterations most likely account for the functional differences between ILR1 and sILR1. The sILR1 mRNA transcript was found to be expressed in *A. suecica* tissues at the highest levels at age 5 with slight decreases at 10 and 15 days. At 1 and 2 days of age, sILR1 expression was not detectable in seedlings (data not shown), while 18S control expression in 1 and 2 day old plants was similar to the older seedlings. The expression of the ILR1 in *A. thaliana* at days 5, 10, and 15 is low compared to sILR1 expression; additionally, ILR1 expression can not be detected at days 1 and 2 (data not shown). We are presently examining *A. suecica* tissues for sILR1 tissue-specific expression. These studies should lead us to a better understanding of molecular evolution in closely related species.

Effects of the Heavy Metal Copper on Mitochondrial Oxygen Consumption in the American Oyster, *Crassostrea virginica.* Wendy Barreiro, Jonven Attia, Kameika Samuels[1], Margaret A. Carroll[1] and Edward J. Catapane[1], Kingsborough Community College and [1]Medgar Evers College. Faculty Mentor: Margaret Carroll.

We showed last year that *Crassostrea virginica* spats transplanted to Jamaica Bay accumulated copper and other metal pollutants. Copper is a required trace metal in most cell systems, but excess soluble copper ions cause prooxidant effects. Mitochondria are sensitive to increased oxidative stress caused by metal toxicity. We studied the effects of copper on O_2 utilization in oyster gill mitochondria. *C. virginica* obtained from a local fish market were treated with copper and mitochondrial respiratory rates were monitored. Copper treated animals were more sensitive to additions of copper to the respiration buffer, with decreases of O_2 utilization in excess of 34% with a 5 mg copper addition and an almost complete inhibition with a 50 mg addition. The study shows copper has a deleterious effect on mitochondrial O_2 utilization *in vitro* and short term exposure of oysters in the lab to copper heightens this deleterious effect. This could be of physiological significance to the growth and health of oysters in waters with high copper content.

W. Barreiro is an undergraduate research participant. K. Samuels and J. Attia are student participants in the CSTEP and MEC/KBCC Bridges to the BA Program, respectively. This work was supported by grants 0516011058 of the CSTEP Program of NYS Dept. of Education, 1R25GM62003 of the Bridges to the BA Program of NIGMS, the Groundworks Program of CUNY, grant 64262-00-33 of the PSC/CUNY Research Award Program and a NIH Extramural Associates Research Program. We thank Flowers and Sons, Inc., Oyster Bay, NY for supplying oysters.

Performing Biological Experiment in *Silico* . Ledion Bitincka, Montclair State University. Mentor: Dr. Charles Du.

Genomics is a new and fascinating area of biology enabled through the large-scale DNA sequencing efforts of many public and private organizations, including the Human Genome Project. Genomics is producing huge amounts of data unprecedented in biology at the level of the whole genome. But how to manage, store, and interpret all these data, the answer lies in a growing new discipline within genomic sciences called bioinformatics. Bioinformatics provides a way in which to manage and store huge amounts of data, and to create statistical tools for analyzing it. Bioinformatics, the merger of biotechnology and information technology, will enable scientists in many fields to find an incredible wealth of information, and to find answers that range from which genes affect human disease to what makes tree grows. Montclair State has set up the infrastructure for bioinformatics study. There are two super power sun blade server dedicated to computational biology research. We also installed the most popular public databases on our local database server. There is a sun workstation lab for undergraduate students to learn the computing software packages, such as GCG and SAS. The pipeline of data flow from wet lab, Internet data searching to data mining will be set up soon.

Analysis and comparison of chlorophyll content in *Z. marina* L. grown in a laboratory microcosm. P.A. Calder, A.M. Stavroulakis, M.T. Ortiz and A. Zeitlin, Kingsborough Community College, Brooklyn, N.Y.

A common seagrass found in the North Atlantic and Pacific Oceans is *Zostera marina* L. (eelgrass). Eelgrass provides shelter and food for a number of marine organisms. Water clarity is improved, and sediment is stabilized where there is eelgrass growth. Even though Z. *marina* can be found in a variety of places in New York, it does not grow in Jamaica Bay, which is adjacent to Kingsborough Community College. This research is part of a larger project whose goal is to restore eelgrass to Jamaica Bay. Eelgrass still grows along the southern shore of Long Island. In eastern Long Island, at Smith Point, growth is abundant. Chlorophyll content of plants taken from Smith Point and placed in Jamaica Bay laboratory microcosms were compared to those grown in Smith Point conditions. Differences detected in chlorophyll levels could relate to the plants photosynthetic activity (rate) and productivity. Chlorophyll pigments were extracted from the leaves, which were ground with a mortar and pestle in spectroanalyzed acetone then in 95% ethanol. Extracts were analyzed spectrophotometrically at 663nm (A_{663}) for chlorophyll *a* and at 645nm (A_{645}) for chlorophyll *b*. Differences in chlorophyll content between plants grown in Smith Point and Jamaica Bay environments were detected over the experimental period. This could be an indication of plant productivity and survival potential in the Jamaica Bay environment. Alternatively, the differences detected between plants may be attributed to the microcosm environment. Additional experimentation and fieldwork comparisons should provide information to confirm this observation. The results from this work may aid in the restoration efforts of *Z. marina* to Jamaica Bay, NY.

Aquatic Gastropods of West Point: Comparative Analyses between Habitat and Location. Eric J. Chapman and Robert S. Prezant, Montclair State University.

A two-year semi-quantitative survey was conducted on the United States Military Academy Property in West Point, New York. Molluscs collected during the survey reveal a diverse assemblage of species that varies by habitat (lentic versus lotic). A total of 21 described species of gastropod were collected, along with a single new taxon of planorbid-like gastropod. Results showed the highest diversity of gastropods was found in lakes and ponds with a total of 17 species. Lowest diversity of molluscs recorded was from ephemeral ditches containing 7 species of gastropods. These survey data were compared with 2 other regional surveys to determine if the similarity of species found within different areas of the county (Orange County, NY) had comparable communities. A total of six species were found in common by all three surveys, but we also found five gastropod species previously unreported from Orange County. Similarity indices show a commonality of species with a coefficient of 63.56 for all surveys.

Bioinformatic Analysis of Cyanophage AS-1. Tin-Chun Chu, Shi-Fang Hsu and Pat Platner, Montclair State University. Mentors: Dr. Charles Du, Dr. Lee Lee, Dr. Jack Gaynor, Dr. Quinn Vega, and Dr. Bonnie K. Lustigman.

