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Abstracts

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Alphabetical by title

2018 FIELD SURVEY: FOLLOW-UP SPOTTED TURTLE (CLEMMYS GUTTATA) CENSUS AT IRA MARSH

Dr. Peter A. Rosenbaum, Kasey Barber, Kaitlyn Talmage and Matthew Gorman. *SUNY Oswego*

Ira Marsh in Cayuga County, NY is home to a spotted turtle (*Clemmys guttata*) population (a New York State Species of Special Concern) (NYSDEC, Spotted Turtle Facts Sheet; Klemens et al., 2000). Research at this site was initiated in 1986 by David E. Collins, then senior keeper of reptiles and amphibians at the Syracuse Burnett Park Zoo, who used the technique of “headstarting” and captive rearing in hopes of observing a positive outcome from the release program. This was done in order to potentially further implement these kinds of conservation efforts in hopes of augmenting higher-risk species populations, such as the bog turtle (*Glyptemys muhlenbergii*) (Collins, 1987). The current study was a follow-up census of past research efforts executed at this site (Collins, 1987; Czech, Flite & Sumner, 1995; Czech, 1998; Hunkele, 1997; Pryor & Brown, 1994). Radio telemetry was used to assess seasonal movements, potential nesting sites, and habitat use. Morphometric data was recorded and venipuncture was performed on all turtles. The current study aimed to evaluate the impact of headstarting and habitat alteration on a native spotted turtle population at Ira Marsh. Seven spotted turtles were hand captured through the duration of this study, all of which were either classified as juveniles or females with no male spotted turtles found. Thirty baited traps were staged in the marsh to potentially increase the capture frequency. However, no turtles were captured using this technique. After one week of no findings, the traps were removed and all future captures were performed by hand.

3D MODELING OF A BRITTLE STAR VITELLARIA LARVA.

Guy Azriel, Jack Nelson, Madison Lenhart, *Rochester Institute of Technology*

There is a great deal of diversity in brittle star development. The vitellaria larva is found as a developmental stage in five families of brittle stars, although this stage is not well-studied. The formation of coelomic cavities play a major role in establishing the body plan of the organism, which drives research to model their formation and differentiation. Vitellaria larvae from *Ophioplocus esmarki* were imaged with confocal microscopy and consequently modeled in Autodesk Maya, a computer animation and modeling software, where derivatives of the coelomic cavities can be easily viewed and manipulated in three dimensions. These representations can be overlaid to give spatial awareness of the derivatives of the cavities, and provide a greater understanding of the layout of the organism. 3D modeling technology has countless applications in biology and can further our understanding of the natural world.

3D MORPHOMETRIC ANALYSIS OF DIVERSIFICATION IN PYGOPODID SKULLS AND CORRELATION WITH HABITAT

George Gurgis, Jennifer Olori, *SUNY Oswego*

Pygopodids are a group of miniaturized, elongate, and limb-reduced geckos found throughout Australia and New Guinea. Although there are only 7 genera with some containing only one species, the group has a wide variety of skull morphologies, habitat use, and locomotor abilities that can vary between or even within genera. In order to assess potential relationships between skull morphology and ecology, CT scans for 17 specimens covering six genera were used for 3D morphometric analysis. Landmark Editor was used to record 29 landmarks, which were subjected to Generalized Procrustes Alignment in Geomorph. Disparity in skull shape was visualized through Principal Components Analysis, and a MANOVA was used to test for an association between shape and habitat. After, a subset of 14 specimens with well resolved relationships were used to generate a

phylomorphospace and conduct phylogeny corrected MANOVA. When all specimens were included without phylogenetic correction, habitat ($p = 0.0234$) was significant. PC1 (skull depth, orbit shape) explained 46% of the variation whereas PC2 (snout elongation, occipital shape) explained 14%. However, phylogeny-corrected MANOVA showed that habitat ($p = 0.9609$) was not significantly correlated with skull morphology. The phylomorphospace showed a clear correlation with phylogeny as members of the same genera tended to cluster together, although a few closely related taxa did not fit that pattern. Some closely related *Aprasia* were split along PC2, as were both *Delma* specimens. Similarly, both individuals of *Pygopus* were split along PC1. Our results demonstrate that across genera, phylogeny has a strong effect on the morphology, but it may be due to small sample size because some taxa have few or only a single species. However, because some closely related taxa are significantly spread across the morphospace, habitat, or some other untested ecological factor, may cause the variation within genera.

3D PROSTATE TUMOR FORMATION IN VITRO.

Alaa Abdelmageed Ahmed, Janice B. Fung, Brenda C. Lara, Amany E. Elsharkawy, Irene M. Evans,
Rochester Institute of Technology

In living tissue, tumor cells exist in a 3D microenvironment with intricate cell-to-cell and cell-matrix interactions. To simulate this 3D microenvironment, cellular matrices (such as Matrigel) were manipulated to allow cancer cells to grow in a spheroid shape. Spheroids in Matrigel mimic live environmental in vitro conditions compared to a two-dimensional cell model. This model is useful in the study of physiological and structural changes of cells. The conditions that allow prostate cancer cells C4-2 (PSMA+) and PC3 (PSMA-; for control) to form spheroids were studied and it was found that dilution of the Matrigel matrix is important in the spheroid formation. Spheroid culture methods along with the binding of Targeted Molecular Imaging Agents (TMIA) allow visualization of cancerous cells using the confocal microscope. TMIA are able to selectively stain cells of interest, and they can be used in precise, post-metastatic therapy techniques by placing a chemotherapeutic or photoimaging agent on the TMIA. Formation of spheroids was observed over time with different concentrations of Matrigel. During and after the spheroid development, prostate cancer cells formed bridges between two spheroids; these structures resemble micro-metastases formation which may indicate cell-to-cell signaling. The TMIA tested in prostate cancer cells growing as spheroids have the potential to significantly impact cancer research and treatment.

A

A HOST OF MUTATIONS: GENETIC ANALYSIS OF GIANT SALMONELLA VIRUS SPN3US

Zein Haider and Julie Thomas, *Rochester Institute of Technology*

Bacteriophages replicate by infecting a specific bacterial host and commandeering that bacterium's mechanisms of replication. We study the giant Salmonella phage SPN3US as a model for related phages, which infect bacteria of clinical and agricultural significance. Little is understood regarding how these phages as the majority of their genes are functionally uncharacterized. Our current major focus is the virion of SPN3US, which like that of all tailed phages, consists of a head and a tail. However, the SPN3US virion is much larger than that of many other types of tailed phages, and highly complex, containing >80 different proteins. We are particularly interested in determining which proteins have structure/assembly roles versus proteins that are ejected into the Salmonella cell and have a role in host takeover. To determine the roles of different virion proteins we have isolated SPN3US mutants after chemical mutagenesis and sequenced them via Next Generation sequencing. We are currently attempting to cross two of our sequenced mutants, one of which has a mutation that prevents tail formation and the other has a mutation that prevents head maturation. We believe that the combination of

these two mutations will allow us to study highly pure head assembly particles using high resolution microscopy and mass spectrometry. We have demonstrated that these two mutants can rescue one another via classic genetic complementation tests. However, although theoretically feasible, the isolation of a specific double mutant after a cross has yet to be achieved. Therefore we aim to develop a methodology for the selection of double mutants that will be valuable with this pair of mutations, and can also be employed for other useful combinations of mutations. In addition, in the future we plan to utilize targeted gene editing techniques to assist our studies of SPN3US structure and infection.

A PHYLOGENETIC ANALYSIS OF DARRIWILIAN GRAPTOLITES, SUBORDER AXONOPHORA

Michael R. Grenier, *SUNY Buffalo*

Ordovician and Silurian stratigraphic identification and correlation as well as fine timescale resolution is highly dependent upon the identification of graptolite fossils found in the strata. Taxonomic identification is greatly aided by an understanding of the evolutionary history of the taxa. The Axonophora, a suborder of the Graptoloidea, arose in the Darriwilian Stage of the Middle Ordovician and became the dominant planktic graptolites during the Late Ordovician. Although evolutionary relationships within the Late Ordovician Axonophora are well-established, their early phylogenetic history has been unresolved. In this study, I have used morphological analysis of thirty-nine previously uncoded axonophoran taxa to develop a phylogenetic matrix of discrete codes, melded with pre-existing character sets from other researchers. Several qualitative characters have now been quantified using continuous measurements. TNT 1.5 phylogenetic software analysis resulted in over 1 trillion trees being generated and assessed. Analysis consistently produced a single most parsimonious tree (MPT) that was highly resolved. Results of several previous studies are confirmed, but several other published hypotheses are not supported. This study provides a more detailed and highly supported resolution of axonophoran clade phylogeny and evolution.

A STUDY OF THE RR LYRAE-AB VARIABLE STARS IN THE SMC AND LMC.

Brett Meerdink, Matthew Sodano, Shashi Kanbur, *SUNY Oswego*; Susmita Das, Harinder Singh, *University Enclave, Delhi, India*; Anupam Bhardwaj, *Peking University, Beijing*

Variable stars are stars whose geometries and luminosities change periodically. RR Lyraes are a type of variable star and are used as standard candles to measure intergalactic and extragalactic distances and geometries of galaxies and galactic objects. According to previous research, it is unclear if the period-color (PC) relation at minimum color (the apparent magnitude of a star at one band minus that of the star at another band) for the Small Magellanic Cloud has a slightly negative or zero slope for RR Lyraes of the fundamental mode (type ab). Using the fourier decomposition method to analyze the light curves of RR Lyrae-ab from the OGLE-IV catalog, PC relations at minimum color for the RR Lyrae-abs of SMC and LMC were produced. The robustness of the of these relations were evaluated by making cuts to the data. We found the SMC PC relation at minimum color to be slightly negative, statistically significant and very robust however the LMC PC relation at minimum color was found to have a slightly statistically significant, robust, positive slope.

ADDITION OF MCH INHIBITS VDR WHEN MCHR1 LOCALIZES TO TRANSIENT PRIMARY CILIUM DURING ADIPOCYTE DIFFERENTIATION.

Bianca Camillaci, Dr. Laurie Cook, The College at Brockport

Melanin Concentrating Hormone (MCH) is a neuropeptide involved in the regulation of appetite, sleep-wake cycle and energy balance. MCH binds to the G-protein coupled receptor MCHR1, found in the brain, thymus and interestingly, adipocytes. In our current research, we aim to understand the importance of MCH in adipogenesis, and what genes are regulated by MCH using developing 3T3-L1 adipocytes. Our previous studies have

demonstrated that on day two, differentiating adipocytes develop a transient primary cilium where MCHR1 localizes, and is thought to alter cell signaling. Additionally, on day two of adipogenesis, RNA Seq analysis has demonstrated that Vitamin D Receptor (VDR) displays the most significant change, indicating decreased expression with the addition of MCH. The Vitamin D Receptor, which is a nuclear receptor, is primarily known for its importance in calcium absorption when bound to its ligand calcitriol, the active form of Vitamin D. Furthermore, some studies have shown that VDR serves as an important transcription factor in adipocytes differentiation, yet conflicting data is present on its significance. The objective of the present study is to further understand the role of MCH on VDR, using Quantitative PCR (qPCR) over the full ten-day process of adipocyte differentiation. A ten-day differentiating protocol was used to take the cells from pre-adipocytes to adipocytes, where the experimental group was treated with MCH for 6 hours prior to RNA harvest. RNA was harvested from both the control and experimental adipocytes every two days, starting at day zero. The extracted RNA was used to make cDNA in order to track VDR expression with qPCR over the ten days. The qPCR data was analyzed using delta delta CT, with a polymerase II reference gene control. At this time, the results of this experiment show the highest level of VDR expression occurs at day two. Additionally, consistent with RNA Seq data, the qPCR results indicate notable inhibition of VDR with the addition of MCH only on day two, when MCHR1 localizes to the transient primary cilium. Future experiments will explore possible pathways which MCH regulates VDR and VDR's specific significance in adipogenesis.

ALGINATE MICROPARTICLES AS BIOSIMULANTS.

Rachel Czerwinski, *SUNY College of Environmental Science and Forestry*; Meghan Ramsey, Frances Nargi, Trina Vian, Benjami Ervin, *MIT Lincoln Laboratory*

Biological sensors have a wide range of applications, from environmental to agricultural to industrial to medical. In order to test their sensitivity and range, sensors are generally triggered by simulants. The ideal simulant is something that not only resembles the particle of interest and can trigger the sensor detection technology, but is safe and physically and chemically stable. As there are many different biological detection technologies, different simulant properties may be needed to trigger each sensor. While microbes can be used to test any sensor utilizing biological detection technologies, the perceived or actual safety risks associated with working with biological materials can make it difficult to get approval for their use in all circumstances. Here, we describe initial efforts in the production of micron-scale particles that can be used to test or calibrate biological sensors. The product should be monodisperse in size and shape, safe for release, and functionalizable to enable testing of diverse sensor technologies. Alginate, a safe, naturally occurring copolymer of guluronic acid and mannuronic acid found in seaweed, was chosen as the polymer of interest after a survey of materials due to its safety, its water solubility as a salt with a monovalent cation (e.g. sodium) and its crosslinking gelation in the presence of divalent cations (e.g. calcium). The method of particle production chosen was microfluidics. Microfluidic systems allow for precise control over droplet size and shape, producing a highly homogeneous product. An initial proof of concept study was performed using methods described in the literature in order to justify further methods development efforts.

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ALLELIC HETEROZYGOSITY IN THE CANDIDA ALBICANS BIOFILM TRANSCRIPTION FACTOR, ROB1.

Julia Rak, Megan McGraw, Virginia Glazier, *Niagara University*

Candida albicans is a dimorphic opportunistic pathogen capable of growing both as yeast and filamentous cells. While residing harmlessly as a commensal in the gastrointestinal tract of humans, *C. albicans* maintains responsibility for >50% of all systemic fungal infections. *Candida albicans* is diploid in nature and has a limited parasexual cycle, which has resulted in allelic heterozygosity at a given gene loci. One gene with allelic heterozygosity is *ROB1*, which plays a role in transcription regulation responsible for providing *C. albicans* with ability to initiate hyphal growth. The hyphal phenotype is a virulence factor, and *C. albicans*' ability to penetrate tissue, colonize organs, and form biofilms (on implanted medical devices) can be attributed to hyphae formation. The deletion of one and/or both of the alleles of *ROB1* has been found to affect the production of the biofilm and the rate of filamentous growth. Our findings indicate that allelic heterozygosity of *ROB1* results in desperate transcriptional profiles depending on which allele is deleted. Here we show that the *rob1ΔA/ROB1B* has reduced filamentation and provide evidence to suggest that *TLO10* may be required for filamentation in the *rob1ΔA/ROB1B* mutant.

ALTERNATIVE SPLICING DURING ADIPOCYTE DIFFERENTIATION

Peter Giangrasso, Dr. Laurie Cook, and Dr. Rongkun Shen, *The College at Brockport*

In mammalian cells, one single gene may produce multiple transcripts leading to protein isoforms, which is called alternative splicing. This leads to the large proteome using a limited number of genes within a genome. We obtained the expression data of the RNAs of pre-adipocytes and post-adipocytes using the cutting-edge next-generation sequencing technology (RNA-Seq). We used the new Tuxedo suite to identify differential expression of genes as well as novel transcript isoforms in the mouse (mm10 assembly) genome. Alignment was completed using HISAT2, StringTie was used for assembly, detection of novel isoforms, and quantification, and Ballgown for differential expression analysis. 46 gene isoforms were differentially expressed between the samples. We suggest that the significant changes in splicing and expression between the control adipocytes and the adipocytes treated with melanin concentrating hormone (MCH) have a relation to obesity. The resulting BAM files were visualized in UCSC genome browser. Python scripts were written to web scrape the UCSC genome browser evidence of the novel gene isoforms. Further analysis with more biological replicates and deeper sequencing will be completed in the future to further support these findings.

AN INVESTIGATION INTO NANOSCALE OLIGOMERIZATION OF AMYLOID BETA PEPTIDE AT THE INTERFACE OF GOLD AND ICE.

Justin Slovak, Brianna Paulino, Shreyya Malik, Sakura Hamazaki, Kazushige Yokoyama, *SUNY Geneseo*

Formation of oligomers of amyloid beta ($A\beta$) is regarded as a critical onset stage of Alzheimer's disease. While oligomers are often produced as a heterogeneous ensemble of different types of oligomeric forms, (e.g., dimers, trimers, tetramers, etc.), the presence of a certain sized nanoscale surface may selectively produce a specific oligomeric form. The order of oligomer was considered to be increased proportionally to that of the size of nanoscale surface available. For example, dimer, trimer, and tetramer units were selectively produced as the gold size increased from 10 nm to 100 nm. In order to establish a new methodology to probe a specific oligomeric form, the fluorescence dynamics of a fluorescein-attached $A\beta$ 1-40 monomer (FA β 1-40) were investigated. The fluorescence decay times of FA β 1-40 for various sizes of gold nanoparticles, ranging between 10 nm and 100 nm in diameter, were observed as the folded and unfolded conformations of the monomer prevailed which was induced by altering the pH between 10 and 4, respectively. Faster dynamics were observed in acidic environments as well as in the presence of the larger gold colloids, implying that larger oligomer units provide a higher density for nonradiative channels than their smaller counterparts.

AN INVESTIGATION OF COMMENSAL-IMMUNE INTERACTIONS ALTERED BY ORAL PATHOGENS.

Authors: John Lepore, *SUNY Geneseo*; Sarah Metcalfe, Megan Jones, Michelle Panasiewicz, Michelle Visser, Jason Kay, *SUNY Buffalo*

Pathogenic bacteria alone cannot lead to periodontitis in model systems. However, when combined with commensal bacteria the synergy between the bacteria allows disease to develop. Our previous studies found that macrophages are less able to kill the commensal *Streptococcus gordonii* when activated, suggesting that in a disease context this normally commensal bacterium may be able to act as an accessory pathogen. Here we begin to examine the role the traditional oral pathogen *Porphyromonas gingivalis* may play in disrupting macrophage-commensal interactions. A sterile air pouch was created on the dorsal side of mice via a subcutaneous injection of sterile air to replicate the subgingival environment. Groups of fMLP, fMLP+IL4, and fMLP+IFN γ /LPS were injected into the air pouches of different mice to recruit phagocytes for 24 hours. *S. gordonii* were injected into each grouping and were incubated for 2 hours. In addition, varying combinations of *S. gordonii* and *P. gingivalis* were given to human macrophages and were studied with a “sandwich” type ELISA to determine the levels of the cytokines TNF and IL-1 β released. Flow cytometry of the fMLP, fMLP+IL4, and fMLP+IFN γ /LPS groups indicated a noteworthy presence of neutrophils in addition to macrophages at the 24-hour time point. Due to the similar role of neutrophils and macrophages in the degradation of bacteria, it is difficult to determine to what extent each leukocyte’s role was in the destruction of the bacteria. In respect to the TNF ELISA, the difference in release between 100% *P. gingivalis* and the combination of 20% *P. gingivalis* and 80% *S. gordonii* was statistically significant with a $P < 0.05$ thus indicating the possibility of increased propagation of periodontal disease in the presence of this combination of the bacteria, as opposed to solely *P. gingivalis*. With respect to the IL-1 β ELISA, the difference in IL-1 β release between the 100% *P. gingivalis* and the combination of 20% *P. gingivalis* and 80% *S. gordonii* and the difference between 100% *P. gingivalis* and 100% *S. gordonii* are statistically significant with $P < 0.05$. This suggests a synergy of *P. gingivalis* and *S. gordonii* that may further propagate periodontal disease more than the pathogenic *P. gingivalis* does alone. In agreement with previous research, our study suggests that relative to *P. gingivalis*, more cytokines are produced when there are two bacterium present as opposed to a single bacterium—supporting the hypothesis that commensal bacteria in combination with pathogenic bacteria play a crucial role in furthering periodontal disease.

