RAS SCIENTIFIC PAPER SESSION MONROE COMMUNITY COLLEGE NOVEMBER 9, 2019

ORAL PRESENTATION ABSTRACTS

FOUR YEARS OF MANUAL REMOVAL OF CATTAILS (TYPHA) MAINTAINS HABITAT STRUCTURE IN A SENSITIVE PEATLAND Koty Kurtz, Kathryn Hunt, Faith Page, and C. Eric Hellquist Department of Biological Sciences, State University of New York Oswego, Oswego, NY 13126. Invasive cattails (Typha spp.) can alter habitat structure and nutrient availability in Great Lakes wetlands. At Silver Lake (Oswego County, NY), Typha angustifolia is colonizing a sensitive floating mat of a poor fen peatland complex. Deposition of Typha leaf litter can provide a competitive advantage over native plants by creating dense thatch. One species jeopardized by thatch deposition in Menyanthes trifoliata (bog buckbean), the primary food source of the endangered bog buckmoth (Hemileuca sp1.). Over the last four years, we have used manual control methods to limit the expansion of Typha on the floating mat. To assess what time of year is most effective for Typha removal, we cut Typha in the spring (n=12) and in the fall (n=12) to monitor regrowth. Since 2016, spring harvests of Typha have reduced living stems by 2x. Dead stem counts in the spring have decreased 12-fold since 2016. Fall harvests of living stems were reduced 1.8x since 2016, while dead stems were reduced by 59x. Since 2016, fall harvests reduced living biomass by 1.5x while dead biomass was reduced 6x. Our work indicates that spring is the most effective time to cut Typha. Spring removal requires reallocation of carbohydrates to resprouting ramets and also prevents the formation of inflorescences. However, regrowth of Typha stems from rhizome systems has prevented large reductions in stem counts over four years. However, the removal of these stems is a worthwhile effort because it has virtually eliminated the deposition of Typha litter that gradually becomes a layer of thatch on the floating mat. Thus, the open hollows of pooled water that are important microhabitats for Menyanthes have been maintained, a benefit for both Menyanthes and its herbivore, the bog buckmoth.

A SURVEY OF THE CUTANEOUS BACTERIA OF THE SPOTTED SALAMANDER (AMBYSTOMA MACULATUM) Richard T. Stevens, Department of Biology, Monroe Community College, 321 State St., Rochester, NY. 14608 Amphibian skin has been found to be host to a diverse community of microorganisms and there is evidence that amphibians manipulate the composition of this community by the secretion of antimicrobial substances such as peptides. Cutaneous bacteria are thought to play a role in preventing the chytrid fungus and other fungal diseases in amphibians. While there has been a recent increase in studies researching the microbiome of amphibians, there have been relatively few studies investigating the skin microbiome of salamanders and only one small study of the microbiome of ambystomid salamanders. This study attempts to provide insight into the components of the cutaneous microbiome of spotted salmanders, Ambystoma maculatum. We identified colonies collected from 10 spotted salamanders, including 7 adults, one juvenile, and two larvae. Bacteria were cultured on R2A agar in the lab and identified using sequencing of the 16S rRNA gene. A total of 9 distinct bacteria from 6 genera were identified. Two bacteria were identified to family but genus could not be identified. Bacterial diversity was greatest among adult salamanders. Among the bacteria found was Janthinobacterium, which is known to prevent chytrid

fungal infection and is even used to inoculate amphibians reintroduced to sites where they have been extirpated from chytridiomycosis. The majority of bacteria identified from salamanders had some known antifungal properties.

MECHANISMS OF BISPHENOL A DISRUPTION OF LIPOLYSIS IN DROSPHILA MELANOGASTER. Maura Connorton, Edward Freeman PhD and Todd Camenisch PhD St. John Fisher College, Department of Biology and Wegmans School of Pharmacy, 3690 East Ave, Rochester, NY 14618 Obesogens are chemicals that promote obesity by acting as endocrine disrupting chemicals (EDCs, 1). Obesogens may increase adipose content, reduce calories burned at rest, favor calorie storage, or alter appetite and satiety signaling (2). Based on this and published work, our lab conducted studies to evaluate the impact of bisphenols on larval fat deposition in Drosophila melanogaster. These studies have demonstrated that embryonic and larval exposure to BPA results in statistically increased lipid deposition levels (unpublished). Our lab proceeded to conduct RT-PCR on cDNA synthesized from these larvae to evaluate potential methylation of Bmm, Brummer lipase (main control gene of triglyceride break down in Drosophila) and upregulation of Kr-h1(a transcription factor that inhibits Brummer lipase transcription) transcription via an estrogenic receptor. BPA can methylate DNA and can act as an estrogen mimic (1). It was found that relative expression of Kr-h1 significantly increased in BPA treated larvae and Bmm relative expression was significantly decreased in BPA treated larvae (unpublished). All collected Ct values were normalized to Beta-1 tubulin. To further evaluate whether this decrease in Bmm transcription was due to increased expression of Kr-h1 transcription factor via BPA upregulation or whether the Bmm promoter region was methylated via BPA DNA methylation, methylation assays were conducted. DNA was synthesized from larvae using a DNeasy Blood and Tissue Kit (cat. 69504). A bisulfite conversion was performed using an EpiTect Fast DNA Bisulfite Kit (cat. 59824). Using a Pyro sequencer, a PyroMark PCR kit (cat.978903), and PyroMark Q24 Advanced Reagents (cat. 970902) methylation assays were run for both methylation of the Bmm promoter region and global methylation (for future gene candidates). Methylation of the Bmm promoter region would further support the decreased relative expression of Bmm from RT-PCR experiments. A lack of methylation of the Bmm promoter region would suggest an upregulation of Kr-h1 transcription factor via BPA estrogenic properties. This would concur with the increased relative expression of Kr-h1 in the RT-PCR trials. These results would allow for the development of future folic acid rescue experiments (folic acid is a potential candidate to inhibit BPA DNA methylation).

GENETIC INVENTORY OF MICROBES PRESENT ON SPACECRAFT AND SPACECRAFT ASSOCIATED SURFACES. Paula Fogel, Cornell University, Lisa Guan and Parag Vaishampayan, Jet Propulsion Laboratory, California Institute of Technology The Mars 2020 mission, which will cache Mars soil and core samples for possible future return, requires that a â€œGenetic Inventoryâ€ of potential microbial contaminates on the spacecraft be compiled. Since any future return samples would likely be analyzed for indicators of the presence of life, including nucleic acids, the Genetic Inventory (GI) project will catalog the DNA present on the spacecraft and spacecraft associated surfaces of the Mars 2020 mission prior to launch in order to mitigate any false-positive findings of biological material from return samples. This will be the first genetic inventory study of spacecraft to use whole genome sequencing and amplicon sequencing for taxonomic analysis. In addition to

informing the analysis of return samples, comprehensive genetic data about the microorganisms present in cleanrooms may also help inform the development of new bioburden reduction techniques in the future. However, due to the unique constraints of microbiome and nucleic acid studies in a Planetary Protection context, traditional environmental sampling kits could not be used for our purposes. Therefore, a new protocol was developed to process the low-biomass samples that come from spacecraft sampling. The current recommendation for the GI Project is to concentrate samples using 50kD Amicon filters (Millipore Sigma, Burlington, MA), pre-treat DNA using a pre-treatment involving bead-beating, and extract DNA using the QIAampÂ® UCP Pathogen Mini Kit (Qiagen, Hilden, Germany), and with the QIAcube (Qiagen, Hilden, Germany) set to a 100uL elution volume.

A MULTI-PERSPECTIVE CONSIDERATION OF OBESITY.
Edward Freeman and Cassandra LeClair, St. John Fisher College
Obesity is a global health concern. Although it is clear that diet and exercise affect an individual's weight and overall health, these parameters are influenced by more than just these two factors. Recent work has suggested that obesity levels are also impacted by genetics, environmental conditions, and socioeconomic status. An understanding of each risk factor and their complex interplay is necessary for proper interventions, lifestyle planning, and public awareness. Much effort has been dedicated to studying these risk factors individually. This talk will highlight this work and make the argument that these factors need to be studied in a more comprehensive manner with an emphasis on interdisciplinary approaches that consider multiple risk factors simultaneously.

ASYMMETRIC CYCLOPROPANATION OF ARYLDIAZOACETATES USING CHIRAL COMMERCIALLY AVAILABLE N-HETEROCYCLIC CARBENE LIGANDS COMPLEXED TO GROUP 11 TRANSITION METALS. Peyton Kunselman, Nathan Johnson, Michael Coleman Ph. D. Rochester Institute of Technology, 1 Lomb Memorial Drive, Rochester, NY 14623 The scientific value of cyclopropane motifs in organic molecules is vast. Cyclopropane rings have a uniquely rigid geometry that lends to their use in improving the pharmacokinetics of pharmaceutical compounds and in the ligand design of chiral molecular architectures. Reactions using carbenic precursors offer a practical and robust methodology to construct these cyclopropyl-containing organic compounds. Catalytic asymmetric cyclopropanation reactions are a classic benchmark reaction for evaluating the reactivity and selectivity of novel chiral ligand/metal complexes. This work explores stereoselective cyclopropanation reactions using safer environmentally-benign and inexpensive Group 11 â€˜coinage metalsâ€™ complexed with commercially available chiral imidazol(in)ium salts afford an operationally simple single-step protocol resulting in a green and sustainable catalytic asymmetric cyclopropanation reaction in good yields, high diasteroselectivity, and promising enantioselectivity.

UNDERSTANDING THE GENETIC DIVERSITY OF SCAEVOLA ON PUERTO RICO. Abigail Wine and Susan Witherup PhD Department of Biology, Ithaca College, 953 Danby Road Ithaca, NY 14850 The genus Scaevola in the family Goodeniaceae consists of 130 species of tropical flowering shrubs. Though the genus originates from Australia, 40 species have dispersed and reached areas such as Hawaii, Polynesia, Puerto Rico and other islands in the Pacific and Atlantic Oceans (Howarth et al. 2003). Dispersal events gave rise to two of the most widespread species outside of

Australia, Scaevola plumieri and Scaevola taccada. Both occur on the islands of Puerto Rico, though S. plumieri is the endemic species and S. taccada is an invasive species thought to have been introduced as an ornamental plant for commercial businesses. Previous studies to understand the relationship between these two species observed the disruption of the natural growth of S. plumieri due to comparatively more successful seed dispersal by S. taccada, as its seeds are able to float (Finkle and Elliott 2011). The introduction of new non-native species to islands impacts biological and genetic diversity of established native species (Paulay 1994). Island species are especially sensitive to introductions of non-native species (Finkle and Elliott 2011). Some non-native species may be invasive, meaning they can cause habitat destruction, the extinction of native species, and the loss of biodiversity (Hejda et. al, 2009). Invasive species not only lack predators, parasites, and competitors, they are also able to spread quickly and out-compete native species (Finkle and Elliott 2011). Studying the genetic diversity in island plants, especially between native and recently introduced non-native populations, is important in understanding the influence of introduction events on endemic species. Studies done to assess the impact of invasive species on biodiversity often utilize microsatellite simple sequence repeats (SSRs) to produce quantifiable measurements of genetic diversity to characterize how vulnerable a species may be to extinction (Abdelkrim et al., 2009). Analysis of SSRs aids in the management of invasive species and the conservation of the organisms they affect by indicating genetic variation, variability between and among populations, inbreeding, and modes of reproduction (Ellis and Burke, 2007). Microsatellites are short tandem repeats of DNA ranging from 1 to 6 nucleotides long that are capable of repeating between 5 to 40 times in a single sequence (Selkoe and Toonen 2006). The amplification of microsatellite regions allows for the analysis of variability between and among both individuals and whole populations. Data from microsatellites produces peaks representing the different fragment lengths or alleles from the amplified region. The analysis of the data collected from both S. plumieri and S, taccada on Puerto Rico will allow us to understand the variation across the sampled populations. As a result, it will be possible to determine the genetic diversity present in Scaevola on Puerto Rico and whether it correlates to geographic distance. This research explores the genetic diversity of two coastal shrubs of the genus Scaevola that may be found on Puerto Rico and its surrounding islands. Plants in this genus are distributed across many tropical islands in both the Pacific and Atlantic Oceans (Finkle and Elliott 2011). On the islands of Puerto Rico, the native species Scaevola plumieri co-occurs with an invasive species, Scaevola taccada, that is thought to have originated from the Indo-Pacific region. Since its introduction to Puerto Rico, S. taccada has begun to encroach on many S. plumieri populations across the island and threatens to out-compete it. Previous research has shown the ability of S. taccada to prosper in the presence of S. plumieri and disrupt the growth of the native species (Finkle and Elliott 2011). The purpose of this research is to understand the genetic variation and diversity in, among, and within the populations of S. plumieri and S. taccada on Puerto Rico. Additionally, the distances between beaches at which sampling took place are taken into account to determine whether genetic diversity has any correlation to distance. It was hypothesized that the native S. plumieri would be more diverse than its invasive counterpart S. taccada because of its longer inhabitance on the islands of Puerto Rico. â€ƒ Literature Cited Abdelkrim, J., Robertson, B.C., Stanton, J.-A.L., and Gemmell, N.J. (2009). Fast, cost-effective development of species-specific

microsatellite markers by genomic sequencing. BioTechniques 46, 185â€“192. Finkle, A.J., and Elliott, N.B. (2011). Status of Endemic Scaevola plumieri and Invasive Scaevola taccada on San Salvador Island, Bahamas. Proceedings of the Thirteenth Symposium on the Natural History of the Bahamas. Eds. Baxter and Cole: 46-51. Hejda, M., PyÅ¡ek, P., and JaroÅ¡Ãk, V. (2009). Impact of invasive plants on the species richness, diversity and composition of invaded communities. Journal of Ecology 97, 393â€“403. Howarth, D.G., Gustafsson, M.H.G., Baum, D.A., and Motley, T.J. (2003). Phylogenetics of the genus Scaevola (Goodeniaceae): implication for dispersal patterns across the Pacific Basin and colonization of the Hawaiian Islands. American Journal of Botany 90, 915â€“923. Paulay, G. (1994). Biodiversity on Oceanic Islands: Its Origin and Extinction. Integr Comp Biol 34, 134â€“144. Selkoe, K.A., and Toonen, R.J. (2006). Microsatellites for ecologists: a practical guide to using and evaluating microsatellite markers. Ecol. Lett. 9, 615â€“629.

Development of a Markerless Allelic Exchange Method for the Genetic Modification of Acetobacter Bacteria. Christopher Murphy and Peter Newell Genetic modification has been utilized in bacteria since 1973 when Boyer and Cohen first introduced recombinant DNA into an E. coli. Since then the process has been refined and expanded across the domain, but most bacterial mutations still utilize antibiotic resistance markers to make selection for mutated bacteria less challenging. Removing these resistance genes allows the use of recombinant organisms in a broader set of industrial applications, as well as more nuanced genetic studies. As of yet, no method for creating markerless mutations has been reported for Acetic acid bacteria. In this study we developed a method of markerless allelic exchange for Acetobacter fabarum, an acetic acid bacterium isolated from wild Drosophila. The method utilizes two plasmids: a suicide plasmid containing the modified allele to be introduced into the chromosome, and a replicating plasmid with an arabinose-inducible I-SceI meganuclease that targets a sequence in the suicide plasmid. Once the first plasmid is integrated into the chromosome at the target locus via homologous recombination, the second plasmid is introduced and I-SceI expression is induced. Cleavage of the integrated plasmid leaves a double-stranded break, killing cells that fail to complete a second homologous recombination event at the locus. Successful allelic exchange leaves only mutant or wild type sequences, effectively removing antibiotic resistance gene. Later, the replicating plasmid can be cured from the strain leaving no resistance genes via counterselection. We chose two genes for inactivation based on their putative role in uric acid metabolism, which has been implicated in the adaptation of Acetobacter to its host Drosophila melanogaster. After implementing the allelic exchange method, PCR and sequencing confirmed the desired genomic changes. Functional analyses of the mutants are ongoing. The ability to implement allelic exchange within Acetobacter fabarum will allow for better analysis of gene function, and result in a better understanding of the role of uric acid metabolism in symbiosis with Drosophila. Acetic acid bacteria have a wide range of uses within the food and beverage industry, and with the ability to implement new mutations without introducing any new resistance genes, the efficiency, and function of these bacteria can be improved.

EVALUATING THE IMPACT OF ROADSIDE DITCHES ON IN-STREAM EROSION AND RELATED GEOMORPHOLOGICAL PROCESSES IN CENTRAL NEW YORK. Emma Payne, Rebecca Schneider, PhD, Kalena Bonnier-Cirone, Alexander Goddard, and Brian

Rahm, PhD. Cornell University and the New York State Water Resources Institute, Ithaca NY 14853 Roadside ditches are shallow depressions which parallel every road, constructed to carry away stormwater from the road surface. However, recent research has documented that the extensive network of ditches in each watershed actually intercepts about 20% of all runoff from the adjacent hillslopes, as well as roads. This flow is rapidly shunted to nearby streams where it contributes to flooding and water pollution. In an average central New York watershed, there are 94 connections between streams and ditches and 63 percent of all ditches discharge into streams. We hypothesized that the high volumes of water potentially contribute to in-stream erosion, with associated negative impacts on water quality, such as increased sediment and phosphorous transport leading to harmful algal blooms. Despite their prevalence and capacity to interrupt natural hydrological processes, little research exists on the impact of roadside ditches on stream ecological processes and geomorphology. The goal of this project was to determine the effects of roadside ditches on streams, by comparing stream geomorphologic features immediately above and below the stream-ditch confluence. Nine sites, each consisting of a first order stream intercepted by a road with lengthy roadside ditches, were sampled across Tompkins and Schuyler Counties in central New York. At each site, a cross-sectional profile and longitudinal slope were measured using a transit and stadia rod; substrate texture was analyzed using the Wolman Pebble Count; and bank stability was assessed based on percent vegetative cover and occurrence of eroding substrates, undercuts and exposed roots. There were significant changes in the cross-sectional profiles downstream for almost every stream, although some exhibited widening while the others became more incised. 7 of the 9 streams exhibited a decrease in slope along one downstream bank, associated with more extensive floodplain development. The extent of exposed bank face increased downstream in most sites. Substrate texture also differed downstream, but varied among sites with some having increased bedrock exposure, while others had an increase in the incidence of larger pebbles, cobbles and rocks. Cumulatively these findings suggest that roadside ditches are a major geomorphic driver in stream networks, and contribute to significant amounts of sediment transport to water bodies downstream.

ARE MICROPLASTICS FOUND WITHIN LAKE ONTARIO SPAWNING SALMON? Ryan Bailine1, Derek Kuhn1, Casey Raymond1, and C. Eric Hellquist2 1-Department of Chemistry, State University of New York Oswego, Oswego, NY 13126 2-Department of Biological Sciences, State University of New York Oswego, Oswego, NY 13126. In 2019, New York salmon stocking targets for Lake Ontario were over 1.0 million chinook salmon and over 0.20 million coho salmon. In 2007, the economic impact of this fishery was $63 million, of which $43 million contributed to local economies of New York shoreline communities. Like all water bodies, Great Lakes ecosystems are under an ever increasing threat from plastic pollution. We sampled microplastics from the stomachs of chinook (n=40) and coho (n=33) salmon from Lake Ontario. Microfibers and micro fragments were recovered from both species, but the overwhelming majority of plastics were microfibers. We used fourier transform infrared (FTIR) spectroscopy to confirm that the microlitter recovered from salmon was plastic, and to identify the types of plastic entering Lake Ontario salmon. Three filament samples were tested using FTIR spectroscopy that produced a spectrum identical to that of a widely used consumer plastic, PET (polyethylene terephthalate). Of the 40 chinook salmon sampled, 92% contained microplastics.

Similarly, 100% of the coho salmon contained microplastics. Larger chinook salmon ingested more microplastics, but no correlation between fish size and plastic ingestion was found with coho. Our data confirm that plastics are found in nearly all Lake Ontario salmon sampled, and that plastics remain in the digestive system of salmon even when individuals are not actively feeding during spawning.

IMPACT OF SLENDER FALSE-BROME (BRACHYPODIUM SYLVATICUM) ON PLANT COMMUNITIES IN NEW YORK STATE. Megan Aubertine and Kathryn Amatangelo The College at Brockport, SUNY 350 New Campus Dr., Brockport, NY 14420 Invasive species disrupt native plant communities, altering patterns of species assemblages. Ecologists use co-occurrence studies to help identify patterns of species assembly in different systems and how invasive species may interrupt these assemblages. Slender false-brome (Brachypodium sylvaticum) is a perennial bunch grass native to Eurasia and North Africa that has invaded ecosystems in the United States and Canada. Little is known about B. sylvaticum and its impact on plant communities. To investigate how this invader disrupts communities, I used co-occurrence analyses to help identify the impacts of B. sylvaticum on native plant communities within New York. At two sites where B. sylvaticum is present, I ran evenly spaced transects with evenly spaced 1 x 1 m quadrats along each transect. In each plot, vegetation was identified down to the lowest possible taxonomic group and I estimated percent cover for each. The vegetation data were analyzed using the Pairs program by putting them into a species presence-absence matrix and calculating C-scores. Of the species pairs found at the two sites, 7 percent were significant at the first site and 20 percent were significant at the second site. Eight pairs were significant at the first site, six of which were disassociations. At the second site, nine out of the fourteen significant pairs were disassociations. These results indicate which species in New York are negatively impacted by the presence of B. sylvaticum and where B. sylvaticum may occur based on the species it is associated with.

EFFECTS OF HYDROLOGY, MANAGEMENT AND PAST LAND-USE ON CARBON AND MICROBIAL COMMUNITIES IN RESTORED WETLANDS. Benjamin Hamilton, Carmody McCalley Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, Rochester, NY 14623 Multiple wetland ecosystem services such as carbon sequestration and nutrient removal are influenced by microbial communities and dissolved organic matter (DOM). We examined DOM composition, carbon metabolism, and microbial communities in three created wetlands to characterize patterns in these factors across created systems. The wetlands have distinct hydrology, vegetation and antecedent land-use, including a gravel mine repository, agricultural field, and cow pasture. Porewater and soil were collected from each wetland in spring, summer, and fall. DOM was analyzed using NMR spectroscopy, soil microbial community composition was analyzed using 16S ribosomal sequencing, and CO2 and CH4 production rates were measured in anaerobic soil incubations. Structural DOM composition varied significantly between the three wetlands but did not vary seasonally. Distinct differences in the microbial community composition of each wetland were shown and phylogenetic differences in microbial community composition appear to be driven by hydrology. Average CH4/CO2 production ratios were approximately 1:1 for all sites in the spring and summer and approached 3:1 in the fall, with no differences in gas production between sites. This suggests that while DOM characteristics and microbial

communities in restored wetlands are impacted by site characteristics, these differences have less effect on carbon metabolism.

EFFECTS OF SURFACE COMPOSITION ON DICTYOSTELIUM ADHESION AND MECHANOSENSATION. Authors: Michelle Urman, Yulia Artemenko Highly motile cells of the Dictyostelium discoideum social amoeba are commonly used as a model system for the study of directed cell migration. Mechanical cues, such as shear flow, can induce directed migration of various cells, including Dictyostelium; however, molecular mechanisms that allow cells to sense mechanical cues are poorly understood. Although integrins have been implicated in mechanosensation, Dictyostelium lacks integrins and attaches to substrate in large part due to non-specific interactions mediated by Van der Waals forces. The purpose of this study was to test whether reducing integrin-independent adhesion of cells to the surface would affect Dictyostelium mechanoresponse. To reduce adhesion of cells we used bovine serum albumin (BSA), which has non-specific binding domains that can interfere with electrical charge interactions that bind the cell to the surface. We evaluated cell mechanosensation by measuring actin polymerization in response to very brief, 2 sec, exposure to shear flow on the surfaces coated with various concentrations of BSA. Mechanical stimulation response of Dictyostelium cells grown on a bacterial lawn, which are known to produce a robust response in this assay, was the same on BSA compared to control coating. Interestingly, when we tested adhesion of bacterially-grown cells, there was no significant difference on BSA compared to the control surface, in contrast to previously published literature. Indeed, standard axenically grown cells on BSA-coated surface showed a significant decrease in adhesion and a corresponding increase in velocity during random migration. These results suggest that cells in different stages of Dictyostelium growth and development respond differently on surfaces of differing chemical compositions. Efforts are currently underway to find surface modifications that reduce attachment of bacterially-grown cells to allow for examination of their mechanoresponse under reduced adhesion conditions.

GENERATING A PIPELINE TO CHARACTERIZE ALLOSTERY IN DHFR, Juan Sepulveda, Previous work introduced allosteric regulation to the metabolic enzyme dihydrofolate reductase (DHFR) by inserting a light sensing domain from plants (LOV2). Through in vivo experimentation, certain amino acid mutants were found to have a profound effect on the light sensitivity of this chimera. In order to confirm these findings, it is critical to characterize these mutants biochemically and through x-ray crystallography. To accomplish this, we developed and refined a set of protocols to produce a large quantity of pure and active chimeric DHFR-LOV2 protein. This necessitated changes to the chimeric. using mutagenic primers and restriction free PCR. Protein purification methods were also optimized by utilizing chemical or sonication means to lyse the cells. Our final protocol incorporated sonication lysis for higher yield, cleavability and protein activity. With our established methodologies we will efficiently create, purify and characterize the mutant constructs. Understanding the impact of these mutations will shed light on how proteins evolve to fine tune allosteric regulation.