Cyanophage AS-1 is a virus that infects cyanobacteria *Anacystis nidulans* and *Synechococcus cedrorum*. Both of these cyanobacteria are freshwater unicellular cyanobacteria (blue-green algae) that frequently cause algal blooms. Genomic libraries of cyanophage AS-1have been generated and many clones have been characterized. Some fragments of AS-1 DNA have been sequenced using ABI310 DNA sequencer. The sequences have been aligned and sent to GenBank for BLASTN and BLASTP searches. Open reading frames have also been identified. Phylogenetic analysis of AS-1 sequences were carried out by comparing the homology of nine AS-1 clones forward and reverse DNA sequences and AN35 to previously reported DNA sequences of marine cyanophage capsid assembly protein (g20), Cyanophage P60, cyanobacterium stanieri, and Encephalomyocarditis virus. All the DNA sequences were aligned by multiple sequence alignment package Clustalx. Phylogenetic trees were constructed by aligning sequences using GCG software. Tajima-Nei distance method was chosen for the distance correction. Tree construction uses the neighbor-joining algorithm, a distance matrix method, that produces an unrooted tree without the assumption of a molecular clock. Five clusters were drawn from the tree. The majority of AS-1 clones and AN35 are clustered together. Cyanophage P60 and AS1_395 are in one group. The entire Encephalomyocarditis virus falls in one cluster. AS1_360, AS1_395, and Cyanobacterium stanieri are closely linked together. Marine cyanophages all clustered into one clade, but have relatively far genetic distance from AS1 clones. From our sequence data, it seems that the DNA sequences of AS1 clones have no close relationship with marine cyanophage sequences. Further DNA sequences from AS1 virus will search against GenBank for homology. More tree building algorithms will be applied to all the DNA sequences to obtain the consensus tree.

Development of Bioinformatics Software Tool for Mapping Conserved GRS Elements in human pre-RNAs. Garrett Dancik, Bioinformatics Group, School of Theoretical and Applied Sciences, Ramapo College of New Jersey. Faculty Mentor: Dr. Paramjeet Bagga.

We have previously identified a 14 base, conserved, 'G-Rich Sequence' (GRS) that mediates efficient 3'end processing of mammalian pre-mRNAs through interaction with an RNA binding protein of hnRNP H family[1,2]. Current research efforts in our lab are aimed at mapping GRS elements in a large number of human genes. Studying the distribution of this conserved sequence in the human genome will aid in understanding its role in regulating RNA processing events of human gene expression. Mapping small elements like GRS in large genomic entries could be a laborious and time consuming process. In order to automate our analysis, we have developed a prototype of GRS-Mapper, a windows based computer program. It provides connectivity to three major public databases for human genomic sequences. The user is able to search individual or any combination of databases with a unique ID or by using keywords from a variety of fields. Prototype GRS-Mapper reads the retrieved file and maps GRS elements on an interactive gene diagram. The prototype program also computes a variety of information about GRS elements and their distribution near RNA-processing sites in the gene. The fully developed program will be very useful for an efficient and productive analysis for GRS elements in a large number of human genes. GRS-Mapper will also be employed to populate a database of RNA processing sites in the future.

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2. Arhin, G.K., Boots, M., **Bagga, P.S.**, Milcarek, C., and Wilusz, J. (2002) Nucleic Acids Res. **30**: 1842-1850.

Study of the effect of AS-1 Virus on its host *Anacystis nidulans* Cyanobacteria. Schakia Eze and Paola Reveco, Montclair State University. Faculty Mentor: Dr. Lee H. Lee and Dr. Bonnie K. Lustigman.

Anacystis nidulans is cyanobacteria usually found in the water of lakes and ponds. When infected by the cyanophage AS-1, it has been found that the rate of photosynthesis in the *A. nidulans* is greatly decreased. The cyanophage AS-1 is a virus that infects *Anacystis nidulans* cultures causing cells to become clear within 5-7 days due to cell lysis. At room temperature, the AS-1 viral lytic cycle lasts 12-16 hours. The flourometer, an instrument that measures the rate of photosynthesis, can determine to what extent the AS-1 affects the host cell cultures. Infected cultures were also examined by hemocytometer and a spectrometer 20 to determine the cell count and turbidity of the infected *A. nidulans* culture over a 7-day period. This study makes it possible to see the deterioration of the *Anacystis nidulans* cell population in relation to the presence of the AS-1 through its lytic cycle. In this preliminary study, the *A. nidulans* cells were infected with the AS-1 virus. Samples of the *A. nidulans* culture were taken for cell counts, flourometer, and spectrometer readings every 2 hours for an intensive 12 hours period. The infected culture was then monitored daily by the same methods for 7 days. The decline in photosynthetic activity in the cultures was steady through the life cycle of the virus. The cell count increase on the first day of the study and then steady decline, this may be due to the replication of the uninfected cells at the beginning of the infection. All the cells had been infected, and lysed after 7 days. The results from the turbidity study are very similar to that of the direct count. The number of virus presence was monitored by titering of the infected culture. Plaques of AS-1/*A. nidulans* infected cultures were observed in each 2-hour time interval.

A Senior Seminar Course Utilizing the Case Study Method. Patrick Field, Kean University.

Incorporating a case study format into a senior seminar course is a novel method for teaching the components of a successful seminar. Within this format, seminar presenters familiarize the audience with relevant background information, present the case study, divide the class into discussion groups to answer case questions, and then facilitate a discussion that encompasses the entire class.

Transcription Induced a Mutagenic Response during Amino Acid Starvation in *Bacillus subtilis.* Nakia Gray, Audry Hamphery, Edwards Shorn and Samar Ayach, New York City College of Technology. Faculty Mentors: Dr. Walied Samarri, and Dr. Rivka Rudner.

A correlation was found between the reversion rates of auxotrophs and the increase level of the stringent factor (ppGpp). The stringent factor accumulates in the absence of the required amino acid or in the presence of agents like serine hydroxamate (SH) known to induce the stringent response. To investigate the relationship between operon derepression and mutation rates, two isogenic strains of *B. subtilis* were examined, the BD79 (*leuB1-*, *pheA1-)* and BD170 (t*hrA5-*, *trpC2-*) differing only in their *relA* background. These were: a wild-type (*relA*$^+$), a knockout (Δ*relA::mls*), and a *relA* over producer that is a IPTG - inducible as *amyE::spac-relA-cat* construct integrated at the *amyE* locus. A positive correlation was reported during leucine or threonine starvation between the following: i. The reversion rates in the *leuB* or *thrA* genes (measured by colony count), ii. (p)ppGpp levels (measured by thin-layer chromatography plates), and iii. The increased levels of *leuB* or *thrA* mRNA produced during nutritional stress (measured by RNA isolation and Slot Blot Analysis). During leucine or threonine starvation or SH treatment for 45-60 min in the *relA*$^+$ over producer strains and the parental strain, the levels of *leuB* and *thrA* mRNA increased 2.8-2.2 and 1.8-2.1 fold respectively. Starvation conditions as well the treatments with SH in the knockout strains revealed a considerable decrease in mRNA of 65-85% compared to the vegetative level. It was concluded that micro-organisms have the potential to speed their own evolution.