ANATOMY AND MICRO-MORPHOLOGY OF THE STYLAR UMBRELLA OF SARRACENIA PURPUREA (NORTHERN PITCHER PLANT).

Authors: Chad Halson, Jinyan Guo, *SUNY Oswego*

The genus of North American Pitcher Plants, *Sarracenia*, are well known for their unique carnivorous pitcher-shaped leaves, while little research has focused on their flowers. *Sarracenia* flowers have a unique umbrella-shaped style, a portion of the female reproductive organ that consists of the distal regions of five fused carpels. Two regions make up the stylar umbrella, a flat stylar canopy and stylar stalk, which is unlike most other flowers with filamentous styles. We hypothesized that the flattened umbrella-shaped style plays an important role in attracting pollinators while still maintaining its function as a part of the transmitting tissue and compared structures on the petal and leaf to the style. Mature samples of petals, styles, and leaves of *Sarracenia purpurea* were imaged with both a light microscope and a scanning electron microscope to observe anatomy and micro-morphology. We found that both surfaces of the stylar canopy have convex epidermal cells with and without reticular cuticular striations, unicellular trichomes with striped cuticular striation, secretory glands, and stomata. Convex epidermal cells are similar but less round than cells on the distal end of the petal and may provide visual cues for pollinators. Trichomes are similar to those on the pitchers lid and may provide tactical cues for pollinators. Secretory glands are similar to secretory glands found in lower regions of the pitcher found in previous work and may provide olfactory cues for pollinators. The presence of stomata may indicate a possible photosynthetic role; however, further research is needed to identify if chloroplasts are also present. The regions

of transmitting tissue (stigma, stilar canal, and stilar stalk) do not display these cues for pollinators that are seen on the stilar canopy. These regions are all characterized by flat elongated epidermal cells with reticular cuticle striations. Thus, our anatomical and micro-morphological data indicates that the unique umbrella-shaped style of *Sarracenia purpurea*, while still maintaining its role as apart of the transmitting tissue also provide visual, tactile, and olfactory cues for pollinators.

ANOCTAMIN 1 & ANOCTAMIN 2 AT THE MOLECULAR LEVEL

Alexandra Flint, Bailey Majtyka, Christina Abraham, Cori Mainville, Iesha DeLesline, Adam Rich, *The College at Brockport*

Background: Anoctamin 1 (ANO 1) and anoctamin 2 (ANO 2) are calcium activated chloride channels (CaCCs). CaCCs are necessary for cellular physiology including epithelial secretion of electrolytes and water, sensory signaling, neuronal regulation, and regulation of vascular tone. In cystic fibrosis ANO1 deficiencies can contribute to viscous mucous accumulation. Additionally, ANO1 is an important marker for ICC, which is important to produce the electrical slow wave in the gastrointestinal tract. ANO2 is suspected to be important for sensory signaling in the eye and in the olfactory apparatus. Previous research done in Systems Physiology classes have shown ANO1 or ANO2 expression in the brain, gut, and eye of zebrafish. Aims: The overall goal of this experiment was to determine the presence of ANO 1 and ANO 2 in the eye, retinal pigment epithelium (RPE), olfactory bulb, and gastrointestinal tract in *Danio rerio* (zebrafish) through isolation of ANO1 and ANO2 mRNA in zebrafish. Methods: Zebrafish mRNA was isolated by dissecting tissue samples from the gastrointestinal tract, eye, RPE and olfactory bulb, performing further RNA isolation using Qiazol. The product was used to synthesize cDNA via RT-PCR and further amplified through PCR. Amplified DNA was visualized on agarose using gel electrophoresis. ANO 1 and ANO 2 bands formed using different primers, were compared to bands formed through B-Actin and Kit A controls and Quickload purple 100bp DNA ladder. Results: ANO 1 and ANO 2 RNA is expressed in the whole eye and specifically, the retina of Adult zebrafish. ANO 1 RNA is expressed in adult zebrafish GI tissues. Current experiments are examining ANO 1 and ANO 2 RNA expression in the olfactory apparatus. Conclusion: ANO 1 and ANO 2 are expressed in the whole eye and in the retina of adult zebrafish. Only ANO1 is expressed in the GI tract of adult zebrafish.

APPLICATIONS OF CRISPR-CAS9 TECHNOLOGY ON WNT5A IN DANIO RERIO EMBRYOS

Andreia Cadar, Guy Azriel, Rachel Fasiczka, Jeremy Kane, *Rochester Institute of Technology*

Clustered Regularly Interspaced Short Palindromic Repeats, or CRISPR, are genomic elements found in many prokaryotic genomes. These components were discovered in the bacterial defense against bacteriophages and the capabilities of the CRISPR-Cas9 system inspires a promising new technology for controlled in vivo gene editing. This technology uses highly specific guide RNA molecules that selectively bind to targeted genetic sequences. When bound to a programmable nuclease such as Cas9, the sgRNA-Cas9 complex targets and cleaves this genetic sequence. This study seeks to utilize the CRISPR-Cas9 system to modify a model system, *Danio rerio*, or zebrafish. sgRNAs were created in Benchling to target exons 2, 3, and 4 of the *wnt5a* gene, an important developmental gene found in zebrafish that controls kidney, pancreas, neck, tail, and fin development. This gene was amplified with primers designed in IDT PrimerQuest, and the sgRNA was complexed with Cas9 protein in vitro, which creates a ribonucleoprotein complex that was visualized when run on a polyacrylamide gel electrophoresis. With this result, the sgRNA-Cas9 complex can be injected into zebrafish embryos, where it is expected to create deleterious mutations that do not express *Wnt5a*, thus inhibiting certain stages in the development of the organism.

ASSESSING SALT MARSH VULNERABILITY, RESILIENCE, AND BLUE CARBON POTENTIAL THROUGH THE USE OF HIGH RESOLUTION HYPERSPECTRAL IMAGERY

Sarah Goldsmith, Rehman Eon, Christy Tyler, Charles Bachmann, Christopher Lapszynski, David Osgood,
Rochester Institute of Technology

Coastal wetlands provide the greatest number of ecological services of any coastal environment, including support for coastal fisheries, habitat, protection from storm surges, reduction of nutrient loading to coastal waters, and carbon sequestration at rates that are potentially an order of magnitude greater than that of terrestrial forests. However, carbon storage within marshes is highly variable on very small spatial scales and there is still a great deal of uncertainty regarding salt marsh carbon sequestration due to this heterogeneity. Additionally, salt marshes are vulnerable to a variety of anthropogenic impacts such as human manipulation, land conversion, invasive species, and global climate change, which may be related to acute die-off within salt marshes. To evaluate the vulnerability and resilience of marshes at a large scale requires technologies such as high-resolution remote sensing techniques. We evaluated the physiological response and resulting hyperspectral signature of *Spartina alterniflora* (smooth cordgrass), the dominant plant in salt marshes along the US east and Gulf coasts, subjected to relevant stressors in both a greenhouse setting and across natural environmental gradients in the field. Vegetation indices were applied to develop a spectral library of marsh states that can be used to determine marsh vulnerability in the field using remote sensing techniques. The ability to predict marsh stressors and marsh state may be an important tool for determining the vulnerability of marshes and could aid in conservation efforts by identifying the most essential locations for conservation and assist in evaluating how stressors impact critical ecosystem services such as carbon sequestration potential.

B

BACTERIAL EXPRESSION OF CHIMERIC ESCHERICHIA COLI AND TRYPANOSOMA BRUCEI DNA METHYLTRANSFERASES.

Cassandra C. Taber, Kevin T. Militello, *SUNY Geneseo*

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. The plasmids were re-isolated after three hours of growth. They were then digested with various restriction enzymes blocked by methylation. Each digestion was run on an agarose gel with DNA from an uninduced cell as a control. All four proteins were produced at 20 degrees C but the proteins with the TbDmt DNA binding domain were less soluble than the other two. EcDcm methylated at its expected site, 5'CCWGG3', but TbDmt showed no signs of methylation at any of the sites tested. To date, it appears that the chimeric protein with the EcDcm DNA binding site and TbDmt enzymatic domain is methylating at 5'CCWGG3', the same site EcDcm methylates. This suggests that TbDmt is a DNA methyltransferase, but the sequence it methylates is potentially not 5'CCWGG3'. Further work will be done in improving the conditions in

which the chimeric proteins are produced to enhance folding of the potential DNA methyltransferases. In summary, this work contributes to our limited knowledge of epigenetic regulation in bacteria and protists.

BEAVER FORAGING PREFERENCES AND IMPACTS ON FOREST STRUCTURE IN NEW YORK'S ADIRONDACK MOUNTAINS

Michael J. Mahoney, John C. Stella, *SUNY Environmental Science and Forestry*

Beavers (*Castor canadensis*) are ecosystem engineers, causing changes at the landscape scale due to a combination of their damming and foraging behaviors. While these behaviors – and the impacts they have on riparian communities – have been well studied in several forest regions, they are poorly understood within the forests of northeastern North America. Field surveys at 19 beaver locations throughout New York's Adirondack State Park assessed beaver foraging preferences and the impacts of beaver activity on forest structure and composition. Forest canopy closure decreased with proximity to beaver impoundments, and forest structure and composition also varied along this gradient. Beavers preferentially harvested stems between 2 and 10 cm diameter, with the 2 to 5 cm size class most generally preferred. Deciduous species were also preferentially harvested, with typically disfavored species such as American beech (*Fagus grandifolia*) harvested at higher rates than in studies from other regions. Logistic regression models showed clear foraging preferences for stems closer to the impoundment of intermediate sizes for all modeled groupings and species. Understanding the impacts beavers will have on riparian forests in the Northeast is critical as beaver continue to recolonize their historic range, creating new management challenges and opportunities in years to come.

BEHAVIORAL DIFFERENCES EXHIBITED IN ZOO-HOUSED SOCIAL AND SOLITARY FELIDS.

Abigail Robinson and Susan Margulis, *Canisius College*

Lions, tigers and snow leopards have long been classified as either social or solitary by nature, with tigers and snow leopards being solitary and lions being the only social member of the genus *Panthera*. These big cat species are often seen in zoos, and these labels dealing with sociality may impose some limitations on how we assess the different effects of zoo housing on these species. This study aims to explore the ways in which different species of *Panthera* (two solitary, one social) are influenced by, and behave in the zoo environment. Data were collected for three to twelve months on twelve subjects from two zoos in Western New York (7 lions, 2 tigers, 3 snow leopards). Lions were found to exhibit less stereotypic behaviors than the tigers and snow leopards despite the fact that all species were housed in species-typical groups. This was especially noticeable in the tigers. We suggest that sociality may buffer animals from stress related behaviors in a zoo environment. These results highlight the value of multi-institutional studies in a zoo setting.

BIOSTRATIGRAPHY, SEA LEVEL CHANGE, AND DISCONFORMITIES IN THE UPPER DEVONIAN CHATTANOOGA SHALE OF WESTERN TENNESSEE BASED ON CONODONTS AND MAGNETIC SUSCEPTIBILITY (PRESENTED AT GSA 2017 IN SEATTLE, WA)

Josephine Chiarello, Emily Hauf, D. Jeffrey Over, SUNY-Geneseo; Jin-Si R. Over, University of Victoria, Victoria, BC
Thomas J. Algeo, *University of Cincinnati*

A drill core in Humphreys County, western Tennessee on the western side of the Nashville Dome in the Illinois Basin contained 14 m of predominantly organic-rich Chattanooga Shale that lies unconformably on the Middle Devonian Sellersburg (Pegram) Limestone and is overlain by carbonates equivalent to the Sunbury Shale in the Appalachian Basin. Conodonts were recovered from 78 horizons; bulk magnetic susceptibility was measured at 5 cm intervals. Conodonts indicate that the base of the Chattanooga is Frasnian Zone (FZ) 3; three Frasnian conodont zone intervals are discernable. The Frasnian-Famennian boundary is disconformable, characterized by thin sandstones and a lag bed, where crepida Zone strata lie on FZ 13 strata. Famennian strata are divisible into

five conodont zone intervals, the Protosalvinia interval is recognized above the first occurrence of *Palmatolepis glabra distorta* and *Palmatolepis grossi*, which indicate the utahensis Zone through granulosus Zone; the Devonian-Carboniferous boundary seems to be disconformable, however this interval of the core had poor recovery. A medium gray muddy carbonate interval above the last Famennian fauna yielded a rich siphonodellid fauna typical of the Sunbury Shale and assigned to the sandbergi Zone. Magnetic susceptibility shows six major and 27 minor trends. Abrupt shifts are attributed to eight significant disconformities in the strata which correspond to increases in organic content and decreased MS values over the disconformity interpreted as deepening/flooding events.

BITE FORCE ANALYSIS OF THE HUMAN MANDIBLE.

Harrison Moses, *SUNY Geneseo*

Describing the capabilities and limitations of jaw morphology throughout evolutionary history provides a clear picture of what human ancestors were capable of eating, and how they processed their food. Specifically, bite force, or the force used to break down food, reflects the strength of the jaw, and thus may influence dietary preferences. The chewing and maximum biting capabilities of 15 individuals were assessed with a bite force pressure gauge. Known skeletal correlates of bite force, including length of the ramus and body of the mandible, the magnitude of the gonial angle, and occlusal surface area of the lower dentition were also measured. These data were compared with corresponding skeletal measurements taken from casts of *A. afarensis*, *Homo neanderthalensis*, and *Homo heidelbergensis* to approximate their maximum bite force and chewing capabilities. The resulting correlations between maximum bite force, the gonial angle, and occlusal surface area were significantly stronger than those found for the chewing force. This study evaluates the usefulness of considering both maximal bite force and chewing force in dietary research methods. Further, implications of the data are considered in terms of food choice throughout evolutionary history.

BLACK SOLDIER FLY LARVAE COMPOST VIABILITY STUDY

Dawn Carter (PhD), Sarah Brownell (PhD), Shwe Sin Win (PhD), Brian Thorn, Lennon Cavanaugh-Gordon, Nicole Cavanaugh, Vince Darmohray, *Rochester Institute of Technology*

Composting is an extremely valuable way to get rid of unwanted waste while enriching the nearby environment. Black Soldier Fly (*Hermetia illucens*) larvae are an excellent organism to facilitate compost systems, however they are native to southern climates. This experiment is being done to see whether BSF larvae can be used in an urban food waste composition system for a community such as RIT. This would help RIT meet its goal to become waste and carbon neutral by 2030. One of the advantages of BSF larvae is that they can reduce waste volume up to 40% in comparison to other compost methods. They also consume usually neglected materials such as meats and oils and have the possibility to create other useful bioproducts such as biodiesel, fertilizer, and methane. This experiment will have a system built specifically for BSF larvae and measure the mass and energy balance. A closed stirred tank reactor with equal air flow in and out and a fan inside to keep the air well mixed will be monitored for temperature and humidity differences to understand if such a system is viable for a northern environment. A shed is also being constructed to house the BSF larvae during the harsher New York State winter.

BUFFALOPTERUS WITHIN THE LATE SILURIAN BERTIE GROUP OF NEW YORK AND ONTARIO, CANADA.

Samuel J. Czurca, Jr., Stephen Mayer, Wayne Davey, Tod S. Clements

The Silurian strata preserved in the northern Appalachian Basin are, amazingly, replete with eurypterid horizons each bearing a distinctive biota. The Bertie Group, in particular is the repository of the best known eurypterid faunas (extinct sea scorpions) in the world. While there are 'common' eurypterid species known from certain

units within the Bertie Group (viz. Phelps Waterlime and stratigraphically higher Williamsville Formation), some forms are exceedingly rare including the bizarre *Buffalopecterus pustulosus* (Hall, 1859). We report here for the first time the occurrence of *Buffalopecterus* within the Phelps Waterlime and the discovery of a large carapace by Stephen Mayer in the Canadian Williamsville Formation ('A' Member) at Ridgemount Quarry South in Fort Erie, Ontario, Canada. The specimen from the Phelps Waterlime was found among a small collection of carapaces kindly given to one of us (SJC) in the 1980s by Allan Lang from his quarry in the Fiddlers Green Fm. The specimen is currently in the collections of the Peabody Museum of Natural History. The Canadian (Mayer) specimen is an unusually large carapace and may represent the first known occurrence of the genus in the Canadian Bertie Group. One of us (TSC) was able to saw the specimen out of the bedrock. The counterpart of this specimen is also now in the eurypterid collections of the Yale Peabody Museum. Ironically, shortly after the discovery of the Mayer specimen, extraordinarily, Tod Clements discovered another specimen in the Canadian quarry (Clements specimen). This was totally unexpected as this bed (Williamsville 'A' Waterlime) has been searched for decades without even a trace of visible evidence. Aside from our knowledge of the type specimen (see Clarke & Ruedemann, *The Eurypterida of New York*, 1912), little is known about appendages of this form. The telson, as originally and erroneously interpreted, is so strange that this eurypterid was once thought to be a pterygotid. Clarke & Ruedemann reported a probable length of a living animal at about 1.0 meter. *Buffalopecterus* is one of several types of strange eurypterids of which we know little to nothing about their habitat or why we find pieces of this arthropod where we find them. Added Notes, carapace measurements: (length vs. width measured at base): Mayer carapace l=12 cm., w = ~19.5 cm. Clements carapace l=8.0 cm., w=~13.8 cm. James Hall (type) carapace l=6.7 cm., w=12cm. Pohlman carapace l=5.0 cm., w=9.3 cm

C

CAN THE OAK TWIG PRUNER BEETLE (*ANELAPHUS PARALLELUS*) BE SEXED?

Jesse Freeling Brundage, William Brown, Luciana Cursino, *Keuka College*

Antennae of female oak twig pruners (*Anelaphus parallelus*) rarely extend beyond the elytra, while male antennae more often do. The aim of this work was to better quantify this generality, identify other morphological characteristics by which this species could be sexed, and develop a fast molecular sexing method. For each of 48 specimens, total antennae length was measured and divided by the total body length to determine an antennae : body length ratio. A histogram of the antennae to body length ratio revealed two groups: one group with antennae length often longer than the body length, assumed to be males, and the other group with antennae length seldom longer than the body length, assumed to be females. DNA was obtained and PCR using *dxs* gene primers was tested but no sex-specific bands were identified. Without positive control specimens, we cannot infer more from these preliminary findings. We intend to rear adult beetles from pruned twigs and, hopefully, identify males and females from behavioral characteristics. Once sexed positive controls have been obtained, efforts will continue to sex the beetles through morphological and molecular methods.

CARBENE LABELING MASS SPECTROMETRY-CONTINUED OPTIMIZATION OF A TOOL FOR BIOPHYSICS.

Ellirose Edwards, Sahara Javner, *Houghton College*

Protein biophysics is an important field where it enables one to study protein folding, association, and dynamics. Some diseases associated with protein miss folding and miss aggregation are Creutzfeldt-Jakob disease, fatal familial insomnia, multiple systems atrophy, and Alzheimer's disease. Much is still unknown about these diseases and few treatment options exist. The overarching goal of this work is to explore amyloid-beta aggregation that is associated with Alzheimer's disease. To better understand protein miss folding, we are developing a new mass spectrometry-based technique. This involves rapidly labeling proteins as gas-phase ions

(produced by electrospray ionization) using an aggressive omniphilic reagent, carbene. This technique adds another new way to study proteins. The main focus of our efforts was to continue optimizing this technique using affordable samples of aspartame and synthetic melittin. Using melittin, having a solved x-ray structure, allows for the comparison of our results with published data. Our results were promising showing that we were able to optimize the yield of methylene labeling using aspartame. Labeled melittin data was significantly more complex than that for aspartame, but was somewhat consistent with the previously published solved melittin homotetramer structure.

CARBENE LABELING MASS SPECTROMETRY.