Title: ISOLATION AND IDENTIFICATION OF TINEA PEDIS CAUSING DERMATHOPHYTES FROM COLLEGIATE RUNNERS. Authors: Liga Astra Kalnina, Stephanie Guzelak, DPM, Maryann Herman Ph.D. St. John Fisher College, Rochester NY Abstract: Tinea pedis,

also known as athleteâ€™s foot, is a very common superficial cutaneous fungal infection in humans caused by several dermatophytes, especially Trichophyton rubrum, Trichophyton mentagrophytes, and Epidermophyton floccosum. All forms of tinea pedis are pathogenic and are selective symbionts to the soles and toe webs of feet. Within the three forms of tinea pedis there is a varying degree of presentation on the host, from mild scaling and fissures, to vesicles and bullae, or being asymptomatic. Various risk factors contribute to the likelihood of one contracting tinea pedis, especially several factors unique to competitive runners. This includes the use of occlusive footwear, common locker rooms, and submission of feet to constant maceration, trauma, sweating, and having a depressed immune function. Research has shown that runners in particular are twice as susceptible when compared to the general population to have tinea pedis, and the infection is known to infect up to 70% of people worldwide at least once in their lifetime. This is significant because tinea pedis manifestation can become very resistant to treatment or even lead to secondary complications such as cellulitis and onychomycosis and severely impact the performance of runners and athletes alike (4). The dermatophytes found on collegiate runners were collected, isolated, and morphologically characterized in 2014. Isolates will be sequenced to confirm molecular identification and data will be presented in a primary research article.

SURFACE MODIFICATION OF POLYBENZIMIDAZOLE (PBI) WITH UV PHOTO-OXIDATION FOR USE IN HIGH-TEMPERATURE PROTON EXCHANGE MEMBRANE FUEL CELLS (HT-PEMFCS). Devon Shedden, Kristen Atkinson, Ibrahim CissÃª, and Dr. Gerald Takacs Polybenzimidazole (PBI) is a material of interest for various membrane applications. PBI has strong mechanical, chemical, and thermodynamic properties that can withstand the stresses within a High-Temperature Proton Exchange Membrane Fuel Cell (HT-PEMFC). PBI has one major drawback in poor hydrophilicity. Phosphoric acid is used as a dopant to increase the proton conductivity of PBI. This research seeks to modify the surface of PBI to increase phosphoric acid adhesion and therefore boost overall fuel cell efficiency. Ultraviolet photooxidation (UVPO) is one such method shown to form polar oxygenated functional groups that better adhere to the hydrogen of phosphoric acid. Upon treatment, surface modification and hydrophilicity are investigated using X-ray Photoelectron Spectroscopy (XPS), Atomic Force Microscopy (AFM), and water contact angle, among other verification methods. Phosphoric acid adhesion is later verified using Thermal Gravimetric Analysis (TGA).

THE CORVUS CORAX; RELATIONSHIPS WITHIN POPULATIONS. -Catherine Lyke- The Corvus corax, also known as the common raven is a very intelligent species that populates regions in the northern hemisphere. The population of research is located in the Revillagigedo Islands of Clarion and Socorro and Mexico, the C. corax are not a native species in these locations. Mitochondrial DNA is used to dive deeper into the population genetics of the organisms living in these regions. Extractions were completed from 47 C. corax which we then completed Polymerase chain reaction (PCR) and sent the samples for sequencing. These samples were analyzed for similarities and differences within the non-coding region of the mitochondrial genome. Leading to the idea that the C. corax found in these new sampling locations are more closely related to the California clade rather than the Holarctic clade of the C. corax supporting our hypothesis. More data is needed to prove this idea.

EXPRESSION AND PURIFICATION OF APOLIPOPROTEIN E ISOFORMS. Brooke Morrisseau1 and Kestas Benidictas2 1Jephson Science Center, Natural Sciences Division, Keuka College, Keuka Park, NY 14478. 2SUNY Oswego, 7060 State Route 104, Oswego NY 13126. Since the discovery of ApolipoproteinE (ApoE) 4 association with Alzheimerâ€™s disease, many in vitro experiments with ApoE isoforms 2, 3, and 4 have been performed. Alzheimerâ€™s patients with an ApoE 4 gene are known to have an increased concentration of copper and zinc. The ApolipoproteinE isoforms have been hypothesized to have different binding affinities to lead, due to their difference in amino acid sequence. All three ApoE isoform genotypes were expressed in a plasmid vector. The ApoE plasmids were transformed into E.coli cells and IPTG was used to induce expression. The ApoE induced cells were lysed, and partially purified by using Ni- NTA Column Chromatography, C3 Protease and DDT. Here we demonstrate an efficient protocol for the expression of ApoE 2, 3, and 4 isoforms. With large scale quantities of the ApoE pure isoforms, experiments that test the isoforms binding affinities to lead will be later performed. These protocols may facilitate future studies that could potentially make ApoE a biomarker for lead toxicity.

SCALING DOWN WOOD CHIP BIOREACTORS FOR USE IN ROADSIDE DITCHES TO FILTER NITRATE FROM AGRICULTURAL RUNOFF. Steven Dunn and Rebecca Schneider, PhD, (Cornell University, Ithaca NY) and Eric Chase (PA Center for Dirt and Gravel Roads) Nutrient runoff is receiving increased attention nationally, as a potentially key driver that triggers harmful algal blooms in lakes and oceans. In the Midwest, the strategy of capturing agricultural runoff in large, field-scale wood chip bioreactors has proven successful for filtering out dissolved nitrate through microbial denitrification. Our research investigated the potential of using scaled down versions of these bioreactors directly within roadside ditches, which have been shown to efficiently capture and transfer runoff from agricultural fields and septic systems to nearby streams. Two bioreactors, each measuring five meters in length by one meter in width by 0.2 meters in depth, were placed in series in a ditch in rural Bradford County, Pennsylvania in March 2018. Samples of ditch water were collected upstream, downstream, and between the two bioreactors approximately biweekly, and analyzed for dissolved nutrients, pH and electrical conductivity. Dissolved oxygen concentrations dropped incrementally downstream of each of the two bioreactors, a necessity for denitrification and an indication that both bioreactors were functioning similarly. Precipitation and discharge were monitored continuously during the growing seasons of 2018 and 2019. At peak performance, the combination of the two bioreactors removed 100% of the nitrogen load flowing through the ditch, but only during low flows. During higher discharge, water overtopped the bioreactors, bypassing the majority of the filtering system, and much less nitrate was removed. Gradual build-up of sediment and clogging of pore spaces within the woodchip matrix increased the frequency of overtopping. Under appropriate conditions of low flows and minimal sediment loads, use of a series of wood chip bioreactors installed directly within roadside ditches can be an effective, low cost tool for removing dissolved nitrate.

THE COMPARATIVE STUDY OF EGGSHELLS OF PASSERINE BIRDS. Muhammadzohir Hidoyatov, Daniel T. Baldassarre, and Poongodi Geetha-Loganathan* Department of Biological Sciences, 30 Centennial Drive, SUNY Oswego, Oswego, NY 13126 In an

ovipositor egg, all the extracellular matrix layers around the albumen are referred to as the eggshell. Eggshells serve as multifunctional shields for successful embryogenesis, providing protection, moisture control, and thermal regulation. As most of our understanding of avian eggshells come from studies on the domestic chicken, differences in morphology and composition of eggshells of other bird species are been neglected in the literature. Here, we describe the ultrastructure of eggshells of five different Passerine bird species (Order: Passeriformes). Eggshells collected from the Rice Creek Field Station were washed, air-dried and mounted on aluminum stubs with double-sided carbon tape. The shells were then subjected to gold sputter plating followed by imaging using a Scanning Electron Microscope. The thickness of the eggshells was 141.32 Î¼m for House Sparrow, 132.09 Î¼m for American Robin, 106.42 Î¼m for Northern Cardinal, 130.34 Î¼m for Eastern Bluebird and 89.07 Î¼m for Tree Swallow. The basal caps of mammillary bodies of all the speciesâ€™ eggshells were perfectly placed on the eggshell membrane and each tip of the basal caps was attached to the membrane. The membrane of eggshells is composed of an interwoven meshwork of fibers intertwined in all directions that were parallel to the eggshell surface. Our study will provide the first comprehensive analysis on eggshells of perching birds, exhaustive morphological and composition description provide common characters for Passerine eggshells, as well as unique features of each species.

EXPLORING THE EFFECTS OF INVASIVE SLENDER FALSE-BROME (BRACHYPODIUM SYLVATICUM) ON TEMPERATE FOREST ECOSYSTEM PROCESSES. Andrew Leonardi and Kathryn Amatangelo Nonnative plants can impact native plant communities, ecosystem conditions, and ecosystem processes. Slender false-brome (Brachypodium sylvaticum) is a perennial bunch-grass native to Eurasia and North Africa that has invaded the United States and Canada. Environmental conditions such as soil moisture, soil respiration, root biomass, and soil bulk density can be altered by the presence of a monoculture-forming species such as B. sylvaticum. In two forests, I found plots with and without B. sylvaticum that were paired based on canopy type, canopy cover, and slope. In these plots I measured soil respiration, bulk density, and vegetation cover. I also placed probes in a subset of these plots to measure volumetric water content. These parameters were measured to assess the influence of B. sylvaticum on invaded areas and to look for abiotic boundaries that might inhibit further spread. Preliminary results suggest the presence of B. sylvaticum is not the only factor influencing soil moisture. Other factors such as soil type and canopy cover will be measured to determine if the presence of B. sylvaticum has a significant influence on environmental conditions.

ACID WHEY AS A VIABLE FEEDSTOCK FOR SUBMERGED FERMENTATION OF GANODERMA SPECIES.
Harshal Kansara, Sarad Parekh, Christopher Cater, Thomas Trabold and Jeffrey Lodge
Dairy waste pollution is a major challenge New York State faces, of which a subset is waste whey rich in lactose. Fungal species like Ganoderma have a variety of pharmaceutical and health applications, and there has been a growing interest to look at large scale submerged fermentation because of its obvious benefits. The project involved valorizing primarily Greek yogurt whey (40 g/L lactose), by demonstrating the feasibility of propagating 2 species of Ganoderma in shake flasks, a 2L stirred tank reactor (STR) and later scaling up to a 5L STR. Other growth

media evaluated were milk permeate (120 g/L lactose) and goat feta-cheese whey (40 g/L lactose). Initial trials were conducted in 2L STR on standard - lactose, yeast extract (YE), peptone media, then on acid whey, YE, peptone and finally on stand-alone acid whey. Next, the project involved scaling up to 5L STR. HPLC analysis showed a lag phase of 3-4 days (no lactose consumption) between inoculation and start of lactose consumption. The media needed additional nitrogen supplementation to achieve complete lactose consumption. Low cost nitrogen sources were also tested, from which corn steep liquor (CSL) gave the best results. The final media makeup of Greek yogurt whey (Lactose - 40g/L), with CSL (30 g/L),magnesium sulphate (0.5 g/L) and potassium phosphate (1.5 g/L) gave best results with dry mycelium wt. of 6 – 9 g/L after complete lactose conversion.

Title: GENETIC INTERACTION BETWEEN ADHESION REGULATORS RAP1 AND KINASE RESPONSIVE TO STRESS B IN DICTYOSTELIUM DISCOIDEUM Authors: Gengle Niu, Bianca Fernandez, Yulia Artemenko Abstract: Cell adhesion to the substrate influences a variety of cell behaviors and its proper regulation is essential for migration. Social amoeba Dictyostelium discoideum is an extensively and commonly used model organism, whose movement is very similar to that of other amoeboid cells, such as neutrophils and metastatic cancer cells. Although we know many components of the signal transduction network that regulate directed migration, details of the pathways regulating cell adhesion during migration are lacking. Rap1 is a small GTPase that regulates adhesion in Dictyostelium cells in part via its effects on myosin II and talin. Kinase responsive to stress B (KrsB), a homolog of mammalian tumor suppressor MST1/2 and Drosophila Hippo, also regulates cell adhesion and migration, although the molecular mechanism of KrsB action is not understood. Since KrsB has been shown to interact with active Rap1 by mass spectroscopy, we decided to investigate the genetic interaction between Rap1 and KrsB. Cells lacking KrsB have increased contact with the substrate and are difficult to detach from the surface, which leads to reduced movement. Expression of constitutively active Rap1G12V increased cell adhesion, and inactive Rap1S17N reduced cell adhesion even in the absence of KrsB, suggesting that Rap1 does not require KrsB to mediate cell adhesion. However, Rap1S17N reduced cAMP-induced KrsB phosphorylation, whereas expression of Rap1G12V raised basal KrsB phosphorylation, suggesting Rap1 regulates KrsB activation. Surprisingly, chemoattractant-induced activation of Rap1, as assessed by transient cortical localization of the biosensor RalGDS, was impaired in krsBÂ¯ cells, possibly due to increased basal activity of Rap1. Thus, Rap1 appears to activate KrsB, which may function in a negative feedback loop to shut off Rap1 signaling, allowing for precise regulation of cell adhesion during migration.

ROLE OF DIFFERENCES IN CELL MECHANICAL PROPERTIES, VARYING CELL SIZE AND CELL SPEEDS IN SELF-ORGANIZATION OF BINARY CELL POPULATIONS. Peter Letendre We seek to better understand how binary cell populations interact and migrate over a range of time scales. To this end, we stimulate a system consisting of two cell types with varying mechanical properties and cell self-propulsion speeds. In our simulations, we model the two cell types as deformable particles in two dimensions that can propel themselves and interact with neighbors upon contact. We characterize the organization and migration of the system using configuration snapshots, trajectories, and mean squared displacements of the two cell types. Our results will help depict how different Youngâ€™s Moduli, self-propulsion speeds and

varying cell size distributions affect the collective behavior of binary cell populations.

SOLVATION OF PHOSPHONIUM IONIC LIQUIDS IN SUPERCRITICAL CARBON DIOXIDE. Zackary C. Putney and Mark Heitz* Department of Chemistry and Biochemistry, The College at Brockport, State University of New York, Brockport, New York, NY 14420, USA; zputn1@brockport.edu (Z.C.P.) *Correspondence: mheitz@brockport.edu; Tel.: +585-395-5586 We present steady-state and time-resolved spectroscopic data derived from coumarin 153 (C153) in a binary solution of trihexyltetradecylphosphonium bis(trifluoromethylsulfonyl)imide (THTDPSA), tributylmethylphosphonium bis(trifluoromethylsulfonyl)imide (TBMPSA), or trihexyltetradecylphosphonium chloride (THTDPCl) with supercritical CO2 (scCO2). The steady-state excitation and emission peak frequency data in neat scCO2 and IL/scCO2 diverged at low fluid density (Ï□r = Ï□/Ï□c < 1). The prominent spectral differences at low fluid density provided clear evidence that C153 reported different microenvironments, and suggested that the IL is solubilized in the bulk scCO2. Heterogeneity of the C153 microenvironment is readily controlled by scCO2 density. C153 dimers have been reported in the literature and this formed the basis of our hypothesis that dimerization is occurring in scCO2. Time-dependent density functional theory (TD-DFT) electronic structure calculations yielded transition energies that were consistent with excitation spectra and provided supporting evidence for the dimer hypothesis. Time-resolved fluorescence measurements yielded non-exponential decays with time constants that further supported dimer formation. The associated fractional contributions showed that the dominant contribution to the intensity decay was from C153 monomers, and that in high density scCO2 there was negligible contribution from C153 dimers.

PHYLOGENETIC ANALYSYS BY DNA BARCODING OF TWO CLOSELY SPECIES OF LONGHORN BETTLES FROM NY. Luciana Cursino, William Brown and Robert Salerno. Closely related species pose a great challenge for phylogeny reconstruction and species identification using DNA barcoding due to their overlapping genetic variation. In this work we used 56 samples of Anelaphus longhorn beetles from two different but closely related species: A. paralellus and A. villosus. We tested the cytochrome oxidase I barcoding (5P-COI) as a single marker using five different phylogenetic analysis methods, Maximum Likelihood (ML), Maximum Parsimony (MP), Minimum Evolution (ME), Neighbor-joining (NJ) and the Unweighted Pair Group Method with Arithmetic mean (UPGMA). Our results show that a single genetic marker not is sufficient to completely separate these related species in two distinct phylogenetic groups but one of the methods was the most appropriate to separate part of the individuals tested.

A NEWLY DOCUMENTED GLACIAL ADVANCE NEAR THE YOUNGER DRYAS/BOLLING-ALLEROD CLIMATIC TRANSITION, OR GREENLAND INTERSTADIAL (GI-1b), IN WESTERN NY: POTENTIAL IMPLICATIONS FOR THE HISTORY OF GLACIAL LAKES IROQUOIS AND AGASSIZ. Young, Richard A., Department of Geological Sciences, SUNY, Geneseo, NY, 14454 Widespread evidence of an unrecognized late glacial advance that crossed preexisting moraines in western New York is confirmed by 40 radiocarbon ages and several new optically stimulated luminescence (OSL) analyses between the Genesee Valley and the Cattaraugus Creek basin (Buttermilk Creek) of eastern Lake Erie. The Late Wisconsin chronology of the region has long been

inadequately constrained by a lack of dates for moraines between the Pennsylvania border and western Lake Ontario. Few published 14C ages are related to distinct events, unlike the evidence compiled for the upper Great Lakes, Wisconsin, Ohio, and Pennsylvania. The new 14C ages on wood collected from glacial tills in the Buttermilk Creek basin near Springville, NY, and recalibration of numerous 14C ages from earlier investigations in the Genesee Valley document a significant glacial advance into Cattaraugus and Livingston Counties between 13,000 and 13,300 calendar years Before Present (cal yr BP), near the Greenland Interstadial (GI-1b) cold interval leading into the transition from the warmer Bolling-Allerod episode to the Younger Dryas cooling. The chronology from four widely distributed sites indicates that a Late Wisconsin advance through a forested landscape deposited thin glacial till irregularly over the present surface without significantly modifying the preexisting glacial topography. A short-lived advance by a partially grounded ice shelf best explains the evidence. The ice advance, ending 43 km south of Rochester and a similar distance south of Buffalo, overlaps the recently revised age of glacial Lake Iroquois, now considered to have existed from ca. 14,800 to 13,000 cal yr BP. The radiocarbon samples have an age range similar to the famous Two Creeks forest bed, and thus demonstrate that the advance correlates with the well documented Two Rivers advance in Wisconsin. Accordingly, the data provide an important new link between late glacial events in the upper and lower Great lakes. The western NY evidence is also relevant to the proposed alternative drainage routes for glacial Lake Agassiz, especially major meltwater discharge events of interest through the St. Lawrence Valley, the Champlain lowlands, and the Hudson Valley.

BIODEGRADATION OF POLYCAPROLACTONE AND STARCH BLENDED POLYMERS Abigail Rolston Single-use plastics are heavily utilized across many industries. From medicine to food service, plastic is being produced to be used only momentarily, but then to persist for hundreds of years post disposal. To address the environmental havoc caused by plastic pollution, the flow of conventional plastic production needs to be disrupted. If conventional plastics were replaced with biodegradable plastic-alternatives, this would allow for continued use of convenience-based packaging, while also bypassing energy-intensive recycling. However, finding a balance between mechanical function of material and desired biodegradability rates has led researcher to consider a wide array of materials to create these biodegradable materials. Polycaprolactone (PCL) is a polymer with a slow rate of biodegradation. Starch is a natural polymer, a renewable resource, and highly biodegradable. Blended polymer composites were created with varying ratios of PCL and starch content in the Packaging Science Department at RIT by the Diaz-Acosta lab group. To identify the biodegradation rates of these novel composites, soil burial experiments were conducted. Future expansions of this research will incorporate CO2 flask as an additional method of measuring decomposition rates. Disposal environments featuring food waste will also be utilized to explore potential benefits food waste may possess when trying to create a microbial environment to maximize material degradation. Also, microbial cultures of samples will be done to identify microbial groups that are involved in degradation of these specific materials.

UNDERSTANDING MILE-A-MINUTEâ€™S (PERSICARIA PERFOLIATA) PHENOLOGY AND TREATMENT CONTROL METHODS IN WESTERN NEW YORK. Erica Mackey and

Kathryn Amatangelo Department of Environmental Science and Ecology The College at Brockport, State University of New York 350 New Campus Drive Brockport, NY 14420 Invasive species are recognized as a major threat to natural ecosystems and a leading threat to biodiversity. Mile-a-minute (Persicaria perfoliata) has become a serious invasive species in western New York due to its ability to grow up to 15 cm per day, be a prolific seed producer, and its ability to form dense, tangled mats that climb over shrubbery and understory vegetation. The purpose of this experiment was to determine the best management strategy for mile-a-minute and measure the speciesâ€™ phenology and fitness in western New York. Three study sites were chosen in western New York where mile-a-minute had previously been found in 2017 and 2018. In early summer, quadrats were laid on transects and mile-a-minute phenology and cover was recorded. In mid-summer, plots were divided into control, mechanical, herbicide and both herbicide and mechanical treatments and then treated accordingly. Treatment areas were monitored every other week for percent cover, number, fitness, and phenological measurements of mile-a-minute. We predicted that mechanical and herbicide treatments would be equally effective at reducing mile-a-minute cover in treatment plots. Preliminary results show that herbicide is the most effective at killing mile-a-minute and then preventing it from coming back up. For mile-a-minuteâ€™s phenology, preliminary results show that the higher the light there is (% PAR), the earlier this plant will flower which can have a profound effect on when it will then produce seed. Next steps include evaluating how much of the stem left is needed for mile-a-minute to regrow and the timing of when the treatments are implemented.

PREVENTION OF POSTHARVEST DISEASE OF ASIAN PEARS (PYRUS PYRIOFOLIA) USING THE BACTERIAL BIOCONTROLS, PSEUDOMONAS FLUORESCENS AND PANTOEA VAGANS Yaroslav Grynyshyn*1, Ruairi McHugh*1, Morgan Pimm1, Taylere Herrmann1, Daniel Stein2, Maryann Herman Ph.D.1 *Co-first authors 1St. John Fisher College, 3690 East Avenue, Rochester, NY 14568 2Ontario Pear, 1050 Lake Road, Ontario, NY 14519 Fresh produce is susceptible to rot-causing fungi that can infect while growing, at harvest, during handling, storage, transport and marketing, or even after purchase by the consumer. Postharvest produce losses are estimated between 10 to 30% per year, despite use of modern storage facilities, sanitation techniques, and fungicides. Concerns regarding food safety, environmental harm, and fungicide resistance are driving a need for alternative control measures. Biological control (biocontrol), using an organism to suppress damaging activities of another organism, can effectively inhibit growth of postharvest fungi. During the summer of 2017, 256 bacterial strains were isolated and identified from leaves, fruit, and soil of Asian pears (cultivar â€˜Olympicâ€™) at Ontario Pear Farm in Ontario NY. Pseudomonas fluorescens and Pantoea vagans, two known species of biocontrol bacteria, were selected to test control of two prevalent postharvest fungal pathogens, Rhizopus stolonifer and Botrytis cinerea. Biocontrol efficacy was assessed in vivo using Asian pear cultivars â€˜Shinsekiâ€™ and â€˜no known kindâ€™. P. fluorescens and P. vagans effectively controlled both R. stolonifera and B. cinerea, suggesting application of bacterial biocontrol species on Asian pears could reduce fruit losses as from postharvest disease and provide another tool for Asian pear growers in the region.

EFFECTS OF ENVIRONMENTAL MODIFICATIONS ON DICTYOSTELIUM ADHESION AND MECHANOSENSATION. By: Sara Fuller and Yulia Artemenko Dictyostelium

discoideum is a social amoeba used as a model organism to study cell migration. Due to their lack of genes coding for integrin, these cells can adhere non-specifically to a variety of surfaces. The question we are addressing is whether a change in adhesion will make a difference in the ability of D. discoideum cells mechanical stimuli. Due to their non-specific method of adhesion, cells have a reasonable percent adhesion on a non-coated surface, and can respond to a shear flow. We have been studying the effects of Glucose, and Glycine to test whether they alter adhesion, and if so, how that will affect mechanosensation. Sugars and amino acids have been previously shown to inhibit adhesion of D. discoideum. Mechanosensation of cells treated with glucose showed no effect. From there, using axenic cells in an adhesion assay showed no reduction in adhesion. Cells that were grown on Ka though showed a vastly different result to the anexic cells; preliminary evidence suggests that in our assay only addition of glucose or a combination of glucose and glycine, but not glycine itself lowered cell adhesion. In the future, comparing the diameter of cells before and after stimulation and comparing anexic cells to Ka during random migration.

MODIFICATIONS TO THE HOUGHTON XRD. Sarah Olandt and Brandon Hoffman Department of Physics, Houghton College, One Willard Ave Houghton, NY 14744 Modifications have been made to the Houghton College X-ray Diffractometer (XRD) which will be used for analysis of thin films. The Bragg-Brentano theta 2-theta XRD contains a Phillips-Norelco x-ray source powered by a 40 kV power supply. A Vernier student radiation monitor is mounted to a Lin Engineering 101411 stepper motor to collect data that is analyzed using LoggerPro software. Adjustments have been made to the LabVIEW program used to control the stepper motors for the radiation monitor and the thin film sample in order to maintain consistency and accuracy as they rotate along a semi-circular path. Safety modifications have also been completed, including shielding and interlocks for the apparatus to protect the surrounding room as x-rays are directed towards the sample.