Evolution of Seven-helix Transmembrane Proteins. Nicole Green, and Rashida Henry, Brooklyn Campus, Long Island University. Faculty Mentor: Dr. Carole S. Griffiths.

Phylogenetic analysis of proteins can generate much information about the evolution of protein structure and function. G-Protein Coupled Receptors (GPCRs) are a group of seven helix transmembrane proteins. The function of these proteins is to transmit signals from a variety of molecules such as hormones, neurotransmitters, and mediators, from the extracellular environment to the intracellular environment of a cell. We are examining the evolution of four proteins from two different subfamilies of GPCRs within classes of vertebrates. Nucleotide sequences of the genes coding for these proteins will be subjected to phylogenetic analysis. Sequences will be translated into the corresponding proteins and amino acid changes will be mapped onto the phylogenies. A three-dimensional model of one of these proteins, rhodopsin, will then be used to correlate amino acid changes with structural regions of the protein. We are reporting preliminary results.

Diminished Food Resources, Delayed Reproduction and Increased Mortality in Brood-Bearing Terrestrial Isopods, *Armadillidium vulgare*. Anaiseh Hashemi, Montclair State University. Faculty Mentor: Dr. Scott L. Kight.

Female terrestrial isopods (Crustacea: Oniscidea) carry eggs and early instars in a ventral brood pouch. We investigated reproductive expenditure of female *Armadillidium vulgare* Latreille under the condition of restricted food resources. Regardless of food availability, few cases of spontaneous termination of care were observed and most gravid females either successfully produced offspring or died while still bearing eggs. There were no differences in pre-hatching maternal mortality between food-restricted and non-restricted groups, but females exhibited significantly higher post-reproductive mortality when food availability was heavily reduced after oogenesis. This did not occur when food was restricted prior to oogenesis, but in this case females delayed the onset of reproduction. An association between mortality and past reproduction was further supported by high laboratory mortality, regardless of food availability, in non-gravid females field-captured late in the reproductive season. Maternal investment in *A. vulgare* thus appears to be energetically expensive. Despite the ability to terminate care, however, females continue to invest heavily in reproduction even when resources are scarce and the likelihood of mortality is high.

Getting to the Root of the Problem: Kinetics and Macromolecules of Attachment in the *B. japonicum*-Soybean Symbioses. Deneen A. Jackson[1], Nathan W. Oehrle[2], and David W. Emerich[2], Faculty Advisor: Anthony DePass[1], [1]Long Island University (Brooklyn) and [2]University of Missouri (Columbia).

The interaction between *Bradyrhizobium japonicum*, a dimorphic soil bacterium and its host plant, soybeans, is beneficial for plant growth. Rhizobium-leguminous plant symbioses result in the formation of nodules on the root of the plant. It is through these nodules that symbiotic nitrogen fixation occurs using nitrogenase, a bacterial enzyme, to convert dinitrogen to ammonia employing 16 ATPs. This process is the major source of nitrogen from the biosphere. To understand what limits nitrogen fixation and consequently plant growth and development, it is necessary to look closely at the initiation of symbiosis by examining the mechanisms of attachment of *B. japonicum* to the soybean root. Through in vivo attachment assays where soybean roots were incubated in the presence of *B. japonicum* for various points in time, we discovered that bacterial attachment to the soybean root hair is a multi-phased process. Initially the bacteria binds to the soybean root loosely and without specificity. Eventually, with the assistance of proteins, tight binding occurs and it is suspected that a cap formation develops where the bacteria accumulate at the attachment site. Using in vitro analysis procedures, we were also able to confirm the presence of a protein believed to be involved in this crucial attachment process.

Comparison of Urea and Silver-Conjugated Urea Nanoparticle Uptake *In Vivo*. Elie Jarrouge, College of Staten Island/CUNY. Faculty Mentor: Dr. Valerie Pierce.

We are studying urea tolerant *Drosophila melanogaster* populations that are known to have a slower rate of urea uptake than wild-type populations. This suggests that how urea crosses the gut wall may be important. We propose using silver-conjugated urea nanoparticles to visualize the crossing of urea into the body under electron microscopy. First, we have to determine the toxicity of silver-urea and its effect *in vivo* as compared to regular urea. The viability of the urea tolerant and wild-type flies was assessed both in the presence of silver-urea and regular urea. Additionally, we measured the concentration of urea in the hemolymph of third instar larvae to see if silver-urea accumulates to the same levels during development as regular urea. There was no difference in viability between urea tolerant flies reared on urea food versus silver-urea food. Also the same percentage of wild-type larvae reached the pupal stage on both food types, with virtually none eclosing. These results suggest that silver-urea has the same level of toxicity in both populations as regular urea. The urea assay showed that both urea and silver-urea led to the same urea concentrations in the hemolymph. The wild-type larvae showed an average of 110 mM urea in their hemolymph on both urea and silver-urea food, while the tolerant larvae showed an average of only 85 mM on both urea and silver-urea food. As expected the tolerant population had a significant lower concentration of urea. We didn't see any significant difference between regular and silver urea, which indicates that silver-urea tends to behave *in vivo* the same way as regular urea.

Preliminary Results on the Isolation and Identification of Novel Marine Bacteria Which are Epiphytic on Seaweeds of the New Jersey/New York Coast. Eli Klein and Melissa Birken, Montclair State University. Faculty Mentors: Dr. Bonnie Lustigman and Lee H. Lee.

The marine environment represents an area of interest in the development of new antimicrobial substances. Marine seaweeds contain epiphytic bacteria that have been difficult to culture in the past. Recently, new media development has allowed for the growth of these organisms in the lab. In this study, we have cultured, isolated and begun preliminary identification of marine bacteria in order to identify antimicrobial substances they might produce. Seaweed samples (*Chondrus crispus, Polysiphonia , Fucus vesiculosis, Enteromorpha intestinalis,*) were placed in 50ml of seawater and brought to the lab, where they were rinsed with sterile seawater. Samples of approximately 2 cm were cut from the fronds and prepared for Transmission Electron Microscopy. The seaweeds were swabbed and this was then streaked on minimal marine agar made of seawater and agar. The plates were kept two weeks at ambient temperature. Individual colonies were isolated and streaked to new minimal marine agar plates. Pure marine bacterial cultures were gram stained and photographed. Electron micrographs were prepared from the isolated colonies. Challenges of the marine bacteria were initiated with *Escherichia coli* and *Staphylococcus epidermidis* and zones of inhibition were measured. Thirteen of the isolates produced marked zones of inhibition against the challenge organisms.

STEP at Kingsborough Community College: A Science Enrichment Program for Minority Students. Dr. Georgia J. Lind, Kingsborough Community College.