Ellirose Edwards, Dr. Paul Martino, *Houghton College*

Aggregated proteins are often difficult to study due to their amorphous structure. Many of our current methods are not adequate to deal with all proteins. One such protein of interest is Amyloid Beta. This protein is expected to have an influence on the senile plaques produced by Alzheimer's Disease, but since it is difficult to image Amyloid Beta proteins, this cannot be confirmed. We attempted to rectify this problem with a labelling method using electrospray. Our current focus has been on refining the process and attempting to test the process on model systems. Our results indicate that we indeed were able to label peptides and optimize this chemistry, but that our structural results on a model system were more complex to elucidate than originally anticipated.

CHARACTERIZATION OF FSD-1 MUTANT ALLELES IN NEUROSPORA CRASSA.

Mark Soto, Elizabeth, Hutchison, *SUNY Geneseo*

NDT80 is a key meiotic transcription factor in *Saccharomyces cerevisiae* and NDT80 homologs are present in filamentous fungi. *fsd-1*, a homolog of NDT80, has been identified as an integral regulator of sexual development in *Neurospora crassa*. *N. crassa*, a well-studied model organism, is a filamentous ascomycete fungus that can undergo asexual or sexual reproduction. To further understand the *fsd-1* gene and its role in *N. crassa*, we will construct mutant alleles of *fsd-1* and assess whether these mutations affect *fsd-1* function. In *S. cerevisiae*, several Ndt80 loss-of-function mutations have been shown to exhibit a decrease in both DNA binding and sporulation. This study focuses on mutating amino acid residues located within the DNA binding domain and the carboxyl terminus. To accomplish this, primers will be designed and used in double-joint polymerase chain reaction, a method used to construct alleles that target to the native locus without the need for subcloning. Along with the mutation is the green fluorescent protein (GFP) tag for protein localization study and hygromycin resistance for selection purposes.

CHARACTERIZATION OF NOVEL GIANT BACILLUS THURINGIENSIS SIPHOVIRUSES RELATED TO B. ANTHRACIS PHAGE TSAMSA.

Benjamin Hall, Breanna Laber, Ei Thinzar Phyto, Mohamed Mohamed, Julie Thomas, *Rochester Institute of Technology*

Bacteriophages are naturally occurring bacterial viruses that appear in abundance in nearly every ecosystem and are estimated to be the most abundant biological entities on the planet. We recently isolated the novel bacteriophages MnM and Onix from soil samples from Buffalo, NY and Bavaro, DO. Both phages infect the soil bacterium *Bacillus thuringiensis*. Our analyses of MnM and Onix have shown that both are siphoviruses with unusually long tails (~400nm). Sequencing of the MnM and Onix genomes determined them to be ~160 kb long and 73% similar to one another at the nucleotide level. Bioinformatic analyses of the two phage genomes identified the most closely related phage to be that of the giant siphovirus Tsamsa, which was isolated in Namibia and infects *B. anthracis*. A combination of bioinformatic strategies, including HMM-based tools, were utilized to identify a module of head genes, as well as the genes encoding the main components of its long tail.

In these phages, there are only a few virion genes that have a known function, including the DNA packaging enzyme and tape measure protein, which has a significant role in determining the length of the tail. Our goal is to further characterize MnM to enhance the understanding of this group of novel giant phages. We plan to confirm and expand upon our identifications in further studies by using mass spectrometry of purified virions. This knowledge will be relevant to understanding how these, and related phages, interact with their bacterial hosts, which include the human pathogens *B. anthracis* and *B. cereus*, and also their roles in the environment.

CHARACTERIZATION OF THE SARRACENIA PURPUREA INQUILINE MICROBIAL COMMUNITY.

Kelsey Barrus, Jacquelyn Lewis, Jason Bintz, and Jamie Potter, *Houghton College*

Much of ecological theory generates predictions about number of species and their abundance. Testing these predictions is challenging as populations and communities are not easily manipulated, the relevant spatial and temporal scales are usually very large, and it is unrealistic to categorize everything. To overcome these obstacles, there has been a long history in ecology of using microcosms as model systems for testing ecological theory. The Northern Pitcher Plant (*Sarracenia purpurea*) is a useful model system as it has well defined communities, short generation time, discrete and easily manipulated individuals, and lives at a variety of spatial scales. The current characterization of the bacterial community in the plant is incomplete, thus the goal of this project is to quantify and characterize the bacterial community using standard microbiological techniques. Samples were collected from four groups of plants based on location and age. Samples were diluted with saline solution to 10³ and 10⁵ then plated on Luria-Bertani (LB) and Plate Count Broth (PCB) media. Plates were incubated at 30°C and growth was checked at 16, 40 and 60 hours. Colony forming units were counted as a representation for the number of individuals in the community; morphotypes (i.e. color, shape, size, margin and texture) were used to identify species. Gram stains and digital imaging were used for further characterization. There were 45 morphotypes found on PCB and 29 on LB. Additionally, greater diversity in species was found in samples obtained farther from the shore line and greater abundance of individuals was found in samples from older pitchers. Further research will include molecular identification of bacteria using 16S RNA sequencing, analysis of biochemical growth requirements of bacteria using standard microbiological techniques, and additional identification and comparison of bacteria in other communities and at different time scales throughout the seasons. This will allow for further characterization to use the data for testing ecological mathematical models.

CHARLES LYELL'S VISIT TO WESTERN NEW YORK - MASTODON, FOREST AND SOCIETY.

Russell Judkins, *SUNY Geneseo*

On his first trip to North America, in the year 1841, Charles Lyell visited several areas of Western New York and recorded in his journal of that trip observations which still have research interest for the region today in the fields of Anthropology, Social History and Geography, as well as in his own field of Geology. These observations focus, first, upon mastodon remains in Western New York, second upon the nature and character of the native forest as it was then being cleared and removed for agriculture, and third upon a visitor's notes on social changes wrought by the then still relatively new American democracy and its attendant social behaviors. First among these, Lyell recorded specific contacts with mastodon fossils at Niagara Falls and Rochester, and utilized them in forming local chronological estimates and comparisons, relative to ancient stream bed levels, index fossils, and the hypothetical presence of the human species. Later developments in paleontology would fully validate Lyell's early awareness of the mastodon and its importance in NYS scientific research. Even more importantly however - and especially noteworthy for those in attendance at the RAS Meetings held this year in Geneseo - Charles Lyell left a brief and intriguing account of his own supervision of a mastodon re-excavation in the Village of Geneseo. From this re-excavation he determined the actual position of the animal's burial in

relation to modern fresh water shell remains, which were one of his special research interests and which resolved a discrepancy in the report of the original excavation. Secondly, in addition to his ancient probosidian observations, Lyell offered an account of his own informal albeit brief study of the age of the ubiquitous forest cover of Western New York, as sampled at Bath. His estimates show a surprising recency for the forested land he traveled through and observed being removed. Its age was substantially less, by his estimates, than even the period of Iroquois occupancy of the region. Finally, Lyell's keen observational skills offer insights regarding the social, interpersonal behavioral, and religious systems of New York's western frontier at an era of population transformation, major growth from the impact of canal building, the social ferment of the Second Great Awakening/Burned Over District period, and the dawning of the second half of the nineteenth century. Charles Lyell's observations remain relevant and a delight today, as they were when originally published in 1855.

COELOMOGENESIS IN A BRITTLE STAR VITELLARIA LARVA

Jackie Moser, Guy Azriel, Christina Ideman, Taylor Kovar, Melissa Barton, Nasreen Jaff, Hyla Sweet, *Rochester Institute of Technology*

One type of abbreviated development in ophiuroids includes the vitellaria larva, which is found within five families. The vitellaria has many differences from the ophiopluteus, including the lack of feeding and digestive structures, and metamorphosis in as early as 3-5 days. The coelomic cavities generate much of the internal body systems of the juvenile brittle star, and thus one would expect many differences in development in a nonfeeding larva with fast development to the juvenile stage. Embryos and larvae from *Ophioplocus esmarki* were fixed, cleared, and examined with confocal microscopy. We found that the early aspects of coelomic cavity development are very different in the vitellaria compared to the ancestral ophiopluteus larva. Most of the archenteron is subdivided into an anterior axocoel, middle hydrocoel, and posterior somatocoel. The posterior-most portion of the archenteron forms the rudiment of the stomach. The early coelomic cavities are not paired. The single axocoel forms subdivisions, which may be homologous to the left and right axocoels in the ophiopluteus. A single hydrocoel forms on the left. The somatocoel begins as a single archenteron compartment on the left. Ectodermal invaginations form the right somatocoel and a portion of the left somatocoel. At this stage, the somatocoels are paired on either side of the stomach. Later aspects of development are similar in the vitellaria and the ophiopluteus. The migration of the hydrocoel, left somatocoel, and right somatocoel follows a similar pattern in the two types of larvae, and contribute to the same juvenile tissues. Overall, the early aspects of coelomogenesis include a restructuring of the archenteron to produce mostly mesoderm and a small amount of endoderm, and there is an unusual contribution of the ectoderm to the posterior coeloms.

COMMON STUDENT MISCONCEPTIONS IN PHYSICS CLASSES: MECHANICS

Kyle Bautista, Carolina C. Ilie, *SUNY Oswego*

Physics is an important and amazing field of study. However, Physics can be a complicated subject for some students. There are several different topics and areas of physics where students seem to develop or have previously acquired misconceptions. It is possible for these common misconceptions to be found by taking a closer look at what a students' rationale is when they are answering a question. To do this, a Physics survey was created based on several topics in the introductory mechanics unit covered in a college-level physics course. Participants will be asked to answer ten questions covering a range of topics including graphs of motion, force, and mechanical energy. Answers to the survey are multiple choice along with a required brief explanation with each answer to better identify the cognitive process of participants and diminish guessing. The surveys will be collected and all responses will be analyzed for any common errors. From this, we hope to create and implement new pedagogical strategies aimed to clarify physics concepts students struggle to understand. Some

say Physics can be a challenging subject to learn, but with the appropriate student-centered classroom techniques, it is possible for anyone to not only succeed, but find a greater passion for the field.

COMPARISON OF PREY FISH FATTY ACID SIGNATURES AMONG THE FINGER LAKES

Matthew Beers, Tom Bianchi, Matt Futia, and Jacques Rinchar, *The College at Brockport*

The Finger Lakes are home to a mixture of native (yellow perch) and non-native (alewife and round goby) prey species that compose the majority of the forage base for predators such as lake trout. However, the availability of these prey species varies in each Finger Lake: alewife can be found in all the lakes except in Skaneateles Lake, round goby is only currently present in Cayuga Lake, and yellow perch is present in all the lakes. The objectives of my research were to (1) characterize fatty acid signatures (FAS) of yellow perch, round goby, and alewife collected from the Finger Lakes, and (2) to compare alewife FAS among lakes. Alewife, yellow perch, and round goby were collected from Keuka, Seneca, Canandaigua, Cayuga and Skaneateles lakes using seine and gill nets during the summer of 2017 and 2018. Lipids were extracted from whole body fish and fatty acids were then transmethylated and separated using a gas chromatograph/mass spectrometer. Our results indicate that FAS differed significantly among the three different species (ANOSIM, Overall $R = 0.726$, $P < 0.001$). The major fatty acids responsible for differences among species were 16:1n-7, 18:1n-9, 20:5n-3, and 22:6n-3. In addition, alewife FAS differed significantly among the lakes they are present in (PERMANOVA, pseudo $F = 8.87$, $P < 0.001$). The major fatty acids responsible for differences in alewife FAS among lakes were 18:1n-9, 22:6n-3, 16:0, and 18:4n-3. These data will be used for comparisons with lake trout FAS to determine lake trout diet based on the principle “you are what you eat”.

COMPARISON OF THE SYNTHESIS OF CURCUMIN ANALOGS USING MICROWAVE AND TRADITIONAL HEATING METHODS.

Kiersten Kennedy, *Le Moyne College*

Curcumin and its analogs, which are commonly found in the spice turmeric, have been shown to exhibit extensive biological activities, such as anti-cancer, anti-oxidant, anti-inflammatory, and anti-microbial effects. However, their efficacy as potential drug candidates is limited by poor bioavailability and aqueous solubility, so much research has been conducted to effectively synthesize analogs with better properties. To expand knowledge on the organic synthesis of these curcuminoids, microwave-assisted synthesis and traditional oil bath synthesis were used to compare the yield and purity of two curcumin analogs. Yield measurements were calculated based on filtration and isolation of solid product, and thin-layer chromatography was used to assess purity. The synthesis proceeds through a modified Knoevenagel mechanism between a cyclic diketone and a substituted benzaldehyde, with the use of a boric anhydride protecting group to prevent deacetylation and ring cleavage. We demonstrated that in concentrated reaction mixtures, microwave heating produces much greater yields than traditional heating. The kinetics of this synthesis were then analyzed under both heating conditions by comparing rate of product appearance using UV-VIS spectroscopy. This was feasible due to the highly conjugated nature of curcuminoids. We found that under the dilute conditions used to measure kinetics, the synthesis occurred at similar rates for both heating methods, despite the apparent increase in yield with microwave heating. Further analysis of kinetics and order of this reaction with respect to different reactants is currently being conducted to better understand the varying effects of microwave and oil-bath heating on the synthesis of different curcuminoids.

CRITICAL BONE FRACTURE REPAIRS: A COMPARISON OF POROUS PROPERTIES OF CHITOSAN BIOACTIVE CEMENT AND PIG BONES.

Medina Sabrina, Uddin Sabiha, Gabriel Justin, Gikonyo Barnabas, *SUNY Geneseo*

Previously, the most effective method for supplementing/replacing a bone was an autograft. This method comes with risks as a result of the invasive nature the autograft procedure ensues by removing a small section of bone and using it as a bone simulant at the fractured site. This study aims to develop an alternative system to replace an autograft. For these initial studies, we use pig fibula to compare the properties of our novel cement system. Calcium Phosphate Cement (CPC), a biocompatible bone substitute composed of Hydroxyapatite (HA), a major component of human bone, is a base ingredient for the cement. Due to the successful ability of these cements to osseointegrate and initiate bone growth, we focus our efforts in the challenges of adequate porosity size with the use of different concentrations of chitosan and sodium bicarbonate. Results were found that showed the sample most similar to the bone sample was the chitosan sample.

CRITICAL BONE FRACTURE REPAIRS: A COMPARISON OF THE MECHANICAL PROPERTIES OF CALCIUM PHOSPHATE BIOACTIVE CEMENT AND PIG BONE PART II.

Mark Soto; Yen Linh Le, Barnabas Gikonyo, *SUNY Geneseo*

Understanding the mechanical properties of bone is critical to the design of materials that are to be used in repair of bone fractures. The mechanical properties of the materials in turn determine the behavior of the body under a load or force. This study compares the mechanical properties of Calcium Phosphate Cement (CPC) to pig bone with the aim of determining its suitability and applicability for use on load bearing bone fracture sites. CPC has been reported to be a bioactive and biodegradable material with potential resorbability, molding capabilities, and easy manipulation. It is composed of hydroxyapatite (HA), a major component of human bone, and a base constituent of the continuing efforts are geared toward addressing challenges of adequate mechanical strength of the cement to ensure compatibility to human bone. The cement was synthesized and characterized using published methods, mechanical strength tested and the data obtained is presented and discussed herewith.

D

DECT-BASED QUANTIFICATION OF BMAT AND AN ANALYSIS OF VARIABILITY WITHIN THE LUMBAR VERTEBRAE

Angela J. Kubik, Katelyn A. Greene, Kyle McNamara, Kristen M. Beavers, J. Keenan Brown, Leon Lenchik, Daniel P. Beavers, Denise K. Houston, Ashley A. Weaver, *SUNY Geneseo*

Introduction: Bone marrow adipose tissue (BMAT) is inversely associated with bone mineral density (BMD), and increasingly recognized as an independent risk factor for fracture [1]. Traditionally, BMAT is assessed using Magnetic Resonance Spectroscopy (MRS) or histological evaluation [1,2], but the cost, availability, and invasive nature of these methods limit their clinical research utility. Alternatively, dual energy computed tomography (DECT) can be used to quantify BMAT, although prior studies have been limited to the 2nd lumbar vertebra in middle-aged, osteoporotic subjects with obesity [3,4]. The purpose of this study was to apply an existing method for obtaining BMAT measurements using DECT to assess the variability of BMAT measurements across all lumbar vertebrae in older, non-osteoporotic adults with obesity. Materials and Methods: Fifteen lumbar DECT scans of older adults with obesity were collected at 80 kV and 140 kV energy levels with a bone calibration phantom (v.3 Mindways, Austin, TX) and processed using ImageJ (v.1.46r NIH, Madison, WI). An elliptical region of interest (ROI) was placed in the center of each of the L1-L5 vertebral bodies on the 80 and 140 kV images. Hounsfield unit measurements within the ROIs and the phantom calibration slopes were used to compute a subject-specific average basis material composition, or BMC. This value was represented relative to a bone model triangle displaying BMC of red and yellow marrow computed from energy-dependent mass attenuation coefficients by the Photon Cross Sections Database, XCOM (v.1.5 NIST, Gaithersburg, MD). The derived subject measurements were then plotted in the basis material space and projected onto a marrow reference using a focal-based projection. Percent BMAT for each lumbar vertebra of each subject was obtained by applying the assumption

that 0% and 100% BMAT corresponds to red and yellow marrow references respectively. A one-way ANOVA and Bartlett's test were used to determine statistically significant differences in percent BMAT between the lumbar vertebrae. Results and Discussion: Subjects in this study were 70.7 ± 3.3 years of age, with a BMI of 33.9 ± 4.0 kg/m². Average percent BMAT across L1-L5 was $56.7 \pm 26.8\%$, with no statistically significant difference in means or variances across the vertebrae (ANOVA: $p > 0.05$; Bartlett's test: $p > 0.05$). Conclusions: There was no significant variability in percent BMAT across L1-L5. In future studies, BMAT may be accurately described using either an average L1-L5 value or as previously reported using a single vertebral level. The results could be utilized to standardize a protocol in larger clinical studies concerning weight loss and bone health. Acknowledgements: This study was funded by NSF (REU Award #1559700) and NIH (R01 AG050656). References: [1] Schwartz AV. *Front Endocrinol.* (2015) 6: 1-6. [2] Suchacki KJ. *Curr Opin Pharmacol.* (2016) 28: 5056. [3] Arentsen L. *Bone.* (2015) 72: 118-122. [4] Bredella MA. *Radiology.* (2015) 277: 230-235.

DERMAL BACTERIA OF AMBYSTOMA MACULATUM AND AMBYSTOMA JEFFERSONIANUM

Annie M. Stevens, *SUNY College of Environmental Science and Forestry*; Kristen E. Fellows, *University of Delaware*

Dermal bacterial communities have been shown to be important in amphibians and may keep pathogenic organisms such as the chytrid fungus under control. However, few studies have looked at naturally occurring bacterial communities in salamanders, and no studies have examined these communities in ambystomid salamanders. We investigated the cutaneous bacterial communities of the spotted salamander, *Ambystoma maculatum* and Jefferson's salamander, *Ambystoma jeffersonianum*. In March 2017, we captured 5 male and 7 female spotted salamanders as well as 3 female Jefferson's salamanders during the annual migration to breeding pools at Mendon Ponds Park in Pittsford, NY. Captured salamanders were measured, weighed, and rinsed three times in distilled water after sex was determined. Skin swabs were taken on both dorsal and ventral sides and cultured on TSA plates. Subcultures were taken to obtain pure cultures, then gram stained and examined using BioMerieux API 20E test kits to determine identity of bacteria. The average number of bacteria species on spotted salamanders was 3.08. Significantly more bacterial colonies were found on males than females. Each TSA plate contained large mucoid colonies which were identified as *Pseudomonas aeruginosa*. *P. aeruginosa* has been shown to have antifungal properties in previous studies and may be important in preventing infection with chytrid.

DESIGNING AN ARDUINO WATER QUALITY SENSOR.