INTERFERENCE OF IONIC LIQUIDS ON THE BRADFORD ASSAY: A SPECTROSCOPIC STUDY Tyler Johnston,* and Mark P. Heitz Department of Chemistry and Biochemistry, The College at Brockport, SUNY, 228 Smith Hall, 350 New Campus Drive, Brockport, NY 14420 With the growing popularity of ionic liquids (ILs) for use in industrial applications, these substances are inevitably entering the environment. As these liquid salts become more widely used, it is essential that the interactions between these liquids and biomolecules are characterized. The Bradford assay is a UV-vis absorption method used for protein quantification that relies on the specific interactions between protein and Coomassie Brilliant Blue G-250 (CBBG) dye, which absorbs at 595 nm. Using known protein concentrations to produce a standard curve, unknown protein concentration can be determined. However, the Bradford assay is susceptible to interference from surfactants and other chemical denaturants. The structural similarities between surfactants and ionic liquids (ILs) suggests that ILs may also perturb the accuracy of the Bradford assay. The focus of our study is the spectroscopic measurement of the effects of imidazolium chloride ILs ([Imx,1]+ Cl-, x = 2,6,10) on the Bradford assay. Our results show that in neat IL, there is a systematic increase in the CBBG absorbance at 595 nm indicating that the dye responds to presence of ionic liquid. Additionally, the level of interference was positively correlated to the hydrophobicity of the imidazolium chloride IL. The response of CBBG to both protein and [Imx,1]+ Cl- creates a problem in that the

presence of IL results in a measured protein concentration that appears to be higher than what is actually present in solution.

FINITE ELEMENT ANALYSIS OF FOSSORIAL PYGOPODID SKULLS (GEKKOTA). George Gurgis1, Jennifer Olori1, Juan Daza2, Ian Brennan3, Mark Hutchinson4, and Aaron Bauer5 1Department of Biological Sciences, State University of New York (SUNY) Oswego, NY 2Department of Biological Sciences, Sam Houston State University, TX 3Division of Ecology & Evolution, Australian National University, Australia 4Biological and Earth Sciences, South Australian Museum, SA 5Department of Biology, Villanova University, PA Pygopodids are limb-reduced, miniaturized geckos endemic to Australia and New Guinea. Pygopodids are mainly terrestrial and commonly associated with grass-swimming behaviors; however, Aprasia species are highly fossorial and further miniaturized, converging on similar ecology and morphology to typhlopid snakes. Additionally, Aprasia from eastern/central and western Australia exhibit distinct skull shapes, possibly due to the functional demands of burrowing in different soil types. Another pygopodid genus, Ophidiocephalus, was described as fossorial with morphology most similar to eastern Aprasia species; however, ophidiocephalus more commonly utilizes existing tunnels and thus may experience a different pattern of cranial stress when digging. The burrowing mechanics of pygopodids have never been studied; however, we propose that mechanical stress is distributed outwardly as a shell across the expanded nasals, rather than along an anterior-posterior central column as suggested for other head-first burrowing squamates. To test how differences in morphology may be related to differing functional demands, Finite Element Analysis was implemented by applying and comparing both face loads and point loads of 20N onto 3D solid meshes of the skulls of one eastern/central and one western Aprasia, and one Ophidiocephalus. The resulting stress and strain were low in all taxa and appeared to be evenly spread out across each axis; however, Ophidiocephalus experienced slightly higher average stress than either Aprasia. Although anatomically divergent, each lineage appears to have independently converged on a similar level of biomechanical performance.

TRANSCRIPTOMIC ANALYSIS AND NEURAL TRANSCRIPT IDENTIFICATION IN THE BRITTLE STAR OPHIOPLOCUS ESMARKI. Alexandria Shumway, Hyla Sweet Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, 85 Lomb Memorial Drive, Rochester NY 14623 Ophioplocus esmarki is one species within a family of brittle stars that includes an abbreviated mode of development with a non-feeding, vitellaria larva. This development contrasts to the ancestral mode that produces a feeding, ophiopluteus larva. These two different developmental modes provide an opportunity to compare gene expression and function, with a focus on neural development. This project aims to complete functional annotation of the O. esmarki transcriptome and to provide a comparison of gene expression in both the vitellaria and juvenile stages of development. Illumina sequencing was performed at the University of Rochester Genomics Center. The sequence results were then quality checked and assembled through Trinity, FASTQC, and Trimmomatic tools. Functional annotation was performed using Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and EuKaryotic Orthologous Groups (KOG) tools. The next portion of the research focused on identifying neural transcripts of interest. To begin, candidate transcripts from the model sea urchin, Strongylocentrotus purpuratus, were identified and run against the de novo

transcriptome using a local tblastn search to find similar sequences in O. esmarki. Future work will use this information to show differences in gene expression in both the vitellaria and juvenile nervous systems.

DOES STAKEHOLDER ENGAGEMENT IMPROVE ECOSYSTEM RESTORATION OUTCOMES? Sydney VanWinkle and Christy Tyler Thomas Gosnell School of Life Sciences, Rochester Institute of Technology, Rochester, NY 14623 Ecosystem creation and restoration are increasingly common techniques to replace ecosystem functions and services lost to human development. Project success is typically determined by metrics of ecosystem functionality, measured during a set period following restoration actions. The ecological factors that contribute to the outcome of restoration projects are well studied. However, the role of the local human community is not as well understood. How do the number of stakeholders and their level of involvement affect the success of restoration outcomes? We have qualitatively assessed the role of stakeholders in four restoration projects in the Lake Ontario Watershed to identify relationships between stakeholder involvement and restoration outcomes. Through semi-structured interviews with town engineers, local volunteers, and project leaders, we assessed peopleâ€™s goals and rationales for involvement. These qualitative results will be compared to quantitative ecological measurements of restoration outcomes gathered using a rapid assessment method to determine ecological function, measuring invasive species cover, intended hydrology and plant community composition. The results are then cross examined using an analysis of the intrinsic and extrinsic landscape features in each case study. These features include but are not limited to determining if the sites have public access, how close surrounding human populations reside, whether or not trails exist throughout the sites, and what the siteâ€™s proximity to roads are. These comparisons give a holistic view of how both social and ecological factors impact restoration outcomes.

MCH-MEDIATED EXPRESSION OF CIRCADIAN RHYTHM GENES THROUGHOUT PRE-ADIPOCYTE DIFFERENTIATION Shane Walters and Laurie B. Cook Department of Biology, The College at Brockport, State University of New York, 350 New Campus Drive, Brockport, New York 14420 Melanin-concentrating hormone (MCH) is a hormone known for stimulating appetite. Its effects are most studied in the brain, where it serves as a neurotransmitter, but our lab focuses on its effects in fat cells, particularly its influence over the differentiation process of 3T3-L1 pre-adipocytes. The differentiation of these cells takes ten days, over which MCH has been shown to mediate changes in gene expression. Day 2 is of interest due to the discovery of a primary cilia to which MCHR1 localizes. The data suggests that transcription of certain circadian rhythm genes respond to MCH, which may be a residual effect of its role in REM sleep. This connection may help describe the relationship between sleeping, eating habits, and metabolic efficiency. We aimed to study the regulatory role MCH has in relation to circadian rhythm in fat cells, particularly in the expression of Period genes. Period genes are involved in their own transcriptional regulation, and an increase in expression of these genes results in a shorter cellular rhythm as it is able to suppress itself faster, while a decrease in expression leads to a slower beat and a longer circadian rhythm. On a tissue level, these rhythms are synchronized by a variety of hormones including other appetite related hormones including leptin and ghrelin. MCH is now implicated in this synchronization. Preliminary data focused on Period gene expression at days 0 and day 2 of

differentiation; this study examined Period gene expression out to day 10. Different experiments seem to support different results as well. For example, RNA Seq data says that MCH decreases the expression of Per1, while qPCR in general supports the idea that MCH increases expression of that same gene. This semester, research data suggest that if any changes are occurring at all, they are developmental, or after Day 10. Factors such as the method of detection and low level of basal gene expression may be complicating sensitivity.

POSTER ABSTRACTS

STUDENT LED FABRICATION OF MICROFLUIDIC PETL DEVICES. Alex Martinez, Fabio Sacco and Fernando Ontiveros Biology Department, St. John Fisher College. Microfluidic devices are valuable tools in the fields of chemistry, biology and engineering. Student access to this technology can not only make them aware of it, but may facilitate learning of foundational concepts in the laboratory. Microfluidic devices with different purposes were designed and fabricated by students in a classroom setting. This was achieved using materials and equipment available at office supply stores. One device that was made was able to perform size-based microsphere separation. These devices are a first step towards the ability to separate distinct cell populations in blood, like circulating tumor cells (CTCs). We were able to enrich microspheres similar in size to CTCs. A second device that was fabricated applied controlled mechanical stimuli at the microscale for gene expression studies in Drosophila melanogaster embryos. The last device that was fabricated was used to separate DNA through electrophoresis techniques. It was found that through the use of one 9V battery, separation was achieved in the device. Using PETL methods, devices like these were made by students in a classroom setting and serve a promising role in the future of microfluidic education.

PROTEIN SECONDARY STRUCTURE PREDICTION USING DEEP LEARNING. Tom Mousso and Rongkun Shen Department of Biology, The College at Brockport, State University of New York, Brockport, NY Protein function is solely based on its structure. Although there are multiple experimental approaches to solve protein structure, there is an increasing gap between the number of proteins and the know structures. Computer predictions provides a convenient way to solve proteins when their structures are not available. Within the structure prediction, the secondary structure is crucial for higher level prediction. There have been several machine learning approaches such as classical neural network, nearest neighbor, support vector machines and so on. Our lab used conditional random fields to predict secondary structures and it outperformed all the above methods. Recently, deep learning emerged and performed remarkably well on many tasks including GO game and natural language processing. Since protein secondary structure is a sequential problem for machine learning, the recurrent neural network (RNN) is best suited for this task. We built the position-specific scoring matrix (PSSM) profiles from the published dataset as the input data. We are applying RNN in Tensorflow and Keras as the learning model to predict the secondary structure. We expect that the deep learning approach would improve the prediction accuracy.

INVESTIGATING VOC EMISSONS AS A POTENTIAL MECHANISM OF POLLINATOR PREFRENCE IN SCAEVOLA SPP. Mason J. Awe, Susan Swensen Witherup Floral volatile organic compounds (VOCs) have long been known to have an effect on plant-pollinator interactions, though the scope of understanding has remained limited until recently. With newer technology and analysis techniques, these compound profiles can be more accurately quantified and analyzed. This information can give insight into what gives plants an advantage or disadvantage in attracting pollinators, therefore influencing a plantâ€™s reproductive success. Initial testing examining different color morphs of S. aemula showed no notable differences in volatile profiles between the two, but allowed us to fine-tune collection and analysis procedures. Following this proof-of-concept testing utilizing

S. aemula, we have expanded the scope of this project to analyze this dynamic relationship in the context of two species of Scaevola in Puerto Rico, the native S. plumieri and the introduced S. taccada, which has become invasive. Samples were taken from populations of both species on the island using a volatile collection system and a VOC trap containing a porous absorbent polymer. The samples were analyzed via gas chromatography and mass spectrometry. Analyzing the resulting data qualitatively through gas chromatography has given us a base set of volatile compounds produced by both species to examine further, though no significant qualitative differences have been found. As the project develops further, we will begin analyzing samples quantitatively, which will give us valuable information about how differing VOC profiles might contribute to invasive ability and reproductive success in these two species, and by extension how these patterns may be present elsewhere in nature.

THE NUTRITIONAL QUALITY OF NATIVE AND INVASIVE BERRIES FOR MIGRATORY BIRDS. Authors: Jenifer Rosete*, Victoria Kwasinski*, Erica Delles, and Susan Smith Pagano *Presenting Authors; jxr5567@rit.edu, vak4777@rit.edu Affiliation: Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, 85 Lomb Memorial Drive, Rochester, NY 14623 Migratory songbirds rely on plentiful food resources at stopover sites in order to successfully refuel and complete their long-distance journeys between breeding and wintering grounds. During the fall, native wild fruits provide an important source of nutrition for migrants, but there may be nutritional implications if invasive fruit-bearing plants invade these critical habitats. This project summarizes the nutritional and biochemical characteristics of fruits from several native and invasive plant species found in habitats used by migratory birds in western NY and the Northeast region. We aimed to determine whether invasive fruits will provide adequate nutrition for migratory fueling compared to native fruits. Fruits were collected in autumn at peak ripeness in several locations, frozen until analysis, and then dissected to remove the seeds before freeze drying the fruit pulp and skin. Analyses on the dry mass of fruits included energy density, crude fat content, acid detergent fiber content, and Â°Brix in the juice of whole fruit. We also measured antioxidant capacity and total phenol content in extracts of fruit. There was a possible trend toward lower quality (energy and fat) in the invasive fruits compared to the native fruits in this region. The data suggests that the continued spread of many invasive fruit-bearing plants may decrease the quality of food resources available to birds at important stopover sites.

INVASIVE AND NOXIOUS PLANT DENSITY IS NOT SIGNIFICANTLY CORRELATED WITH BEE ABUNDANCE IN NY ROADSIDE HABITATS. Alyssa Schoenfeldt, Virginia Aswad, Shereef Ghoneim, Debmalya Ray Choudhuri, Kaitlin Stack Whitney Highway roadsides may be a suitable habitat for pollinating insects, as they have a diversity of native wildflowers. Yet roadsides are also disturbed, edge habitats that have been shown to be ideal for invasive plants, which may not provide the same quality habitat as native plants. Our research objective was to examine if the amount of invasive and noxious plants in roadsides was correlated with the abundance of honeybees and wild bees. To test this question, we surveyed plants and pollinating insects along 30 NY highways in 2019, for a total of 160 observations. We used line intercept transects to sample vegetation density and the Xerces Streamlined Bee Monitoring Protocol to sample bees. We hypothesized that sites with more invasive and noxious plants would have lower pollinator abundance. We analyzed wild bee

abundance, honeybee abundance, and total bee abundance as a function of the proportion of invasive/noxious plants in vegetation transects using mixed-effects linear regression. We also examined the contribution of temperature and wind speed to bee abundance. Our results to date do not find a statistically significant association between the amount of invasive/noxious plants and our bee abundance measurements. Understanding the relationship between roadside plants and bee abundance can inform roadside management strategies that aim to help conserve pollinating insects.

EVALUTATING OPTIMAL ENVIRONMENTAL CONDITIONS FOR MILE-A-MINUTE (PERSICARIA PERFOLIATA) GROWTH AND REPRODUCTION. Hannah Schuler and Kathryn L. Amatangelo Mile-a-minute (Persicaria perfoliata), a problematic invasive vine species, has recently been discovered in Western New York, but there is little information available for this species locally. We studied whether mile-a-minute grew better when something was available on which to twine, and how light affected plant growth. Three sections of forest edge at Oak Orchard Wildlife Management Area in Genesee County, New York were selected due to differences in light availability. Five square meter quadrats were placed in each section, and each quadrat was divided in fourths. Each sub-quad was assigned to control or received one of three treatments: â€˜competitionâ€™ (removal of all but three mile-a-minute plants), â€˜stickâ€™ natural or added woody vertical sticks) or â€˜trellisâ€™ (a small garden trellis). Weekly measurements were taken in sub-quads on height, percent cover, herbivory, and phenology of the mile-a-minute over five weeks. We expected plant height and reproduction to be greater in natural or artificial trellis treatments, herbivory to be even, and mile-a-minute to be most successful in sunnier sections. Supporting our predictions, height was greatest in the trellis treatments and percent cover and reproduction were both highest in the sunniest section. However, herbivory damage was greatest in the competition treatments and treatment did not affect flowering. This project adds insight to the question of what affects the growth and success of a new invasive species in Western New York.

VASCULAR PLANTS OF THE GLENNALLEN, AK AREA. Vivian Chappell and James Wolfe Department of Biology, Houghton College, Houghton, NY 14744 Hulten (1968) listed some 1500 vascular plants for the entire state of Alaska, including the Arctic, Aleutian Islands, and Southeast Panhandle. A survey of vascular plants of Mount Fairplay off the Taylor Highway in the Interior by Wolfe et al. (2105) listed 74 species, including those typical of high elevation tundra. We surveyed the Glennallen AK area for vascular plants in the late summer of 2017. Glennallen is located in the Copper River Valley and the junction of the Glenn and Richardson highways, major routes for transportation in southcentral Alaska, and close to the entrance of the Wrangell-St. Elias National Park. Plants readily accessible to these highways were photographed and identified according to Hulten (1968), local keys, and the USDA plant database. Some 120 species in 34 families were found, including such invasive species included oxeye daisy, common dandelion, and butter and eggs (toadflax). Comparatively rare plants such as monkshood, cloudberry and dwarf dogwood occurred in more natural areas with either spruce forest or successional shrub communities. This survey provides some baseline data for local conservation groups and interested tourists traveling through the Glennallen area.

RAS 2019 Abstract 2019 - Poster Title: Anoctamin 1 and mucus secretion in Zebrafish larvae. Authors: Pasoon Ahmad and Adam Rich Address: 350 New Campus Drive, Brockport, NY 14420 Anoctamin 1 is a calcium activated chloride channel that influences membrane potential in gastrointestinal pacemaker cells, total solute transport in epithelial cells, and mucus secretion in the respiratory system in mice. Our goal is to determine if Ano1 functions in zebrafish gastrointestinal mucus secretion. Goblet cells secrete mucins and epithelial cells secrete water, resulting in mucus production. Ano1 is involved in mucin and water secretion. We predict that Ano1 inhibition will reduce mucus secretion. Goblet cells in zebrafish larvae were identified using alcian blue staining and dextran sodium sulfate treatment was used to stimulate inflammation and mucus production. The amount of mucus in zebrafish intestine, as well as the total number of goblet cells will be measured in control, DSS treated larvae, and DSS-treated larvae with Ano1 inhibition. Reduced goblet cells and mucus after Ano1 inhibition will suggest a functional role for Ano1.

IMPROVING VESICULAR STOMATITIS VIRUS AS A CANCER THERAPY: IMPACT OF MUTATIONS IN THE M PROTEIN ON NF-ÎºB ACTIVATION IN VIRUS-RESISTANT PROSTATE CANCER CELLS. Alaa Abdelmageed Ahmed1, Amanda N. Weiss1, and Maureen C. Ferran1. Rochester Institute of Technology, Rochester, NY 14623 Â Â Â To block vesicular stomatitis virus (VSV) infection, the host cell tries to induce expression of the interferon (IFN) protein, which establishes an antiviral state to protect the cell. Our previous work indicates that the VSV M protein evades the IFN response in mouse L929 cells by preventing activation of NF-ÎºB, a transcription factor that is essential for expression of the IFN gene. The IFN pathway is perturbed in the majority of human cancer cells, leaving them susceptible/sensitive to oncolytic (cancer-killing) viruses such as VSV. Since the IFN response remains intact in healthy cells, non-cancerous cells are protected from infection. Unfortunately, some cancer cells are resistant to killing by VSV, likely because portions of the antiviral response remain intact. Therefore, it is important to understand why some types of cancer cells are resistant to VSV infection and to develop recombinant strains of virus that can successfully kill all cancer cells. Similar to our observations in mouse cells, we found that the wild type M protein blocked NF-ÎºB activation in VSV-sensitive human prostate cancer cells (LNCaP). Viruses encoding a mutant M protein activated this transcription factor. The goal of this study was to determine the role of the M protein on killing of VSV-resistant prostate cancer cells (PC3). NF-ÎºB activation in PC3 cells was monitored by immunofluorescence after 0, 4, and 8 hours post-infection (hpi) and at three different multiplicities of infection (MOI). Importantly, we determined that NF-ÎºB is constitutively active in mock (uninfected) PC3 cells. This may explain why these cells have a constitutively active antiviral response and are resistant to oncolytic viruses. In contrast to our results in L929 and LNCaP cells, NF-ÎºB was activated in many cells infected with viruses containing a wild type M protein at 4 hpi. The percentage of cells with activated NF-kB increased further by 8 hpi, and similarly, with higher MOI. Infection with M-mutant viruses did not result in significant nuclear localization of NF-ÎºB at 4 hpi, however the number of cells exhibiting NF-kB activation did increase slightly by 8 hpi. Real Time PCR will be used to determine if NF-ÎºB activation correlates with the production of IFN mRNA in VSV-infected LNCaP and PC3 cells.

Examination of Cell Signaling in gef-Mutant Zebrafish William Meyer, Rico Amato, Elena Kleinhenz, and Travis J. Bailey Ph.D. The zebrafish good effort (gef) mutation

results from a 3 base pair deletion in exon 3 of the gene chaf1b, which codes for a histone loading protein. After a period of normal development, retinal progenitor cells (RPCs) which normally differentiate into the different cells of retina begin to die resulting in stunted eye development. Some hypothesize that this is caused by activation of the tp53 pathway leading to apoptosis. However, previous studies in the Bailey laboratory suggest that this may be an incomplete mechanism of cell death. We hypothesize that the cell death seen in gef-mutant zebrafish results from faulty signaling pathways leading to RPCs not receiving signals to differentiate. After a period of limbo, apoptosis is initiated. To test this hypothesis, we performed fluorescent in-situ hybridization for genes corresponding to proteins cell differentiating signaling pathways to determine if these pathways are impaired by the gef mutation.

Molecular Cloning of Dictyostelium discoideum Î±-Actinin Stephanie Arcello & Yulia Artemenko Cells can directionally migrate in response to a variety of cues, including mechanical stimuli such as shear flow. Dictyostelium discoideum is a social amoeba commonly used for the study of directed cell migration. Actin cytoskeleton appears to play a key role in the response to shear flow, although how this mechanical stimulus is perceived and transmitted is not known. This led us to question whether actin crosslinking proteins, such as Î±-actinin, can be involved. We hypothesized that when Î±-actinin is removed, Dictyostelium cells will not respond to mechanical stimulation as well as cells with Î±-actinin. To test the response of cells with and without Î±-actinin in mechanosensation, we will express mCherry-tagged Î±-actinin or empty vector in Î±-actinin-null cells. Efforts are currently underway to generate an expression vector with mCherry-tagged Î±-actinin. The Î±-actinin gene has been amplified successfully by PCR, and both the PCR product and the vector have been digested with appropriate restriction enzymes and ligated. We are currently screening for potential positive clones. Once molecular cloning of the new Î±-actinin plasmid is complete and the cells are successfully transformed with the plasmid, we will begin testing their response to mechanical stimulation. Examining cellular response to brief mechanical stimulation using Dictyostelium cells will aid in understanding the originating actions necessary for shear flow-induced motility.

THE GENETIC MANIPULATION OF FULL-LENGTH AND TRUNCATED VAN GOGH GENE. Jenna Baer and Huey Hing, The College at Brockport The establishment of cell orientation and differentiation influencing tissue and organ development is determined by Planar Cell Polarity (PCP) signaling in an organism. PCP plays a role in the orientation and development of bundles of neural circuits contained within glomeruli in the olfactory bulb of the brain in Drosophila. Working along with PCP, Wnt is a signal gradient that induces orientation of developing structures. In our current research, we aim to understand the importance of PCP component genes Van Gogh (Vang) and Derailed (Drl). Vang is a 4-pass-transmembrane protein located on the presynaptic axon, and Drl is a receptor tyrosine kinase located on the postsynaptic dendrite. Our previous studies have shown that glomeruli containing neural connections with only Vang are repelled to the PCP-Wnt gradient, inducing a repulsion rotation of those glomeruli. Glomeruli that contain neural connections with both Vang and Drl are in contrast attracted by the PCP-Wnt gradient, inducing an attractive rotation of those glomeruli. The resulting antagonistic interaction leads us to believe that Drl inhibits Vang function. To investigate the mechanism by which Drl inhibits Vang, we have used Crispr/Cas9

technology to create truncated versions of the Drl and Vang proteins. This process resulted in the insertion of an eye marker which had to be excised. In this report we describe the excision of the eye marker using genetic crosses followed by confirmation using molecular techniques. Further testing will be done to analyze the functions of the truncated Vang and Drl proteins in neural circuit development, once the excised eye marker has been excised.

EXPRESSION AND FUNCTIONAL CHARACTERIZATION OF GALECTINS 1 AND 3 IN A SODIUM-TRANSPORTING MOUSE EPITHELIAL CELL LINE. Kourtney Baker, Bernardo Ortega Department of Biology, The College at Brockport, State University of New York; 350 New Campus Drive, Brockport NY 14420 The sodium channel (ENaC) mediates sodium reabsorption through epithelia. A family of extracellular proteins named galectins, have been proposed to help retain ion channels at the cell membrane. Using a specific inhibitor, here we investigate if Galectin 1 (Gal-1) and Galectin 3 (Gal-3) could be involved in retaining ENaC at the apical membrane of the ENaC-expressing mpkCCDc14 cell line. This knowledge may help identify a new target for inhibiting ENaC expression at the plasma membrane.