Minority students are historically underrepresented in the scientific professions. This may be due in part to lack of early exposure to good quality science programs, and perhaps also to lower levels of encouragement to train for and enter research and health-care professions. Both of these possibilities are addressed in a program for minority high school students run out of Kingsborough Community College, The Science and Technology Entry Program (KCC-STEP). Twenty to fifty students meet for two hours on Saturday to participate, and we lead one activity on each Saturday from November through May. During the week, the students can meet for an additional two hours with a faculty member from their high school whose orientation is to encourage them to stay with a scientific career path, and to facilitate that path however they can. This can include additional activities, counseling or other advisement. Our activities have included hands-on research and laboratory-based activities in biology, physics, chemistry, engineering, anthropology, field ecology, and mathematics. The mandated participants in this program are African American, Hispanic or economically underprivileged, and most of them are in science classes in their high schools, so STEP prepares activities that enrich, rather than repeat, basic high school curricula. In this poster, I present a thumbnail sketch of the students, the activities, and the excitement that this program has brought to the high school freshmen and sophomores of our area. We can do this because of a grant from the State Education Department of The University of the State of New York, the support of the KCC Administration, the faculty and staff of the KCC Biological Sciences Department, and our wonderful high school faculty, for all of which we are very grateful.

The Effects of Physical Stress on Reproductive Success in the Terrestrial Isopod *Porcellio laevis*. Meydar Nevo, Montclair State University. Faculty Mentor: Dr. Scott L. Kight.

Female *Porcellio laevis* were induced to become gravid with the use of an incubator by programming favorable temperate conditions as well as increased hours of daylight. From the instant the experimental females were observed to be gravid, they were subjected to physical stress for 5 minutes daily. This activity was imposed to determine if excessive physical activity disrupted the normal reproductive cycle. The pouch of each female was examined daily for detection of any physical abnormalities caused from the strenuous physical activity. The results indicate a strong response to this regimen of activity where the experimental females exhibited a shorter gestation period as compared with the control group as well as a trend indicating the production of fewer young. There was also a significant correlation between gestation and body size of the experimental females.

Mitochondrial Gene Rearrangements in Diaspidids (Armored Scale Insects). Ifedayo Nicholson and Benjamin B. Normark[1], Kingsborough Community College and [1]University of Massachusetts, Amherst. Faculty Mentor: Edward J. Catapane.

Scale insects (order: Hemiptera, superfamily: coccoidea) are notorious pests of agricultural crops, trees, and ornamental plants. Diaspide is the largest (approximately 2,370 species worldwide) and probably most economically important coccoidea family because they have the largest host range that includes many agricultural crops. Our project focused on the molecular systematics of Diaspidids. We sequenced approximately 1200 bp fragment of the mitochondrial genome (which included part of CO1, all of the t-RNA leucine, and part of the CO2, genes) of several Diaspidids and used the sequences (along with sequence aligning and tree building software) to infer evolutionary relationships among them and with other scale insects. When the sequences of 1200 bp region of Diaspidids mt DNA were aligned with the sequences of other scale insects, we found that the Diaspid sequences were missing the sequence for the t-RNA leucine gene (usually found between the CO1 and CO2 genes in most animals and almost all insects). This finding is significant because animal gene arrangement often remains unchanged over long periods of evolutionary time, and is highly conserved (with few exceptions).

Ifedayo Nicholson is a student participant in the MEC/KBCC Bridges to the Baccalaureate Program of Medgar Evers College grant 1R25GM62003 of NIGMS and a participant in the Summer Research Internship Program in Ecology at the University of Massachusetts, Amherst.

Transposon Rearrangement in pCMVFLAG GFRa-1, a RET co-receptor. Cristina Ochoa, Maria Velasco, Teresa Leja, Kelvin Caban and John Smalley, Montclair State University. Faculty Mentor: Dr. Quinn Vega.

GFRa-1 is a co-receptor for the receptor tyrosine kinase, RET. The co-receptor, in association with a ligand, GDNF, activates RET. This association activates cellular processes leading to either cell division or differentiation. GFRa-1 is required for kidney development and neuronal survival. In an attempt to identify the critical regions of the co-receptor, a transposon was inserted randomly into the co-receptor sequence. This procedure involves the insertion of a 1.7 kb fragment into the vector followed by the removal of all but 15 bp, causing the addition of 5 amino acids to the final protein product. The initial transposon reaction resulted in over 250 colonies. The initial screen of these colonies has resulted in approximately 6% of the positives containing transposons within the co-receptor. However, further analysis of the colonies yielded a small fraction containing two transposons and roughly half of the plasmids lacking a transposon, presumably through a recombination reaction. Possible reasons for the recombination will be discussed.

Study of Combined Effect of Cadmium Chloride and Ferric Chloride on the Growth of Cyanobacteria *Anacystis nidulans.* Tope Olufade and Devin R. McDonald, Montclair State University. Faculty Mentors: Dr. Lee H. Lee and Dr. Bonnie Lustigman.

Anacystis nidulans is a unicellular cyanobacteria, which lives in fresh water. *A. nidulans* has been used as an indicator for the presence of different levels of pollutants in the environment. This particular cyanobacteria has been used to study the effects of iron, manganese, selenium and cadmium etc on its growth. A preliminary study of the combined effects of cadmium and ferric chloride has been carried out. In this study 50 mg/L of ferric chloride ($FeCl_3$) was combined with 5, 10, 20, 25, and 30 mg/ L of Cadmium Chloride ($CdCl_2$). The growth was monitored by direct count using hemocytometer and turbidity studies using spectrophotometer at 750 nm. 5 and 10 mg/L of $CdCl_2$ with 50 ml $FeCl_3$ enhanced the growth of the *A. nidulans* when compared to the control. The culture inoculated with 20 mg/ L of $CdCl_2$ and 50 mg/L of $FeCl_3$ was slightly inhibited. 25 mg/L of $CdCl_2$ combined with 50 mg/L of $FeCl_3$ indicate severe growth inhibition. It was also observed that a combination of 30 mg/L of $CdCl_2$ and 50 mg/L of $FeCl_3$ almost completely inhibited the growth of the cyanobacteria. This suggests that ferric chloride may act as an antagonistic agent to reduce the toxicity of cadmium at low concentration. However, when the concentration is higher, there is a strong synergistic effect that resulted from the combination of both metals.

ENVIRONMENTAL CHANGES IN MAHWAH, N.J. 1986 - 1997. Ryan Ortiz, Rockland Community College. Faculty Mentor: Susan Brydon Golz, Ph.D.