Elizabeth Moore, William White, Ileana Dumitru Ph.D., Peter Spacher Ph.D., John Halfman, Ph.D, Lisa Cleckner, Ph.D., *Hobart and William Smith Colleges*

The Finger Lakes are very important to New York State in many ways. It is vital that these eleven lakes are kept clean and unpolluted. The Finger Lakes Institute and Hobart and William Smith Colleges (HWS) regularly monitor various lakes and streams in the Finger Lakes Region. It is critical that these measurements are taken consistently and close to the same times. This enables us to make comparisons of the data and track how the water is changing over time. However, with so many lakes and streams in the Finger Lakes Region, it can be challenging to get to all of these locations on a consistent basis and take measurements. Therefore we designed a system that is able to record different measurements of lakes and streams, specifically temperature and dissolved oxygen levels, and transmit the results through a cellular network. This will benefit researchers who are studying lakes and streams in the Finger Lakes Region because multiple systems can be built and placed in a variety of areas.

DETERMINING EFFECTS OF MELANIN-CONCENTRATING HORMONE ON INSULIN-SIGNALING PATHWAY COMPONENTS.

Dayanara Torres and Laurie B. Cook, *The College at Brockport*

It's well known that appetite is controlled by a variety of hormones, however, a link between hormones that stimulate appetite and the regulation of glucose uptake by cells is unclear. Preliminary observations in our lab suggests a connection between MCH signaling and GLUT4 translocation to the plasma membrane in adipocytes. The aims of this project were to quantify GLUT4 translocation in adipocytes treated with or without MCH, insulin, or both and explore the connections between MCH signaling and insulin-pathway genes via qPCR. Through protein localization, 3T3-L1 adipocytes were treated with and without MCH, insulin, or both, and immuno-stained for GLUT4 glucose transporter. Fluorescence microscopy images showed intense GLUT4 staining of cells. With NIH ImageJ, fluorescence intensity line scans were generated to better discern differences across treatments. Line scans indicate that MCH facilitates GLUT4 translocation to the plasma membrane when co-treated with insulin, but not on its own. To further investigate MCH's role in the insulin-signaling pathway, qPCR fold changes of insulin-signaling genes, *gas7*, *sned1*, and *igfbp4* were calculated from preadipocytes and ciliated developing adipocytes. *Gas7* and *sned1* showed transcripts that were upregulated by MCH in 3T3-L1 non-ciliated cells but abrogated in ciliated cells. *Igfbp4* fold changes remained relatively stable in both treatments. These results provide the first evidence to suggest a link between the appetite regulatory hormone, MCH, and insulin signaling in cells. While MCH is known to effect energy homeostasis, the molecular mechanisms are as yet unclear. For adipocytes, MCH seems to prepare the cells for an influx of nutritional glucose for long-term storage as fat. Future experiments will include conducting a glucose uptake assay to confirm that MCH improves glucose uptake in 3T3-L1 adipocytes.

DETERMINING THE INTERACTIONS BETWEEN DOUBLE STRAND BREAK PROCESSING AND NON-HOMOLOGOUS END JOINING DURING DIRECT REPEAT-MEDIATED DELETION EVENTS IN THE MITOCHONDRIA OF BUDDING YEAST.

Imran Tahir, Andrew Connolly and Rey A. Sia, *The College at Brockport*

Mitochondria are well recognized as the powerhouses of eukaryotic cells due to their essential role during oxidative phosphorylation. The mitochondrial DNA (mtDNA), exists independently from the nuclear genome and encodes the proteins required by the electron transport chain. mtDNA is susceptible to mutations which occur in an age dependent manner and can manifest into metabolic diseases, neuromuscular disorders and symptoms of aging. Furthermore, two-thirds of mtDNA deletions are flanked by directly repeated sequences. The mechanisms for these direct repeat-mediated deletions (DRMDs) are not understood. Non-homologous end joining is the default repair pathway of double strand breaks (DSBs) in the nucleus of higher eukaryotes. The specific goal of this investigation is to determine the roles the nuclear genes *KU70* and *KU80* play in mitochondrial DRMD events. The products of these genes are involved in the nuclear double strand break and non-homologous end joining (NHEJ) repair pathways. The lab has developed a set of strains that can measure spontaneous and induced DRMD events in strains lacking one or more of these genes. The data will be compared to a wild type strain to determine the effects loss of these genes have on spontaneous and induced DRMD rates.

DEVELOPING AND TESTING AN EXPERIMENTAL SYSTEM FOR SMOOTH MUSCLE WOUNDING AND RECOVERY.

Keegan Frenya, Ransom H. Poythress, *Houghton College*

Electrical stimulation (ES) on skeletal muscle is a novel technique utilized by many physical therapists. ES in skeletal muscle has been shown to improve blood flow, stimulate protein synthesis, reduce edema, and promote cellular migration and white blood cell activity. Currently, there is little research that investigates ES as a therapeutic modality for smooth muscle recovery. Our research involved developing and testing an ES

experimental system for smooth muscle wounding and recovery. The efficacy of ES was tested in scratch wound assays of cultured rat aortic smooth muscle cells. We found that 10V and 35V of direct current produced the maximum growth in micrometers when compared to our untreated controls.

DEVELOPMENT OF THE AXIAL COMPLEX IN THE BRITTLE STAR OPHIOPLOCUS ESMARKI

Nasreen Jaff, Dr. Hyla Sweet, *Rochester Institute of Technology*

The *Ophioplocus esmarki* is a sea organism part of the echinoderm phylum. Although it's a very common invertebrate, little is known about its developmental process. The embryos transition from bilateral to five-fold symmetry. During this process, an enigmatic structure known as the axial complex, develops in one location of the animal. Minimal research has been conducted on the development of this organ. In this project, the structure and development of the axial complex was analyzed through continued observation at different stages. Brittle star embryos and juveniles were stained with neural and muscle markers and examined using confocal microscopy. We found that the axocoel divides into three parts. The posterior lobe connects with the esophagus and the other parts contribute to the axial complex, which also includes a neural component. To better understand the relationships between the different tissues of the axial complex, 3D models were created as well.

DIFFERENCES IN MOISTURE PROFILES BETWEEN FIELD AND FOREST MICROCLIMATES.

Adrianna N. Kremer, *SUNY Brockport*; Kristine M. Chen, *University of Oklahoma*; Neil F. Laird, *Hobart & William Smith Colleges*

Microclimate studies provide insight into small-scale surface influences on mass and energy balances that translate into the deeper planetary boundary layer. Specifically, comparisons of field and forest microclimates indicate differences between complex forest conditions and less complex field conditions. Given the prevalence of forest biomes, findings from field-forest microclimate comparisons have the potential to be widely applicable. While past studies have reported on a variety of aspects related to field and forest microclimates, none have examined vertical moisture profiles. The current study quantifies the diurnal variability of low-level moisture profiles at an interior forest site and adjacent field site, as well as explores contributing factors to this variability ranging from large-scale to microscale conditions. Data was collected at the Hanley Biological Preserve in the Finger Lakes Region of New York, where weather stations in the field and forest recorded measurements at 1 m, 2 m, and 3 m heights during multi-month periods in the autumns of 2012 and 2017. Analyses were grouped by the Spatial Synoptic Classification (SSC) to examine influences linked to the large-scale atmospheric environment. Results indicate that SSC type and cloud cover strongly influenced the diurnal pattern, magnitude, and variability of both the field and forest DPT profiles. Under less cloudy conditions, daytime DPT profiles increased with height in the forest and decreased with height in the field. This suggests that transpiration from the foliage canopy (surface vegetation) in the forest (field) were important contributions to DPT profiles and had important interactions with large-scale atmospheric conditions distinguished by SSC type. Future work will examine additional factors that may influence variability in DPT profiles, including wind speed and direction, precipitation, and foliage changes.

DISTRIBUTION OF SULFUR-CYCLING BACTERIA IN FAYETTEVILLE GREEN LAKE.

Joy M. O'Brien, Kaleigh R. Block, William J. Edwards, Ph.D., Cassandra L. Marnocha, Ph.D., *Niagara University*

A meromictic lake is a lake that is permanently stratified. Fayetteville Green Lake is a meromictic lake near Syracuse, NY and is of particular interest for sulfur-cycling studies because of its deep water chemistry. This lack of mixing allows for distinct distributions of bacteria throughout the layers of the lake. Previous work has shown that purple sulfur bacteria dominate in the chemocline. We hypothesized that the presence of sulfide in the

chemocline would play a role in the distribution of bacteria with different sulfur-cycling metabolisms. To investigate, we collected samples from different depths of the lake for chemical and DNA analyses. Our data showed a significant difference in microorganisms between the chemocline and the rest of the lake's layers. We also found a significant increase in the abundances of sulfur-cycling bacteria within the chemocline. Our results indicated that there is a more diverse group of sulfur-cycling bacteria than was previously thought. For example, members of the Chlorobi (green sulfur bacteria) were nearly as abundant as purple sulfur bacteria. Chemotrophic sulfur-oxidizers also made up a significant amount of the chemocline community. The presence of these bacteria in the chemocline may suggest that there is competition for electron donors or a more complex sulfur cycle.

DOES COMMUNITY ENGAGEMENT IMPROVE ECOSYSTEM RESTORATION OUTCOMES?

Sydney VanWinkle, *Rochester Institute of Technology*

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 an important factor that is not well understood. The most effective restoration may happen when numerous stakeholders with a wide range of goals are involved. I have qualitatively assessed the role of stakeholders in four restoration projects to identify relationships between stakeholder involvement and restoration outcomes. Through semi-structured interviews with stakeholders such as town engineers, local activists, and project leaders, I assessed individuals' goals and rationale for involvement. These qualitative results will be compared to quantitative measurements of ecological function, including invasive species cover, intended hydrology and plant community composition.

DYNAMIC CHELATION BEHAVIOR IN NEUTRAL HYPERCOORDINATE DIORGANOSILICON COMPLEXES OF 1-HYDROXY-2-PYRIDINETHIONE.

Erin R. Tiede, Bradley M. Kraft, *St. John Fisher College*; William W. Brennessel, *University of Rochester*

A series of diorganosilicon complexes containing the OPTO (1-oxo-2-pyridinethione) ligand were synthesized and characterized by ^1H , ^{13}C , and ^{29}Si NMR spectroscopy and X-ray crystallography. The crystal structures of a series of silacycloalkane complexes of the form $(\text{CH}_2)_x\text{Si}(\text{OPTO})_2$ ($x = 3, 4, 5$) and $\text{Me}_2\text{Si}(\text{OPTO})_2$ were examined to probe the influence of ancillary ligand characteristics on the chelate strength of the OPTO ligand. Variable-temperature ^{29}Si and ^{13}C NMR studies revealed dynamic chelation equilibria involving dissociation of the $\text{Si} \leftarrow \text{S} = \text{C}$ bond in all of the complexes. The carbon resonances of the OPTO ligand in various complexes were identified with ^1H - ^{13}C HMQC NMR experiments with their relative positions dependent on temperature and the substituents bonded to silicon.

DYNAMICS OF MTDNA POPULATIONS IN MAMMALIAN CELLS

Brandon Bogner, Kellianne Kornick, Rebecca Zathang, Leo Sutter, and Moumita Das, *Rochester Institute of Technology*

Mitochondria are organelles found in almost all eukaryotic organisms. They are highly dynamic and once formed, they can undergo changes in size and content via the processes of fusion, fission, and mitophagy. Mitochondria are famously known as the powerhouse of the cell for their role in cellular energy production. They are also essential for cell signaling and apoptosis, and have their own DNA, called mtDNA, which is maternally inherited. The same cell can have multiple variants of mtDNA, and harmful alterations in mtDNA can accumulate over time, resulting in pathological changes in mitochondrial function and have been linked to

several diseases. We develop and study a mathematical model to understand and predict the population dynamics of mtDNA and how it is correlated to changes in mitochondrial bioenergetics. We examine the time evolution of populations of healthy and dysfunctional mitochondria subject to mitochondrial biogenesis, fission, fusion, mitophagy, and changes in the mitochondrial membrane potential, and determine the relative impact of these processes on mtDNA population dynamics. Our results may provide insights into how different mtDNA populations survive and evolve under different selection pressures, and the origins of mtDNA disorders.

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ECOLOGICAL IMPACTS OF FOOD WASTE DIGESTATE DISPOSAL

Shradha Shrestha, Christy Tyler, *Rochester Institute of Technology*

Food waste is a serious global problem; one-third of the food produced in the world is never eaten. Anaerobic digestion (AD), a process to convert bio-waste (e.g., food waste, crops, manure, sewage) to energy, generates biogas and digestate as end products. This valorization solution to the food waste problem is a potentially sustainable option, but the ecological and economic effects of digestate disposal are not well understood. In particular, the liquid digestate has agronomic value and is used as a soil amendment and organic fertilizers. However, after repeated applications, additional uncertainties exist as the mineral-N goes through NH₃ volatilization, nitrification, and nitrate leaching. To study this, we developed a preliminary case study at a co-digestion facility (Synergy Biogas) and associated row-crop agricultural operations in the Genesee River Watershed. We also initiated bi-monthly measurements of digestate composition and greenhouse gas fluxes from digestate storage. We captured gas samples from a lagoon storage pond and analyzed following dilution on a Shimadzu Greenhouse Gas Analyzer. In Summer 2018, emissions was roughly 54% (30-74%) methane, 25% (16-32%) carbon dioxide, and <1% nitrous oxide. Additionally, a geospatial model- Long-Term Hydrological Impact Analysis (L-THIA) was developed, with a focus on the Pearl - Oatka Creek watershed to identify potentially vulnerable regions where an ecological risk of digestate containing runoff may occur. This hydro-ecological approximates runoff potential using Land use land cover, crop types, slope and soil hydric categories and rainfall intensity. In the future, historical soil fertility records of co-digestion facilities would be used for a series of measurements in agricultural fields to subsequently compare the proximity of digester facilities to identify vulnerabilities and potential solutions. We conducted a series of empirical measurements at a digester level (Food waste: 70% and Manure: 30%) to study characterization and predict (and thereby minimize) potential environmental impacts. Additionally, we developed alternative digestate disposal pathways to evaluate the environmental footprint of the waste to energy recovery (WtE) options for food waste disposal facilities.

EFFECT OF ARGININE METHYLATION ON THE ENZYMATIC ACTIVITY AND FUNCTIONS OF TBLPN, A LIPIN HOMOLOGUE FROM TRYPANOSOMA BRUCEI.

James Illingworth, Alyssa Raichel, Elizabeth Green, Rebecca Rossier, and Michel Pelletier, *SUNY Brockport*

Human African Trypanosomiasis, also known as African sleeping sickness, is a vector-borne devastating disease caused by the parasitic protozoan *Trypanosoma brucei*. This parasite is transmitted between mammalian hosts by the tsetse flies of the genus *Glossina*. According to the World Health Organization (WHO), sleeping sickness threatens over 60 million people in 36 countries of sub-Saharan Africa. During recent epidemics in several villages in the Democratic Republic of Congo, Angola, and Southern Sudan, the prevalence of the disease has reached 50%, and sleeping sickness was considered the first or second greatest cause of mortality, ahead of HIV/AIDS. Besides its great health and economic importance, *T. brucei* represents an exceptional tool for the study of cell physiology/biology. We recently identified a protein homologous to yeast and human lipin, a

phosphatidate phosphatase involved in membrane biogenesis, energy metabolism, and adipose tissue development. We have shown that TbLpn catalyzes the dephosphorylation of phosphatidic acid (PA) to diacylglycerol (DAG), with a potential role in phospholipid biosynthesis. In addition, as predicted from this in vivo interaction, it was found that TbLpn contains methylated arginine residues. In order to better understand the role of arginine methylation in TbLpn functions, we are carrying out site-directed mutagenesis of arginine residues that are predicted to be methylated in vivo. The mutated TbLpn proteins will then be transfected into procyclic (insect stage) and bloodstream form (mammalian stage) *T. brucei*, and the effect of the mutation on cell growth, cell morphology, and enzymatic activity will be determined.

EFFECT OF DIETARY MAGNESIUM MANIPULATION ON THE GASTROINTESTINAL MICROBIOME OF A MOUSE MODEL OF ULCERATIVE COLITIS

Christopher Carlson, Bernardo Ortega, *The College at Brockport*

Ulcerative colitis is a disease characterized by inflammation of the GI tract, which disturbs the mucosal lining and hinders magnesium (Mg²⁺) absorption. Research has shown that increasing the dietary intake of Mg²⁺ decreases the severity of the colitis symptoms, but there is no data on the effect this has on the microbiota of the GI tract or the blood. We found that, in DSS-treated mice, the amount of bacteria in the colon increases with a decrease in dietary Mg²⁺, and that the concentration of bacteria in the spleen increases with a decrease in dietary Mg²⁺.

EFFECT OF DIETARY MAGNESIUM ON THE MICROBIOME OF THE SPLEEN IN A MOUSE MODEL OF ULCERATIVE COLITIS.

Josiah Seaburg, Taylor Schultz, and Michel Pelletier, *The College at Brockport*

Magnesium (Mg²⁺) is a mineral utilized by virtually every organ in the human body, and plays a crucial role in physiological functions such as protein and nucleic acid synthesis [3]. Mg²⁺ deficiency has been shown to activate a pro-inflammatory response [1], which in turn contributes to the development of conditions including, but not limited to, endothelial dysfunction, hypertension, anxiety disorders [2], and type 2 diabetes. While previous studies have investigated these aspects of Mg²⁺ deficiency, little is known about how the gut microbiota is affected by insufficient quantities of this abundant cation. For this study, we wanted to examine the effects of a Mg²⁺ deficient diet in comparison to a control diet on the gut microbiota, using an ulcerative colitis (UC) mouse model. Dextran sodium sulfate (DSS)-induced colitis is widely used because of its simplicity and many similarities with human UC. DSS is a water-soluble negatively charged sulfated polysaccharide (40-50kDa) with anticoagulant properties that induces damage in the epithelial monolayer lining the large intestine. It is believed that increased mucosal permeability allows dissemination of proinflammatory intestinal contents, such as bacteria and their products, into the underlying tissue model. We hypothesized that not only would the microbiota be altered, but also that host biological functions would be affected consequently.

EFFECTIVENESS OF PEPPERMINT OIL ON HUMAN AND PLANT PATHOGENIC BACTERIA.

Dan Kaplan, Maryann Herman, *St. John Fisher College*

This project investigated the effectiveness of peppermint (*Mentha piperita*) essential oil against five human and six plant pathogenic bacterial strains. Bacterial inhibition was determined using a Kirby-Bauer disc diffusion assay, using two antibiotics for comparison. This work demonstrated that peppermint oil has antibacterial properties against pathogenic bacteria. Most promising control was seen with *A. tumefaciens*, *C. michiganensis*, *X. perforans*, and *K. pneumoniae*. Future work will investigate MIC and MBC with promising pathogen-peppermint combinations.

EFFECTS OF COCONUT OIL AND COCONUT OIL-PULLING ON STREPTOCOCCUS MUTANS

Samantha Tardugno, Maryann Herman, *St. John Fisher College*

As people look for alternatives to western medicine, it is important that the natural techniques they turn to are safe and effective. One emerging trend is a technique called oil-pulling, which involves swishing coconut oil inside the mouth for 15-20 minutes then spitting it out. Health claims include improved oral health by decreasing gum inflammation, cavities, and gingivitis. Previous studies have shown that oil-pulling can be as effective as rinsing with an antiseptic mouthwash on decreasing *Streptococcus mutans* and other common mouth bacteria. This study will explore the effects of coconut oil on one of the causative agents of dental caries (cavities), *Streptococcus mutans*.

EFFECTS OF SURFACE MODIFICATION ON DICTYOSTELIUM ADHESION AND MECHANOSENSATION

Allison Hearn, Sara Fuller, *SUNY Oswego*

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 to sense 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 Poly-L-Lysine (PLL), Glucose, and Glycine to test whether they alter adhesion, and if so, how that will affect mechanosensation. PLL is a chemical that has been shown to increase adhesion in mammalian cells. By coating surfaces with PLL we have found evidence that the same may be true in *D. discoideum* cells. In contrast to PLL, sugars and amino acids have been previously shown to inhibit adhesion of *D. discoideum*; however, preliminary evidence suggests that in our assay only addition of glucose, but not glycine lowered cell adhesion. Future studies will examine whether coating a surface with PLL or treating cells with glucose can alter response to mechanical stimulation.