EFFECTS OF THIORIDAZINE ON CAPSULE FORMATION IN THE FUNGAL PATHOGEN CRYPTOCOCCUS NEOFORMANS. Sean Carrigan, Virginia E. Glazier, PhD Niagara University The fungus Cryptococcus neoformans has the capability to be pathogenic with life threatening effects to individuals with a compromised immune system. In resource limited countries, there is a greater need for affordable yet effective drugs that treat C. neoformans because of the high rates of infection due to immunocompromising infections such as HIV/AIDS. Repurposing a drug that has already been approved by the FDA not only saves money as these drugs are off-patent, it also saves time trying to discover a new drug that would have to go through FDA regulations before it is safe for human use. Drugs such as Thioridazine have been identified to have antifungal effects in previous studies, however their mechanisms of action are still not clear. We have found that thioridazine appears to influence capsule formation, a key component in Cryptococcus neoformans pathogenesis.

EFFECTS OF CARBON DIOXIDE ON DRUG SUSCEPTIBILITY IN CRYPTOCOCCUS NEOFORMANS AND CANDIDA ALBICANS. Kristen N. Donovan, Virginia E. Glazier Niagara University Cryptococcus neoformans and Candida albicans are fungal pathogens capable of causing life threatening infections in humans. The morbidity and mortality risks of these fungi have made the need for more effective and affordable treatments of high global importance. We are interested in the effects of carbon dioxide on two already used antifungal drugs, fluconazole and caspofungin. We are examining fluconazole susceptibility in C. neoformans and C. albicans and caspofungin susceptibility in C. albicans. The effectiveness of fluconazole and caspofungin were tested under high carbon dioxide conditions because both of these pathogens can be found the lungs where CO2 levels are high. We hypothesize that carbon dioxide will enhance the efficacy of fluconazole and caspofungin. In order to determine the effects of CO2 on drug activity, MIC, FIC and e-test results were be compared at 37Â°C, or at 37Â°C in the presence of CO2. Observing effects under these conditions will lead to a deeper understanding of how physiologically relevant conditions adjust the functions of antifungals. This information will be

helpful in the development of better treatment options for C. neoformans and C. albicans.

MUTATIONAL POSITIONING WITHIN THE N-TERMINAL DOMAIN OF Î’-ACTIN AS A CONTRIBUTING FACTOR IN DIFFUSE LARGE B-CELL LYMPHOMA (DLBCL) PATHOGENESIS. Alexander Ille*, Hannah Lamont*, John Fischer Dâ€™Youville College, 320 Porter Ave, Buffalo, NY, 14201, U.S.A. *Co-first authors ABSTRACT Diffuse large B-cell lymphoma (DLBCL) is the most prevalent type of non-Hodgkinâ€™s lymphoma in adults. DLBCL can present with either a singular enlarged mass or dissemination at multiple sites. Exome screening of patients with DLBCL identifies a specific pattern of Î²-actin gene mutations localized in the N-terminal domain. In humans, Î²-actin is a cytoskeletal protein involved in intracellular signaling, cellular motility, and focal adhesion. These attributed functions garner interest in the various mechanisms by which Î²-actin is involved in oncogenicity. The N-terminal domain of Î²-actin normally interacts with various co-translational and post-translational processing enzymes. The absence of these interactions results in various cytoskeletal abnormalities, including an increase in the ratio of filamentous to globular actin, increased filopodia and lamellipodia formation, and accelerated cell motility. Here we employed computational modeling to explore variation between wildtype Î²-actin and mutant variants of Î²-actin as documented in DLBCL. Methods used for computational modeling include both homology-based and ab initio structural prediction. Our results reveal remarkable N-terminus irregularity in DLBCL mutant variants of Î²-actin, accompanied by irregular hydrogen bonding with N-terminal processing enzyme NAA80. Furthermore, mapping of these variants demonstrates their mutational position is within the N-terminal Î²-sheet.

CHARACTERIZATION OF NOVEL STAPHYLOCOCCAL BACTERIOPHAGE. Manpreet Singh, Christopher Clark, Rachel Wager, and Mark Gallo, PhD. Niagara University Staphylococcus aureus can cause a number of diseases, with one of the major concerns being methicillin-resistant Staphylococcus aureus (MRSA). Today, the main treatment for MRSA is to use antibiotic drugs. MRSA is difficult to treat due to the lack of effective antibiotics against this pathogen. An alternative is to use bacteriophage to control Staphylococcus. A number of novel phage have been isolated from the nares of white tail deer, Odocoileus virginianus. Recent DNA sequence analysis indicates that they belong to the Siphoviridae family. This research explores the host range of these phage against strains of Staph.

ISOLATION OF BACTERIOPHAGE AGAINST STAPHYLOCOCCUS. Hannah Fahs, Alexus Okun, and Mark Gallo, Ph.D. Niagara University Bacteriophage, otherwise known as bacterial viruses or phage, infect bacteria and in some cases can kill the host. There is the possibility to use phage when treating bacterial infections, as many bacteria have become resistant to nearly all known antibiotics and hence are ineffective. One agent in particular, MRSA (methicillin resistant Staphylococcus aureus), can produce particularly damaging infections, oftentimes leading to death. This research will analyze primary samples isolated from white tail deer, Odocoileus virginianus, to search for phage that are capable of killing S. aureus.

SEARCHING FOR ENZYMES TO PRODUCE UNIVERSAL O TYPE BLOOD. Jesse Kozub, Jeff Sommerfield, Jiyeon Ryu, Molly Balbierz, Amanda Belmona, Pavel Kovtunov and

Mark Gallo, Ph.D. Niagara University Blood transfusion is a medical procedure that is vital to modern medicine. Although the procedure is very common there are certain considerations that may prevent the timely administration of donor blood to a patient. The main obstacle is the compatibility of blood type. This results from the presence of sugars on the surface of the blood cells that are responsible for its antigenic properties. These sugars distinguish the three blood types as A, B, and O. Given that these sugars on the blood cells itself are the cause of this incompatibility, it is proposed that by removing these sugars that a universal blood could be produced. This research involves the identification of potential enzymes for this process and strategy for cloning the genes and expressing in E. coli.

NOVEL LONG NON-CODING RNA DETECTION FROM RNA-SEQ DATA. Peter Giangrasso, Laurie Cook, and Rongkun Shen Department of Biology, The College at Brockport, State University of New York, Brockport, NY Long non-coding RNAs (lncRNAs) are transcripts with more than 200 nucleotides that are not translated into proteins. LncRNAs play important roles in many biological processes and disease progression. Since most lncRNAs have poly(A) tails, they are sequenced by regular mRNA-Seq along with the transcripts of coding genes. In this study, we use the RNA-Seq data from mouse 3T3-L1 preadipocyte cells to detect novel lncRNAs that have not been annotated. Two novel lncRNAs have been identified from our data manually, located at chr15:90882505-90883884 and chr15:64068336-64069062. We are employing the Tuxedo suite to align the RNA-Seq reads to mouse mm10 (GRMC38) assembly with the guidance of mouse GENCODE annotation. Meanwhile, we allow Cufflinks (part of Tuxedo suite) to detect the more novel transcripts. The coding potential for each novel transcript will be assessed using Coding-Non-Coding-Index (CNCI), Coding-Potential-Assessing-Tool (CPAT), Coding-Potential-Calculator (CPC) and PhyloCSF. The remaining novel lncRNA candidates will be validated using real-time qPCR. We hope to discover more novel lncRNAs involved in adipogenesis. In the future, we will also design and implement machine learning approach to predict novel lncRNAs in the genome.

MOLECULAR CLONING OF TRUNCATED FILAMIN CONSTRUCTS LACKING KEY REGULATORY DOMAINS.
Colin Harrington and Yulia Artemenko
The model organism Dictyostelium discoideum is commonly used to study directed migration because it shares many similarities with mammalian cells, yet is easier to handle and manipulate genetically. Filamins are large actin binding proteins that stabilize three-dimensional actin webs and link them to cellular membranes. Filaminâ€™s Actin Binding Domain (ABD) and the Dimerization Domain (DD) work together to ensure filamin binding and cooperation on the cellular cytoskeleton. It is currently unknown how D. discoideum will respond to mechanical stimulation if a construct was developed without their Actin Binding Domain and Dimerization Domains. It is currently known that without the ABD, filamin will not be able to bind to the actin Without the DD, filamin will not be able to dimerize together. Preliminary evidence from our laboratory suggests that filamin may be required for the cellâ€™s ability to respond to mechanical stimulation by shear flow. To understand how filamin is involved in sensing mechanical stimuli, we will be generating filamin constructs without the ABD or without the DD. D. discoideum cells lacking filamin will then be transformed with mCherry-tagged filamin without

ABD or DD. The constructs will then be assessed for their ability to respond to mechanical stimuli. The cloning of the two constructs is ongoing.

IDH1 AS DNA DAMAGE RESPONSE REGULATOR IN HIGH CYCLIN E HIGH-GRADE SEROUS OVARIAN CANCER. Qingyuan Jia1,2, Erika S. Dahl1, Kelly E. Leon1, and Katherine M. Aird1 Cellular and Molecular Physiology, Penn State College of Medicine, Hershey, PA1 Department of Biology, University of Rochester, Rochester, NY2 Ovarian cancer is the most lethal gynecological malignancy. High grade serous ovarian cancer (HGSOC) is the deadliest histological subtype of ovarian cancer. The oncogene CCNE1 (encoding cyclin E) is amplified or overexpressed in approximately 20% of HGSOC patients and is correlated with reduced overall survival. Overexpression of cyclin E in fallopian tube (FT) cells, the proposed cell-of-origin of HGSOC, is an initiating event that contributes to the pathogenesis of HGSOC. Previous reports have demonstrated that overexpression of cyclin E increases DNA damage response (DDR) gene expression. Up-regulation of the DDR may allow for these cells to tolerate the replication stress and DNA damage induced by cyclin E, which would lead to transformation and tumorigenesis. However, the molecular mechanism by which cyclin E-high cells upregulate DDR gene expression remains unclear. We previously published that the TCA cycle enzyme, wildtype isocitrate dehydrogenase I (IDH1) is critical for the proliferation of HGSOC cells with high cyclin E. Additionally, we observed a correlation between high cyclin E status and IDH1 expression in both HGSOC cell lines and patient samples from The Cancer Genome Atlas (TCGA). IDH1 overexpression phenocopied cyclin E overexpression in DDR genes, including the homologous repair protein BRCA2. Here, we aimed to determine whether cyclin E is upstream of IDH1 and the subsequent role of IDH1 in regulating the DDR in cyclin E-high HGSOC cells. Towards this goal, we knocked down cyclin E using shRNA in Ovcar3 HGSOC cells, which have high cyclin E expression. Knockdown of cyclin E decreased both IDH1 and BRCA2, suggesting both proteins are downstream of cyclin E. To further demonstrate that cyclin E cells rely upon IDH1 activity for proliferation, we knocked down cyclin E in Ovcar3 cells and subsequently treated them with an IDH1 inhibitor (IDHi) to test colony-forming ability. Cyclin E-high cells were more sensitive to IDH1 inhibition than cells with low cyclin E, further confirming cyclin E-high cells depend on IDH1 for proliferation. Next, to determine whether increased IDH1 is necessary for limited DNA damage upon cyclin E expression, we stained for Î³H2AX and 53BP1, markers of DNA double-strand breaks, in cells with cyclin E overexpression with or without knockdown of IDH1. As expected, we observed an increase in Î³H2AX and 53BP1 foci in cyclin E overexpressing cells. Interestingly knockdown of IDH1 further increased Î³H2AX and 53BP1 foci, suggesting that IDH1 is critical for repairing DNA DSBs in cyclin E overexpressing cells. Together, our data suggest that IDH1 downstream of cyclin E plays a critical role in the homologous repair of DNA and is essential for proliferation of these cells. HGSOC patients with high cyclin E are homologous repair proficient, and therefore resistant to DNA damaging agents in the clinic. Thus, targeting IDH1 in cyclin E-high HGSOC patients may be an effective therapy in combination with DNA damage agents for this patient population.

INVESTIGATION OF A COMPOUND TO POTENTATE TOPOISOMERASE 2 POISON ACTIVITY. Joseph Karboski, Deanna Berg, William DePasquale, Jonelle Mattiacio, and Jonathan Millen Topoisomerase 2 (Top2) is an enzyme essential to relieve strain in DNA while it is being unwound in preparation for replication. Doxorubicin, a

commonly used chemotherapy agent, is a known topoisomerase 2 poison which interferes with transcription to cause cell death. We discovered that a compound (X1) works to increase the potency of Doxorubicinâ€™s cytotoxic effect in cancer cell lines. In-vitro this compound increased the cytotoxicity of Doxorubicin on in S. cerevisiae (yeast) and in a human fibrosarcoma cell line (HT1080). Quantification was completed by visualization in yeast growth assays and by the survival assays in the cell line. Increasing concentrations of the compound in the presence of Doxorubicin, decreases cell viability in a concentration-dependent manner.

TITLE: GENETIC SCREENING FOR NOVEL PARTNERS OF AN ADHESION REGULATOR - KINASE RESPONSIVE TO STRESS B (KRSB) AUTHOR: Ali Khan, Swin Ratnayake, Yulia Artemenko ABSTRACT: Dictyostelium discoideum social amoeba is a well-established model organism for the study of amoeboid-type migration, which is the type of movement seen in neutrophils and metastatic cancer cells. Cycling between active and inactive forms of the serine/threonine kinase responsive to stress B (KrsB), a homolog of mammalian tumor suppressor MST1/2 and Drosophila Hippo, contributes to the dynamic regulation of cell adhesion that is needed for proper cell adhesion and chemotaxis in D. discoideum. However, the exact mechanism by which KrsB affects the cellâ€™s ability to adhere is unclear. The goal of this project is to find new regulators or effectors of KrsB using a genetic suppressor screen. Cells lacking KrsB were transformed with a cDNA library and mutants that exhibited either a rescue or an enhancement of the original phenotype were isolated. Cells lacking KrsB have a distinct phenotype when they form plaques on a bacterial lawn, with an enlarged region of cells in streams and an uneven expanding front of vegetative cells, which makes krsBÂ¯ plaques appear to have rough edges. During the first round of screening, 150 plaques were identified, 48 of which showed a phenotype that was different from krsBÂ¯: 30 plaques had smooth round edges similar to wild-type or cells rescued with KrsB, and the rest had phenotypes that differed from krsBÂ¯ or wild-type cells, such as plaques that completely lacked aggregating cells. Thus, the first round of screening demonstrated that the cDNA library may provide genes that can compensate for the lack of KrsB. Efforts are underway to expand our collection of mutants and to isolate plasmids with the cDNA library inserts to identify the genes responsible for the rescue of the krsBÂ¯ phenotype or for making the phenotype more severe. Identification of these genes will give us a better understanding of the molecular mechanism of KrsB function in cell adhesion and migration.

DETERMINING THE SIGNIFICANCE OF THE MICOS PROTEIN COMPLEX ON THE FREQUENCY OF SPONTANEOUS CELLULAR RESPIRATION LOSS IN SACCHAROMYCES CEREVISIAE. Skyler LaCoss and Rey Sia The mitochondria are essential organelles to the survival of cells due to their important role in cellular respiration. Mitochondria have their own set of DNA (mtDNA), which encodes proteins needed for the execution of successful oxidative phosphorylation. One of these gene complexes, known as the MICOS complex, contains six genes and is responsible for encoding proteins needed for the maintenance of the inner architecture of the organelle. Oxidative phosphorylation is only possible due to the proton gradient that is produced across the inner mitochondrial membrane. The MICOS gene complex encodes proteins that facilitate the building of the inner and outer membranes of the mitochondria, as well as the cristae junctions, which are required for a sufficient rate of cellular respiration. The lab has developed a set of mutant strains that each

represent a single gene knockout from the MICOS complex. Specifically, the mic19Î” mutant strain will be compared against the wild type strain, MIC19, in a respiration loss assay to develop an understanding of the significance of the MICOS complex on cellular respiration. Rich growth media containing dextrose as the carbon source were used to monitor spontaneous respiration loss in both the MIC19 and mic19Î” strains. When plated using dextrose as the sole carbon source after growth on glycerol media, the mic19Î” strain demonstrated an increase in cellular respiration loss compared to that of the wild type. This shows that Mic19p plays a significant role in maintaining a functional mitochondrion.

ACTINOMYCIN-D INDUCES APOPTOSIS IN HELA CERVICAL CANCER CELLS. Kalya Lilly, Anthony DiCecca, Logan Slother Eric Benfey, and Dr. Robert Greene Niagara University, NY 14109 Cervical cancer is the fourth most prevalent variety of cancer found in women worldwide. Cervical cancer arises from abnormal cell growth in the cervix. Treatment of the HeLa cervical cancer cells line with Actinomycin-D directly stimulates apoptosis. Actinomycin-D is a chemotherapy medication produced from Streptomyces parvullus which inhibits transcription by binding DNA at the transcription initiation complex and prevents elongation of the RNA chain by RNA polymerase. We treated HeLa cervical cancer cells with Actinomycin-D to better understand the mechanism for how induces apoptosis. Various concentrations of Actinomycin-D were used to determine the most effective apoptotic treatment for the HeLa cells. The treatments were performed for 24 hours and then analyzed for efficacy. We also treated HeLa cells over the course of 72 hours using a single concentration to determine the effectiveness of Actinomycin-D over an extended treatment time. Future research could be performed using Actinomycin-D in conjunction with phototherapy to more effectively induce apoptosis in cervical cancer cells.

DNA Damage-specific Regulation of Cell Cycle Checkpoint by Î³-H2AX Zhengfeng Liu and Xin BiÂ Â Â Â Â DNA lesions trigger the activation of DNA damage checkpoints (DDCs) that stop cell cycle progression and promote DNA damage repair. Î³-H2AX is an early chromatin mark induced by DNA damages such as double-stranded DNA break (DSB) that is recognized by a group of DDC and DNA repair factors.Â As such, Î³-H2AX has long been believed to promote DDC and DNA repair. However, our lab recently made the surprising discovery that Î³-H2AX have a DNA damage-specific roles in DDC. We further found evidence suggesting that Î³-H2AX regulates DDC and DNA repair by mediating the competitive recruitment of DDC mediator Rad9 and DNA repair factors to sites of DNA damage.

EFFECT OF THE FDA APPROVED DRUGS THIORIDAZINE AND TRIFLOUROPERAZINE ON VIRULENCE AND HOST TEMPERATURE ADAPTATION IN CRYPTOCOCCUS NEOFORMANS. Megan E. McGraw, Virginia E. Glazier, PhD Biology Department, Niagara University Cryptococcus neoformans is a fungal pathogen that targets individuals with compromised immune systems. In resource limited countries such as Africa, the rate of infection is high due to the large number of the population who have HIV/AIDS. C. neoformans infects and kills about 500,000 individuals every year. Due to this, there is a great need for effective and affordable drugs to treat C. neoformans. Repurposing drugs that have been approved by the FDA saves time and money that would go into discovering new drugs that would later have to be determined safe for humans. Previous studies have identified several FDA drugs

that have been shown to kill C. neoformans, specifically two antipsychotic drugs, Thioridazine hydrochloride and Triflouroperazine. We speculate that drugs that have both antifungal activity and target known virulence factors would be better able to treat C. neoformans infections than drugs with antifungal activity alone. Therefore, to determine the potential of certain FDA approved drugs as C. neoformans treatment options, their effects on C. neoformans virulence factors was observed. We are looking at growth at both 30 and 37 degrees Celsius after treatment with thioridazine hydrochloride and trifluoperazine. Both in vitro and in vivo trials are studied to see the effect that the growth rate and virulence of C. neoformans. The in vivo trials are performed in larvae of Galleria mellonella which are known biological model for fungal infections.

FECAL MAGNESIUM EXCRETION REMAINS STABLE UPON DSS INDUCTION OF ULCERATIVE COLITIS IN MAGNESIUM-DEPRIVED MICE. Emily Odell, Bernardo Ortega Department of Biology, The College at Brockport, State University of New York; 350 New Campus Drive, Brockport NY 14420 Ulcerative colitis (UC) is an inflammatory disease of the colon. Magnesium (Mg) waste is common in UC, and Mg deficiency has been found to exacerbate inflammation in UC patients. Dietary Mg deprivation may affect UC patients by triggering a systemic proinflammatory state, or by limiting the Mg available to the bacteria located in the lumen of the gastro intestinal tract. Studies on UC are often performed using mice treated with the Dextran Sodium Sulfate (DSS). However, in this model, intestinal bleeding may contribute to increasing luminal Mg, thus hindering the reliability of this model. Here we show that fecal samples from mice fed a Mg-deficient diet, and treated with a 0.5% DSS solution to induce UC, have no higher Mg content than fecal samples from DSS-untreated animals. Thus, a mouse DSS UC models constitutes a valid tool in order to investigate the contribution of dietary Mg to UC.

EFFECTS OF SULOCTIDIL AND THIORIDAZINE ON BIOFILM FORMATION IN CANDIDA ALBICANS. Julia Rak and Virginia E. Glazier, PhD Niagara University Candida albicans is an opportunistic pathogen capable of growing both as yeast and filamentous cells. While residing harmlessly as a commensal in the gastrointestinal tracts of most humans, C. albicans maintains responsibility for >50% of all systemic fungal infections. C. albicans possesses the ability to initiate hyphal growth; a virulence a factor that allows for the penetration of tissues, colonization of organs, and formation of biofilms. Eradication of these biofilms significantly reduces the pathogenic effects of C. albicans, and the goal of our research is to repurpose FDA approved drugs for the treatment of candidiasis. Our findings indicate that treatments with Suloctidil (a peripheral vasodilator) and Thioridazine (an antipsychotic) both show reduction C. albicansâ€™ ability to form biofilms. Here we provide evidence that both drugs have the potential to be used in the eradication or prevention of candidiasis in high-risk individuals.

ANOCTAMIN 1 EXPRESSION IN ADULT ZEBRAFISH RED BLOOD CELLS Porshya Shani Kithsiri, Keri Furness, Skyler Lacoss, Jenna Baer, and Adam Rich Background: The overarching goal for our Group is to determine if Anoctamin 1 (Ano1), a calcium activated chloride channel, is expressed in zebrafish red blood cells (RBC). We hypothesize that Ano1 contributes to pH and volume regulation in RBC. Further understanding the role for Ano1 in RBC will contribute to our overall understanding of pH and volume regulation in human RBC and may contribute to finding cures for

pathologies associated with RBC. Aims: The overall goal for our Group is to determine if ANO1 is expressed in adult zebrafish red blood cells. The goal for our Team is to isolate blood from adult zebrafish, develop blood smears, identify different cell types, and to use immunohistochemistry to probe for Ano1 expression. Experimental Approach: Blood was obtained from adult Zebrafish, cell density was determined using a hemocytomoeter, and blood smears were prepared. Cell morphology was determined using a Wright-Giemsa Stain. Anti-Ano1 antibody will be used on acetic acid- ethanol fixed blood smears to determine Ano1 expression. Results: We can isolate approximately 10 Âµl from one adult zebrafish. It was necessary to add heparin to prevent immediate clotting. A 1:4 dilution with 0.9X PBS and 0.5 mM EDTA was used to avoid blood clotting, and to obtain a suitable cell density for blood smears. Conclusion: Wright Giemsa staining has been inconsistent preventing morphological characterization of zebrafish blood cells. Experiments are underway that will refine the protocol. In addition, experiments to identify Ano1 expression with anti-Ano1 antibodies are planned.

ANOCTAMIN 1 EXPRESSION IN ZEBRAFISH PRIMITIVE AND DEFINITIVE RED BLOOD CELLS Cassandra Jackson, Kristen Sacchitella, Thzin Say, Mckenzie Tu, and Adam Rich Department of Biology, The College at Brockport, Brockport, NY Background: Anoctamin 1 (Ano1), a calcium activated chloride channel, is well known for its role in the gastrointestinal tract, insulin secretion, saliva production, smooth muscle contraction in the airway and the reproductive tract, and in neurons involved in sensory signal transduction. We hypothesize that Ano1 is present in zebrafish primitive and definitive red blood cells (RBCs). Zebrafish and human RBC are similar and zebrafish have been used as a model for human diseases. Aims: The overall goal for our group is to determine if Ano1 is expressed in zebrafish RBCs. The goal for our team is the to determine if Ano1 is expressed in both primitive and definitive zebrafish red blood cells during early zebrafish development. Methods: Zebrafish red blood cells were collected by mashing larvae of different ages ranging from 2dpf to 12dpf, in a glass well plate in a minimal volume of 0.9X PBS with 0.5mM EDTA. Additional PBS EDTA was added and the suspension was filtered using a 40 Âµm nylon mesh. Centrifugation allowed the zebrafish embryonic cells and blood cells to separate from the tissue by spinning at high and low speeds. Pellets were re-suspended in small volume of PBS EDTA and stained with the Wright-Giemsa stain. Smears were examined under the microscope. Results: Very few blood cells have been identified in smears and separating blood cells from tissues has been inconsistent. Next Steps: Collecting blood from zebrafish embryos and larvae using methods in published reports has been unsuccessful. New experiments will focus on using a transgenic fish line that expresses red fluorescent protein in blood cells so that we can visualize the cells in each step. We plan to use the Wright-Giemsa stain to differentiate and visualize cell morphology. After successful blood smears are made will use immunohistochemistry to visualize Ano1 expression.