The purpose of this project was to use Geographic Information System technology to map the environmental effects of rapid increase in development within the Township of Mahwah, N.J. between 1986 and 1997. The maps will be used by the Mahwah Environmental Commission to study the effects of deforestation, loss of wetlands and increase in impermeable surface on the Township's drinking water supply. The maps will be a significant resource in future planning for preservation of open space. ARCView 3.2 was used to create maps of land use and land cover based on data collected by the N.J. Department of Environmental Protection in 1986 and 1995/97. Land use/land cover determinations were provided by aerial Color Infrared (CIR) stereo-paired imagery. Three maps were developed to illustrate the significant environmental impact of this ten year period of development: 756 acres of deforestation loss of 141 acres of wetland and an increase in impervious surface of 300 acres. Much of this change occurred in vital areas of aquifer recharge and critical wildlife habitat. Maps were also generated to identify important areas for open space preservation.

This project was funded in part, by a grant from the NJDEP.

The Effects of Water Turbulence on Eelgrass Growth and its Epiphytic Associations. D. Perdicaro, M.T. Ortiz, A.M. Stavroulakis and A. Zeitlin. Kingsborough Community College, Brooklyn, New York.

Eelgrass (*Zostera marina* L.) is a marine flowering plant that grows and lives along coastal areas worldwide. This plant plays an important role in marine ecosystems as a food source, sediment stabilizer and shelter for other species. Eelgrass is no longer found in Jamaica Bay, New York. However, our hope is to restore it back to this location. It grows in other nearby areas such as Smith Point, Long Island, where water is not as turbulence as in Jamaica Bay. We investigated whether turbulence had an effect on eelgrass growth and it's epiphytic associations. Plants were collected from Smith Point and placed in laboratory microcosms simulating the Jamaica Bay environment under calm and turbulent water conditions. Aquaria were set up with water flow rates of 0.48, 0.9, 1.5 miles per hour (mph), respectively. Microscopic examination of epiphytes was conducted at the beginning and conclusion of the experiment. Water turbulence had a negative effect on eelgrass growth. Concomitant changes were observed in the epiphytes. Water turbulence may potentially decrease eelgrass growth. Our results have implications for selection of remediation locations in Jamaica Bay.

Effects of Two Pollutants, Copper and p-Nonylphenol, on Glutathione-S-Transferase Activity in the American Oyster, *Crassostrea virginica.* Surujnie Persaud, Kawasi Lett[1], Siema Cox, Margaret A. Carroll and Edward J. Catapane. Medgar Evers College and [1]Kingsborough Community College. Faculty Mentor: Margaret Carroll.

Jamaica Bay (JB) contains pollutants in levels higher than NYS Water Quality Standards. Our lab showed that *Crassostrea virginica* spats transplanted to JB accumulated copper and other metal pollutants despite excellent survival and growth. Bivalves are frequently used for heavy metal monitoring and bioaccumulation kinetics studies but little is know about their biochemical responses to metal accumulations. We studied the effects of copper and p-nonylphenol (p-NP) on Glutathione S-transferases (GST), an inducible enzyme, important in detoxification. GST uses the endogenous antioxidant glutathione to conjugate hydrophobic, electrophilic xenobiotics. Oysters which had been transplanted into JB, oysters from Cape Cod, and oysters from a local fish market were treated with p-NP or copper. p-NP was found to induced GST activity up to 268%. Copper treatments resulted in a 65 and 54% drop in GST activity. The study shows the presence and inducability of GST in oysters and suggests oysters growing in a copper polluted environment may experience physiological difficulties if challenged by pollutants requiring detoxification by GST.

S. Persaud, S. Cox and K. Lett are student participants in the CSTEP of MEC and the MEC/KBCC Bridges to the BA Program, respectively. This work was supported by grants 1R25GM62003 of the Bridges to the BA Program of NIGMS, 0516011058 of the CSTEP Program of NYS Dept. of Education, 64262-00-33 PSC-CUNY, the CUNY Groundworks Program and a NIH-EAR Program grant. We thank Frank M. Flower & Sons, Inc., Oyster Bay, NY for supplying oysters.

Professional and Organizational Ethics of Medicine in America Today. Rosanna Pittella and Dr. Donald Dorfman, Monmouth University.

The ethics currently governing American medicine were not born of the altruism at the heart of the Hippocratic oath. The operating philosophies of today's managed care organizations, hospitals, and doctor's offices have originated in accounting books and legal tomes. Those empowered in today's medical world hold degrees in accounting and law and demote those with medical degrees renaming them Service Providers. Ironically, Physicians alone are equipped to revitalize America's medical industry. The American Medical Association's Physician Code of Ethics, heavily based on the Hippocratic Oath, is the standard by which physicians and other caregivers are expected to act. Sadly, in today's medical landscape, manifestations of these principles have all but disappeared. Decisions made within health care organizations are not designed to support such ideals with respect to controversial issues including: nondiscriminatory access to care, assisted suicide/euthanasia, genetic mapping/engineering and cloning, and organ harvesting/transplantation. Today's health care system is propelled by conditions, circumstances, and principles designed for business. This study first outlines the ethics of the modern medical industry and the breadth of its divergence from Hippocratic standards, secondly suggests areas in which Hippocratic philosophy can no longer be applied, and finally provides practical suggestions for the revitalization of American medicine.

Genome Project of Cyanophage AS-1 and Cyanobacteria *Anacystis nidulans.* Patricia Platner, Shi-Fang Hsu, Kisha Vilecus and Inna Nutanson, Montclair State Univerity. Faculty Mentors: Dr. John J. Gaynor, Dr. Lee H. Lee, Dr. Quinn Vega and Dr. Bonnie K. Lustigman.

Anacystis nidulans is a freshwater unicellular cyanobacteria (blue-green algae) that frequently causes algal blooms. These blooms pose a threat to aquatic ecosystems, causing oxygen depletion and eutrophication in freshwater lakes. No satisfactory means for their prediction or prevention is currently available. It has been suggested that cyanophage (cyanobacteria virus) is a regulatory agent and may be responsible for the disappearance of algal blooms. Cyanophage AS-1 infects *Anacystis nidulans* and *Synechoccus cedrorum* (another unicellular cyanobacteria). The effects of Clorox and Parvosol on AS-1 were studied and the results suggest that AS-1 is very resistant to both disinfectants. This establishes the possibility of using this virus as an environmental probe. In addition, establishment of probes for *Anacystis nidulans* is necessary for earlier detection of algal bloom. Our goal is to synthesize duplex environmental probes to detect both AS-1 and *A. nidulans*. DNA from cyanophage AS-1 and cyanobacteria *A. nidulans* were isolated and purified. DNA fragments were generated by cutting the DNA with restriction enzyme *Eco*RI. Restriction fragment analysis was carried out using the agarose gel electrophoresis. The phagemid vector pBluscript SK (+/-) was also cut with the same restriction enzyme. The genomic libraries of AS-1 DNA and *A. nidulans* DNA were compiled by using the phagemid pBluescript SK(+/-) as a vector and host *E. coli* (SOLR cells). Many clones have been selected and stored. Some clones were characterized by isolating the phagemid using the Qiagen mini prep. The sizes of the inserts were then determined by agarose gel electrophoresis. The sequences of the inserts were then determined using the ABI 310 DNA sequencer. These sequences will be sent to Genbank for a Blastn search.