EFFECTS OF THE PARASITE OPHRYOCYSTIS ELEKTROSCIRRHA ON THE PAINTED LADY BUTTERFLY, VANESSA CARDUI (LEPIDOPTERA: NYMPHALIDAE)

Joseph McCarthy, Department of Biological Sciences, *SUNY Oswego*

The protozoan parasite *Ophryocystis elektroscirrha* (OE) is known to infect three species of butterflies, all members of the genus *Danaus*. There are no documented cases of other butterfly species hosting OE, and no research has been done on its effects on other species. In the three *Danaus* hosts, OE infections can lead to shorter lifespans, reduced flight ability, lower fecundity rates, and an overall reduction in body sizes. I studied the effects of OE on a non-host species, the painted lady butterfly (*Vanessa cardui*), to determine if OE could complete its life cycle or impact the development of the painted ladies. Preliminary data from cross infections found that high levels OE exposure lead to a reduction in adult and pupal body mass and an increase in amount of time between larval and pupal eclosion. A replicate study with less OE inoculant showed no significant trend, which could indicate that high numbers of OE are necessary to see a response in the painted ladies. Histological samples of larval and pupal specimens were prepared to compare the progress of the OE life cycle in both monarchs and painted ladies.

EFFECTS OF THIORIDAZINE HYDROCHLORIDE ON CRYPTOCOCCUS NEOFORMANS VIRULENCE FACTORS

Valerie Garcia-Batiz, Tiffany Arrington, Virginia Glazier, *Niagara University*

The fungal pathogen *Cryptococcus neoformans* infects and kills 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. This results in a greater 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* including thioridazine hydrochloride. However, it is not yet clear how thioridazine hydrochloride kills *C. neoformans* and whether the mechanism of action includes effects on known virulence factors. 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 thioridazine hydrochloride as a *C. neoformans* treatment option, we will be looking at the effects of thioridazine hydrochloride on *C. neoformans* virulence factors which include capsule formation and melanization at human host body temperature.

ELECTRICAL STIMULATION IMPROVES SCRATCH WOUND RECOVERY IN CULTURED SMOOTH MUSCLE CELLS.

Kirsten Blakeslee, Keegan Frenya, Ransom H. Poythressm, *Houghton College*

Despite its broad and varied use as a therapeutic modality in skeletal muscle recovery, the effects of electrical stimulation on other systems remain largely unknown. The efficacy of electrical stimulation in scratch wound healing assays in cultured rat aortic smooth muscle was examined as well as changes to inflammatory response and cytokine release through ELISA analysis and real time quantitative PCR. A single, hour-long low voltage treatment significantly improved scratch recovery time in this system. Additionally, ELISA and QPCR have yielded preliminary promising candidate proteins for further experimentation.

ENTANGLED TRAJECTORIES HAMILTONIAN DYNAMICS FOR TREATING QUANTUM NUCLEAR EFFECTS

Brendan Smith, Alexey V. Akimov, *SUNY Buffalo*

A simple and robust methodology, dubbed Entangled Trajectories Hamiltonian Dynamics (ETHD), is developed to capture quantum nuclear effects such as tunneling and zero-point energy through the coupling of multiple classical trajectories. The approach reformulates the classically-mapped second-order Quantized Hamiltonian Dynamics (QHD-2) in terms of coupled classical trajectories. The method partially enforces the uncertainty principle and facilitates tunneling. The applicability of the method is demonstrated by studying the dynamics in symmetric double well and cubic metastable state potentials, as well as a variety of 2-dimensional model potentials. The methodology is validated using exact quantum simulations and is compared to QHD-2. ETHD calculations agree well with the quantum results, suggesting that ETHD may be a simple and inexpensive way of including quantum nuclear effects in molecular dynamics simulations.

ENVIRONMENTAL STRESS RESPONSE AND COMPARISON OF BIOFILM FORMATION OF BACTERIAL ISOLATES.

Maryah Glover, Milky Abajorga, Dr. Seema Thomas, *Rochester Institute of Technology*

Environmental factors play a significant role in directly and indirectly affecting cellular processes. Bacteria exercise various mechanisms to form biofilms more specifically based on the conditions of their micro environments such as pH and temperature. The study focuses on the effect and comparison of various pH (5.0, 7.0 and 8.0) and temperature (23oC, 30oC, 37oC and 45oC) conditions on the formation of biofilm in *Pantoea agglomerans* and *Citrobacter freundii*. Mid-log phase of the cultures grown in tryptic soy broth, adjusted to an optical density of 1.0 were used. The microplates were incubated at the said temperatures, followed by crystal violet assay. The amount of biofilm formed in both the strains was dependent on pH than on temperature. The strains recorded higher biofilm formation at lower temperature of 23oC and an alkaline environment of pH 8, whereas exhibited a relatively lower threshold for heat resistance at a higher temperature of 45oC. Though comparison analysis showed that *P. agglomerans* is robust in biofilm production than its counterpart, *C. freundii*, it is concluded that both the strains were either slow or partially resistant to biofilm formation depending on factors such as their motility or were in early stages of attachment to the substratum.

EVALUATING THE PROMISE OF CALCIUM PHOSPHATE CEMENTS TO TRANSFER PROTEINS TO FRACTURED BONE SITE PART 1: DIFFUSION STUDIES

Simran Singh, Pema Sherpa, Barnabas Gikonyo, *SUNY Geneseo*

Bone defects caused by trauma, tumors, and inherent genetic disorders require the use of grafting materials to facilitate bone regeneration at the affected site. However, the lack of bone supply and donor site morbidity associated with autografting pose significant challenges. A promising alternative approach to autograft is the use of bone cement prepared with Calcium Phosphate Cement (CPC). An effective synthetic bone cement establishes an equilibrium between porosity, mechanical strength, and the rate of diffusion. The overall objective of this project is to design a diffusion monitoring system that can track the diffusion of proteins and other biological materials from CPCs to the site of fracture to aid in the bone repair process. The diffusion of copper sulfate from copper sulfate loaded CPCs is monitored using absorption spectroscopy over varying time intervals to assess the potential of the CPCs to deliver proteins to the fracture sites. The results are presented and discussed hereafter.

EVALUATION OF CO-OCCURRENT ACTIONABLE GENES AND CORRESPONDING DRUG POTENTIAL USING LARGE-SCALE CANCER GENOMIC DATA

Briana Kubik; Zi-Ming Zhao, Ph.D; Jeff Chuang, Ph.D, *SUNY Geneseo*

The ability to predict how a patient will respond to various targeted therapies is an important step in precision oncology. While significant contributions have been made towards the development of therapies that target single genomic alterations, less evidence has been seen in situations where more than one actionable mutation occur together. Lack of research in this area makes it difficult for molecular tumor boards to make informed clinical decisions for patients with these genomic characteristics. In an attempt to identify co-occurring aberrations with the highest potential for clinical implication, this study proposes a computational tool to systematically assess co-occurrent tendencies of altered, actionable gene pairs in large public clinical genomic databases. A pan-cancer assessment of 48 actionable genes for their mutation, copy number alteration (CNA), and fusion data obtained from AACR Project Genomics Evidence Neoplasia Information Exchange (GENIE) revealed 973 significant co-occurrences. Further analysis of the top two gene pairs suggests a non-uniform co-occurrent tendency across tumor types and variable clinical evidence associated with each gene. Decisions regarding single-agent or combination therapeutic approaches for combating these co-occurring aberrations can be tested experimentally using patient-derived xenograft (PDX) models and preclinical outcomes can be further validated and used to help clinicians optimize treatment decisions for currently understudied genomic configurations.

EXAMINATION OF NEUROD4 IN RETINOGENESIS

Alexis Saunders, Dr. Travis Bailey, *SUNY Geneseo*

Zebrafish exhibit eye development similar to that of humans. The neurod4 gene encodes a transcription factor that may be important in neuroretinal development. neurod4 is also moderately conserved from zebrafish to humans, and might have an equally important function in the cell cycle. We generated a neurod4:GFP transgene and compared the reporter gene expression with endogenous neurod4 expression detected by in situ hybridization. The transgene contains 2.1 kb of the upstream genomic sequence and includes the first exon of the neurod4 gene, ending before the first intron. Gross morphology analysis showed GFP expression from the neurod4:GFP transgene closely matched in-situ data already published, and indicated that the transgene displayed similar expression from the endogenous gene. Because neurod4 is expressed in the retina during

embryogenesis, we tested its requirement on cell proliferation in the retinal during the regeneration following constant intense light damage to photoreceptors by anti-PCNA immunostaining. We electroporated zebrafish retinas with neurod4-morpholino to cause loss-of-neurod4 expression and subjected them to light damage for three to four days. The results of these experiments suggest a requirement of the neurod4 gene to exit the cell cycle during zebrafish retinal regeneration.

EXPLORATION OF KALANCHOE DAIGREMONTIANA PHYTOCHEMICALS FOR ANTIMICROBIAL PROPERTIES

Brianna Walworth, Xayathed Somoulay, Grace Stoklosa, Sridhar Anand, Jonelle Mattiaccio, Maryann Herman, *St. John Fisher College*

Kalanchoe daigremontiana is a tropical plant traditionally used to treat infections, decrease inflammation, and promote wound healing. Prior work on a related species, *Kalanchoe pinnata*, has demonstrated significant inhibition of fungal and bacterial pathogens. This project aims to test effectiveness of organic extracts of *K. daigremontiana* against a range of human pathogens. We have cultivated *K. daigremontiana* under controlled conditions (soil, pH, water, light). At three- and six-month time points in their growth, the aerial parts of the plants were dried, macerated, and exhaustively extracted using organic solvents of increasing polarity. Each solvent extract was evaporated under reduced pressure, and the resulting biomass was weighed. Samples at the nine- and 12-month points will also be acquired. Extracts will be tested against several human pathogens (*Pseudomonas aeruginosa*, *Escherichia coli*, *Staphylococcus aureus*, and *Candida albicans*) using a disk diffusion assay. Factors for future consideration are modifying the sample acquisition time and the use of abiotic stress factors to upregulate secondary metabolite production.

EXPRESSING A. THALIANA SR45 AND SR45 RRM IN E. COLI.

Anna, Hu, Nick, Jodush, Dr. Xiao-Ning, Zhang, *Saint Bonaventure University*

SR45 is a splicing regulator in *Arabidopsis thaliana*. It has been shown to associate with transcripts from a variety of genes; including those involved in immunity, growth and development. SR45 has an RNA Recognition Motif (RRM), which is able to recognize and bind to RNA sequences. In SR45, the RRM is flanked by two RS domains, which are for protein-protein interaction. Although SR45-interacting proteins and RNA motifs have been reported, the details of these interactions are still unconfirmed. In order to study these interactions, the soluble form of SR45 protein must be produced. Here, it was achieved through the expression of SR45 RRM and SR45 in *E. coli*. However, in order to do so, the codons for 35% of amino acids of SR45 had to be altered to account for codon bias in *E. coli*. The DNA sequences for SR45 RRM and SR45 were inserted into pET16b and pMAL-c2 expression vectors, respectively, and a variety of conditions were tested for optimization. MBP-fused SR45 RRM was expressed as a soluble protein, but His-tagged SR45 RRM was only expressed as inclusion bodies, which was solubilized later to obtain soluble His-tagged SR45 RRM. Currently, we are in the process of expressing MBP-fused SR45 full length protein. With the availability of soluble SR45 RRM and SR45 protein, future research includes confirmation on protein-protein and protein-RNA interactions involving SR45.

EXPRESSION OF NOTCH PATHWAY GENES IN GEF MUTANTS.

Amanda Young, Sara Feinland, Dr. Travis Bailey, *SUNY Geneseo*

A mutagenesis screening of *Danio rerio* (zebrafish) produced the good effort (*gef*) mutant, characterized by an underdeveloped retina by 3 dpf and lethality at 7 dpf. It is known that *gef* mutants have a deletion in the *chaf1b* gene. *Chaf1b* loads histones and it has been postulated that DNA exposure leads to cell death. If *chaf1b* is mutated, failure for histones to load properly could affect transcription of genes and may cause the small eye phenotype in *gef* mutants. Following comparative deep-RNA sequencing, DAVID bioinformatic analysis revealed common-pathway genes that are downregulated in the *gef* mutant. Two genes, *notch1a* and *her15.1*, were

identified to be downregulated and are normally expressed in the spine, head and retina during early stages of development. These genes are part of the Notch pathway, which is essential for retinal development. Since these genes were found to be down-regulated in gef mutants, loss-of-expression might contribute to the gef mutant phenotype, and we expect them to be expressed less in the affected cells of gef mutant embryos when compared to wild-type embryos. We performed in situ hybridization to analyze whether the gene expression was altered in gef mutant embryos compared with wild-type in affected cells.

F

FACTORS THAT INFLUENCE ROADKILL DETECTION PROBABILITIES

Liana Raguso, *The Lawrenceville School*, William Brown, *Keuka College*, Marion Zuefle, *Cornell University*

Variability in species detection probabilities may be due to differences among species, observers, habitat, or other conditions. To further explore this variability, we examined detection probabilities for roadkill surveyed in central New York State from a moving car. In addition to whether the driver, passenger, or both detected the roadkill, location and size of roadkill were recorded. As an initial attempt at data exploration, detection probabilities among observers were assumed to be the same. Detection probabilities for size classes and locations of roadkill were estimated using a conservative model in DOBSERV software. Larger roadkill were detected with greater likelihood than smaller roadkill. Roadkill were more likely to be detected on the passenger's side or in the center of the road than the median or driver's side of the road. These results may generalize to surveys of living animals detected from moving vehicles.

FALSE CONCEPTS AND FAILING APPROACHES: AN ANALYSIS OF POVERTY IN THE DEVELOPING WORLD

Alexander Findeis, *SUNY Geneseo*

The UN Millennium Development goals set out to reduce poverty at \$1.25 per day by 50% between 1990 and 2015 – a goal that was reached. However, is \$1.25 per day an accurate measurement of poverty? In order to fight poverty effectively, it is necessary to have a clear understanding of what it is and how it relates to other socio-economic factors. This research project examines 31 developing countries over the course of 2000-2010, using data from the World Bank. By comparing socio-economic factors such as GDP, exports, FDI, HDI, and the Freedom House Index, the relationships between key variables can be identified. Through this analysis of key factors and differing measurements of poverty, this paper will show that current understandings of poverty, and proposed solutions for it, are lacking in accuracy and viability. Only by beginning to re-imagine the methods of measuring poverty can a constructive conversation be held on how to eradicate it.

FOLIAGE CANOPY INFLUENCES ON DIURNAL TEMPERATURES.

Adrianna N. Kremer, *SUNY at Brockport*; Kristine M. Chen, *University of Oklahoma*; Neil F. Laird, *Hobart & William Smith Colleges*

Deciduous forests experience seasonal changes of foliage cover with leaf growth in the spring and leaf loss in the autumn. These changes in foliage cover can substantially influence the atmospheric microclimate of the forest. This study examines the influence that spring transition from no foliage to full foliage has on under-canopy forest temperatures by comparing interior forest to adjacent field atmospheric measurements. Data was collected during two multi-month spring seasons by weather stations located at the Hanley Biological Preserve in the New York State Finger Lakes region. In addition to atmospheric measurements, hemispherical fisheye photographs were collected to quantify forest foliage cover throughout the measurement periods. The periods of transition in foliage cover were determined through fisheye image analysis and examination of the ratio of

solar radiation between the field and forest. As the foliage cover increased throughout the season, the amount of solar radiation that was received at the forest site decreased and the range between the daily maximum and minimum temperatures became notably different than the range measured at the field site. During the no foliage period, the daily temperature range between the field and forest sites were similar. During foliage transition and full foliage periods, the daily temperature range in the field became greater compared to the daily temperature range in the forest. Future research on this project will explore the influence of foliage cover on the variability of other microclimate variables, such as moisture and winds.

G

GENETIC SUPPRESSOR SCREEN IN DICTYOSTELIUM CELLS LACKING KRSB.

Swin Ratnayake, Yulia Artemenko, *SUNY Oswego*

Social amoeba *Dictyostelium discoideum* 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 KrsB contributes to the dynamic regulation of cell adhesion needed for proper cell adhesion and chemotaxis in *D. discoideum*. However, the exact mechanism by which KrsB affects the cell's ability to adhere is unclear. The goal of this project was to discover novel regulators and/or effectors of KrsB using a genetic suppressor screen, where 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. Identification of the genes responsible for the phenotype will give us a better understanding of the role and regulation of KrsB in cell migration, a process that is important both for normal physiology, as well as in a host of pathophysiological conditions, including atherosclerosis and cancer metastasis.

GEOTECHNICS OF EARTHWORM LOCOMOTION: AXIS SYMMETRIC TESTS

Vivia Amanda Fastiggi, *Wells College*; Rodrigo Bolera, Prashanth Vangla, Dr. David Frost, Atlanta

Geotechnical investigation via Cone Penetration Testing (CPT) in the present day is constrained in many aspects. Testing is limited to accessible areas, is costly and time consuming and data can only be obtained in the vertical direction. A solution for these limitations would be a self-propelled device that could characterize soil in any direction. Earthworms (e.g. *Lumbricus terrestris*) are a great bio-inspired idea for this solution due to their ability to easily and quickly propel themselves through the soil. To obtain a better understanding of the soil response to earthworm locomotion 3D printed ABS Worm body segment analogs representing the peristaltic shape at different ratios were used in an axis-symmetric device and translation resistance and displacement were measured. In the results we observe that all of the earthworm analogs showed an increase in the translational resistance as there was an increase in confinement pressure. There also showed to be a correlation between the increases in the expansion of the radius there is an increase in translation resistance at both relative densities. From the results a conclusion can be drawn that as the radius of the earthworm analog increases, the expanded analog in the axis-symmetric device encounters more soil and more passive resistance as well as the interfacial friction resistance already present on the analog. This accounts for the increase in the translation resistance and is a major principle in the anchorage of the earthworm.

GO OR GROW? STUDYING FITNESS OF CELL POPULATIONS USING A MATHEMATICAL MODEL.

Noah Reuter, Moumita Das, *Rochester Institute of Technology*

It has been observed that many types of cells and organisms either favor expansion and growth or rapid and distant migration. This is referred to as the go or grow hypothesis. We test this hypothesis using a computer simulation of two types of cells modeled as active self-propelled particles, and interacting via the Johnson-

Kendall-Roberts force when in contact. The two cell types have different self propulsion speeds and death rates, and the simulation assumes that the faster cells have shorter life spans. We investigate the migration and phase separation in this system and look to see which population is more successful in reaching the periphery. Ongoing work and future outlook involves incorporating cell proliferation, and investigating how that may impact the organization and dynamics in the system.

I

IDENTIFICATION AND CHARACTERIZATION OF POLYMERIC SUMO-2/3 CHAIN MODIFICATION AT THE SPINDLE MIDBODY DURING CYTOKINESIS.