EXPRESSION OF ANO1/TMEM16A IN ZEBRAFISH HEMATOPOITIC CELLS Solan Sooriakumar, Bohdan. Smich, Mathew Borrelli, Cody Compton, Adam Rich Department of Biology Sciences, The College at Brockport SUNY Background: Anoctamin 1 (Ano1) is a voltage-sensitive calcium-activated chloride channel that is expressed in smooth muscle and epithelial cells. The function of Ano1 is well documented for these tissues and has roles in epithelial chloride secretion, volume regulation, and membrane potential regulation. Based on the observation of a

transgenic Ano1-knockout zebrafish we hypothesize that Ano1 may also be expressed in zebrafish erythrocytes. The expression and function of Ano1 in zebrafish erythrocytes as well as human erythrocytes is currently unknown. Aims: The overall Group goal is to identify the presence of Ano1 in zebrafish erythrocytes. Our teamâ€™s specific objective is to identify when Ano1 is expressed in cells during hematopoiesis in adult zebrafish. Experimental Approach: The kidney was dissected from adult zebrafish and pulverized through a nylon mesh filter to dissociate the tissue and release hematopoietic cells. Cells and tissue debris were separated using a centrifuge. An improvised, 3D printed, cytospin-like apparatus was developed to deposit a concentrated monolayer of cells onto a slide. Cells were identified after a Wright Giemsa stain. Results: Isolation of hematopoietic cells from kidney tissue has been inconsistent, leading to large amounts of debris in blood smears. Conclusion: We are continuing to refine our protocol to isolate hematopoietic cells from the cellular debris. Our efforts are focusing on â€˜trackingâ€™ the hematopoietic cells through multiple centrifugation steps to optimize washing cells from tissues. Next steps include using immunohistochemistry with anti-Ano1 antibodies to determine Ano1 expression. We also plan to use transgenic Ano1 Knockout animals that express red fluorescent protein in place of Ano1.

THE ROLE OF ARF6 IN MCH MEDIATED ACTIN REARRANGEMENTS IN 3T3-L1 PRE-ADIPOCYTES Bohdan Smich and Laurie B. Cook Department of Biology, The College at Brockport, State University of New York, 350 New Campus Drive, Brockport, New York 14420 Obesity has become a pandemic in our society. One potential method to alleviate this crisis is the use of pharmaceutical therapy to manage how our bodies metabolize the energy that we consume. The pathways involved in the motility of pre-adipocyte cells are important in understanding how our bodies interpret and react to specific biochemical signals. Our laboratory is focused on a pathway that activates the expansion and migration of pre-adipocytes. Melanin-concentrating Hormone (MCH) is a neuropeptide that is known for regulating appetite and metabolism within adipocytes through the G protein-coupled receptor, MCHR1. MCHR1 is known to act through a Gq pathway to rearrange actin. Our proposed pathway is that MCHR1 activates ARNO, a guanine nucleotide exchange factor, and Arf6, ADP-ribosylation factor 6, in succession resulting in destabilized actin in murine 3T3-L1 pre-adipocytes and increased motility. A pharmacological inhibitor of Arf6, NAV-2729, was used to determine if Arf6 was indeed a downstream signaling component in this pathway. Fluorescence microscopy was used to visualize the actin stress fibers and morphology of the cell and a scratch wound assay was performed to determine if the migration rate was affected. Preliminary results from our fluorescence stain show that the structure of actin was affected by NAV-2729 after MCH addition.

DETERMINING EFFECTS OF MELANIN-CONCENTRATING HORMONE ON INSULIN-SIGNALING PATHWAY COMPONENTS. Dayanara Torres and Laurie B. Cook Department of Biology, The College at Brockport, State University of New York, 350 New Campus Drive, Brockport, New York 14420 Itâ€™s well known that appetite is hormonally controlled, however, a link between appetite- stimulating hormones (like MCH) and the regulation of glucose uptake by cells is unclear. Preliminary observations in our lab suggest a connection between melanin-concentrating hormone (MCH) signaling and GLUT4 translocation to the plasma membrane in

adipocytes. We explored the connections between MCH signaling and GLUT4 translocation in 3T3-L1 adipocytes treated -/+ MCH and insulin using two techniques; immunofluorescence microscopy and a glucose-uptake assay. Immunofluorescence microscopy was used to track GLUT4 glucose transporter location in these cells. NIH ImageJ, fluorescence intensity line scans were then generated to discern differences across treatments. Data suggests that MCH facilitates GLUT4 translocation to the plasma membrane when co-treated with insulin, but not on its own. Glucose uptake assays measured the fluorescent intensities of tagged glucose molecules entering adipocytes. In these experiments, MCH diminished insulinâ€™s ability to increase glucose uptake by these cells, however these experiments did not reach statistical significance. In conclusion, we explored the potential effects of short-term MCH signaling on insulin-mediated GLUT4 translocation in adipocytes and determined there to be no discernable effect. There is a possibility that long-term sustained MCHR1 activation may influence the insulin pathway and although there was no statistically significant change there still might be an MCH effect which could be due to glucose movement via a different glucose transporter but this remains to be investigated.

EFFECTS OF VITAMIN-D TREATMENT ON MCF-7 LUMINAL BREAST CANCER CELLS. Amanda Ventrella, Audrey Dunn, Eric Benfey, Dr. Robert Greene Niagara University, NY, 14109 Breast Cancer begins when the cells in the breast tissue begin growing uncontrollably, forming a benign tumor and eventually spread and grow enough, turning into a malignant tumor. There is growing evidence that treatment of the MCF-7 luminal breast cancer cells line with Vitamin-D directly stimulates apoptosis. Vitamin-D is a fat-soluble vitamin that can be obtained from the diet, as well as a seco-steroidal prohormone that is produced in the skin by UV-light. However, the precise mechanism of Vitamin-D-induced apoptosis on Breast Cancer cells is still poorly understood. To better characterize this effect, we treated MCF-7 cells with 100nM vitamin-D and assessed the degree to which vitamin-D induced apoptosis over 8 hours. We also exposed vitamin-D treated MCF-7 cells to UV for 30 minutes, and assessed whether that affected the rate of apoptosis. We found that while MCF-7 cells treated with vitamin-D underwent apoptosis over the course of 8 hours, those treated with UV and vitamin-D were more quickly and severely apoptotic.

TROPHIC CASCADES AND AERATION IN LAKES: EFFECTS ON WATER QUALITY AND ZOOPLANKTON COMMUNITY STRUCTURE. Katelyn Brown, Dan Beers, Isidro Bosch, and Michael Chislock. This study focused on the effects of three installed aeration devices in Lake Lacoma, a small, hypereutrophic lake in western New York. Artificial aeration is predicted to â€˜trapâ€™ phosphate in sediments by creating an oxygenated environment from the surface to the bottom of the lake. A hypothesized indirect effect of aeration is facilitation of large-bodied zooplankton by creating a cold, well-oxygenated deep refuge from potential fish predators. It was found that phosphorus concentrations remained high over the summer months; however, the zooplankton community had increased in response to aeration.

FIVE NEW PARASITOIDS AND COMMENSALS OF THE OAK TWIG PRUNER BEETLE, ANELAPHUS PARALLELUS. Jesse Freeling Brundage, William Brown, and Luciana Cursino (Advisor) Keuka College, Division of Natural Sciences and Mathematics Keuka Park, NY 14478 Oak twig pruner beetles (Anelaphus parallelus (Newman); Coleoptera: Cerambycidae) spend the majority of their two-year lifecycle as wood

boring larvae. Commensal arthropods may inhabit the twig hollowed out by the larva and parasitoids may develop on or within a larva, eventually killing it. This study compiled known parasitoid and commensal associations of A. parallelus and identified new associations based on DNA barcoding of emerged specimens acquired in Pennsylvania and New York from 2010 to 2018. Associated parasitoids in Braconidae (Hymenoptera), Ichneumonidae (Hymenoptera), and Tachinidae (Diptera) were previously described. Here, we sequenced the mitochondrial COI-5P region of 28 samples for DNA barcoding and constructed a molecular phylogenetic tree of the results. We corroborated previously described associations and identified five new commensal or parasitoid associations with A. parallelus, mostly at species level, using BLASTn (â‰¥90% identities) and BOLD ID (â‰¥97% similarity): Hymenoptera: Messatoporus compressicornis (Ichneumonidae), Xylophrurus fasciatus (Ichneumonidae), Ancistrocerus adiabatus (Vespidae), Epistenia coeruleata (Pteromalidae); and Diptera: Dexiinae sp. (Tachinidae).

Title: Assessing the toxicity and burial of microplastics in freshwater lake sediments Authors: Kristina Chomiak, Matthew Hoffman, Nathan Eddingsaas, and Christy Tyler Abstract. The mass production of single-use plastics and microplastics has led to increased plastic waste entering landfills and water bodies. In aquatic ecosystems, accumulations of these materials can present lethal or sublethal impacts on organisms. Recent models of plastic movement in the Great Lakes predict that certain plastics sink to the bottom sediments where their fate is unknown. This contamination poses a risk to benthic invertebrates that are the key drivers of ecosystem function with potential impacts at both the organismal and ecosystem levels. At the same time, invertebrates have potential impacts on the movement of microplastics in the benthos. Bioturbating invertebrates play a key role in the burial and resuspension of sediments and organic matter, suggesting the potential to translocate plastic particles and impact their ultimate fate. This study uses Lumbriculus variegatus, an important freshwater ecosystem engineer, as a model organism. We use standard toxicological experiments to assess lethal and sublethal impacts of microfibers and measure the role of L. variegatus in the burial and resuspension of microfiber particles. Our findings suggest significant mortality and sublethal impacts at high densities of microfibers, and that the toxicity may be driven in part by the presence of dyes. We also demonstrated that L. variegatus rapidly buries polyester microfibers, leading to permanent removal from the pelagic ecosystem. These reciprocal interactions are a key component to achieving a more complete understanding of transport, impact and fate across the microplastic life cycle in the environment.

USE OF FILAMENTOUS BACTERIAL GROWTH ON STREAM MACROINVERTEBRATES AS AN INDICATOR OF NUTRIENT ENRICHMENT. Madelynn Edwards, The College at Brockport Non-point source pollution from fertilizer runoff has had a significant impact on the quality of the waterways in the US. Increased nitrogen and phosphorus levels in waterways can have long-term, negative impacts on aquatic life, including macroinvertebrates. Previous studies suggest that the presence of filamentous bacteria (Leptothrix spp. and Sphaerotilus spp.) on macroinvertebrates is directly related to nutrient enrichment in streams and could be used as a bioindicator for water quality. The objectives of this study are to (1) investigate differences in the density and biomass of macroinvertebrates in nutrient enriched and non-enriched streams in western New York and (2) determine if there is a

relationship between nutrient concentration and bacterial coverage in Odonata and Plecoptera. Three enriched and three non-enriched streams were sampled for macroinvertebrates and nutrient concentrations during summer 2019. In addition, bacteria were cultured from enriched sites to determine growth rate in response to the addition of compounds containing P, N, and NaCl. There was no significant difference in the number of insects infected with bacteria between the enriched and non-enriched sites. N concentrations were significantly greater at the enriched sites ($p = 0.013$). P concentrations did not differ between the groups. Initial lab experiments on bacterial growth in response to differing nutrient concentrations suggest the absence of N hindered growth. This preliminary information will be used to inform future sampling and microcosm experiments.

Title: Methane Emissions from Stormwater Ponds Authors: Brianna Pollard, Carmody McCalley Thomas H. Gosnell School of Life Sciences Rochester Institute of Technology Rochester, NY 14623 Abstract: Methane (CH_4) is a powerful greenhouse gas that has a global warming potential 28 times larger than carbon dioxide (CO_2) on a 100-year horizon. Methane emissions from inland freshwater sources are not as well understood than those from other natural sources; however, current estimates suggest that they account for a significant portion of global CH_4 emissions, releasing more than 103 Tg of CH_4 per year. Emissions from inland waters are difficult to measure due to their high spatiotemporal variability, leading to high levels of uncertainty and a need for more CH_4 flux data from these freshwater systems. Increased runoff associated with urbanization has led to construction of man-made inland waters called stormwater ponds. Methane emissions estimates for stormwater ponds are very limited and are therefore typically excluded from global methane budgets. In order to reduce the uncertainty in global CH_4 budgets and to understand how urbanization is impacting greenhouse gas emissions, there is a need to characterize CH_4 emissions from stormwater ponds. High temperatures associated with thermal pollution coupled with high nutrient and sediment inputs suggest that stormwater ponds could potentially support high rates of methanogenesis. We used bubble traps to quantify CH_4 emissions from five stormwater ponds in Henrietta, NY. Stormwater ponds released on average 347.3 mg CH_4 m^{-2} d^{-1} during the growing season and emissions showed strong spatial and temporal variability, suggesting that pond characteristics and weather patterns play an important role in determining emissions. Future work to quantify sediment and water chemistry as well potential CH_4 production and oxidation rates will help identify key drivers of observed CH_4 emission patterns across ponds.

ABUNDANCE OF MICROPLASTICS IN THE SOUTHERN TRIBUTARIES SEDIMENTS OF LAKE ONTARIO. Cameron Snell, Tammy Bleier, and Michael Chislock. The focus of my project is microplastics in sediments of southern Lake Ontario Tributaries (Oak Orchard River to Irondequoit Creek). There is extensive research on microplastics in open water of the Great Lakes, but only one on the sediments. Microplastics float, so studies are done on the surface; however, it is believed that the longer they are in water they grow a film due to algae. This film may cause them to sink leading to a miscount of microplastics. I have taken samples from multiple locations using a dredge and have used density separation to remove all organic matter and identify the microplastics.

Title: The Influence of Herbivory on Submerged Macrophytes and Nitrogen Retention in Created Wetlands. Evan N. Squier, Kimberly A. Lodge, Delanie Spangler, Christy Tyler, Carrie McCalley, and Nathan Eddingsaas Wetlands are frequently created for nutrient removal and improvement of water quality. However, wetlands are complex systems and the abiotic and biotic interactions that determine functionality are not fully understood in natural wetlands, and even less so in created wetlands. This may lead to shortcomings in meeting desired restoration outcomes. Herbivory is an important indirect control on nutrient cycling and other biogeochemical processes in wetlands through top-down controls. Herbivores can significantly decrease plant biomass and community structure, potentially altering nitrogen immobilization by plants, denitrification, nitrogen fixation and regeneration of inorganic nutrients in the sediments. Caged and uncaged plots were established in two created wetlands in Western New York State, and the impact of grazer exclusion on vegetation community structure and nitrogen cycling processes assessed. Herbivores, predominantly waterfowl, selectively removed emergent vegetation, leading to significantly higher submerged macrophyte cover in uncaged plots where light availability was greater. Potential denitrification was enhanced in the absence of grazers where emergent plants dominated, perhaps due to increased organic matter availability. We hypothesize that enhanced nitrogen fixation and benthic nitrogen release in uncaged plots may exacerbate the negative influence of grazers on nutrient removal capacity. Our results suggest that control of large grazing waterfowl in created wetlands will enhance nutrient retention and removal services and improve downstream water quality.

THE IMPACT OF HERBIVORE EXCLUSION ON METHANE EMISSIONS IN WETLANDS Briana Stringer, Carmody McCalley, Christy Tyler, Delanie Spangler, Kimberly Lodge, Ben Hamilton, Evan Squier Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, Rochester, NY 14623 Wetlands provide ecosystem services but are threatened by urbanization, prompting the need for created wetlands. Replicating the functions of natural wetlands has proven difficult and created wetlands often have lower plant diversity and productivity. This study explores the implementation of herbivore exclusion as a management approach in a created wetland in Western, NY. Changes in carbon gas fluxes were quantified in plots with and without the influence of large grazers. In-situ measurements of methane (CH_4) and carbon dioxide (CO_2) fluxes were quantified, soil incubations quantified anaerobic CH_4 and CO_2 production potentials and rates of CH_4 oxidation, and a clipping mesocosm quantified grazers impact on plant-mediated transport. Herbivore exclusion resulted in a net increase in summertime CH_4 emissions, despite no change in production potential and a trend towards higher potential oxidation rates. This suggests that high plant biomass during the summer growing season facilitates efficient transport of CH_4 to the atmosphere and impacts the role of oxidation of CH_4 in sediments. Clipping mesocosm results support the important role of plant-mediated CH_4 transport. These results suggest that grazers play an important role in wetland vegetation dynamics and shift greenhouse gas emissions in wetlands.

OPTIMIZING GROWTH CONDITIONS FOR BIOMASS AND LIPID ACCUMULATION IN C. REINHARDTII. Natalie Guzelak and Noveera Ahmed There is a rising discrepancy between the availability of renewable fuel sources and the rate at which they are

being used. Fossil fuels are under scrutiny for the significant amounts of environmental pollution that they produce, unpredictable prices and lack of sustainability, therefore, microalgae are being examined for their potential as biofuel reserves. The unicellular alga Chlamydomonas reinhardtii, in particular, has been evaluated for its potential use as a sustainable biofuel due to its relatively high lipid concentrations. C. reinhardtii will produce and store lipids in response to stress conditions and disruption of the starch biosynthesis pathway. We are exploring media additives that will increase biomass by increasing both the growth rate and longevity of C. reinhardtii while also maximizing lipid accumulation. Nile red dye was used to visualize neutral lipid content in three strains of C. reinhardtii using fluorescent microscopy and quantified by image analysis under several growth conditions. The conditions with the highest yield can then be used to grow C. reinhardtii as an inexpensive and easily replenished biofuel source.

RV1700 ADP-RIBOSE HYDROLASE FROM MYCOBACTERIUM TUBERCULOSIS. Nana Aikins, Thomas Hynes, Cassi Martin, Kevin Oâ€™Donovan and Suzanne F. Oâ€™Handley School of Chemistry and Materials Science, Rochester Institute of Technology, Rochester, NY Mycobacterium tuberculosis (Mtb) currently infects ~1/4 of the worldâ€™s population, kills ~1.5 million annually, and there are many highly antibiotic-resistant strains, thus investigating potential novel antibiotic targets is essential. We have been systematically discovering the activity for and characterizing the Nudix hydrolases from Mtb as potential drug targets due to their ability to hydrolyze important metabolites. One Nudix hydrolase from Mtb that we have been studying is the ADP-ribose hydrolase Rv1700. ADP-ribose can spontaneously modify macromolecules; uncontrolled ADP-ribosylation due to excess ADP-ribose is detrimental to the cell, and thus Rv1700 may help control this process. It has been reported that ADP-ribose hydrolases confer tellurite resistance to cells. Thus far we have been able to show that E. coli containing a plasmid producing another ADP-ribose hydrolase (MJ1149) from the archaea Methanococcus jannaschii can grow in higher levels of tellurite than the E. coli alone, similar to what has been determined by others previously. Currently, we are testing to see if this is also true for Rv1700 from Mtb. and Orf209 from E. coli, to show that Rv1700 has the same activity in vivo as other ADP-ribose hydrolases, and thus we may be able to use tellurite resistance as a phenotypic marker for ADP-ribose hydrolase activity in vivo.

TYPE OF HOST PLANT DOES NOT INFLUENCE HORIZONTAL TRANSFER OF Wolbachia sp. TO OAK TWIG PRUNER LARVAE Sarah Bresette, William Brown and Luciana Cursino (Advisor) Jephson Science Center, Natural Sciences Division, Keuka College, Keuka Park, NY 14478. Insects may acquire intracellular symbionts, such as the bacteria Wolbachia sp., from plant hosts. Our goal was to test whether the type of host plant would play a role in horizontal transference of Wolbachia sp. in larvae of A. parallelus, the oak twig pruner beetle (Cerambycidae). Larval A. parallelus from red oak twigs (Quercus rubra) were removed and reintroduced into pre-drilled black walnut (Juglans nigra) or red oak twigs and stored in mesh bags for six months. Similar methods were followed for larvae collected from black walnut. One leg was collected from each of the 108 adult A. parallelus that emerged and DNA was extracted from leg tissue. The presence of the conserved wsp gene was used to identify the presence of Wolbachia sp. End-point PCR was then performed using WSP_F1 and WSP_R1primer. Wsp obtained PCR products (602 bp) were

electrophoresed, sequenced and aligned to construct an unrooted phylogenetic tree. Forty total specimens (11 from the oak to oak treatment, 11 from walnut to oak, 9 from oak to walnut, and 9 from walnut to walnut) tested positive for Wolbachia sp. and belonged to the same strain, regardless of the host plant. These results suggest there is no correlation between type of host plant and transmission of Wolbachia sp. in A. parallelus.

COMPARATIVE BIOFILM ANALYSIS OF OTITIS MEDIA OTOPATHOGENS BETWEEN PH 7.0-8.0. Andreia Cadar, Vincent Darmohray, Diksha Thakkar and Robert Osgood Middle ear infections (otitis media) are common, affecting over 22 million people in the United States annually. These infections frequently become chronic due to the biofilm growth by the organisms that initiate the infections. In effect, these biofilms serve as a barrier between the infection and the treatments provided. As a model to further explore biofilm growth under environmentally germain conditions, an epithelial cell line, D562 has been conditioned to grow in liquid cell culture conditions that mimic the middle ear for further exploration. We hypothesize that the formation of biofilms produced in the middle ear is caused by the adhesion of bacteria to cells in the middle ear during infection conditions. Experiments include the introduction of Streptococcus pneumoniae (S.pn) and Moraxella catarrhalis (M.cat) into pH adjusted cell culture media for a short period of time to investigate their potential to form biofilm. A combination of a live/dead stain and confocal microscopy are then utilized in order to comparatively investigate density, composition and other structural characteristics of the biofilm at pH points of 7.2 and 8.0. This insight will allow us to compare biofilm formation under clinically relevant pH conditions and better understand the favorable conditions for biofilm formation of the different bacteria. Genomic DNA and total RNA will be isolated for use in subsequent gene expression analysis. The analysis is needed to understand which genes are expressed exclusively under pH 8.0 versus the pH value of 7.2. This can further help us understand which genes may be relevant for biofilm formation for some strains under given pH conditions. This information is needed for consideration of the changes that are taking place in the epithelial cells that have been conditioned to grow at pH 8.0 versus 7.2. Our intention is to highlight changes in the bacteria that may be useful as potential targets for treatment of chronic middle ear infections.

THE QUEST TO COMBAT ANTIBIOTIC RESISTANCE: ISOLATION, SEQUENCING, AND ABRIBACTERIAL PROPERTIES OF RIT452. Nicole Cavanaugh, Anutthaman Parthasarathy, Narayan Wong, KayLee Steiner, Megan Hallenbeck, and AndrÃ© O. Hudson Bacteria are becoming resistant to the antibiotics that were historically effective in clinical settings. The goal of this study is to identify bactericidal/bacteriostatic compounds produced by bacteria isolated from the environment. We have employed bioprospecting approaches to identify unique bacteria from the environment. The variable 3 (V3) regions of the 16S rDNA were amplified using polymerase chain reaction (PCR) followed by nucleotide sequencing. A selection of these unique isolates were subjected to whole genome sequencing using the Illumina MiSeq sequencer including the strain RIT452. RIT 452 was shown to produce a variety of secondary metabolites in addition to bactericidal compounds. Disk assays were employed to test the inhibitory effects of organic compounds isolated from RIT452 against other bacteria. Fractions were collected

using FPLC chromatography to facilitate the identification of the compound/s that are responsible for the antibiotic effect.

OPTIMIZING GROWTH CONDITIONS FOR BIOMASS AND LIPID ACCUMULATION IN C. REINHARDTII. Natalie Guzelak and Noveera Ahmed There is a rising discrepancy between the availability of renewable fuel sources and the rate at which they are being used. Fossil fuels are under scrutiny for the significant amounts of environmental pollution that they produce, unpredictable prices and lack of sustainability, therefore, microalgae are being examined for their potential as biofuel reserves. The unicellular alga Chlamydomonas reinhardtii, in particular, has been evaluated for its potential use as a sustainable biofuel due to its relatively high lipid concentrations. C. reinhardtii will produce and store lipids in response to stress conditions and disruption of the starch biosynthesis pathway. We are exploring media additives that will increase biomass by increasing both the growth rate and longevity of C. reinhardtii while also maximizing lipid accumulation. Nile red dye was used to visualize neutral lipid content in three strains of C. reinhardtii using fluorescent microscopy and quantified by image analysis under several growth conditions. The conditions with the highest yield can then be used to grow C. reinhardtii as an inexpensive and easily replenished biofuel source.

Isolation, Sequencing, and Antibacterial Properties of Paraclostridium sp. Isolated from Soil. Megan Hallenbeck1, Jonathan Chu1, Narayan Wong1, Anutthaman Parthasarathy1 and AndrÃ© O. Hudson1 Bacteria are becoming increasingly more resistant to current antibiotics. The overarching goal of this project is to identify new antibacterial compounds produced by bacteria isolated from the ecological niche of fruit trees on campus, specifically crab apples (both fruits & root zone soil). The bacteria were cultured on agar media and isolated by established microbiological methods. The variable 3 (V3/V4) regions of the 16S rRNA were amplified using polymerase chain reaction (PCR) followed by nucleotide sequencing. Isolates belonging to less common genera were subjected to whole-genome sequencing using the Illumina MiSeq sequencer including RIT 636 (Paraclostridium sp.). RIT 636 was shown to produce various secondary metabolites, including some with antibacterial properties. Disk diffusion assays were used to test the inhibitory effects of organic compounds extracted from the spent medium of RIT 636 against other bacteria. Fractions were collected using reverse phase chromatography to facilitate the identification of compound/s that are responsible for the antibiotic effect.