Antiproliferative Effects of 2-Methoxyestradiol on Breast Cancer Cells. David A. Recinos[1] and Thresia Thomas[2]. Faculty Advisor: June Polak[1], [1]Long Island University, Brooklyn NY and [2]Robert Wood Johnson Medical School New Brunswick, NJ.

Several studies have proven the direct relationship between estradiol and breast cancer. Further studies have found that the estrogen receptor plays a major role in the cause of breast cancer. An estradiol metabolite, 2-methoxyestradiol (2-MeO) can inhibit the growth if breast cancer cells. It is not clear however, at what doses the inhibitory effect begins and if the estrogen receptor plays a major role in its mechanism. We treated estrogen receptor (ER)-positive MCF-7 and ER-negative MDA-MB 453 breast cancer cell lines with different concentrations of 2-MeO (1 nM to 10 μM. DNA synthesis was measured using a [^{3}H]-thymidine incorporation assay after incubation of these cells for 48 and 72 hours. Estradiol was added to MCF-7 cells to promote estrogenic growth. The analysis showed that nanomolar concentrations of 2-MeO had little effect on these cell lines at both time points. At 2.5 to10 μM concentration significant growth inhibitory effect was observed at 72 hrs. An 87% decrease in the growth of MDA-MB 453 cells was observed at 2.5 μM 2-MeO compared to only 35% for MCF-7 cells. These results suggest that the effect of 2-MEO is not mediated by ER, although ER may have a role in the sensitivity of ER-positive cells. Studies on compounds such as this may yield new anti-tumor compounds with potential for clinical application.

Pathology of Testicular Autoimmune Orchitis Using Scanning Electron Microscopy (SEM). Joseph Riggio, Rory Ulloque, Nazish Sayed and Annalia Da Cruz, Montclair State University. Faculty Mentor: Dr Judith Shillcock.

Allergic Orchitis is an autoimmune disease of the testis characterized by reduction of sperm and destruction of the seminiferous tubules. Two experimental groups of five and one control group of four Sprague Drawley rats were used in the study. Testicular tissue from Sprague Drawley rats was emulsified in Freund's Complete Adjuvant (FCA) and then injected into the footpads. Experimental group 1 received 100 mg of testicular tissue per 300 gms body weight, emulsified in FCA. Experimental group 2 received 25 mgs of testicular tissue per 300 gms body weight, emulsified in FCA. The control group received the FCA emulsified in saline. In both experimental groups after 18 weeks, there was total destruction of testis as detected by the SEM. Further studies are in progress to observe the pathology of the disease process from the early stages to total destruction of the normal testicular histology.

Impaired Mitochondrial Respiration and Lysosomal Activation Occur during Apoptosis in MCF7 Human Breast Cancer Cells. Alexander Rios and Cristina Ochoa, Montclair State University. Faculty Mentor: Dr. Reginald Halaby.

Breast cancer is the second leading cause of cancer deaths in women. Many of the currently available treatments for breast cancer are invasive and non-specific, killing healthy cells as well as cancerous ones. It would be desirable to develop therapies that can specifically kill neoplastic cells. We used human breast carcinoma MCF7 cells as a model system for human breast cancer. To elucidate the cellular processes by which MCF7 cells activate the apoptotic machinery, we induced cell death by treating the cells with tumor necrosis factor-α (TNF). Although several reports have addressed the ability of TNF to induce apoptosis in MCF7 cells, the mechanism by which it does so is not well understood. In the present report, we investigated the effects of TNF on lysosomes and mitochondria during apoptosis. Histochemical acid phosphatase studies demonstrated that lysosomes increased in size and amounts in TNF-treated cells. There was a significant difference in cell viability between control and experimental cells. Our results provide evidence that lysosomal enzymes degrade cytoplasmic and nuclear regions of dying cells during apoptosis of MCF7 cells. In addition, the data demonstrate that impaired mitochondrial respiration leads to cell death in the cells.

Studies of *Zostera marina* L. (eelgrass) Growth Rate in Jamaica Bay, New York. E. Rodriguez, A. Stavroulakis, M . Ortiz and A. Zeitlin, Kingsborough Community College, Brooklyn, NY.

Zostera marina L., more commonly known as eelgrass is found in coastal seawater. It is a marine angiosperm, which is very important because it provides food for fish, shellfish and waterfowl. It also prevents shifting of sand and mud banks in harbors. I'm studying eelgrass growth in Jamaica Bay, New York because it no longer grows there. A research group at Kingsborough Community College has initiated remediation studies to reintroduce the eelgrass to Jamaica Bay. The research group transplants eelgrass to aquarium tanks, which contain Smith Point Park, New York water and sediment, where eelgrass flourishes, and Jamaica Bay water and sediment where eelgrass no longer grows. The group was successful in growing the eelgrass in this laboratory microcosm. My research project compared growth rates between Smith Point Park and Jamaica Bay eelgrass transplants in the laboratory microcosms. Eight experimental plants were selected and measured (weight, rhizome length, number of nodes, number of shoots, number and length of mature leaves). Then I used a hole-punch method, which involved puncturing the plant 3-7 centimeters above the rhizome (Zimmerman *et al*., 1995). With this method the growth rate was determined by measuring and graphing the distance the hole punched traveled over time. I placed these plants in two tanks. Four plants were placed in Smith Point Park water and sediment and four were placed in Jamaica Bay water and sediment. So far comparable growth rates were observed. The experiment is still in progress to see if with more time we can see a difference. Learning whether growth rates are different in the plants is important because this would give us more of an idea of whether the plants are growing faster or slower in one area and not the other. This would also give more information and ideas for future experiments with these plants and restoration efforts.

Rehabitation of the American Oyster, *Crassostrea virginica,* in Jamaica Bay, NY, a One Year Report. Rocio Rodriguez, Wendy Barreiro, Gary Sarinsky, Edward J. Catapane[1], Margaret A. Carroll[1] and Ebere Nduka[1], Kingsborough Community College and [1]Medgar Evers College. Faculty Mentor: Gary Sarinsky.

Jamaica Bay (JB) was once abundant with oysters, but in early 1900's oyster beds disappeared and now are rare. Over-harvesting, pressure from predators, parasites and declining water quality are cited as causes. Last year we initiated an project to study growth and survival of *Crassostrea virginica* transplanted into JB. Oysters were placed in Taylor Floats suspended one foot below the water surface. The current project extends the study to a full year period. Oysters were examined biweekly and growth determined by measuring shell length on the anterio-posterial axis. Water temperature, pH, turbidity, salinity, conductivity, chlorophyll-a, and dissolved oxygen also were measured. Oysters continued their growth, attaining a 400% increase in shell length in the one year period. Water quality data is varied, depending on tidal patterns and other environmental influences, but overall is good and consistent with that reported by others. The study thus far continues to show JB water quality is suitable for oyster growth under the conditions of our experiments.