Te-An Chen, Xiang-Dong "David" Zhang, *Buffalo State College*

SUMOylation is an essential post-translational modification that regulates a variety of important cellular processes through covalently conjugating small ubiquitin-related modifier proteins (SUMOs) to hundreds of different protein targets and subsequently affecting their activity, interaction, and stability. There are three main SUMO homologs expressed in mammals: SUMO-1, SUMO-2 and SUMO-3. SUMO-2 and SUMO-3 are 96% identical (referred collectively as SUMO-2/3), while SUMO-1 shares only 45% identity to SUMO-2/3. In contrast to SUMO-1 that is often attached to the lysine residues of target proteins as monomers, SUMO-2/3 are conjugated to target proteins in the forms of both monomers and polymeric SUMO-2/3 chains. To monitor the presence of polymeric SUMO-2/3 chain modification *in vivo*, we transfected human HeLa cells with a plasmid that encodes a green fluorescent protein (GFP) tagged fusion protein containing four tandem repeats of SUMO-interacting motifs, which exhibit a high binding affinity to SUMO-2/3 chains, followed by immunofluorescence microscopy. We found that GFP-SIMs fusion proteins are co-localized with the spindle midbody protein markers, including Aurora B, CENP-E and Tubulin, during cytokinesis. Furthermore, overexpression of GFP-SIMs fusion proteins causes an accumulation of SUMO-1, SUMO-2/3, the SUMO-conjugating E2 enzyme Ubc9, the SUMO E3 ligase PIASy, and the SUMO E3 ligase RanBP2 at the spindle midbody. Lastly, GFP-SIMs transfected cells at the stage of cytokinesis frequently contain chromatin bridge within the cleavage furrow, suggesting that a defect in resolving DNA catenation may block the completion of cytokinesis in these transfected cells compared to untransfected cells. Our studies suggested that polymeric SUMO-2/3 chain modification may play a critical role in regulating the progression of cytokinesis in mammalian cells.

IDENTIFICATION OF ASAP COMPLEX MUTANT LINES IN ARABIDOPSIS THALIANA.

Joseph Hong, Xiao-Ning Zhang, *Saint Bonaventure*

The Apoptosis- and Splicing-Associated Protein complex (ASAP complex) play a large role in RNA metabolism. It is evolutionarily conserved in eukaryotic cells. The ASAP complex can bind to the exon junction complex in which it then proceeds to affect transcription, splicing and translational regulation. ASAP is composed of 3 subunits, RNPS1, Acinus, and SAP18. All 3 subunits are shown to be involved in splicing. RNPS1 is a known splicing regulator. Acinus functions during chromatin condensation of apoptosis along with general transcriptional regulation. SAP18 is involved in transcriptional repression as well as recruitment of histone deacetylase to take acetyl groups off histones. The orthologous genes for these proteins have been identified in the model organism *Arabidopsis* as SR45 (AtRNPS1), AtSAP18, AtACIN and AtHDC1. In order to study the function of ASAP complex in *Arabidopsis*, multiple lines carrying independent T-DNA insertion mutations of these genes were examined. First, homozygous mutants were verified by genotyping. Then total RNAs were extracted from the inflorescence of these homozygous mutant plants and converted into cDNAs. The expression and splicing patterns of AtSAP18, AtACIN and AtHDC1 genes in these mutant lines were analyzed via rt-PCR. The mutant lines with the strongest effect on the RNA level were saved and crossed to a well-studied sr45-1 null mutant. Future research will

examine phenotypes of these Arabidopsis single and double mutants at different developmental stages and their responses to various environmental stimuli.

IDENTIFICATION OF RNA MODIFICATION ENZYMES IN TRYPANOSOMA BRUCEI.

Will C. Schultz, Xiane Smith, Jordan Coffey, Kevin T. Militello, *SUNY Geneseo*

RNA methylation is a type of posttranscriptional modification that plays an important role in controlling gene expression. There is minimal research on this process, especially in Trypanosomes. The organism *Trypanosoma brucei*, the protozoan parasite responsible for Human African Trypanosomiasis, does not seem to have promoter regions or transcriptional regulation machinery. Thus, RNA methylation may play an especially important part in regulating gene expression in this organism. Recently, we have identified seven putative RNA methyltransferase genes in the genome of *T. brucei*. Our research indicates that two of these putative RNA methyltransferases, termed TbCRMT4 and TbCRMT5 (*T. brucei* Cytosine RNA Methyltransferase), are required for maximum parasite growth. Although we suspect these genes to be RNA methyltransferases, we do not have evidence for RNA methyltransferase activity. In this work, we attempt to obtain experimental evidence for RNA methyltransferase activity of TbCRMT4 and TbCRMT5 in vitro. Our main approach involves expression of the CRMT proteins in *E. coli*, protein purification with beads that bind to an N-terminal poly-His tag, and an in vitro methyltransferase assay. CRMT4 was produced in *E. coli* but was difficult to purify. SDS-PAGE results for an N-terminal His tag protein indicate CRMT4 insolubility. Our next step will be to use PCR to create smaller fragments of CRMT4, which may be soluble. CRMT5 was produced in *E. coli* with an N-terminal His tag and purified using a His-affinity gel column. Purified CRMT5 was used in a series of methyltransferase assays using the MTase-Glo™ methyltransferase assay kit (Promega). CRMT5 shows activity in the methyltransferase assay in the presence of cytosine-containing RNA (*T. brucei* total RNA and Poly-IC RNA) and S-adenosylmethionine. There was no activity observed in the presence of RNA that lacks cytosine or when a mock purification from *E. coli* without the CRMT5 gene was used instead of CRMT5. 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 of RNA methyltransferases indicate the presence of a process to create an epitranscriptome in *T. brucei*.

IMMUNE RESPONSE AND SEXUAL ORNAMENTATION TRADE-OFFS IN TELEOPSIS DALMANNI.

Amy Farnham, Nicholas Sidou, Josephine Reinhardt, *SUNY Geneseo*

Little is known about the genetic basis of evolutionary trade-offs. It is believed that sexual ornamentation conveys information to potential mates about the genetic quality of the male. One example of this is how peacocks prefer mates with more extravagant tails. However, these traits may be costly to produce and result in a less productive output of other resources such as immune defense. Our project uses *Teleopsis dalmanni*, Stalk-eyed flies, who get their name from the unique “eyestalk” projections that are on the side of their heads. Males and females can be distinguished by the length of their eyestalks; males tend to have longer eyestalks while the female eyestalks are shorter. Our goal is to determine whether altering the presence of functioning immunology genes will result in longer eye stalks due to freed up energy resources according to the trade-off hypothesis or if those with a higher genetic quality will be resilient to change according to the handicap hypothesis. CRISPR/Cas-9 techniques will be used to create null mutations in immunity genes in *Teleopsis dalmanni*. Using CRISPR it is possible to use the Cas-9 protein to make a cut in a certain gene and cause a mutation to knock out the gene. The two immunity genes were selected due to the immune response they contribute to *Drosophila*, who show genetic similarities to *Teleopsis dalmanni*, with non-lethal mutations having been seen; as well as the correlation shown between these genes and eye stalk disc prevalence and the female bias they present in Stalk-eyed flies. The Black gene will be used to as control due to the phenotypic change it

would cause in the mutants. To date, we have successfully developed constructs for our Black gene, designed assays for colony PCR, and designed PCR primers to genotype mutants.

IMPACT OF INVASIVE JAPANESE BARBERRY ON THE BREEDING PHYSIOLOGY OF OVENBIRDS.

Molly Border, Katherine Hensel, Susan Smith Pagano, *Rochester Institute of Technology*; Chad Seewagen, *Great Hollow Nature Preserve and Ecological Research Center*

Japanese barberry (*Berberis thunbergii*) is a widespread invasive plant that has become prevalent in Northeastern forests. However, little is known about the impacts of this invasive shrub on breeding habitat quality for forest breeding songbirds. We studied Ovenbirds (*Seiurus aurocapilla*) at the Great Hollow Nature Preserve and Ecological Research Center in New Fairfield, CT in order to investigate physiological indicators of breeding habitat. Male ovenbirds were captured using mist nets on their breeding territories in of May 2017 and 2018. Blood was sampled to assess chronic physiological stress via heterophil:lymphocyte ratios, and plasma was assayed for total protein, triglyceride, and uric acid concentrations. Both chronic stress and plasma metabolite levels were used to evaluate the overall physiological condition of each individual in relation to the presence or absence of barberry in their breeding territory. In addition, samples of barberry fruits were analyzed for energy, fat, and total phenol content.

IMPACTS OF MEIOTIC DRIVE ON THE EXPRESSION AND ABUNDANCE OF TRANSPOSABLE ELEMENTS.

Melanie Kirk, Chloe Ladas, *SUNY Geneseo*

This project aims to characterize the abundance and expression of transposable elements (TE's) in the stalk-eyed fly genome, with particular focus on addressing whether the expression of meiotic drive in males leads to transposable element "release" via disruption of piRNA pathways. Based on genomic sequencing data from standard and meiotic drive *T. dalmanni* males, we aim to determine if the abundance of major TE families on the meiotic drive X chromosome is different than on the standard X chromosome, presumably due to accumulation over evolutionary time. Using a bioinformatics-driven approach, this project analyzes RNA sequencing (RNAseq) data from both standard and meiotic drive males to determine if the expression of shared TE copies is higher in meiotic drive males. We are currently using PoPoolationTE2 to uncover the insertion frequencies and positions of TE's as well as to compare TE abundance between population samples. We have obtained results using the program Transposome, run with the intent of estimating TE abundance and diversity. In addition, we will be performing statistical analyses to determine if the differences observed between samples through Transposome are significant. So far, our data indicates that the abundance of TE's is higher in the samples that are known to have drive than in those without drive.

IN SITU EXPRESSION ANALYSIS OF STALK EYED FLY TESTES

Evan McCabe, *SUNY Geneseo*

Heterochromatin Protein 1 (HP1) is a family of proteins that previous research has shown to play a critical role in the organization and condensation of chromatin in preparation for cell division. Often times this protein family has been observed to have newly duplicated in large numbers and localize specifically to the testis in species exhibiting the genetic phenomenon of sex ratio Meiotic Drive; a violation of Mendel's law of segregation of the sex chromosomes in which carriers of drive alleles produce almost exclusively female offspring. The scope of this project is to analyze HP1 expression in stalk eyed flies (*Teleopsis dalmanni*) and to observe its hypothesized disruption of spermatogenesis in pre-meiotic, meiotic, and post meiotic stages. We utilize immunostaining and in situ hybridization techniques in order to detect the localization of HP1 protein and mRNA transcripts in developing testes respectively. So far, we have assessed normal testes development using characteristic cell size, shape, and nuclear morphology, and have cloned and sequenced 4 HP1 gene templates of which antisense

RNA probes are currently being synthesized. Altogether, if our hypothesis that HP1 contributes to irregular meiotic divisions during male meiotic drive is accurate, we expect to find no expression or misexpression of HP1 genes in stalk eyed flies that possess sex ratio meiotic drive, contrasted to the expression pattern of wild type flies.

IN VITRO ASSESSMENT OF A CRISPR/CAS9-MEDIATED, NON-TRANSIENT GENE THERAPY CANDIDATE FOR VARIOUS CANCERS.

Alexander Ille*, Hannah Lamont*, Kimberly Bernosky-Smith, *D'Youville College*

*Co-first authors

The highly specific gene-editing mechanism, CRISPR/Cas9, is emerging as an innovative tool for a wide range of applications within the fields of molecular biology and genetic engineering. Actin-beta (β -actin, encoded by the ACTB gene) is a cellular house-keeping protein involved in cell motility, structure, integrity, and intercellular signalling. Mutations in the ACTB gene play a role in B-cell lymphoma and Becker's melanosis. Moreover, previous data implicates mutant variants of ACTB in mediating the tumorigenic activity at the cellular level. We developed a CRISPR/Cas9 mechanism for the replacement of genomic ACTB with a custom ACTB variant. Our ACTB variant was designed to sustain normal β -actin functionality. In vitro assessment of our mechanism in mammalian cell culture produced successful CRISPR-mediated modification indicated by GFP-reporter expression. Cellular imaging revealed normal morphology of modified cells in comparison to un-modified cells. Our results suggest introductory-level viability of a novel CRISPR-mediated gene-therapy candidate with potential applications for various cancers.

INHIBITION OF SODIUM TRANSPORT BY DECREASED APICAL PH IN THE MOUSE EPITHELIAL KIDNEY CELL LINE MPKCCDC14

Taylor Thompson, Bernardo Ortega, *SUNY Brockport*

The activity and surface density of the epithelial sodium channel ENaC is decreased by acidification of intracellular pH. By contrast, acidic pH enhances activity in A6, an amphibian epithelial cell line. Here we use the mouse cortical collecting duct cell line mpkCCDc14 in order to study the effect of apical acidification on sodium transport in mammalian epithelia. We show that Na^+ transport in mpkCCD cells, as indicated by the calculated short circuit current (I_{sc}), is decreased at a pH of 5.9, likely due to decreased ENaC cell surface density and/or activity.

INORGANIC SPECIES IN FINE AND COARSE PARTICULATE MATTER AND GASES MEASURED IN ST. BONAVENTURE, NY.

Tanya Gupta, *St. Bonaventure University*

Aerosol and gases in the atmosphere can have many detrimental impacts on human health. Emission sources of aerosol and gases include natural and anthropogenic. Natural emissions sources include volcanic gases, soil dust, and forest fires. Anthropogenic sources of emissions include fossil fuels and agriculture. Aerosol particle size also plays an important role in human health because in general smaller particles than fine particulate matter are more hazardous. Fine particulate matter and coarse particulate matter are defined as particulate matter with an aerodynamic diameter of 2.5 micrometer and 10 micrometers, respectively. They are present in the atmosphere for longer durations of time and can enter into the lungs and even the bloodstream which can worsen existing conditions or create new ones. The objective of this research is to determine inorganic species fine particulate matter, coarse particulate matter and gases concentrations in Olean, NY. The site of study is St. Bonaventure University, and the time intervals at which the samples will be collected is every 24 or 48 hours. Fine particulate matter, coarse particulate matter from filters and gas concentrations of ammonium, sulfate, and nitrate will be

collected using denuders and analyzed using ion chromatography. Overall, concentrations of aerosol particles and gases will be determined to characterize air quality in a rural location that has not been studied previously.

INTERFERENCE OF IONIC LIQUIDS ON THE BRADFORD ASSAY: A SPECTROSCOPIC STUDY.

Tyler A. Johnston, Mark P. Heitz, *The College at Brockport*

With the growing popularity of ionic liquids (ILs) in production and industry, inevitably, these substances are entering the environment. As these liquid salts become more widely used, it is essential that the effects and possible interference of these liquids on common laboratory techniques are characterized. The Bradford assay is a UV-vis absorption method used for protein quantification that relies on the specific interactions that occur between a protein and Coomassie Brilliant Blue G-250 (CBBG). Specifically, the assay depends on CBBG's color change when in the presence of protein. The bound form of the dye absorbs at 595-nm. Using known protein concentrations, a standard curve can be constructed. These data points are the baseline against which we can determine unknown protein solution concentration. It has been widely documented that the Bradford Assay is susceptible to interference from a large variety of chemicals, including surfactants and typical chemical denaturants. The similarity of IL structure to surfactants suggests that ILs can perturb the determination of protein concentration via the Bradford assay. Therefore, the focus of our study is the spectroscopic measurement of the effects of 1-decyl-3-methylimidazolium chloride ([Im10,1]⁺ Cl⁻) on the Bradford assay. Our results show that in neat IL solution, there is a systematic increase in the absorbance at 595-nm indicating that CBBG responds to presence of ionic liquid. The similar response of CBBG to both protein and [Im10,1]⁺ Cl⁻ creates a problem in that the presence of IL can result in a measured protein concentration that appears to be higher than what is actually present in solution.

INVESTIGATION INTO THE ROLE OF ACINETOBACTER BAYLYI TSSM, A T6SS COMPONENT, IN BACTERIAL CELL-CELL INTERACTIONS.

John Miller, Kristin Picardo, Ph.D., *St. John Fisher College*

Secretion systems are used by bacterial cells to obtain nutrients, secrete toxic proteins to the environment, or directly act on targets, including eukaryotes, to result in illness. *Pseudomonas aeruginosa* has been shown to use its Type VI Secretion System (T6SS) in a defensive manner. When another bacterium that is T6SS⁺ attacks *P. aeruginosa*, it responds with a counterattack with its own T6SS. This cell-cell interaction with competing bacteria is what allows *P. aeruginosa* to perform its antagonistic behavior. *Acinetobacter baylyi* also contains a T6SS that is more aggressive, meaning it does not require an initial attack to activate its antagonistic behavior. However, the T6SS also has other functions within the bacterial community, such as the proteins secreted by the T6SS being involved in biofilm formation. TssM is a structural protein in the transmembrane portion of the T6SS that is required for the formation of the entire structure and therefore is necessary for a bacterium to have a functional T6SS. Will removal of TssM in *Acinetobacter baylyi* result in reduced biofilm formation as well as decreased lysing of competing bacteria? What effect does the removal of TssM have on *A. baylyi*'s interaction with other bacteria species? Quantitative Competition assays and biofilm assays will be used to analyze the interactions between *P. aeruginosa* and *A. baylyi*. It is predicted that a TssM mutant not having a functional T6SS will result in high survival of *P. aeruginosa* in the Quantitative Competition Assay and a decrease in *A. baylyi* because they would have no mechanism of eliminating the competing bacteria. The TssM mutant would also be predicted to not form a biofilm in a biofilm assay. Learning the specific conditions involved in the usage of the T6SS in bacteria, and how it affects biofilm formation can provide insight into healthy and diseased microbiomes and potential advancements in treatment of infectious bacteria.

INVESTIGATION OF BACTERIAL BIOCONTROL OF FIREBLIGHT (ERWINIA AMYLOVORA)

Maggie Lesch, Maryann Herman, *St. John Fisher College*; Daniel Stein, *Ontario Pear*

Erwinia amylovora is a bacterium pathogenic to Asian pear trees and many other pome fruit. Commonly called fire blight, *E. amylovora*, is very harmful to its host as it can attack and kill all parts of the tree. It disseminates rapidly, making it a disease that can spread throughout an entire orchard given the right conditions, such as abundant rainfall, are present. Orchards in New York State must treat pears early in the season to prevent infection and spread of fire blight, though few options are available. Typically, growers apply preventative antibiotics and bacterial resistance to these products has been found. Investigating biological controls of fire blight, where a natural enemy of the pathogen is used to control its infection and spread, could provide another tool to prevent disease. Known antagonistic bacterial species, isolated from an Asian pear orchard in Ontario, NY have been tested as potential species to control fire blight. Immature pears were collected from a farm in Ontario, NY and infected with fire blight and potential antagonistic species to investigate biocontrol potential.

ISOLATION AND IDENTIFICATION OF CULTURABLE BACTERIAL ENDOPHYTES FROM POISON IVY.

Trevor S. Penix, Peter C. Wengert and Michael A. Savka, *Rochester Institute of Technology*

Poison ivy (*Toxicodendron radicans*) is a poisonous plant known for causing contact dermatitis. The association of bacterial endophytes in the poison ivy plant is largely unknown. Stems and fruitings were sampled from plants growing in Wheatland, NY, surface sterilized, axenically dissected to prepare internal tissue, and internal tissues were inoculated into three different bacterial growth media. After 72 hours of incubation, serial dilutions were prepared and dilutions were plated on growth media agar plates. The plates were incubated and individual colonies were identified and isolated. Nineteen bacterial endophytes were identified displaying a variety of growth morphologies. Genomic DNA was isolated, and V3-V4 region of the 16S rRNA gene was amplified and sequencing. The sequencing results showed species from a variety of genera, including *Curtobacterium*, *Pseudomonas*, *Bacillus*, *Pantoea*, *Streptomyces*, and *Enterobacter*. Future work will include performing bioassays for quorum sensing signals of the acyl-homoserine class and to determine the whole genome sequences of bacterial endophytes.

ISOLATION OF BACTERIOPHAGE IN STAPHYLOCOCCUS SPECIES

Janelle A. Fancher, Maria C. Kajdasz, Shania P.J.M. van Nuland and Mark A. Gallo Ph.D., *Niagara University*

Pathogenic *Staphylococcus* strains that are antibiotic resistant can cause infections that are difficult to treat. The use of bacteriophage in treatment of *Staphylococcus aureus* infection has been proposed as a possible alternative to antibiotics. Isolation and identification of new bacteriophage is an exciting area of research that may yield novel treatments for infections that have been challenging to eliminate by traditional means. One previously unexplored source of Staph and their corresponding phage are strains associated with wild animals. In this study, Staph were isolated from white tail deer, *Odocoileus virginianus*. The resulting bacteria were analyzed for the presence of lytic phage that were active against RN4220, a permissive strain of *S. aureus*. Sixteen independent bacteriophages were detected and their range of activity on other *Staphylococcus* species will be determined. DNA extraction and analysis will be performed.