PHENOTYPES OF NUDIX HYDROLASES Nicolette Kulakowski, Sakinah Abdul-Khaliq, Cara Jones, Luiza Bianco, Thomas Hynes, Colleen Kane, and Suzanne F. Oâ€™Handley Enzymes of the Nudix Hydrolase superfamily are characterized by the ability to hydrolyze substrates containing nucleoside diphosphate linked to some moiety x, hence the acronym Nudix. We are systematically analyzing the E. coli Nudix hydrolase knockouts for phenotypes. MutT is an established antimutator, and we have determined that the other Nudix hydrolases from E. coli are not antimutators. Complementation studies with Nudix hydrolases from M. tuberculosis are being carried out to determine which, if any, are antimutators. Currently we are screening the E. coli Nudix hydrolase knockouts for antibiotic susceptibility.

ISOLATION, WHOLE- GENOME SEQUENCING AND CHARACTERIZATION OF QUORUM-SENSING SIGNAL PRODUCTION IN A POISON IVY BACTERIAL ENDOPHYTE. Trevor S. Penix, Peter C. Wengert, Narayan H. Wong, and Michael A. Savka The Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, 85 Lomb Memorial Dr, Rochester, NY 14623 In the microscopic world, group coordination is a fundamental part of life for many different bacterial species. By communicating and working together, they are able to perform various feats which enable them to survive and thrive in challenging environments. Such feats include the formation of biofilms, the production of toxins, and even the generation of light. This is all mediated by a communication process known as quorum-sensing (QS). This study focuses on a specific class of QS communication signal known as the acyl-homoserine lactones (AHLs). More specifically, this work investigated the structure and synthesis of AHL class QS signals from a strain of endophytic bacteria isolated from poison ivy (PI) vine. The isolate, named PI-S, was whole genome sequenced and identified as Pseudomonas cichorii using the JSpecies platform. Using the antiSMASH platform, the QS signal synthase (luxI) gene was identified and cloned into expression vector pSRKKm. AHL signal separation and detection was performed on PI-S extract using reverse-phase thin layer chromatography in combination with the AHL-sensitive biosensor strain NTL4(pZRL4). PI-S was found to produce at least two different QS molecules. Future work will focus on determining the structure of the signals produced by PI-S bacterial endophyte.

Fish gut microbes: Phylogeny & morphology of Epulopiscium spp. C and J morphotypes Alejandro B Schmieder, Esther R Angert Epulopiscium spp., and related bacteria known as â€˜epulosâ€™, are large, highly polyploid heterotrophs that are morphologically diverse. Additionally, epulos are gut symbionts of surgeonfish and likely influence the digestion of their surgeonfish hosts. Certain surgeonfish host distinct groups of these giant bacteria, and while some Epulopiscium spp. are well-characterized (e.g., the A and B morphotypes), there are several morphologies that we can better understand. For instance, the Cs and Js are fascinating because of their sporulation abilities, reproductive strategies, and morphological diversity; however, the C and J morphotypes are challenging to collect and, thus, little data has been generated on their morphology or genetic information. This research seeks to better understand the diversity of the C and J morphotypes found in surgeonfish hosts Naso lituratus and Naso unicornis. The objectives of this research are twofold: (1) to characterize populations of the C and J morphotypes from N. lituratus and N. unicornis samples from Australia through 16S rRNA gene survey data, and (2) to further investigate the distribution of these morphotypes (and phylogenetic subtypes) in surgeonfish using 16S rRNA probes. We have found that N. lituratus and N. unicornis host different epulo populations. Additionally, epulo phylogeny is determined by morphotype, their host, and the location the host was collected. Overall, the knowledge obtained through this project will help broaden our understanding of epulo morphologies among related fish, to understand the global distribution of epulos, and to provide insight into complex host-microbe systems.

IDENTIFICATION OF AN RNA MODIFICATION ENZYME IN TRYPANOSOMA BRUCEI William C. Schultz, Xiane L. Smith, Cassandra C. Taber, and Kevin T. Militello State University of New York at Geneseo, Department of Biology RNA methylation is a type of posttranscriptional modification that plays an important role in controlling

gene expression. The organism Trypanosoma brucei, the protozoan parasite responsible for Human African Trypanosomiasis, does not seem to have abundant promoter regions or transcriptional regulation machinery. Thus, RNA methylation may play an especially important role in regulating gene expression in this organism. We have identified the presence of 5-methylcytosine in T. brucei RNA using both mass spectrometry and sodium bisulfite sequencing. Recently, we have identified seven putative cytosine RNA methyltransferase (CRMT) genes in T. brucei. All seven CRMTs are expressed in bloodstream and procyclic form parasites, as detected by qRT-PCR. One of the putative CRMTs, termed CRMT5, is required for maximum parasite growth. Although we suspect these genes to be RNA methyltransferases, we do not have evidence for RNA methyltransferase activity. CRMT5 was expressed in E. coli with an N-terminal 6x-histidine tag and purified using a His-affinity column. Purified CRMT5 was used in a series of methyltransferase assays using luciferase activity as a readout. CRMT5 addition resulted in luciferase activity in the presence of cytosine-containing RNA (T. brucei total RNA and Poly-IC RNA). There was little to no luciferase activity observed in the presence of RNA that lacks cytosine or when a mock purification from E. coli without the CRMT5 gene was used. To further our evidence, a CRMT5 mutant was created changing a putative active site cysteine to alanine (C439ðŸ¡ªA). We expect the mutant to show reduced luciferase activity in the methyltransferase assay. Our next step will be to perform a methyltransferase reaction with CRMT5 and subsequently isolate the RNA for bisulfite sequencing to confirm the methylation of cytosine bases. Evidence for the presence of 5-methylcytosine and RNA methyltransferases indicates the presence of a process to create an epitranscriptome in T. brucei.

INVESTIGATING THE LOCALIZATION OF PSEUDOMONAS AERUGINOSA NARG AND NARH USING FUSION PROTEINS. Jaya Manjunath, Jordan McDonald, Melina Recarey, and Johanna Schwingel, PhD Department of Biology, St. Bonaventure University, St. Bonaventure, NY Pseudomonas aeruginosa is a gram-negative bacterium that is involved in biofilm production, which affects immunocompromised individuals such as those with Cystic Fibrosis and burn victims. The nitrate reductase complex used for anaerobic respiration supports robust biofilm development. The nitrate reductase complex components include NarG and NarH which have previously been shown to be associated with the membrane. We aimed to create NarG-GFP and NarH-GFP fusion proteins to serve as controls for future study. The fusions were constructed by overlap extension (SOEing) PCR, ligated into an E. coli vector and transformed into E. coli. The miniprepped plasmids were subjected to restriction digest to check for the presence of the fusion construct and the resulting fusions were confirmed by sequencing. The fusion construct will be cloned into a P. aeruginosa plasmid for future expression and visualization in P. aeruginosa.

ISOLATION, WHOLE-GENOME SEQUENCING AND ANTIBIOTIC ACTIVITY OF PSEUDOMONAS SP. RIT 623. KayLee K. Steiner1, Anutthaman Parthasarathy1, Narayan H. Wong1, Nicole T. Cavanaugh1, Jonathan Chu1, Megan C. Hallenbeck1, AndrÃ© O. Hudson1* 1Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, Rochester NY, USA The rise in antibiotic resistant bacteria has led to increase bacterial infections that are resistant to antibiotics. Slow-growing bacteria, which could be potential antibiotic producers, can be difficult to isolate on rich media due to competition from fast growing bacteria. Pseudomonas sp. RIT 623 was isolated from pond water located on the campus of RIT using pond

water agar. The genome was sequenced and analyzed for potential secondary metabolite gene clusters and antibiotic resistance genes. Antimicrobial production was also tested using extracts from the spent growth medium by means of disk diffusion tests. Fourteen gene clusters were identified as secondary metabolite genes. To date this is the first slow growing aquatic Pseudomonas strain which produces antibacterial compounds. Isolation of the bioactive compounds by liquid chromatography is underway with the aim of identifying the chemical structures and the genes responsible for the biosynthesis.

The Genetic Alteration of Thiomicrospira pelophila as a Solution to Reduce Carbon Emissions in Industry Jordan Stewart1, Samantha Williams2, and Malikiya Hayes3 Dr. Kathleen Scott2, Sarah Schmid2, and Juliana Leonard2 1Cornell University,Â 2University of South Florida, 3Florida A&M University The release of carbon dioxide from the combustion of fossil fuels has led to a decrease in the pH of ocean water, which causes oceanic organisms that are more sensitive to pH changes to perish. It also removes needed calcium carbonate ions from the water, leaving organisms that rely on building carbonate skeletons to most likely die, driving the aquatic ecosystem into chaos. To find a solution to this issue, biologists are studying microorganisms with bicarbonate transporters, specifically bacteria, to find a solution to CO2 pollution. The purpose of this experiment is to discover the mutability of Thiomicrospira pelophila by studying if the species can be mutated into being able to require high CO2 environments to survive. T. pelophila is a chemoautotrophic bacteria that uses its carbon-concentrating mechanism to gain inorganic carbon for its biological processes. T. pelophila was mutated by random knock-out mutagenesis, which inserts a gene randomly into the genome, which interrupts the gene coding for the carbon-concentrating mechanism, leaving the organism unable to survive in low CO2 environments. T. pelophila was mutated by mating with E. coli strain BW20767 carrying pLD27 plasmid and cultured into 96 well plates and replicated to see if the strains were unable to grow in low CO2 conditions. At least four recorded mutant strains of T. pelophila were unable to grow by themselves under low CO2 conditions. Since the T. pelophila can be mutated, we can now decipher its carbon concentrating mechanism, which has the potential to help us construct microorganisms that can produce bioplastics from CO2.

BACTERIAL EXPRESSION OF CHIMERIC ESCHERICHIA COLI AND TRYPANOSOMA BRUCEI DNA METHYLTRANSFERASES. Cassandra C. Taber and Kevin T. Militello State University of New York at Geneseo, Department of Biology Our laboratory is interested in DNA and RNA methylation in E. coli and T. brucei as little is known about this form of epigenetic regulation in microorganisms. One methyltransferase being studied at this time is a putative DNA methyltransferase (TbDmt) from Trypanosoma brucei. The exact function of TbDmt is unknown but the protein strongly resembles bacterial DNA methyltransferases such as DNA cytosine methyltransferase (EcDcm) from E. coli. To test our hypothesis that TbDmt is a DNA methyltransferase, we expressed TbDmt in bacteria and created two chimeric protein sequences switching the DNA binding domain and enzymatic domain of EcDcm and TbDmt. Exchanging the DNA binding domain and enzymatic domain of TbDmt with a known methyltransferase may help us discover the function of the enzyme and, if it is a methyltransferase, what DNA sequence is targeted for methylation. Plasmids were made containing the sequences for EcDcm, TbDmt, and both chimeric proteins where the genes are adjacent to the lac operator. E. coli

were transformed with the plasmids and expression was induced with IPTG. All four proteins were produced at 20C, but the proteins with the TbDmt DNA binding domain were less soluble than the other two. The proteins were denatured using guanidium HCl, isolated using a histidine column and analyzed on a polyacrylamide gel. EcDcm and the chimeric protein with the EcDcm DNA binding site and TbDmt enzymatic domain were successfully purified and were subsequently purified under partial denaturing conditions as well. These proteins will be tested for methylation activity. TbDMT and the chimera with the TbDMT DNA binding domain were not able to be purified using the guanidium HCl denaturing method so new approaches will be tested to purify the proteins. Further work will be done in purifying the proteins under both denaturing and nondenaturing conditions to produce enzymes for activity assays. In summary, this work contributes to our limited knowledge of epigenetic regulation in bacteria and protists.

WHOLE GENOME SEQUENCING AND CHARACTERIZATIONOF BACTERIA ISOLATED FROM AN UNTOUCHED CAVE ENVIRONMENT. Peter C. Wengert, Adam Murtha, Emily Kearney, Narayan H. Wong, Hazel Barton, Andre O. Hudson, Anutthaman Parthasarathy, and Michael A. Savka The Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, 85 Lomb Memorial Dr, Rochester, NY 14623 Microorganisms inhabit every crevasse of our world, being found in the depth of the oceans, the cold of the arctic, and even the upper reaches of the atmosphere. Humanity therefore is in constant contact with the microbial world and can have a great impact on the environments in which these organisms live and reproduce. To gain a greater understanding of the types and properties of bacteria which live unaffected by human activity, bacteria were isolated from an aqueous environment deep within a cavern in Wind Cave National Park in South Dakota. This study primarily focuses on the presence of a known bacterial communication system known as quorum sensing (QS), specifically, the presence of QS systems which utilize acyl-homoserine lactones (AHLs) as a chemical mediator. The organisms isolated had their genomes sequenced, and each species was identified using a tetra-correlation search (TCS) provided by JSpeciesWS. To determine whether or not each isolate was involved in AHL based QS, the genomes were scoured for the presence of acyl-homoserine lactone synthase (luxI homologs) using the antiSMASH platform. They were likewise screened for their ability to detect AHL signals by screening for the luxR genes that encode AHL receptor proteins (LuxR homologs) using tblastn sequence alignment. To verify the functionality of found luxI homologs, a disc diffusion assay was performed using AHL-dependent whole-cell biosensor NTL4(pZLR4). Isolates which both contained luxI in their genome and were shown to produce AHL signals on the disc diffusion assay were further analyzed using reverse-phase thin layer chromatography to determine the number and relative size of the AHL signal(s).

FINITE ELEMENT ANALYSIS OF A FULLY LIMBED SKINK. Isaac Annal and Jennifer Olori Skinks (Scincidae) comprise about 25% of lizard species. They have adapted to niches well, including some species with no limbs and some with well-developed limbs. Many of the limbless species spend a lot of its time burrowing in soil. If the species has developed limbs, it may spend more time above ground. The purpose of my study was to see if limb length is correlated with how well the skull could handle the stress of burrowing. To help solve this question, I investigated a fully limbed skink to determine stress in a more generalized species. The species of interest,

Tropidophorus cocincinensis, spends time on rocks or in crevices near water. Because it spends less time burrowing, I expect it to show poor distribution of stress. To test this, CT scans of the head were loaded into Avizo lite. After selecting only the bones of the skull, 3D stereolithographic models were made and loaded into geomagic. Here the skull was simplified by reducing the mesh size, filling in holes, and smoothing the mesh. The model was then imported into Strand7, where constraints were added to the back of the skull to prevent it from moving or rotating and a 20N force was added to the snout to represent the force of digging into the soil. After running the test, the stress was evenly distributed throughout the skull. Areas that were amplified were around the restraints and where the point pressure was applied. Because the skull showed evenly distributed stress, this species may spend more time in crevices than expected.

SEX OF OAK TWIG PRUNER BEETLES CAN BE DETERMINED WITH TWO MEASUREMENTS. William P. Brown1, Marion E. Zuefle2, and Jesse F. Brundage1 1Division of Natural Sciences and Mathematics, Keuka College, Keuka Park, NY 2Cornell University, NYS IPM, Geneva, NY Distinguishing the sex of oak twig pruners (Anelaphus parallelus, Newman) is important for studies of natural history, ecology, and management. Sex is currently determined by the antenna : body length ratio; males tend to have longer antennae relative to body length than females. Sex determination of prepared specimens is time consuming - it requires measuring body length and the length of 11 separate antennal segments. We wanted to explore potentially easier, more efficient methods of determining sex. We collected 18 body measurements from 72 beetles. Sex of each was determined by dissection. Data were analyzed with a discriminant function analysis. A function based on body length and length of antennal segment 8 correctly determined the sex of all 35 females and 37 males in the sample (100% accuracy for the sample). The antenna : body length ratio accurately predicted the sex of 34 of 35 females and 36 of 37 males (97% accuracy for the sample). The slightly more accurate method was also more efficient: 2 measurements were required for sex determination compared to the 12 required for the antenna : body length ratio.

COMPARING THE INFLUENCE OF TWO SAMPLING METHODS ON THE STABILITY TRENDS IN LONG TERM DEER TICK POPULATION DATASETS. Sofie Christie, Kaitlin Stack Whitney Ixodes scapularis (deer ticks) are primary vectors of Borrelia burgdorferi, the bacteria which causes Lyme disease. Understanding deer tick abundance and population trajectories may inform risks to public health due to their vector status. One challenge is that most biological studies are mostly short term (~3 years). However, the trends observed may not be indicative of longer-term patterns, and could only be a small variation on a much larger temporal scale. In addition, the timing of studies, not just their length, may have a powerful impact on the results of a study. For example, a study done during a drought period could infer results that differ widely from studies done in normal seasons. In order to study deer tick populations, researchers rely on a number of different methods, such as public surveys, dragging, flagging, and CO2-baited traps. Due to this, it can be difficult to standardize results made across different studies, as the methodology can impact the results. Our objective was thus to examine the impacts of the length, timing and sampling approach of studies on deer tick populations. We hypothesized that (1) longer deer tick datasets would have stronger population trends (2) more recent studies on deer tick populations will exhibit more frequent

phase changes (3) studies using dragging will have more consistent trends. We searched for publicly available datasets from observational studies that measured abundance, count, or density data of deer ticks at least annually for 10 or more years. To test (1), we used the â€˜bad breakupâ€™ algorithm in R developed by Dr. Christie Bahlai of Kent State University to model every subset of data greater than 2 years in the dataset and determine whether or not the subset was statistically significant, thus determining the number of years it takes for the dataset to reach a stable pattern. To test (2), we used the â€˜regime shift detectorâ€™ algorithm in R developed by Dr. Bahlai and Dr. Elise Zipkin of Michigan State University, which uses the Ricker model to determine which years phase changes (large, sudden changes that last substantial periods of time) happen. To test (3) we compared the stability patterns between datasets that used opportunistic sampling methods (e.g. people mailing in ticks found on themselves) and datasets that used standardized distance based sampling methods (e.g. dragging and flagging). From our analysis of 4 long term datasets in NY and MA municipalities, we found partial support for our first hypothesis, but no support for our other two hypotheses. For (1) we found evidence that long term datasets were more likely to reach stability. None of the datasets we tested converged in under 5 years, indicating that monitoring longer the 3 year standard is important. For (2) we found no significant patterns in the frequency of phase changes. For (3) we found sampling method had little effect on the trends, and that they both converged by 5 years with similar frequencies. We will continue to add datasets to this analysis, including from additional states (e.g. PA).

PHYSIOLOGICAL CONDITION OF THRUSHES DURING MIGRATION STOPOVER NEAR LAKE ONTARIO. Authors: Erica Delles*, Gretchen Horst, Carter Moleski, Kate Hensel, and Susan Smith Pagano. *Presenting Author; exd8743@rit.edu Affiliation: Thomas H. Gosnell School of Life Sciences, Rochester Institute of Technology, 85 Lomb Memorial Drive, Rochester, NY 14623 Annual migrations are a potentially stressful period of the life cycle of migratory birds. A birdâ€™s body condition is likely to relate to migration success, therefore metrics of physiological condition and health may provide important information about the resource requirements of birds during migration. However, many factors can impact physiological condition of birds, including sex. This study aims to compare the overall condition of migrating thrushes during autumn migration near the south shore of Lake Ontario -- an important stopover site for birds. The species of interest for this study are known migrants in the area- Hermit Thrush, Gray-cheeked Thrush, and Swainsonâ€™s Thrush. Birds were captured and sampled for blood at Braddock Bay Bird Observatory from September through October of 2018. Molecular analysis using PCR of the CHD genes located on the W and Z chromosomes in birds was used to determine the sex of these monomorphic birds. Physiological condition was assessed using plasma assays for triglyceride, uric acid, and total plasma protein, the heterophil to lymphocyte ratios in blood smears, and an overall body condition index. Linking health and condition indices to factors such as molecular sex may improve our understanding of resources necessary for thrushes at important stopover sites like the south shore of Lake Ontario.

INTERACTION BETWEEN DIETARY THIAMINE AND LIPID ON JUVENILE STEELHEAD TROUT. Lillian Denecke and Jacques Rinchard Department of Environmental Science and Ecology, The College at Brockport â€“ State University of New York Thiamine

(vitamin B1) deficiency has been negatively affecting salmonines in the Great Lakes region. This project investigated the hypothesis that thiamine deficiency in steelhead trout is a result of a high lipid diet due to thiamine being used up as an antioxidant to prevent lipid peroxidation. Juvenile steelhead trout were fed four diets (high lipid/thiamine, high lipid/no thiamine, low lipid/thiamine, and low lipid/no thiamine) in triplicate aquaria over a six-week period. Fish were sampled every two weeks to assess survival and growth, and samples were also preserved for biochemical analysis. At the end of the experiment, weight and lipid content of fish fed low lipid diets differed significantly from fish fed high lipid diets regardless of the presence or absence of thiamine in the diet (ANOVA, P

NO DIFFERENCE IN MALE NORTHERN CARDINAL PLUMAGE COLOR BETWEEN RURAL AND URBAN ENVIRONMENTS. Kristie M. Drzewiecki and Daniel T. Baldassarre, SUNY Oswego Dept. of Biological Sciences Humans have drastically altered natural landscapes and it is imperative that we study the effects of anthropogenic change on the evolution of other animals. As a result of human activity, species may exhibit different sexual signals, reproductive output, food intake, or an overall change in behavior. In this study, we explored variation in the sexual signals of two populations of male Northern Cardinals (Cardinalis cardinalis) by analyzing their plumage color. The red plumage color of cardinals is a result of carotenoid pigments that must be obtained from their diet. We compared rural (Rice Creek Field Station, Oswego) and urban (Barry Park, Syracuse) environments because differences in plumage color may be a result of variation in food availability in these areas. In order to detect if there were differences in male plumage color, we collected feather samples from the chest and back of 34 cardinals: 24 from Rice Creek Field Station and 10 from Barry Park. We then examined the feather samples with reflectance spectroscopy in order to quantify the spectral properties of the light reflecting from each plumage patch. We analyzed wavelengths between 300 and 700 nm to account for the UV-sensitive avian visual system. We then processed the reflectance spectra with a mathematical model of the avian visual system to quantify hue, chroma, and brightness as perceived by the bird. We found no major differences in chest or back plumage color between rural and urban environments. This pattern suggests that food availability and carotenoid intake was the same between the two populations, regardless of human presence. Although this system warrants further study, our current results suggest that urban habitats do not significantly affect the mating signals exhibited by male cardinals. This may be one reason why cardinals are able to succeed in human-dominated areas.

THE DEVELOPMENT OF THE COELOMIC CAVITIES AT THE VITELLARIA STAGE. Nasreen Jaff, Guy Azriel, and Hyla Sweet. Rochester Institute of Technology The brittle star Ophioplocus esmarki is a sea organism that is part of the echinoderm phylum. Although it is a very common invertebrate, little is known about the developmental process. The embryos transition from bilateral to five-fold symmetry. The vitellaria stage, part of an abbreviated development, includes aspects different from the ancestral ophiopluteus. Morphogenesis of the vitellaria stage does not include feeding and digestive structures. It also undergoes metamorphosis within several days rather than weeks. In this project, the structure and development of different organs including the hydrocoel, left somatocoel, right somatocoel, pericardial coelem, and pore canal were analyzed through observation at the mid and late vitellaria stages. To better understand the relationships between the

development of the different tissues of the coelomic cavities, 3D models were created. We found that the hydrocoel contributed to the formation of the water vascular system. We were also able to confirm the stone canal connecting to the ring canal between hydrocoels lobes 4 and 5. The contribution of the right somatocoel to an evagination in the axial region that is directed toward and around the esophagus was also seen. Future work will include further analysis of the organisms at later stages as well as making comparisons to other species using similar techniques.

TIMING IS EVERYTHING: VARIATION IN BROWN ANOLE (ANOLIS SAGREI) EGG CHARACTERISTICS OVER A BREEDING SEASON. Caitlin Lawrence, Gabrielle Sawyer, and Christina Schmidt, Wells College Resources allocated to reproduction can vary over time in iteroparous species, which may reflect life history trade-offs. Animals that produce numerous offspring over the course of breeding season often allocate more resources to their earlier offspring. We investigated this potential relationship in brown anoles (Anolis sagrei), which lay a single egg at multiple times over the course of a breeding season. We collected eggs over the course of a breeding season and determined how mass, density, percent fat and percent mineral varied over time. Egg mass decreased over time whereas egg density increased. The percentage of fat allocated to each egg did not change but the percentage of mineral decreased over time. Our results show that brown anoles differentially allocate resources relative to the timing of egg production, suggesting a reproductive strategy to maximize reproductive success for that breeding season and also possibly variation in maternal resource availability over time.

Stephen Loce (spl8@geneseo.edu) A TEMPORAL SURVEY OF BAT SPECIES AT SUNY GENESEO. Bats are among the most prevalent, yet overlooked mammals present in the northeastern United States. They provide numerous ecosystem services including pest control, nutrient cycling, as well as pollination, however, they are tough to study due to their nocturnal behavior, small size, and quick movements. Recording their foraging calls can provide a measure of the richness and diversity of bat species present in a location. For this survey, bats were recorded weekly from early June to late September in order to measure the seasonal changes in richness and diversity of bats across locations on the SUNY Geneseo campus. The sites varied from a woodland terrain (Roemer Arboretum), to grassy areas (Sturges Quad and the College Green), as well as paved areas (Parking Lots B and K). Prior research indicated the most prevalent bat species on the campus to be the big brown bat (Eptesicus fuscus), the silver-haired bat (Lasionycteris noctivagans), and the hoary bat (Lasiurus cinereus), therefore, the survey focused on these three species. We documented a seasonal decrease in the overall abundance of the three species as time progressed from early June to late September. The results of this study will show times of peak bat activity and should prompt the college to take action on the preservation of these important species on the campus.