R. Rodriguez is a student participant in the MEC/KBCC Bridges to the BA Program of Medgar Evers College. W. Barreiro is an undergraduate research participant. This work was supported by grants 1R25GM62003 of the Bridges to the BA Program of NIGMS, the Groundworks Program of CUNY, grant 64262-00-33 of the PSC/CUNY Research Award Program and a NIH Extramural Associates Research Program grant. We thank Frank M. Flowers and Sons, Inc., Oyster Bay, NY for supplying oysters.

Inhibitory Effects of Various Spices on Bacteria. Susana Ruelas-Aguilar and Joseph Sciacchitano, Montclair State University. Faculty Mentor: Bonnie Lustigman and Lee H. Lee.

Spices and herbs come from plants and are used for flavoring foods and beverages. They are also known for usage in preservation of foods. Spices supply chemicals that in small quantities have beneficial effects on digestion, energy metabolism and may assist in the treatment of disease. Uncooked foods contain a collection of microorganisms, which may cause illness. *Escherichia coli, Salmonella* and *Staphylococcus epidermidis* were used as challenge organisms to find if there were inhibitory effects produced by various spices. These organisms were selected because of their role in the development of intestinal disease. The spices include those used in American, Indian and Spanish cooking. Results indicate a wide variety of effectiveness to various spices. Those which produced the largest zone of inhibition were garlic, oregano, chamomile tea, Chinese tea, ginger, adobe powder, cloves and thyme. Garlic by far was the most effective. Different cultures use different spices to flavor their foods, but have some spices in common. The most widely used spices include: onion, garlic and oregano in countries from the Caribbean, Spanish and Italian areas.

Comparison of Placement on Growth of the American Oyster, *Crassostrea virginica,* in Jamaica Bay, NY. Olga Urdanigo, Marlene Tejeda, Juan Luxuma[1], Gary Sarinsky, Edward J. Catapane[1], Ebere Nduka[1] and Margaret A. Carroll[1], Kingsborough Community College and [1]Medgar Evers College. Faculty Mentor: Gary Sarinsky.

Jamaica Bay (JA) once was abundant with oysters until the early 1900's when they disappeared. Our earlier work found oyster spats placed in JB grew well when suspended one foot below the surface. We now examined the influence of placing oysters at the bottom as compared to the surface. Taylor Floats were constructed positioning spats of 20 mm shell length one foot above the sediment as well as one foot below the water surface. Water temperature, pH, turbidity, salinity, conductivity, chlorophyll-a, and dissolved oxygen were monitored at each site. Spats growth was determined by measuring shell length on the anterio-posterial axis. Over a 4 week period spats grew at a similar rate to that observed last year, an approximately 150% increase in shell length. Spats positioned above the sediment grew slightly faster than those at the surface. Water quality varied, depending on tidal patterns and environmental influences, but overall was good and consistent with that reported by other. Survival was good for all samples. The study continues to show JB water quality is suitable for oyster spat growth under the conditions of our experiments.

M. Tejeda and O. Urdanigo are student participants in the MEC/KBCC Bridges to the BA Program of MEC. J. Luxuma is a student participant in Biology-CSTEP of MEC. The work was supported by grants R25GM62003 of the Bridges to the BA Program of NIGMS, 051601105 of CSTEP of NYS Dept. of Education, the Groundworks Program of CUNY, 64262-00-33 of the PSC/CUNY Research Award Program and NIH EARP. We thank Frank M. Flowers & Sons, Inc., Oyster Bay, NY for supplying oysters.

Spatial Properties of IP_3 Induced Ca^{2+}Release in *Tradescantia virginiana* Cells. Joshua I. Wilson[1], Anthony L. DePass[1] and Peter K. Hepler[2], Faculty Mentor: Dr. Anthony L. DePass. [1]Long Island University, Brooklyn and [2]University of Massachusetts, Amherst.

Inositol (1,4,5) trisphosphate (IP_3) is a known agonist that participates in a second messenger signal transduction pathway by mediating Ca^{2+} release from intracellular stores. Studies conducted in animal cells have concluded that the endoplasmic reticulum (ER) is the primary intracellular store that responds to these agonists with receptors identified, cloned, and localized to the ER membrane. By contrast, studies on plant cells indicate that the central vacuole serves as an intracellular store for Ca^{2+}, with the ER being much less important. Numerous reports have identified the vacuole as the target for second messenger agonists such as IP_3. We microinjected *Tradescantia* stamen hair cells were with the ratiometric fluorescent dye fura-2 conjugated to dextran (10kd) and measured cytosolic [Ca^{2+}] after iontophoretic injection of IP_3. Our observations indicate that Ca^{2+} release was concentrated in the cortical and perinuclear regions of the cell with little indication of release from the central vacuole. We interpret these data as Ca^{2+} release from cortical and perinuclear ER, rather than the vacuole, in response to the injection of this Ca^{2+} releasing agonist.

Modern Use of Medicinal Plants on the Eastern Aegean Island Psara (Greece). Christina Won, Long Island University. Faculty Mentor: Dr. George Sideris.

Plants have long been our main source of medicinal compounds. Much of the traditional treatment for injuries and ailments practiced by the ancient Greeks stemmed from folk medicine, a characteristic shared by Greeks and some other societies to this day. Synthetic chemistry has decreased reliance on botanicals as a source of original therapeutic compounds, particularly in the Western world. However, isolated areas may still rely on medicinal plants. Para is a very small island located approximately 190-km northeast of Athens. The island, relatively isolated, has about 500 inhabitants all living in the village of Para located on the southern tip of the island. Considering the remoteness of Para the objective of this project was a study of contemporary medicinal plant usage on the island. Interviews were done with the islands medical personnel and residents and plants were collected from a variety of habitats. Findings indicate that there are a number of known medicinal plants on the island some currently used by residents. For the most part though people rely on modern pharmaceuticals as dispensed and prescribed by the islands doctors. Some remarkable medicinal properties were attributed to some plants which merit further study including chemical analysis.

Cloning the Inositol 1,4,5 Triphosphate Receptor in Plant Cells. Oladapo Yeku[1] and Sabrice Gueirrer[2], Faculty Mentor: Dr. Anthony DePass[2]. [1]Medgar Evers College and [2]Long Island University.