L

LAKE-WIDE COMPARISON OF CHINOOK SALMON CONDITION AFTER PEN-REARING IN LAKE ONTARIO

Josh Noonan, *SUNY Brockport*, additional authors: *New York State Department of Environmental Conservation, Ontario Ministry of Natural Resources and Forestry*

Chinook salmon is the top predator in Lake Ontario supporting a multi-million dollar sport fishery. Each year, New York State Department of Environmental Conservation and the Ontario Ministry of Natural Resources and

Forestry stock millions of Chinook into Lake Ontario at dozens of sites around the lake to maintain the fishery. The Chinook are reared in net pens to increase imprinting and survival. The objectives of this study were to compare growth, condition, and lipid content of Chinook after pen-rearing around Lake Ontario. Pen-rearing was conducted by volunteers at 6 sites in Canadian waters and 9 sites in US waters in April and May 2018 and pen-rearing duration varied among sites (11-38 days). The highest specific growth rates were for Chinook reared in Canadian waters. However, lipid content increased significantly between the initial sampling (prior to stocking) and the final sampling at six US sites and only one Canadian site. In addition, growth of Chinook was limited during the two first weeks after stocking in the pens in both Canadian and US waters. These results suggest the duration of the rearing and potential differences in diet composition (Ewos vs. BioOregon) affect weight gain and lipid content.

LAND-USE IMPACTS WATER QUALITY AND AQUATIC INVERTEBRATE COMMUNITIES IN THE GENESEE RIVER.

Daniel Beers, Courtney McDaniel, and Michael Chislock, *The College at Brockport*

Past studies have repeatedly shown that land usage from human activities can have profound impacts on aquatic ecosystems. Whether it be food-web alterations, emerging contaminants, nutrient loading or habitat destruction, human land use is one of the largest problems facing freshwater ecology and conservation practices. This project aimed to explore how land use in the Genesee River watershed impacts water quality and aquatic invertebrate communities. Two study sites were chosen close to the Genesee River headwaters near the New York - Pennsylvania state line. One was an agriculturally influenced site and one was a forested site. Each site was sampled monthly for aquatic invertebrates and water quality. Field water quality measurements included temperature, specific conductivity, dissolved oxygen, and pH. Water samples were analyzed in lab for alkalinity, suspended solids, turbidity, and nutrients at Brockport's Limnology Lab. Aquatic invertebrates were collected and preserved for identification and community analysis. We predicted that the forested site would have a lower agricultural signature and lower nutrient concentrations than our agricultural site. Results have shown that nutrient concentrations have been higher at our forested site than our agricultural site, most likely due to the heavily agricultural tributary, Cryder Creek, flowing into the river upstream from our forested site. More research needs to be completed on tributaries, including Cryder Creek, to assess nutrient loading from smaller tributaries of the Genesee River, especially in relation to storm events.

LONG-DISTANCE LAKE-EFFECT SNOW BANDS IN THE GREAT LAKES REGIONS.

Neil Laird, Hobart and *William Smith Colleges*

Although less frequent than typical lake-effect events, long-distance lake-effect snow bands have been known to result in unexpected snowfall in areas far removed from the Great Lakes. Little is known about these bands such as how often they occur, how far inland they regularly extend, or what environmental conditions are favorable for their development. A 13-winter time period was examined to identify events and address these questions. During the 13 winters (Nov-Feb) spanning 2003/2004 through 2015/2016, a total of 166 long-distance snow bands were identified throughout the Great Lakes using radar reflectivity composites. These bands reached inland distances of over 600 km from the lakeshore. The project identified several routinely occurring types of long-distance lake-effect band events that seemed to be aided by orography and/or synoptic features, such as a cold surge or Arctic front. The presentation will discuss the occurrence frequency and characteristics of long-distance lake-effect snow bands, as well as highlight some of the possible features that may be aiding their development and maintenance.

MATHEMATICAL MODEL OF THE VITREOUS GEL AND ITS MECHANOBIOLOGY: LINEAR AND NONLINEAR RESPONSES OF THE COMPOSITE NETWORK OF COLLAGEN AND HYALURONIC ACID NETWORKS.

Pancy Lwin, Scott Franklin, George Thurston, David Ross, Moumita Das, *Rochester Institute of Technology*

The vitreous gel in the human eye is a viscoelastic composite network of stiff collagen fibers and softer hyaluronic acid (HA) polymers. Its material properties are critical to vitreous function, and ultimately to that of the eye, and depend on applied stresses, concentrations, and constituent filament stiffness. Although it has long been known to undergo dramatic changes with aging and disease, the key vitreous gel phase transitions and their mechanical consequences are not well understood. We mathematically model and investigate the mechanical response of the primary components of the vitreous gel: (i) a stiff network of collagen fibers, and (ii) a flexible polyelectrolyte network of HA. Our preliminary results, which focus on the stiff network, relate the nonlinear shear and tensile properties and stress-strain relationships of the network to the stiffness, density, and crosslinking of the fibers. Our results may provide insights into the mechanical properties of the collagen network in the vitreous gel.

MCH-MEDIATED EXPRESSION OF CIRCADIAN RHYTHM GENES

Meghan Walters, Laurie B. Cook, *The College at Brockport*

Melanin-concentrating hormone (MCH) is a hormone known for stimulating appetite. Its effects are most studied in the brain, but our lab focuses on its effects in fat cells, particularly its influence over the differentiation process of 3T3-L1 pre-adipocytes. These cells serve as a model for differentiation that we can generalize to mammals, humans being of the highest interest. The differentiation of these cells takes ten days, over which MCH has been shown to mediate changes in gene expression. Preliminary data observed families of genes whose expression was mediated by MCH over the course of two days of differentiation. Day 2 is of particular interest due to the discovery of a primary cilia localizing to MCHR1. The data suggested that certain circadian rhythm genes respond to MCH. Other research has found that MCH may be a key factor in REM-sleep regulation and in the sleep-wake cycle in general. We wished to better study its regulatory role in relation to circadian rhythm in fat cells. The goal of this project was to confirm the data pertaining to six genes related to the circadian rhythm core mechanism and one of its regulatory proteins: Per1, Per2, Per3, Cry1, Cry2, and Csnk1e. Preliminary data suggests MCH does not mediate expression of Per1-3 on Day 0 but decreases expression when treated with MCH on Day 2 of Per1-2; Per3 did not show a significant change. Per1-2 are potential targets of MCH. Cry1-2 and Csnk1e did not show any significant change when treated with MCH and are unlikely to be targets of MCH, but as they are core to the clock mechanism, we wanted to confirm their lack of regulation by MCH. The results of this study mostly match preliminary data. Key differences include significant differences in Per3 expression and Cry2 expression. These differences may simply be explained due to experimental error.

METHOD DEVELOPMENT AND APPLICATION OF POLYMER ANALYSIS.

Jessica Zagari, Markus M. Hoffmann, *The College at Brockport*

Polymers are molecules with defined structural repeat units. It is practically very difficult to synthesize a polymer product that is all of identical number of molecular repeat units. Consequently, the obtained polymer typically consists of a mixture of compounds with varying chain lengths. Such mixtures of polymers are referred to as polydisperse polymers. Polyethylene glycol (PEG), $\text{HO}(\text{CH}_2\text{CH}_2\text{O})_n\text{H}$ is such a polydisperse polymer with n indicating the number of $\text{CH}_2\text{CH}_2\text{O}$ repeat units. PEG is actually commercially available with different average chain lengths such as PEG 400, PEG 1000, PEG 10000, where the number refers to the average molecular weight. Using two separating techniques of gas and liquid chromatography (GC and LC), we were able to analyze the true composition of PEG 200 and PEG 400. PEG 200 was analyzed using gas chromatography and PEG 400 was

analyzed using liquid chromatography. Details of each analysis will be presented. We found for PEG 200 the average molecular weight is 223g/mol, ~10% higher than 200 g/mol, but for PEG 400 we found good agreement with exactly 400g/mol.

MICRORNA TARGET PREDICTION USING MACHINE LEARNING

Neslihan Ari, Dr. Rongkun Shen, *The College at Brockport*

MicroRNAs (miRNAs) are non-coding, single-stranded, 21-23 nucleotide long RNA molecules involved in post-transcriptional gene regulation by target messengerRNA (mRNA) degradation or translational repression. MicroRNA-induced gene silencing impacts important biological processes such as stem cell differentiation, tumorigenesis, neurogenesis, and progression of developmental stages. Experimental approaches to study miRNA-mRNA interaction are time-consuming and costly, thus making computational tools a preferable technique for determining the targets for miRNA molecules. Although current algorithms do exist, there is need for improved sensitivity and accuracy in target prediction. To achieve this, previously prepared training and testing data profiles by Dr. Shen's lab will be used to train a machine learning model, specifically a Deep Learning Neural Network (DLNN), which will be developed as a Multilayer Perceptron within the TensorFlow machine learning system. After training and optimization using various datasets, when the results show reliable target prediction, the miRNA Target Prediction Tool will be shared with scientists around the world to contribute to the study of miRNA-induced gene regulation.

MODELING COMPOSITE BIOPOLYMER NETWORKS USING EFFECTIVE MEDIUM THEORY.

Jacob Wales, Moumita Das, *Rochester Institute of Technology*

The mechanical response of most eukaryotic cells is due to their cytoskeleton, a polymeric scaffold made of two major biopolymer systems, actin filaments and microtubules, with very different mechanical properties. The cytoskeleton is responsible for a number of cellular functions including maintaining shape, rigidity, and facilitating movement. We model cytoskeletal networks as composite networks made of actin filaments and microtubules, using a combination of Rigidity Percolation Theory and Effective Medium Theory to obtain their mechanical response as a function of the concentration of the two filament types.

MODELING US FRESHWATER MACROINVERTEBRATE COMMUNITIES AND ECOLOGICAL HEALTH

Sofie Christie, Kaitlin Stack Whitney, *Rochester Institute of Technology*

Macroinvertebrates are aquatic invertebrates visible without a microscope, including insects, crustaceans, snails, and mollusks. They are important indicators of environmental health sensitive to ecological changes. While many studies examine macroinvertebrate communities at one location, there is a lack of synthesis across space and time. So our objective was to study macroinvertebrate communities at a continental scale. We examined the abundance and diversity of freshwater macroinvertebrates in the phyla Arthropoda and Annelida using publicly available datasets in the United States from any time period. We compiled 2233 records of macroinvertebrate abundance from 1990 through 2018. Using ecoinformatics methods and R statistical software, we modeled macroinvertebrate abundance and functional group community diversity. We tested their correlation with climate-sensitive variables including water temperature, as well as socio-ecological parameters including urbanization and water quality. Our results will help inform conservation of US freshwater macroinvertebrates in a changing climate.

MOTHER-CALF POSITIONING IN SEAQUARIUM-BASED BELUGA WHALES

Natassia Tuhovak and Michael Noonan, *Canisius College*

Understanding the details of the interactions between mothers and their offspring are essential to understanding any species' reproductive and social development. The present study investigated the body positions and postures adopted by mother and calf beluga whales relative to one another, following the birth of five new beluga babies in a seaquarium setting. The calf positioned directly above the mother's dorsal ridge was the most commonly observed dyad posture. The proportion of other positions and postures increased steadily with calf age. It is hoped that these findings regarding these five healthy calves will inform subsequent assessments of new calves observed both in the wild and in human-managed care.

MUTAGENESIS OF DE NOVO GENES VIA CRISPR- CAS9 IN DROSOPHILA MELANOGASTER

Julia Nicosia and Dr. Josie Reinhardt, *SUNY Geneseo*

New genes have always been particularly interesting to biologists because they help explain how organisms have evolved to become increasingly complex over time. There are several ways these new genes can arise including duplication, gene fusion, transposable elements, and de novo. De novo genes are particularly interesting because the gene began coding for a protein only recently in evolutionary history meaning they arose from previously non-coding DNA. The *Drosophila* de novo genes we are studying are expressed mainly in the male testes, and previous work based on RNA interference showed these genes may be essential to male fertility and viability. However, we do not know whether these genes function as proteins, like most genes, or as functional RNAs. We are using CRISPR-Cas9, a gene modification tool, to create null mutations in *Drosophila melanogaster*'s de novo genes to answer this question. CRISPR-Cas9 works by inducing a frame-shift mutation in a gene, but it can also be used to delete a large section of the gene. With a frame-shift, the gene will still be coded into an RNA strand, but the protein translated will be nonfunctional: while the deletion will affect the function of the RNA and protein. By comparing phenotypic and genotypic outcomes of the frameshift and the deletion we can answer the question about how de novo genes perform their functions. We have created CRISPR-Cas9 targeting constructs for multiple de novo genes, designed primers for genotyping of flies post-injection, and have collected data on the survival rate of water injected embryos.

N

NANOSCALE CELLULOSE MICROFIBRILS FROM POTATO, SUGAR BEET AND CELERY PULP AS RHEOLOGICAL MODIFIERS AND BIOCOMPOSITE MATERIALS.

Madeline Hoey, Alixander Perzon, Claire Holland, Peter Ulvskov, Bodil Jørgensen, *University of Rochester*

Annually, agricultural industries generate a substantial amount of cellulosic byproducts that is of great interest due to their potential as a cellulosic reinforcing phase for composite materials and as rheological modifiers. This byproduct waste material consists of roughly one-third cellulose, one-third pectin and one-third hemicellulose. Cellulose comprises the load bearing structure of plant cell walls and consists of up to thousands of β (1 \rightarrow 4) linked D-glucose units, and can be found as intertwined microfibrils in the parenchyma cell wall of sugar beet, potato and celery. Cellulose microfibrils can be extracted from the biomass using a chemical treatment followed by a mechanical treatment to obtain a homogeneous suspension due to the individualization of the microfibrils. We aim to compare the isolated cellulose fibers from potato pulp, sugar beet pulp and celery following alkali and bleaching treatments. Comprehensive microarray polymer profiling (ComPP) indicates non-cellulosic polysaccharides remaining on the surface of the fibrils, and the quantities of these polysaccharides are confirmed by Dionex. Rheological characterization assesses the deformation and flow behavior of prepared microfibrils and the suitability for construction of biomaterials.

OPTIMIZATION OF GROWTH CONDITIONS AND LIPID ACCUMULATION FOR BIODIESEL PRODUCTION USING CHLAMYDOMONAS REINHARDTII

Nate Halsteter, Emily McDermott, and Noveera Ahmed, Ph.D., *St. John Fisher College*

The current rate at which petroleum fuel is being used is unsustainable and, if not corrected, will result in a catastrophic fuel shortage. Scientists are looking at biofuels, fuels derived from living organisms, as a sustainable source of fuel. *Chlamydomonas reinhardtii*, a unicellular protist, has been shown to be a viable source for biodiesel. *C. reinhardtii* produce a relatively large amount of lipids which can be turned into biodiesel using a simple esterification reaction. To increase biodiesel yield, lipid content needs to be increased within algal cells while maximizing cell density. Suen et al (1987) found that *C. reinhardtii* grown under nitrogen-deficient conditions increased lipid droplets with cells. Zabawinski, et al (2001) created a strain that was deficient in ADP-glucose pyrophosphorylase, *sta-6*, and accumulated lipid droplets. It is unclear if these conditions reduce the lifespan of the organism or allow for the same or increased growth rates compared to normal conditions. To identify conditions in which *C. reinhardtii* accumulate lipid droplets, grow at a faster rate, and live longer, three media additives will be tested which have been shown, in our lab, to increase the rate of growth. Vitamin B-12, TPGS, NALC will be added to TAP growth media and growth will be measured by hemocytometer and Evan's blue dye. Lipid droplets will be visualized using Nile Red staining.

Suen, Y., J. S. Hubbard, G. Holzer, and T. G. Tornabene. 1987. Total lipid production of the green alga *Nannochloropsis* sp. QII under different nitrogen regimes. *J. Phycol.* 23:289-296.

Zabawinski, C., N. Van Den Koornhuyse, C. D'Hulst, R. Schlichting, C. Giersch, B. Delrue, J. M. Lacroix, J. Preiss, and S. Ball. 2001. Starchless mutants of *Chlamydomonas reinhardtii* lack the small subunit of a heterotetrameric ADP-glucose pyrophosphorylase. *J. Bacteriol.* 183:1069-1077

OPTIMIZATION OF MICROSATELLITE DNA COMPARISON BETWEEN INDIVIDUAL BELUGAS AS A PROCEDURE FOR GENETIC IDENTIFICATION.

Leanne Walker and Michael Noonan, *Canisius College*

When managing animals in human care, it is extremely useful to determine genetic distinctiveness, particularly when managing breeding populations. The present investigation attempted to exploit inherited chromosomal microsatellite size differences between individuals for identification, using DNA extracted from beluga blood and tissue. The need for considerable procedural variation was encountered between samples in terms of DNA extraction requirements, PCR cycle conditions, amplified product purity, and electrophoresis parameters. Our current research efforts aim to establish whether these procedures, now optimized for whale-to-whale variation, will allow for reliable paternity tests in *Delphinapterus leucas*.

ORIENTATION OF AMYLOIDOGENIC PEPTIDES OVER NANO-GOLD PARTICLES

Kazushige Yokoyama, *SUNY Geneseo*

The surface attachment of amyloidogenic peptides; amyloid beta 1-40 (Ab1-40), alpha-synuclein, and beta 2 microglobulin were investigated over nano-gold particle's surface. The systematic analysis of absorption bands of SPR (Surface Plasmon Resonance) of gold particles extracted the change of surface property caused by a degree of coverage of peptides. The extracted peptide coverage ratio (Theta) was examined with geometric analysis, and it concluded that a peptide holds a "spiking-out" orientation over the gold surface. Based on this orientation, our studies suggest a particular sequence of peptide is responsible for an electrostatic interaction with gold surface. For example, Ab1-40 is considered to be attached to the gold surface with Lysine at 23rd

sequence. Quite interestingly, relationship between (Theta) and diameters of gold particle (d) showed a complex feature and it was fully explainable by physical (but not chemical) interpretation of peptide packing.

ORIGINS OF AN INVASIVE: GEOSPATIAL ANALYSIS OF PLANT DISTRIBUTION AND WIND PATTERNS TO IDENTIFY POSSIBLE ORIGINS OF SCAEVOLA TACCADA IN PUERTO RICO

Taylor Yowan, *Ithaca College*

Scaevola plumieri and *S. taccada* (Goodeniaceae) are two widespread dune-dwelling shrubs found in the Caribbean. We are interested in comparing their patterns of occurrence on the islands of Vieques, Culebra, and Culebrita (Puerto Rico). In particular, we are interested in the potential origins of *S. taccada* which is a non-native species known to be invasive in many locations in the Caribbean where it threatens native species, including *Scaevola plumieri*. Coordinate locations were recorded from previous fieldwork to sample plants in these island habitats. The locality coordinates were loaded into ArcGIS, in combination with digital elevation maps from the United States Geological Survey which were used to determine the aspect of direction for each collection locality. Next, we collected and parsed wind and current data from selected NOAA weather buoys near Puerto Rico to determine prevailing wind and current directions. Combined with the locality aspects, we used the wind and current data to identify possible dispersal routes of the invasive species *Scaevola taccada*. Results from preliminary data analysis suggest *S.taccada* may have dispersed to Puerto Rico from the United States Virgin Islands and St. Croix. The utilization of geospatial analysis has provided us the ability to postulate a source for the invasive species *Scaevola taccada* so that sample collection and genetic analysis can be used to confirm our hypothesis.

P

PACS-2 SUMOYLATION IN RESPONSE TO DNA DAMAGE.