DETERMINING PHYLOGENETIC RELATIONSHIPS OF CORVUS CORAX IN MEXICO AND CENTRAL AMERICA THROUGH MITOCHONDRIAL DNA SEQUENCING. Richard T. Marino III This study explores the different phylogenetic relationships between Ravens from Mexico and if they belong to one of the clades that make up the common raven species (Corvus corax). The clades of the common raven are the Holarctic and California. We obtained our specimens from museum collections. A

small fragment of the specimen is used, such as a small toe clipping, and the DNA was extracted using the Silica Column Protocol. To sequence the mitochondrial DNA, PCR reactions were conducted with certain sets of primers to sequence specific portions of the control region of the mitochondria. Usually, seven samples were ran on the thermocycler with the eighth sample being a negative control containing no DNA. After the PCR was complete, electrophoresis was performed on the samples to see if any section of the DNA was sequenced. A photograph of the gel was taken to add to our records. Once all of the DNA sections are sequenced, we will send all of the samples to a DNA sequencing facility and obtain results. The main goal of this study is to see which species of common raven are more closely related to each other and why these relationships can be observed. Past research within the lab has shown that Mexican samples might be related to the California clade; however, we will have more data to corroborate that hypothesis. I would like to create and present a poster at this conference regarding this study. I believe it would be very informative for people who are interested in this type of topic. Presenting a poster, in my opinion, would be the most effective way for the audience to obtain the information offered to them. I believe this because the audience can follow along with my voice as I draw their eye to the key points of the study. I prefer this style of presenting over a Power Point presentation because it would be more difficult for the audience to follow along with constant clicking through slides. Also, if my speaking speed is a little too fast for the audience, they would not have enough time to process the information that the slides contain. Therefore, a poster would be more efficient because nothing on the print will change and people can examine the poster as often as they would like.

Using Electroretinography to Study Seizure Activity in drosophila melanogaster Mutant Models Charles Morgan and David Deitcher Many strains of drosophila melanogaster that display seizure activity have been used to study the molecular mechanisms of seizures and the circuits involved in epileptogenesis. Performing an electroretinogram (ERG) and such mutants yields valuable information about the differences between a healthy fly and a seizure-prone fly. Using ERGâ€™s, this study shows the abnormalities in ERGâ€™s of various drosophila mutants. Additionally, this study shows seizure activity in response to the ERG experimental method, and offers a technique for studying seizure activity in vivo.

THE EFFECTS OF DISTURBANCE ON THE SUCCESS OF CAVITY-NESTING BIRDS. Kevin Nash and Andie Graham Dept. of Environmental Science and Ecology, The College at Brockport State University of New York, 350 Campus Drive, Brockport, NY 14420 Human disturbance has negatively impacted the survival and reproductive success of many species, including cavity-nesting birds. We conducted a study to determine if disturbance (recreational areas, buildings, roadways, etc.) affected the fledging success of four cavity nesting birds: Eastern Bluebirds (Sialia sialis), House Wrens (Troglodytes aedon), Tree Swallows (Tachycineta bicolor), and House Sparrows (Passer domesticus). We monitored 40 nest boxes placed around the College at Brockport campus from April 2019 to August 2019 using guidelines designated by the North American Bluebird Society. The nest boxes are located in areas with varying distance to disturbance. At each box, we recorded the number of successful fledglings for each species and we measured the distance to the nearest human disturbance from each box. We used linear regression to determine if a relationship exists between the number of successful fledglings for each species and the nearest

disturbance. We found that there was no relationship between the distance from human disturbance to the number of successful fledglings for Eastern Bluebirds, House Wrens, or Tree Swallows. These results suggest that the types of disturbance found on The College at Brockport campus do not negatively affect fledgling rates of these three species. However, we found that House Sparrows actually selected nest sites close to human disturbance ($R2 = 0.52$). This relationship is not surprising, as House Sparrows are invasive species that are known to use human structures for nesting, breeding, and foraging.

TESTING THE ROLE OF MATERNAL HAPLOID IN A DROSOPHILA HYBRID CROSS. Sahana Natesan, Daniel A. Barbash, and Dean M. Castillo Hybrid incompatibility (HI) (such as hybrid sterility or lethality) is a reproductive isolation barrier that contributes to speciation. Genes have been identified whose interaction causes HI; however, identifying the factors (maternal factors, small RNAs, etc.) which drive HI is essential to understanding how these genes function to affect hybrid development. Previous studies have shown that when D. melanogaster female parents are mated with D. simulans male parents, the interaction of two genes - Hybrid male rescue and Lethal hybrid rescue - causes hybrid male lethality. When a D. simulans female parent is crossed with a D. melanogaster male parent we observe the opposite outcome: hybrid female offspring die in the embryo stage while hybrid males live. At this stage, embryonic cells fail to undergo mitosis appropriately. During anaphase, the X chromatids segregate partially or not at all. This abnormal segregation is attributed to the 359-bp satellite DNA in D. melanogaster which maps to the Zygote hybrid rescue (Zhr) locus. Since we know that in a pure D. melanogaster cross, all of the offspring live, we hypothesize that there is a factor which regulates Zhr to allow for normal mitosis to occur. Maternal haploid (Mh) is maternal factor which is an important protease involved in decondensation of the paternal genome during zygote formation. To test whether maternal haploid is a potential factor which drives HI, we created transgenic strains of D. simulans which contained the D. melanogaster maternal haploid protease. We then mated female transgenic flies with D. melanogaster males and compared the hybrid progeny results to that of the control cross. We found that with the presence of D. melanogaster maternal haploid in the genome of the D. simulans fly, the female hybrid viability rate was higher than among the female hybrid progeny of normal D. simulans flies. This shows that maternal haploid is a factor that contributes to hybrid viability.

DEGREE OF CAT SOCIALIZATION EFFECTS LENGTH OF STAY FOR SHELTER CATS. Valerie Stephan and Bill Brown Surveys indicate that cat behaviors, such as degree of friendliness or playfulness, are important to potential adopters. However, there is little data relating degree of socialization with length of stay (LOS) in a shelter. We collected data on behavioral categories (interactive, approachable, and unapproachable), cat age, and LOS from 31 shelters in the Northeastern and Midatlantic United States ($n=645$ cats). Based on a mixed model analysis, which controlled for the effect of shelter, interactive cats had the shortest LOS, followed by approachable cats, and unapproachable cats had the greatest LOS. LOS increased as an effect of age and there was an interaction between age and behavioral categories. LOS of interactive cats, however, was not influenced by age. Further research should explore the effectiveness of cat behavioral modification programs to possibly reduce LOS of shelter cats.

PROTEIN, CARBOHYDRATE AND ASH CONTENT OF SELECT ORGANS OF THE VIRILE CRAYFISH â€“ ORCONECTES VIRILIS. Kylie Robben, Lauren Williamson, and Autumn Bell - Brian W. Witz, Ph.D., Research Advisor - Nazareth College, Biology Department Honeoye Creek is one of the major tributaries of the Genesee River that is influential in the Lake Ontario watershed. For the last two decades, Lake Ontario has been experiencing eutrophication that has led to an increase of algal blooms. This increase in nutrient loading, and associated frequency and severity of algal blooms, has led to habitat destruction and erosion (Makarewicz 2012). In order to decrease nutrient loading into Lake Ontario, we must first attempt to locate the sources of these nutrients. The nutrient loading is primarily from tributary sources (Makarewicz et al 2013). Therefore, the Genesee River and subsequently Honeoye Creek must be studied to identify the sources of nutrient loading in an attempt to manage the algal blooms in Lake Ontario. Although the Genesee River has been well studied since the 1970â€™s, Honeoye Creek has less frequently been researched; our research attempts to advance the knowledge of the conditions in Honeoye Creek, and to create a better sense of where the anthropogenic nutrients in Lake Ontario come from and how this nutrient overload affects organisms such as the virile crayfish Orconectes virilis. This study involved sampling crayfish from three sites along Honeoye creek, and then macronutrient and ash analyses were performed on select organs. We detected significantly greater protein content, on average, in tail muscle tissue than that of both stomach and hepatopancreas. Muscle had significantly greater average carbohydrate content than hepatopancreas, but significantly lower average carbohydrate content than stomach tissue. Finally, exoskeleton tissue had significantly greater ash content than that of both hepatopancreas and muscle. These data will be compared with that of future samples to see if the macronutrient and ash content of O. virilis varies among site along Honeoye Creek.

CALORIC VALUE OF SELECT ORGANS OF THE VIRILE CRAYFISH ORCONECTES VIRILIS COLLECTED FROM 3 STREAM SITES ALONG THE HONEOYE CREEK. Erich Dâ€™Eredita, Rachael Moyles, and Bethany Shaw - Faculty Advisor - Brian Witz, PhD. Annual monitoring of Honeoye Creek in Western New York State is important in order to understand that tributaryâ€™s influence on the Lake Ontario ecosystem; currently, Lake Ontario is threatened with eutrophication due to anthropogenic pollution. It is important to monitor crayfish populations within a lotic system, as they are important bioindicators of overall ecosystem health; they are intolerant to certain pollutants and play important roles at multiple trophic levels, acting as predators, prey, and detritivores. The crayfish diet consists of anything from detritus to small insects and fish. They are best described as â€˜opportunistic omnivores,â€™ eating whatever they can get given seasonal and local availabilities. Crayfish are eaten by fish, turtles, raccoons, mink, herons, cranes, and of course, humans. Due to their importance as both primary and secondary consumers in trophic ecosystems, the absence of crayfish from a stream has the potential to negatively affect the other species present. Understanding how energy is stored in the crayfish is important to understand their physiology, biochemical pathways, and the transfer of energy from one trophic level to another. The focus of this research was to examine caloric values of select crayfish organs: gills, stomach, exoskeleton, hepatopancreas, and muscle. We tested for differences in caloric content among these organs using Studentsâ€™ t-tests. The average caloric value (per gram dry

weight) of hepatopancreas (xÌ… = 27974.5 Â± 167.3) was greatest, followed in turn by that of gills (xÌ…= 20980.3 Â± 144.845), tail muscle (xÌ…= 19695.3 Â± 140.3) , and exoskeleton (xÌ…= 8817.1 Â± 93.9), and the differences among organs are statistically significant (all p

BIOCHEMICAL ANALYSIS OF BROWNING ACTIVITIES IN APPLES. Christian DiBiase, Nathanial Stahl and Poongodi Geetha-Loganathan The aim of this study is to investigate the differential browning mechanisms among various cultivars of apples. The biochemical mechanism responsible for browning activities in apples involves a collection of enzymes called polyphenol oxidases (PPO). These enzymes facilitate the reaction of polyphenolic substrates (PPS) with oxygen to produce benzoquinones, a compound that auto polymerizes to produce melanin, the primary browning agent in apples. In this experiment both the PPO and PPS were extracted from five separate apple cultivars, namely red delicious, fuji, gold rush, rubyfrost, and mutsu. To identify the types of PPO in each subspecies, the reactivity of the extracted enzyme from each cultivar is quantified in the presence of three known substrates, catechol, catechin, and chlorogenic acid using UV-Vis absorption spectrophotometry. The reactivity of the PPO extract with each substrate will be compared across the five apple cultivars to identify the specificity of PPO to type/s of PPS present and to quantify the concentration of PPO present in each species. Also, to determine the concentration and type/s of substrate present in each apple variety, PPS extracted from each cultivar will be analyzed using liquid chromatography-mass spectrometry. Browning activity directly affects the longevity of fruits and vegetables, which is a consistent problem in the agricultural industry. If the biochemical mechanism of browning activity is better understood, improvements could be made to future food production, storage and transportation methods.

ENZYME FUNCTION PREDICTION, DISCOVERY, AND CHARACTERIZATION IN UNDERGRADUATE BIOCHEMISTRY TEACHING AND RESEARCH LABS. Kevin DiMagno, Elizabeth Lucas, Nana Aikins, Katherine Wilson, Minh Le, Kevin Oâ€™Donovan, Spencer Richman, Paul Craig, Jeffrey Mills, and Suzanne Oâ€™Handley School of Chemistry and Materials Science, Rochester Institute of Technology, 85 Lomb Memorial Drive, Rochester, NY 14623 The Structural Genomics Initiative was an effort by consortiums to solve as many unique protein structures as possible; the Protein Data Bank contains a number of enzymes whose structures have been solved, but for which no enzymatic activity has been determined. The Enzyme Function Initiative is an effort to determine as many unique enzyme functions as possible. There are a number of putative NUDIX Hydrolase superfamily members whose structures have been solved, but for which no enzymatic activity has been determined. We have catalogued the structurally-determined enzymes within the NUDIX Hydrolase superfamily using BLAST, Dali, SCOP, and PDB. We then began to characterize these enzymes in the biochemistry teaching laboratory and are finishing their characterization in the research lab. In the biochemistry lab course, the students have expressed his-tagged Nudix Hydrolases (PDB entries 2AZW, 2PQV, 3F13, 3QSJ, 3R03, and 3SON) from plasmids obtained from DNASU, purified the enzymes using nickel affinity chromatography, and then did enzyme assays to determine the substrates. From the assays, the students discovered Nudix Hydrolase activities for four of these enzymes, which we are currently characterizing in the research lab. This project is supported by NSF IUSE 1503811.

USE OF METHYLENE AS A FOOTPRINTING REAGENT FOR THE STUDY OF PEPTIDES. Ellirose Edwards, Hyeok Kim, Gavin Lucky, and Dr. Paul Martino The goal of our research is to develop a new mass spectrometry-based method to study the early events in amyloid-beta peptide aggregation. According to the amyloid cascade hypothesis, it is believed that beta-amyloid aggregation is the trigger that leads to Alzheimerâ€™s disease (AD). One of the difficulties of studying AD is the complex folding pattern of amyloid-beta peptides. Amyloid-beta peptides form an amorphous solid that is not compatible with the current methods of structural elucidation, such as X-ray diffraction, NMR spectroscopy, or even H/D exchange kinetics. In an attempt to make sense of the amyloid-beta misfolding process, our group has developed a new method by which protein structure may be studied. Primarily based off prior work by F. M. Richards, our method uses methylene as a foot-printing reagent. By covalently labelling the protein at all available sites, it is our goal to see the places where amyloid-beta aggregates form which show up as areas that our labelling doesnâ€™t (like a negative of a picture). We will discuss the early stages of optimization of our method, and some alternate strategies that we used in an attempt to solve consistent issues that we encountered. Though this process is not complete, our group hopes to continue making progress and eventually shed light on early events in Alzheimerâ€™s disease and possibly other neurological diseases.

SYNTHESIS OF 8-QUINOLINETHIOL N-OXIDE, A NOVEL CHELATING LIGAND. Nathan J. Halsteter and Bradly M. Kraft St. John Fisher College, Department of Chemistry, 3690 East Ave, Rochester, NY 14618 There are thousands of human health problems. One of these problems is the ingestion and inhalation of inorganic substances such as lead, mercury, and silica. The inhalation of silica can lead to things such as silicosis, lung cancer, and chronic obstructive pulmonary disease (COPD) many of which are incurable. We are attempting to develop varying organic chelating ligands to silicon. This hypothesis driven research compares similar organic silicon chelating ligands to one another. X-ray crystallography allows us to inspect features such as bond length and bite angle which provide insightful evidence on the strength of a chelating ligand. By comparing similar chelating ligands we are learning more about the chelate effect, which may prove useful when attempting to develop chelating ligands to use in vivo to neutralize / remove harmful inorganic compounds from the body.

ADSORPTION AND SURFACE COVERAGE OF MERCAPTOHEXADECANOIC ACID ON SNO2 THIN FILMS. Elizabeth R. Hinterberger and Gregory R. Soja* Department of Chemistry, Dâ€™Youville College, Buffalo, NY The chemisorption and surface coverage of mercaptohexadecanoic acid (MHDA) adsorbed on nanocrystalline SnO2 thin films is presented. MHDA can act as a molecular linker in the attachment of quantum dots to the SnO2 film, which would have applications in sensing and photovoltaic devices. SnO2 thin films were prepared via a low cost doctor blade method, in which colloidal SnO2 is spread across a glass substrate using a Pasteur pipette. Films were immersed in a 2 mM solution of MHDA in THF for at least 2 hours. FTIR spectroscopy was used to confirm chemisorption as well as surface coverage using a modified Beer-Lambert equation. The surface coverage of MHDA on the SnO2 film was calculated to be 1.1 + 0.1 x 10-7 mol/cm2, which closely

agrees with previously reported surface coverages of MHDA on nanocrystalline TiO2 thin films. Future studies will explore the catalytic nature of these SnO2 films.

CARBENE LABELING MASS SPECTROMETRY - A CONTINUATION IN DEVELOPMENT OF A NEW TOOL FOR BIOPHYSICAL INFORMATION. Paul Martino, Hyeok Kim, Ellirose Edwars, Gavin Luckey Proteins, one of the crucial components of the building blocks of body tissue, can also result in various diseases when misfolded. Among them is a disease that has no effective treatment--Alzheimerâ€™s disease. Alzheimerâ€™s disease is thought to be triggered by aggregation of amyloid-beta peptides in the brain and the aggregation of tau proteins (the amyloid cascade hypothesis). The mechanism of misfolding of amyloid-beta peptides that leads to aggregation of amyloid-beta into fibers and plaques has not been discovered. The goal of this research is determining the structure of early amyloid-beta aggregation and changes in protein topography (i.e misfolding) that will lead to the aggregation, through the implementation of a new mass spectrometry technique. Our technique utilizes methylene derivatization of structural relevant peptides (or peptide aggregates) using carbene gas and later analysis by mass spectrometry. We use the carbene gas as a footprinting reagent that selectively derivatizes the structure in a topographical-dependent manner. The analysis of derivative at each amino acid residue requires fragmentation mass spectrometry. During our efforts many problems have arisen that are associated with unexpected fragmentation pathways. To improve the results, we utilized a technique that is used to fix a positive charge at the N-terminus via a trimethylpyrilium (or TMP) modification of the primary amino group. With model peptides, TMP modification resulted in high yields and simplified peptide fragmentation results. We hope to successfully employ TMP modification on larger amyloid-beta aggregates.

PEPTIDE STRUCTURE BY CARBENE LABELING AND MASS SPECTROMETRY. Gavin Luckey, Ellirose Edwards, Hyeok Kim, and Dr. Paul Martino Carbene is a highly reactive, omniphilic reagent that aggressively reacts with amino acids exposed on the surface of a protein. When carbene reacts with the protein, the protein becomes labeled; this is evident in a mass increase of the protein. Using mass spectrometry, singly-labeled protein ions can be examined and structural information about the protein can be acquired based on the location and frequency of labeling. Being able to determine structural information has implications for determining protein structure of Amyloid Beta, a protein that can aggregate in the brain potentially causing Alzheimerâ€™s disease. The research conducted included the replication of a labeling experiment performed by FM Richards. By breaking down diazirine gas using UV light while the gas was being bubbled into a solution containing the peptide to be labeled, carbene was formed which bonded to the peptide. The peptides were then analyzed using mass spectrometry after 3.5, 7.0, and 10.5 minutes of labeling to determine the amount of labeling. It was found that the peptide was being labeled, but increasing oxidative damage occurred as the protein was exposed longer to UV light. While labeling did occur, the yield was low due to the reaction of carbene with water to produce methanol. It was concluded other labeling techniques would be more efficient and yield better results, such as using electrospray ionization which eliminates oxidative damage and methanol production.

UNDERSTANDING THE TRIALS AND TRIBULATIONS OF DISCOVERING A DIELS-ALDER REACTION SUITABLE FOR AN UNDERGRADUATE CHEMISTRY LAB. Molly McMahon and Jeremy Cody School of Chemistry and Materials Science Rochester Institute of Technology 85 Lomb Memorial Drive Understand the trials and tribulations of discovering a Diels-Alder reaction suitable for an undergraduate chemistry lab. Some of the discussion points will be the restrictions to take into consideration given the context that the reaction would be taught within â€“ namely, working with reagents that are easily and cheaply accessible, speed of completion of the reaction, and methodologies that would be accessible to undergraduate students with no prior experience. The Diels-Alder reaction has been well explored and often viewed as a solved problem. As is known to all researchers, things are often not as simple or easy as initially planned.

ANALYSIS OF COPPER NITRATE IN PEG400 SOLUTIONS BY UV VIS SPECTROSCOPY. Jaclyn M. Neubauer and Markus M. Hoffmann The College at Brockport, State University of New York Department of Chemistry and Biochemistry 350 New Campus Drive, Brockport, NY 14420 Polyethylene glycol (PEG) is a surfactant commonly used in soaps and detergents. It is also of interest to use PEG as a solvent due to its ability to dissolve a wide variety of solutes, including inorganic salts. Another benefit of using PEG as a solvent is that it is very benign to the environment as it is nontoxic and biodegradable. PEG has been successfully used in metal organic framework synthesis. Therefore we are interested in determining its metallic salt solubility, specifically copper (II) nitrate. In addition to determining copper (II) nitrate solubility, because it is hygroscopic, we also want to know solubility in the PEG/water binary system. Because nitrate has a UV-Vis feature, we used UV-vis spectroscopy to measure solubility while water content was determined via NMR spectroscopy. Solutions analyzed were prepared by mixing saturated PEG and water solutions. Solutions with higher PEG content appeared green while others were blue. Nitrate content could be obtained for solutions with increased water content but not in neat PEG. Prior to collecting UV-vis spectra for samples, each was diluted with water to ensure nitrate concentration is low enough to avoid saturating the detector. A remarkable observation was made when diluting the initially green saturated PEG solution. It becomes blue upon dilution and an increase in sample temperature was observed. This new blue color slowly faded to green and eventually became colorless over the course of months. These observations are evidence of a surprisingly slow kinetic reaction and deserve future investigations.

Title: HIGHER ORDER CORRELATIONS IN A LEVITATED NANOPARTICLE PHONON LASER. Author: Long Nguyen(1), Kewen Xiao(1), Robert Pettit(2), Nick Vamivakas(2), and M. Bhattacharya(1) (1)School of Physics and Astronomy, Rochester Institute of Technology, Rochester, NY 14623 USA (2)Institute of Optics, University of Rochester, Rochester, NY 14627 USA Email: mxbsps@rit.edu Abstract: From the concept and model of the optical tweezers phonon laser, we systematically investigate the higher order correlations of the laser both theoretically and experimentally. Modulation-evolution of phonon number distribution is obtained by solving the master equation and is also verified by experiments. Subsequently, quantum Langevin equations can be derived from the master equation, which is used to calculate non-equal-time higher order correlations of the phonon laser. The high order correlations reveal the coherence information of the laser which is of the

interesting property of any laser. The theoretical results of correlations match well with experimental data.

Molecular Solvation in Phosphonium Ionic Liquids. Rachel I. Riga and Mark P. Heitz* Department of Chemistry, The College at Brockport, SUNY, 228 Smith Hall. 350 New Campus Dr., Brockport, NY 14420. Abstract: Ionic liquids (ILs) are that are liquid at standard temperature and pressure. ILs are commonly used because of their environmentally friendly properties such as low vapor pressure and high thermal stability. Low vapor pressure is favored, because the IL will not vaporize into the atmosphere as easily as other organic solvents. Even though MeOH is an organic solvent, it can be used in combination with ILâ€™s to decrease the amount of organic solvents being dispersed in the environment. The goal of this work is to characterize the solvation behavior of solvent-modified ILs, including tbmptf2n, thtdptf2n, thtdp2ehp, tbmp2ehp. We measured the following Phosphonium ILs, tert-butyl(methyl)phosphonium (bis)trifluorosulfonylamide, trihexyltetradecylphosphonium (bis)trifluorosulfonylamide, trihexyltetradecylphosphonium 2-ethylhexylphosphate, and tert-butyl(methyl)phosphonium 2-ethylhexylphosphate. We measured the solvation and rotation dynamics of four different IL solutions using methanol (MeOH), ranging from 0.05 to 0.2 mole fraction ionic liquid. Steady-state fluorescence excitation and emission spectra of Rose Bengal was used to probe the solution energetics. The data suggested that the solute emission intensity was most strongly quenched at xIL ~0.1. Excited state intensity decay kinetics were measured, and the lifetime data were in agreement with the steady-state results. Rose Bengal is better solvated at MeOH-rich mole fractions; the selection of Rose Bengal is due to itâ€™s a polarity. If combined with a polar solvent (MeOH), it will be well solvated, which the data is in agreement with.