The Inositol 1,4,5 triphosphate (IP_3) receptor is located on the endoplasmic reticulum in plant and animal cells. It is responsible for Ca^{2+} release in the cytosol in response to a second messenger signaling pathway. Although cloned and sequenced in some animal species, the IP_3 receptor (IP_3R) has yet to be cloned in plants even though there is overwhelming evidence as to its presence and function. Understanding the structure of the receptor will elucidate the condition specific mechanisms of Ca^{2+} release so we are cloning the gene in *Tradescantia virginia*, a plant that that been extensively studied and demonstrated to have an IP_3 sensitive intracellular Ca^{2+} release response. Our cloning strategy utilizes maximum likelihood and maximum parsimony algorithms in the analysis of the amino acid sequences of human, mouse, rat and drosophila IP_3R genes. Additionally, we use the X-Ray crystallography data from a mouse IP_3R fragment to predict amino acid sequences that would likely be represented in the plant IP_3R gene. We then designed degenerate PCR primers based on the predicted conserved sequences, and probed a plant cDNA library. PCR products that match the predicted length are then cloned and sequenced and compared with the sequenced genome of Arabidopsis *Thaliana*. The efficacy of this strategy will be demonstrated using similar proteins with the gene for Actin, a ubiquitous protein vital for the cytoskeletal structure of the plant cell. Products that have been generated using different combinations of our degenerate primers are currently at the sequencing stage.

Fall 2002 Conference Report
by Dr. Carol Biermann

Department of Biology, Kingsborough Community College, Brooklyn, NY

The 35th annual fall MACUB meeting was held at Kingsborough Community College on October 26th 2002. The theme of the conference was "To Be or Not to Be? That is the DNA Question." There were approximately 230 members in attendance. Following an introduction from our President Gary Sarinsky, Kingsborough's President Dr. Byron McClenney welcomed the group. He was impressed by the turnout on a Saturday morning. Wandering around and talking to the students who developed the 44 posters was a stimulating activity for Dr. McClenney.

The first keynote speaker, Dr. Barry Commoner, senior scientist from Queens College's Center for the Biology of Natural Systems, spoke about "Is DNA the Secret of Life or the Other Way Around?" He discussed the mediating role in cellular metabolism (as measured by oxygen consumption) by the DNA molecules. There appears to be an inverse relationship between concentration of DNA in cells (and organisms) and their metabolic activity. In other words, cells with more chromosomes, and therefore more DNA, are less biologically (metabolically active)! A bird would have less DNA than a mammal called the sloth (who just hangs around).

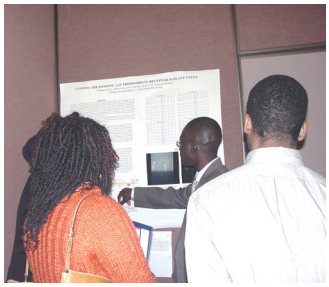
Dr. Commoner also discussed Dr. Francis Crick's statement that the central dogma of biology, DNA to RNA to protein, is a one-way street. He pointed out numerous examples of how the process is an interactive one, with mediation of DNA and RNA activity by proteins. One current example he gave was how prions, which are normal proteins that have gone awry (They are abnormally folded.) become infectious agents. Recent genetic studies using "knockout genes" show that when these genes are inserted into a genome, certain physiological activities should become aberrant, and this has not happened as expected! The hypothesis of Beadle and Tatum, that one gene produces one enzyme has been be modified drastically. The Human Genome Project, completed in year 2000, cannot fully explain how genetic characteristics are produced by the cells. Dr. Commoner pointed to the insertion of genes from one organism into another (genetic engineering and formation of transgenic organisms) as a potentially "dangerous" activity. In many cases there have been undesirable outcomes, which have not been adequately studied.

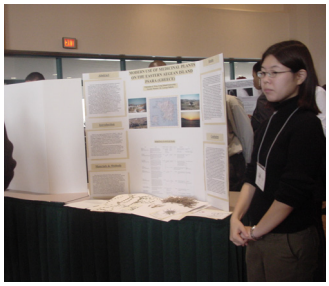
Remarks by Dr. Commoner initiated a lively debate during the questioning session. In response to a MACUB member standing in the aisle and taking exception to many of Dr. Commoner's remarks, Dr. Commoner calmly responded this is what science is all about. It was great for the students in attendance to see this repartee between scientists.

Following lunch, which was delicious, our afternoon keynote speaker, Dr. Adrian Krainer, Senior Scientist at Cold Spring Harbor Laboratory, challenged us with his talk, "Common Cause: RNA Splicing and Human Disease." His first step was to show the audience the central dogma of biology, and then to go about demonstrating how this dogma has been modified by new knowledge concerning the activities of introns upon exon activities. That certain diseases, such as Parkinson's disease, are caused by alternative (abnormal) RNA splicing which has been elucidated and studied recently. Dr. Krainer's talk gave the audience a lot to "chew on." This was a great afternoon dessert!

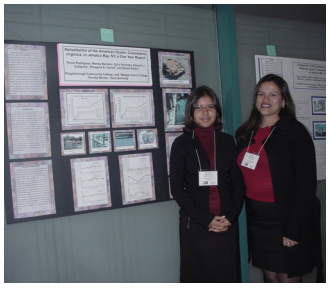
Member presentations and workshops rounded out this remarkable day. There were six member presenters, forty seven student poster presentations, four workshops and a focus session going concurrently. All were well attended. Thanks must go to the executive board of MACUB, especially the hard work of Gary Sarinsky and Paul Russo, for making this day run smoothly. Many others helped, including many faculty, staff and students from Kingsborough, our host institution this year.

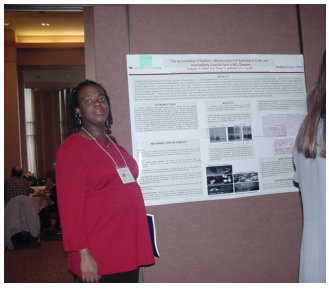


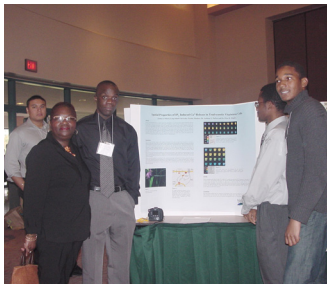
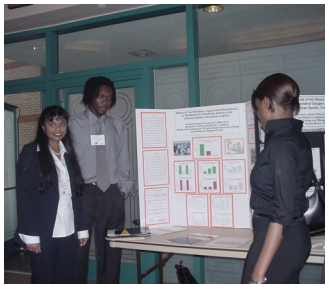


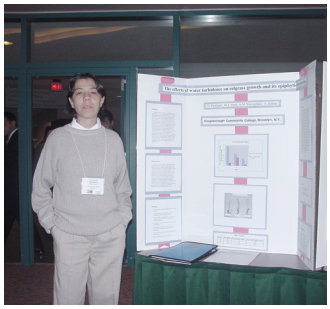



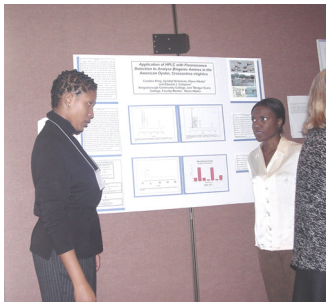

Conference Highlights






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

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