TARGETED MOLECULAR IMAGING AGENTS FOR PHOTOACOUSTIC IMAGING OF PROSTATE CANCER. Alexis Rudesil Prostate cancer is often over diagnosed and over treated due to the low specificity of the current prostate cancer screening test or missed on biopsy due to the low specificity and sensitivity of current imaging techniques. Photoacoustic imaging offers a potential solution using near infra-red (NIR) dyes conjugated to a compound targeting prostate specific membrane antigen (PSMA). The fluorescent and photoacoustic signals of several novel targeted molecular imaging agents (TMIAs) were quantitated and compared to assess the best TMIA candidate to be used when conducting further trials. The fluorescent and photoacoustic signal intensities for all compounds show an increase in intensity as concentration increased. There was no significant difference in the photoacoustic signal of the single labelled fluorophores and sonophores when compared. There was a significant increase in signal intensity when comparing the SNR values of some of the dual labelled compounds to the SNR values of the single labelled compounds they were composed of. As such these compounds were determined to be the best candidates to proceed with for in vivo and in vitro trials.

VISCOSITY-CONTROLLED ELECTRON TRANSFER IN WATER SPLITTING. Justin M. Scheg,* David McCamantâ€ and Mark P. Heitz Department of Chemistry, The College at Brockport, SUNY, 228 Smith Hall, 350 New Campus Drive, Brockport, NY 14420 â€ Department of Chemistry, University of Rochester, Rochester, NY, 14627 Fuel sources produced from the conversion of solar energy-to-chemical energy

offers a form of alternative, clean energy that is seemingly inexhaustible provided the raw materials are always readily available. Among the various forms of â€œsolar energyâ€ under investigation, splitting water to generate hydrogen gas may be a viable alternative as a renewable fuel source, that when combusted produces water vapor as the sole by-product of the combustion reaction. We are studying solar hydrogen production through dye-mediated electron transfer to split water molecules into H2(g) and O2(g). An electron source is required to reduce the H+ ions to H2(g) and we are using immobilized dyes bound to titanium dioxide nanoparticles in an effort to drive electron transfer. A thienyl-rhodamine dye derivative (O-Th) has shown promise in this regard but the electron yield is sensitive to an intramolecular twist within the dye. Methanol/ethylene glycol binary mixtures are used to control solvent viscosity in an effort to determine the optimal solvent properties that maximize electron production. Lifetimes and anisotropies for a phenyl-rhodamine dye derivative (O-Ph) and O-Th in mixtures of xMeOH/ethylene glycol were measured and plotted as functions of the viscosities of these mixtures. The results show that rotational times of these probes increase as solvent viscosity increases. Lifetimes of these probes also increase as solvent viscosity increases, but this trend is less dramatic than it is for rotational times.

POLYMERIZATION OF ANILINE AT GRAPHENE QUANTUM DOTS ELECTRODE. Reeba Thomas, Zaheer Coovadia and K.S.V. Santhanam School of Chemistry and Materials Science, Rochester Institute of Technology, Rochester, NY 14623 The oxidation of aniline has been examined at graphene quantum dot electrode (GQD) (1) with a view of enhancing the formation of polyaniline for greenhouse gas sensors. At GQD electrode, the aniline oxidation occurs in cyclic voltammetry at Epa=0.99 V with the formation of emeraldine green and leucoemeraldine which are reduced at 0.49 V and 0.23 V. However, a notable feature of aniline oxidation at GQD electrode compared with glassy carbon electrode is that the oxidative peak at GQD electrode is shifted towards lesser positive potential and the current is enhanced considerably at the GQD electrode. We carried aniline oxidation, with GQD added into the medium by examining the cyclic voltammetric behavior at glassy carbon electrode. In this situation, the peak current at Epa=0.99 V is reduced due to prior binding of aniline to GQD making the molecule bulkier. This affects the diffusion coefficient of aniline resulting in lower current. Interestingly, this opens a method of making GQD bound polyaniline for sensor applications. In order to conform the mechanism, potential step electrolysis, exhaustive electrolysis and the product examination by Fourier transform infra-red spectroscopy, UV-VIS spectroscopy and Raman imaging spectroscopy are carried out. The data obtained demonstrates that GQD electrode oxidizes aniline lot more efficiently than at glassy carbon electrode. 1. K.S.V. Santhanam, S. Kandlikar, M. Valentina and Y. Yang, US patent No. 9840782, December 12, 2017.

BREAKDOWN OF THE STOKES-EINSTEIN EQUATION IN REVERSE MICELLAR SOLUTIONS. Matthew D. Too and Markus M. Hoffmann The College at Brockport, State University of New York, Department of Chemistry and Biochemistry, 350 New Campus Drive, Brockport, NY 14420 The well-known Stokes-Einstein equation relates the size of a moving particle in solution to its self-diffusion coefficient and the solution viscosity. Prior studies have observed the breakdown of the Stokes-Einstein equation in ionic liquids and in varying concentration solutions of poly(ethylene oxide) alcohol (C10E6) nonionic surfactant in cyclohexane. This study

considered whether an observable breakdown of the Stokes-Einstein equation would also occur in varying water content solutions of fixed concentration of C10E6 in cyclohexane. Therefore, we will present corresponding new experimental results on self-diffusion coefficients and solution viscosity. These data show that the Stokes-Einstein equation breaks also down in these water-in-oil reverse micellar solutions, resulting in unreasonably small average radii and aggregation numbers. However, the ratio of solvent and C10E6 self-diffusion coefficients provided average radii and aggregation numbers consistent with results published by others in the literature. Additional unusual observations will be reported. For example, the ethylene oxide functional group of the C10E6 appears to diffuse at a slower rate than its alkyl chain functional group.

VARIOUS DRYING TECHNIQUES FOR DRYING PEG POLYETHYLENE GLYCOL AND SIMILAR SURFACTANTS. Alex Verrelli and Markus M Hoffmann The College at Brockport, State University of New York Department of Chemistry and Biochemistry 350 New Campus Drive, Brockport, NY, 14420 Water absorbed from the atmosphere is a common contaminant of chemical samples. Drying is a method of purifying liquid samples where water is removed. We investigated several drying techniques for drying polyethylene glycols (PEG) and related surfactants such as C10E6. Recently, PEGs received interest as chemical solvents because they possess green, environmentally friendly characteristics such as being biodegradable and nontoxic. Surfactants in general are large organic molecules with hydrophilic and hydrophobic moieties. Hydrophilic/hydrophobic molecules are polar/nonpolar molecules that interact well with water/oil. Therefore, PEG and related surfactants are great solvents for a wide range of chemicals. For example, PEGs have been used as solvents in synthesis of a variety of compounds including metalorganic substances such as metal organic Frameworks (MOFs). Since some reactants are not compatible with water but water is a common contaminant in PEG, it is important to establish economical and environmentally benign drying protocols for PEGs. The goal of the study is to test the effectiveness of several common drying methods. The four methods tested were: (A) drying with molecular sieves, (B) drying with nitrogen gas with heat and vacuum, (C) using the chemical reaction of 2-2 dimethyloxypropane (DMP) with water in the presence of aluminum oxide and silicon oxide catalysts, and (D) exposure to a drying oven set at 100C. In each method the water content was monitored using a Karl Fischer titrator. Karl Fischer titration is based on a redox reaction that quantitatively consumes water in a sample and in this way reports the water content in parts per million (ppm). To monitor the drying reaction with DMP, Nuclear Magnetic Resonance spectroscopy was used. The NMR data show that the drying reaction proceeds faster with increased amounts of present catalyst. Quantitative analysis of the NMR data is still underway.

SYNTHESIS AND CHARACTERIZATION OF TIO2 Jordan Walker1, Zili Wu2, Zhenghong Bao2, Aditya Savara2, and Alexey Ignatchenko1 1. Department of Chemistry, St. John Fisher College, Rochester, NY 14618 2. Chemical Sciences Division, Oak Ridge National laboratory, Oak Ridge, TN 37831 Recently, interest has centered on the catalytic properties of various on Ti-based nanoparticles as catalysts. The TiO2 nanoparticles were formed by a process called solvathermal synthesis. Ti-101 surface or â€œTruncated Octahedraâ€ was formed by heating the pre-prepared Ti(OH)4 (dispersed in 50% isopropanol) in a Teflon-lined autoclave reactor to 180

Â°C for one day. Ti-010 surface or â€œRodsâ€ were similar to Ti-101, -but included 0.2 g of ammonium sulfate in the mixture. Ti-001 surface or â€œDisksâ€ required the special precursor formed from the Ti(OC4H9)4 hydrolysis; we treated it with hydrofluoric acid in a Teflon-lined autoclave, heated for three days in an oven to 180Â°C . All products were rinsed, centrifuged, dried, and baked within a calcification oven to 300Â°C. Samples of the nanoparticles were characterized by Scanning Electron Microscopy (SEM) and by Diffuse Reflectance Infra-red Fourier Transform Spectroscopy (DRIFTS) to confirm the sample shape. DRIFTS analyses are still in progress, but SEM imaging suggests efforts to create the nanoparticles were successful. DRIFTS of CO2 absorption data remain critical, however, because the fine-grained nature of the particles, being 30 nm in size, makes it difficult to positively identify them even by SEM. Transmission Electron Microscopy (TEM) could also be used to confirm the shapes. The first step of the larger project of mapping the catalytic sites on the alkali promoted anatase TiO2 was to create and verify these particles. If the shapes are confirmed, we can move on to further analysis.

INTRODUCTION OF PIPERAZINE RING INTO CHLOROQUINE ANALOGS FOR EVALUATION IN BREAST CANCER CELLS. Devan R. Warner1, Catherine C. Lincourt1, Dhvani Patel1,2, Peter Cao2, Yasser Heakal2*, Dominic L. Ventura1* 1Department of Chemistry, Dâ€™Youville College, Buffalo, NY. 2Department of Pharmaceutical Sciences, Dâ€™Youville College, Buffalo, NY Chloroquine (CQ) is a chemotherapeutic agent and was also the foremost treatment of malaria for many years. More recently, Chloroquine has recently been investigated in the pharmacological inhibition of autophagy, although in high concentrations. Potentially, chloroquine derivatives may inhibit autophagy of breast cancer cells in much lower concentrations. In this study, we aimed to design and synthesize group of CQ analogs through various methods. Utilizing various amines, we were able to produce a small library of compounds for this study (some examples shown below). Recently, we have found the derivatives containing piperazine rings were able to inhibit autophagy at much lower concentrations than similar molecules without this moiety. Once synthesized, the CQ analogs were tested for inhibition of autophagy in triple-negative breast cancer cells. This part of the project focused on taking advantage of polyamine transporters in targeting and delivering CQ, intracellularly.

USING A LOW-FREQUENCY EPR MOBILE UNIVERSAL SURFACE EXPLORER TO NON-DESTRUCTIVELY ANALYZE MIXTURES OF PAINT ON CANVAS. Elizabeth Bogart, Matina Chanthavongsay, Akul Gupta, Haley Wiskoski, Joseph P. Hornak The study of paint compositions and varieties has been applicable in the fields of historical artifact dating and conservation. For these fields, it is important to analyze samples with as little invasion as possible. This paper outlines the use of a low-frequency electron paramagnetic resonance (LFEPR) mobile universal surface explorer (MOUSE) along with a least-squares regression curve-fitting algorithm to identify and model mixtures of paramagnetic pigments on canvas in a non-destructive manner. This mixture analysis technique using EPR spectroscopy will help art conservators, historians, and the like, with their studies of delicate artifacts.

ALGAE BLOOM DETECTION THROUGH THE USE OF CONSUMER DRONES IN THE FINGER LAKES. Joshua Andrews, William White, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D., and John Halfman, Ph.D joshua.andrews@hws.edu , william.white@hws.edu , dumitriu@hws.edu spacher@hws.edu , halfman@hws.edu

Hobart and William Smith Colleges, Physics Department With the recent commercialization of drones in the United States, many affordable research applications can be explored. The prevalence of Harmful Algae Blooms (HABs) causes many issues to the local population within the Finger Lakes Region. Standard (in-situ) water quality testing to determine the presence of HABs is often time consuming and expensive. The remote sensing by using drones to detect HABs could prove to be a more cost effective and efficient practice. The poster will show how drone imaging data collected through the Finger Lakes are correlated with the algae concentration in the water of the Finger Lakes

REMOTE SENSING TO MONITOR HARMFUL ALGAL BLOOMS. William White, Elizabeth Moore, Ileana Dumitru, Ph.D., Peter Spacher, Ph.D., John Halfman, Ph.D, Lisa Cleckner, Ph.D. william.white@hws.edu, elizabeth.moore@hws.edu, dumitriu@hws.edu, spacher@hws.edu, halfman@hws.edu, cleckner@hws.edu Hobart and William Smith Colleges, Physics Department Harmful Algal Blooms (HABs) occurrence has increased in recent decades. Traditional water monitoring systems are expensive to implement over a large area such as the Finger Lakes. To gain a widespread understanding of lake water quality in relation to HABs, custom water monitoring devices, built in house, can be deployed at a fraction of the traditional water monitoring systemsâ€™ cost. A water monitoring device including a temperature and dissolved oxygen sensor was designed and built. These water monitoring devices were deployed in the Finger Lakes. In order to continuously gather data (the temperature and the content of dissolved oxygen in the lake water), a solar panel and battery powered the sensors. The temperature and dissolved oxygen data together with in-situ water samples determining prevalence of HABs may provide a correlation and help to predict future HABs in the Finger Lakes. The poster will present field data collected by the water monitoring device this summer.

INVESTIGATING WALKING GAIT AND STANCE INTERVENTIONS IN THE ELDERLY TO IMPROVE MOBILITY, BALANCE, AND REDUCE FALL RISK. Alison Pomerleau, and Dr. Jonathan Millen, PhD St. John Fisher College 3690 East Ave, Rochester, NY 14618 As the aging population continues to grow, so does the incidence of mobility, balance, and fall issues in the elderly. A major contributor to this is the change in gait that comes with aging. This study aimed to investigate walking gait and stance interventions in the elderly population that could improve physical health by tracking their exercise regime and other pertinent lifestyle habits. Interventions comprised of various activities and lifestyle alterations that were implemented on a regular basis to help improve balance, strength, mobility, general ambulation, coordination, and so on. Cohorts of senior citizens from St. Johns and Valley Manor, both in the Rochester, NY, participated over a nine-month period and were tracked accordingly. Equipment, including the InBody machine and Xsens wireless motion sensors were integrated throughout the study to provide a body composition and live metric analysis respectively to help quantitatively explain why certain interventions resulted in specific physical changes. The big picture throughout the study remained how could interventions be used to alter a senior citizenâ€™s gait with the intentions of reducing their fall risk. KEYWORDS: gait, balance, interventions, elderly population, fall risk

INVESTIGATION OF THE NEOGENE DEPOSITIONAL ENVIRONMENT OF THE EASTERN HIMALAYAN SIWALIK DEPOSITS THROUGH MULTIPROXY ORGANIC ANALYSIS. AndrÃ© Brunette, Nandini Kar, Richard W. Smith, Suchana Taral, and Tapan Chakraborty The depositional environment of the Neogene Siwalik deposits in the Himalayan foreland basin has been inferred as meandering and braided, exclusively fluvial deposits based on sedimentary facies and fossil analysis. These records mostly come from the Western Himalayas. The Eastern Himalayan Siwalik deposits are not as well studied as Western Himalaya and few studies looking at these deposits reported major differences in facies and fossil assemblages. A recent detailed sedimentological analysis of the Siwalik sediment reported major differences in facies with that of the west. Siwaliks of the eastern Himalaya are characterized by the presence of wave and combined flow structures, dark grey mudstones, brackish water tolerant spore-pollens and marine trace fossils. Based on these evidence, recent studies proposed a marginal marine depositional setting characterized by a river-dominated delta. Our study focuses on reconstruction of the vegetation assemblage, to better understand the Neogene depositional environment, as a marginal marine environment is expected to have a different assemblage compared to a terrestrial environment. We analyzed sediment samples collected from the Tista Valley in the Eastern Siwaliks of India. We present new data of, bulk Î´13C, C/N ratio, and n-alkane chain length. Both bulk Î´13C and Carbon/Nitrogen (C/N) ratio change from terrestrial to marine sources while n-alkane chain lengths vary among different types of vegetation. Comparison of these different proxies can help us to construct a comprehensive record of the Neogene vegetation in the Eastern Siwaliks and ascertain the depositional environment. Terrestrial versus marine affinity of the vegetation has important bearing on the tectonic and paleogeomorphological evolution of the eastern Himalayan Foreland basin.

EARLY DEVONIAN MANLIUS GROUP: EURYPTERIDS, CRINOIDS, OLNEY LIMESTONE AND A DRONE Samuel J. Ciurca, Jr., 2457 Culver Road, Rochester, New York 14609 Joseph LaRussa, 553 Landing Road North, Rochester, New York 14625 After discovering the eurypterid Erieopterus in situ, Ciurca 1978, traced the eurypterid beds around the complete perimeter of Split Rock Quarry, a very large abandoned quarry southwest of Syracuse, New York. At the time, a small area of bedding plane was located that preserved the small crinoid, Lasiocrinus. This crinoid is well known from eastern Helderbergian deposits. The purpose of our current research was to rediscover the crinoid horizon and photographically document the site. LaRussa brought his drone so we could cover photography from above for the first time. While crinoid debris, mostly stems and ossicles, is present in other beds within the Olney Limestone here, only one bedding plane preserves nearly entire specimens. The results were provided to Dr. George McIntosh (Rochester Museum Science Center) as he was involved in reevaluating Lasiocrinus research. While only one new crinoid specimen was retrieved, verifying the original site, stratigraphic measurements were also done. All eurypterid and crinoid specimens collected over many years by Ciurca were given to the Yale Peabody Museum of Natural History in New Haven, Connecticut. Future work includes tracing algal/stromatolite zones around the quarry, especially a thin bed above the crinoid horizon. See also: Ciurca, S.J. Jr., 1978, Eurypterid Horizons and the Stratigraphy of Upper Silurian and Lower Devonian Rocks of Central-Eastern New York. New York State Geological Association 50th Annual Meeting Guidebook, Syracuse University.

VERTICAL FRACTURES IN THE CHAUMONT LIMESTONE IN THE WATERTOWN VICINITY, NY: GLACIAL ORIGIN OR TECTONIC ORIGIN? Michael Delaney and Daisuke Kobayashi, SUNY Brockport There are populations of up to 30 cm-wide, near vertical fractures in limestone pavement of the Chaumont Formation exposed in the moderately vegetated Chaumont Barrens Preserve in Chaumont, New York. Although the common view attributes the fractures to glacial loading, the presence of local deformation structures suggests a potential tectonic origin. In order to determine the responsible mechanism, we quantify the collective orientation and total length of the well-developed fractures in the whole study area, using LIDAR (light detection and ranging) elevation data. The LIDAR data are analyzed with a computer algorithm we developed to locate data points that potentially fall on the bottom of a fracture. Each linear cluster of data points is detected as a fracture, the orientation and length of which are measured. Our result reveals three distinctive fracture sets: NE-SW (~045Ëš), ENE-WSW (~070Ëš), and SE-NW (~125Ëš). The pair of fracture sets of 070Ëš and 125Ëš (2Î¸ = 110Ëš) appear to be the only conjugate fracture set that is physically possible based on the Coulomb fracture criterion, which points to a tectonic origin of the fractures. The third NE-SW fracture population may have resulted from a change in the local stress field; only ~13Ëš of a counterclockwise rotation of the horizonal Ïƒ1 could cause the 045Ëš fracture population. The post-rotation horizontal Ïƒ1 orientation agrees with the maximum horizontal stress around Lake Ontario proposed by a previous study. The orientation of the NE-SW fracture population is consistent with the strike of the local, near vertical faults.

APATITE AS A HALOGEN TRACER IN THE MIGMATITE-GRANITE COMPLEX OF SOUTHERN MAINE. Sarah Rappleye and Paul Tomascak (Geochemistry Program, SUNY Oswego, Oswego, NY 13126; William Nachlas Department of Earth Sciences, Syracuse University, Syracuse, NY 13244) Apatite, Ca5(PO4)3(F,Cl,OH), is a minor to trace mineral that plays a major role in the budgets of several elements in granitic systems, including fluorine and chlorine. The concentrations of these halogens in apatite are a reflection of halogen contents of evolving magmatic systems, so apatite may be used as a tracer. The purpose of this study is to use apatite to compare and contrast halogen contents during the crustal melting process. We use a well-studied sample from a suite of migmatites from southern Maine for this investigation. Migmatites are metamorphic rocks that witnessed some part of the melting process, and so understanding their chemical compositions helps us reconstruct crustal melting and magma transport. We analyzed apatite in situ with wavelength dispersive electron probe microanalysis using the Cameca SX5 at Syracuse University. This study concentrates on apatite from two distinct parts of a single sample from the Devonian migmatite-granite complex, taken in Cumberland, Maine. In this migmatite sample we identify a leucosome dominated by igneous-texture feldspar and quartz and a more gneissose mesosome, enriched in biotite and muscovite. Previous bulk chemical analysis of the two parts of this migmatite sample suggest that the leucosome represents the â€œleft-oversâ€ of the melt transit process: early-crystallized feldspar (primarily plagioclase) that clogged a thermally decaying melt escape network. Apatite grains from both parts of the migmatite range from euhedral to subhedral, slightly elongate with diameters ranging from 0.060 to 0.210 mm. Seven apatite grains (total of 140 spot analyses) from the leucosome yield ranges of F and Cl of 3.76-4.43 wt. % and 0.02-0.24 wt. %,

respectively. Fluorine and chlorine concentrations of two grains (total of 40 spot analyses) from the mesosome were ~3.83 wt. % and ~0.03 wt. %, respectively. All of the halogen concentrations were well above the detection limits of the instrument. The average F/Cl for grains from the leucosome is 24.6 Â± 1.9 (1 sd); mesosome grains average 126.9 Â± 1.9 (1 sd). The grain-to-grain consistency in halogen ratios within a single sub-sample gives us confidence that the local halogen distributions were consistent and hence meaningful in spite of the small number of measurements from mesosome grains. The difference in ratios between leucosome and mesosome suggests a variation in melt composition at the different stages of melting and melt segregation in this rock.

FROST TOWN ARCHAEOLOGY: PRELIMINARY RESULTS FROM THE 2019 FIELD SEASON. Emily Russell, Emily Yahn Frost Town Archaeology is a historical archaeology project that is studying the remains of an 18th-20th century logging town in South Bristol, New York. Once known as Frost Town, the area was first settled at the end of the 18th century by Euro-Americans looking to exploit the areaâ€™s forests for timber. The townâ€™s economy heavily depended on these resources, which they likely shipped to nearby Canandaigua, New York and beyond. In the summer of 2019, the project held its first excavation field season at a site known as the Hall Residence. The residence is south of the townâ€™s now-abandoned cemetery and west of the stream at which saw mills were located. From late July to early August, the Frost Town Archaeology team surveyed the site using shovel test pits and opened a series of trenches to the south of the still-visible foundation. In those trenches, the team found the remains of a possible structure and a wealth of artifacts that hint at the lives of the Pierpont family, who we believe were the last remaining inhabitants of the site before its abandonment in 1914. In this poster we will provide an overview of the findings as well as preliminary results of our first season at Frost Town.

ROCKSAT-C: DESIGNING AND BUILDING A PAYLOAD TO LAUNCH INTO SPACE Shreeya Desai, William Elliman, Victoria Loshusan, James Truley, Ileana Dumitru, Ph.D., Peter Spacher, Ph.D. Shreeya.Desai@hws.edu, William.Elliman@hws.edu, Victoria.Loshusan@hws.edu, James.Truley@hws.edu, Dumitriu@hws.edu, Spacher@hws.edu Hobart and William Smith Colleges, Physics Department For the last five consecutive years, Hobart and William Smith Colleges (HWS) has participated in the RockSat-C program. Working with NASA and the Colorado Space Grant Consortium (COSGC), HWS undergraduate students have designed and built a payload, and launched into space at NASA Wallops Flight Facility, Wallops, VA in June 2019. The payload soared to an altitude of greater than 72 miles (117 km) on a Terrier-Improved Orion rocket. The HWS 2019 payload includes three subsystems: a muon detector, a magnetometer, and a vibration dampening subsystem. The first two systems are heritage elements, and the third one is a novel experiment. Each year, we collect and analyze data that helps the broader scientific community to further understand methods of coincidence/pulse-height analysis for muon detection, and modeling Earthâ€™s geosphere. The collected data also benefits future designers who could use them to enhance and refine the detectors. The vibration damping system collected data on what materials could best dampen vibrations, which could benefit engineers to design technology that is resistant to a rocketâ€™s vibrations. In addition, we continued an outreach program with the local middle school, G-Sat, promoting interest in STEM fields to the youth of Geneva,

New York. The poster will present the analysis of data successfully collected in flight by the HWS payload.

SPECTROSCOPY ON THE FINGER LAKES.

Victoria Loshusan, Amelia McGowan, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D., and John Halfman, Ph.D
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Hobart and William Smith Colleges, Physics Department

Harmful Algal Blooms (HABs) have added toxins to a growing list of New York's waterways. These toxins degrade the water quality and can harm humans and ecosystems. The transient nature of HABs in both space and time result in monitoring challenges, and therefore adds to the difficulty in scientifically understanding the ecological criteria that trigger HABs. This research aims to investigate reflectance spectroscopy as an alternate method of detecting HABs and apply this method for remote sensing using drones. During this summer a small, lightweight spectrometer was used to record reflectance spectra in the wavelength range of 350-800 nm for eight of the Finger Lakes. The poster will present the results and the search for a correlation between these reflectance spectra and the concentration of algae in the lake water.