Patrick Buckley, *SUNY Geneseo*; You Jin Choi, Ph.D., Jonathan Barroso-González, Ph.D. , Laurel Thomas, Gary Thomas, Ph.D., Pittsburgh, PA

Small Ubiquitin-like Modifier proteins, or SUMO proteins, are a family of small proteins that are similar in structure to ubiquitin. These proteins covalently attach and detach to other proteins, such as PACS-2, to modify their function. PACS-2 is a multifunctional sorting protein that was initially identified by its role in mediating secretory pathway traffic and formation of contacts between the endoplasmic reticulum and mitochondria (mitochondria-associated membranes or MAMs) to regulate interorganellar communication and autophagy. Western blot and confocal microscopy analysis has shown that PACS-2 SUMOylation in response to DNA damage leads to the localization of cytosolic PACS-2 to the nucleus. Additionally, PACS-2 has been identified as an inhibitor of SIRT1-mediated deacetylation of p53 following DNA damage. Using western blot analysis, the effect of SUMOylation on the ability of PACS-2 to bind SIRT1 was examined. Experiments were designed to determine if SUMOylation inhibits or aids the ability of PACS-2 to bind SIRT1 and inhibit its p53 deacetylase activity. This investigation aims to provide further insight into the role of PACS-2 following DNA damage and how SUMOylation may act as a modifier of the inhibitory effect of PACS-2 on SIRT1-mediated deacetylation of p53.

PHENOTYPIC EFFECTS OF B-CATENIN BUILDUP IN ZEBRAFISH

Mohammed Alshammary, Laura Branch, Zexuan Jia, Sagan Stanczak, *Rochester Institute of Technology*

CRISPR is becoming one of the most powerful gene-editing tools available. The wide range of potential applications and the precision targeting has made CRISPR attractive to genomic engineering and research. The performance of CRISPR-Cas9 depends on a single-guide RNA (sgRNA). This practice has a high potential to be

applied in the medical field, but beforehand, testing must be done in model organisms. Utilizing CRISPR technology, the genotype of zebrafish can be altered via embryonic injection, i.e., changing the eye morphology; this will be achieved by using the CRISPR-Cas9 system to deactivate the *gsk3b* gene. The sgRNAs were designed using bioinformatics tools including Benchling and CRISPRscan. Four different oligos from exon 1 and 2 of *gsk3b* and two sets of primers were analyzed and designed for in vitro testing. If these results are successful, the next step will be to test in vivo.

POLYMERIC SUMO 2/3 CHAIN MODIFICATION OF PML REGULATES THE SIZE, NUMBER, AND STABILITY OF PML NUCLEAR BODIES.

Robert White, Xiang-Dong "David" Zhang, *SUNY Buffalo State*

The posttranslational modification of promyelocytic leukemia protein (PML) by small ubiquitin-related modifier proteins (SUMOs) mediates the assembly of PML nuclear bodies (PML-NBs) that contain numerous different proteins. Acute promyelocytic leukemia (APL) is caused by a chromosomal translocation, t(15;17), resulting in the fusion protein between PML and retinoic acid receptor alpha (RAR α). APL can be effectively treated by arsenic trioxide. Previous studies have supported a model that arsenic trioxide triggers polymeric SUMO-2/3 chain modification on the PML fragment of the PML-RAR α fusion protein followed by RNF4-mediated ubiquitination and degradation of the fusion protein. The SUMO-targeted E3 ligase RNF4 contains four SUMO-interacting motifs (SIMs) for binding to polySUMO chain signals on target proteins, such as PML and PML-RAR α . To elucidate the exact roles of polySUMO-2/3 chain modification in affecting the size, number, and stability of PML nuclear bodies, especially under the arsenic trioxide treatment, we transfected HeLa cells with a construct encoding GFP-tagged SIMs, followed by immunofluorescence microscopy. We found that compared to untransfected control cells, overexpression of GFP-SIMs reduces the number of PML-NBs, but simultaneously increases the size of PML-NBs. These results suggested that the interaction between GFP-SIMs and polySUMO-2/3 chains may prevent RNF4-mediated ubiquitination and subsequent proteasome-mediated degradation of PML. Our studies may provide insights into the mechanism by which polySUMO-2/3 chain modification mediates the ubiquitination and degradation of PML-RAR α , and may lead to a better therapeutic treatment of APL using arsenic trioxide.

POST-CREMATATION WEIGHT AS AN INDICATOR FOR SEX AND STATURE.

Alexandra Novak, *SUNY Geneseo*

The modern cremation process results in a small volume of finely ground inorganic matter that ultimately renders the standard methods of skeletal analysis impossible. The statures of 50 adult individuals and their post-cremation weights were documented to determine if a correlation exists between the decedent's sex and stature. Thus, influencing the weight of their cremains. The average weight of male cremains was significantly heavier than that of the females (Males averaging 6.55 lb and females averaging 3.54 lb). Stature was determined to have an influence on the post-cremation weight of an individual as well. The average stature recorded (5 ft 7 in) produced a weight of 4 lb 11 oz. The tallest stature (6 ft 4 in), versus the shortest stature documented (5 ft 1 in) produced sample sizes weighing in at 9lb 10 oz and 3lb 1 oz respectively. While sex and stature appear to influence cremation weight, regional variation will likely alter the average values collected within this study.

PRE-DISPERSAL SEED PREDATION IN THE ROEMER ARBORETUM

Tulpen Hansen-Schwoebel, Racheal Devine, *SUNY Geneseo*

Abstract - Many invasive plant species have a detrimental impact on native species through their superior ability to compete for resources, such as fruiting for longer periods of time and drawing away frugivorous seed

dispersers from native plants. Likewise, invasive plant species may increase consumer pressure on native species, creating apparent competition.. Pre-dispersal seed predation by insects can have strong effects on plant population dynamics. Before seeds are dispersed by birds or other dispersal agents such as wind, the seeds inside are still at risk of predation by adult and larval insects. Adult insects lay eggs inside individual fruits, and when the eggs hatch, the seeds inside serve as a food source for the developing larvae. This larval activity renders seeds incapable of germination, which may translate to reduced population growth. During the growing season of 2017, we quantified the relationship between the presence of larvae in fruit and fruiting phenology in both native and invasive plant species in the Roemer Arboretum in Geneseo, New York. We found that the duration of fruiting phenology has a stronger correlation to the presence of larvae for native plant species ($r^2=0.695$) than for invasive plant species ($r^2=0.342$). Fruit crop sizes are larger for invasive species, and this larger volume of fruit production suggests that predator satiation could generate the lack of correlation in the invasive species. Together, a longer period of fruiting and relatively low pre-dispersal seed predation may contribute to the advantages that invasive plant species have over native species. Our presentation will also examine predation rates during periods of overlap in fruit production between native and invasive species.

PREPARATION OF A HETEROBIMETALLIC PHOSPHINE-PYRIDINE COMPLEX WITH THE POTENTIAL FOR METALLOPHILIC INTERACTIONS

Kevin Clark, *SUNY Oswego*

Metallophilicity is the occurrence of an attractive interaction between closed-shell d-10 metals. Complexes showing metallophilic interactions can show a wide range of photoemissive behavior, including thermochromism, solvatochromism, vapochromism and mechanochromism. The unique photoemissive behavior of metallophilic complexes can find use in chemical sensing and optoelectronic systems. Common in the preparation of these complexes is the use of phosphine and/or pyridine derivatives as coordinating ligands. We have synthesized the ligand 2-[2-(diphenylphosphino)ethyl]pyridine, a mixed phosphine-pyridine, for this purpose and have prepared a heterobimetallic complex containing Au(I) and Cu(I). Preliminary results show that this complex exhibits mechanochromic behavior. Grinding in a mortar and pestle causes a visible change in emission which is also observed in fluorescence experiments. This and other preliminary results will be presented and the role of metallophilic interactions on the luminescence behavior of the bimetallic complex will be discussed

PREPARATION OF SMALL LACCASE (SLAC) FOR IMMOBILIZATION VIA CLICK CHEMISTRY AND BIOREMEDIATION APPLICATIONS

Bellina Mushala, *Wells College*; Corey M. Johnson, *Samford University*

Contamination of wastewater by synthetic and natural estrogens threatens aquatic biodiversity. Laccase is an enzyme secreted by some fungi and bacteria that is capable of remediating estrogenic pollutants. To date, most bioremediation applications have utilized fungal laccases that are free in solution. While laccase immobilized on a surface has shown increased efficiency in other applications, this advantage has not been exploited in bioremediation. In recent reports, laccase from the bacterium *Streptomyces coelicolor* (SLAC) has exhibited unprecedented stability and activity, yet has not been tested against estrogenic pollutants. In this study, we take the initial steps toward the design of a bioremediation system using covalently-immobilized SLAC. A recombinant form of SLAC that is capable of incorporating a noncanonical amino acid (phenylalanine azide; AzF) will be attached to a surface alkyne via click chemistry. In order to build this system, a plasmid containing SLAC-AzF was co-transformed into *E. coli* host cells with another plasmid containing the essential tRNA synthetase. SLAC-AzF was overexpressed and purified using Ni-NTA affinity chromatography. Mass spectral analysis for incubations of estrogens in the presence of SLAC-AzF exhibit a variety of soluble, oxidized products. In-gel

fluorescence indicates successful incorporation of the phenylalanine azide (AzF) and the ability of SLAC-AzF undergo cycloaddition via click chemistry. These results enable the development of an effective enzymatic system for bioremediation.

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PREVALENCE OF TOXOPLASMA GONDII IN THE SYRACUSE URBAN DEER POPULATION.

Gabriella Oliva, Jason Lusier, Emily D Ledgerwood, *Le Moyne College*

Toxoplasma gondii is a parasitic protozoan that causes the disease toxoplasmosis in its host. It lives worldwide and is capable of infecting any warm-blooded animal, but is only able to reproduce in cats. The presence of this parasite has been studied in the domestic cat before, as well as other hosts, but there is little literature published on the role of other hosts in transmission. Studies have found the presence of antibodies to *Toxoplasma gondii* in white-tailed deer, suggesting that deer can be infected. These data suggest that deer may contribute to the transmission of this parasite to cats, potentially as an intermediate host, and could therefore also pose a potential health risk to humans if deer can carry and spread *Toxoplasma gondii*. Twenty-six samples of deer feces were collected from six city parks across Syracuse and the DNA was extracted from twenty-one of the samples to determine the prevalence of *Toxoplasma gondii*. Primers specific to *Toxoplasma gondii* were designed and PCR was used to detect oocysts of *Toxoplasma gondii* present in nine of the samples of extracted DNA. The PCR products of these nine samples were separated by size using gel electrophoresis. One of the nine samples was determined to be weakly positive for *Toxoplasma gondii* DNA. Current and future research will focus on optimizing the PCR protocol, screening remaining and new samples for the prevalence of *Toxoplasma gondii* DNA, and sending any positives for commercial DNA sequencing. The data will then be used to map the deer in Syracuse to determine the prevalence of deer infected with *Toxoplasma gondii* across the city, which will help establish an understanding of the health risk that deer pose in transmitting this parasite to the human population of Syracuse.

PREVALENCE OF WOLBACHIA SP. IN THE OAK TWIG PRUNER (ANELAPHUS PARALLELUS) FROM TWO DIFFERENT HOST PLANTS

Sarah Bresette, William Brown, and Luciana Cursino, Keuka College

We tested for the differential presence of an intracellular bacteria, *Wolbachia* sp., in a wood-boring beetle, the oak twig pruner (Cerambycidae; *Anelaphus parallelus*), collected from red oak (*Quercus ruba*) and black walnut (*Juglans nigra*) trees. DNA was extracted from beetle leg tissue using the NucleoSpin Tissue Kit (Macherey-Nagel). The conserved *wsp* gene was used to identify the presence of *Wolbachia* sp. PCR was performed using WSP_F1 and WSP_R1 primers. Wsp PCR products (602 bp) were electrophoresed, sequenced, and aligned to construct an unrooted phylogenetic tree. Of 80 total specimens, 33 tested positive for *Wolbachia* sp. None of 28 oak twig pruners collected from walnuts were infected with *Wolbachia* but 63% of 52 individuals from red oaks were positive. Based on DNA sequencing, the *Wolbachia* species from *A. parallelus* belongs to its own specific subgroup. Our next goal is to experimentally determine whether black walnuts suppress *Wolbachia* infections and, if so, explore chemical reasons for this phenomenon.

PROBING THE DIFFUSION RATE AND INTERNAL PEPTIDE DYNAMICS: TEMPERATURE AND PH-DEPENDENCE STUDIES OF A FLUORESCENCE-TAGGED AMYLOID BETA PEPTIDE AND THIOFLAVIN T IN A SOL-GEL MATRIX

David Akanonu, Gus Formato, Manami Endo, Kieran Brown, Kazushige Yokoyama, SUNY Geneseo

Hydrogels are very popular, serving as an advanced drug delivery method to carry and release drugs to specific parts of the body. Our group is attempting to design a silica sol-gel material-based drug delivery capsule similar to hydrogels with sensitivity-controlled diffusion rate parameters. Inserting a peptide into the sol-gel suppresses solvent diffusion rates because it changes conformation in order to enter into the gel cavities where solvent normally diffuses through. However, extracting the expression of the structural changes occurring is a challenging study. To probe the peptide dynamics in the gel matrix, Thioflavin T with A β 1-40 or FAb (fluorescein attached to A β 1-40) is encapsulated into a sol-gel matrix and subject to fluorescence and lifetime decay assays at different temperatures and pH levels to determine both the solvent diffusion rates and the peptide structural changes occurring. The diffusion rates and peptide dynamics were found to be sensitive to pH and temperature change, which implies that the stable conformation at each pH or temperature level reflects on the coverage of the cavity, which in turn affects the solvent diffusion rate.

PROGRESS TOWARDS BUILDING AN EXTERNAL-CAVITY DIODE LASER (ECDL)

Gregory Abbass, Sachintha Herath, Priyanka Rupasinghe, *SUNY Oswego*

Semiconductor diode lasers are widely used in spectroscopy applications due to their ease of use, compact size, robustness, availability, and affordability. Among those, external-cavity diode lasers (ECDL) are even more attractive within the scientific community due to wide range of frequency tunability and high frequency resolution. Based on an existing design and some modifications, Atomic & Optical Physics Lab in the physics department aim to build an external-cavity diode laser which helps to achieve its long-term goals which include precision atomic structure measurements. Most of these experiments require two-step excitation of atoms which can be conveniently achieved by two ECDLs. With this poster, we present the progress of building such a laser at home.

PROTEIN EXPRESSION OF ANOCTAMIN 1 AND ANOCTAMIN 2 IN VARIOUS TISSUES OF THE ZEBRAFISH

Claire Makowsk, Brian Smith, Clarissa Steier, Brook Scott, The College at Brockport

Background: Immunohistochemistry (IHC) identifies proteins using antibodies specific to those proteins. Here, IHC is used to verify Anoctamin 1 and Anoctamin 2 expression in *Danio rerio* (zebrafish). Anoctamin 1 and Anoctamin 2, also called TMEM16A and TMEM16B, are calcium activated chloride channels that we hypothesize are involved in the functions of the following four tissues: retinal pigmented epithelium, neuromast,

gastrointestinal tract, and olfactory apparatus. The retinal pigmented epithelium, or RPE, is a thin cell layer between the photoreceptor layer of the retina and the choroid. It functions to bring nutrients to the photoreceptors and detoxify waste from the photoreceptor layer. The neuromast is a mechanosensory system located on the lateral line that functions to provide sensitivity to the environment of the fish. The GI tract and olfactory apparatus function similarly in zebrafish and humans. Primary and secondary antibodies specific to ANO1/2 antigens will be used to fluoresce ANO1/2 proteins, which we will then visualize in each of the four tissues using fluorescence and confocal microscopy. Aims: (1) Confirm anoctamin 1 protein expression in the retinal pigmented epithelium, neuromast, gastrointestinal tract, and olfactory apparatus in the zebrafish and (2) confirm anoctamin 2 protein expression in the same four tissues. Methods: We used immunohistochemistry to visualize protein expression of ANO1 and ANO2 in the zebrafish gastrointestinal tract, the olfactory bulbs, the neuromast and the retina. ANO1 and ANO2 specific antibodies were used in pair with fluorescently tagged secondary antibodies to label the ANO1 and ANO2 antigens in various tissues of the zebrafish. Whole mounts and sectioned tissues were used in staining and imaging. Confocal and fluorescence microscopy was then used to view and image the tissues. Expected Results: ANO1 is abundantly expressed in the adult zebrafish gastrointestinal tract. ANO2 is expressed in the retina of 6 dpf zebrafish larvae. *ANO1 is additionally expressed in the olfactory apparatus in pair with ANO2. The neuromast also shows expression of ANO2. Conclusion: Expression of anoctamin 1 was verified in the gastrointestinal tract. Anoctamin 2 was expressed in skin, ocular tissues (retina), and neuromast. Both anoctamins were expressed in the olfactory apparatus of the zebrafish. Further studies need to be done to identify in which area of the retina anoctamin 2 is expressed.

Q

QUANTIFYING POST-DISTURBANCE DAMAGE OF SCAEVOLA PLUMIERI AND SCAEVOLA TACCADA.

Miranda W Ella, Susan S Witherup, and Peter Melcher, *Ithaca* College

Studying the impacts of hurricanes and other significant disturbances on island ecosystems is an important way to learn more about overall plant community dynamics by identifying how different species respond to wind and water damage. This is useful in understanding the native-invasive relationship between *Scaevola plumieri* and *Scaevola taccada* on the beaches of Puerto Rico. As a frontline dune species, *Scaevola* face the full force of the disturbance; subsequently protecting other plants behind them from sustaining too much wind and water damage. Both species are expected to sustain similar amounts of damage, but we expected the invasive, *S. taccada*, to regenerate more effectively than *S. plumieri* six months after the impact of category 4 Hurricane Maria. Data were collected from aerial photographs processed using ImageJ, and light fraction measurements comparing ambient light to light penetrating the bush canopy. At the time of data collection, we expected to be measuring regeneration; however, a massive swell event the week prior to collection created results that instead more accurately described damage sustained. Analysis of these data indicated that *S. plumieri* suffered more canopy damage than did *S. taccada*. While this answered questions regarding how these species fare immediately after natural disturbances, future directions of this research include tracking plant regeneration between the species as well as comparing the impacts of different storms such as hurricanes, swell events, and high winds.

QUATERNARY LIZARDS FROM CATHEDRAL CAVE, WHITE PINE COUNTY, NEVADA.

Nicole Spangenburg, *SUNY Oswego*

The Quaternary Period, which includes the past 2.6 million years, was a time when most modern species started to appear in the fossil record. Because the Quaternary Period was so recent and species from this time appeared to be taxonomically and geographically stable, the Herpetofaunal Sustainability Hypothesis was tested by

comparing modern extant taxa to recovered specimens. Specimens from Cathedral Cave in the Great Basin region in White Pine county, Nevada were recovered in 2003 from Quaternary cave deposits. Cave 2 of Cathedral Cave contained mammalian, reptilian, and amphibian specimens. The reptilian specimens included *Aspidoscelis*, *Crotaphytus*, *Gambelia*, and *Phrynosoma*. Previous research narrowed specimens 115-124 to *Phrynosomatidae* based on jaw structure. These specimens were further identified as *Phrynosoma* specimens using dentary and maxilla apomorphies. Identification used a combination of unique traits including number and position of mental foramina, number and position of teeth, and shape of jaw to differentiate between different taxa. Three specimens that have been further identified are similar to the current *Phrynosoma* species found in western North America, and specimen 117 shows strong similarities to *Phrynosoma hernandesi*. The specimens found at Cathedral Cave currently favor the Herpetofaunal Sustainability Hypothesis, but since few specimens have been further identified, more research is needed to conclude if other fossils currently identified as reptilian also favor stability in the Great Basin Region.

R

RATE OF PLASMID LOSS WHEN SELECTIVE PRESSURE IS REMOVED: USE IT OR LOSE IT

Jack Klem, Jessica Nguyen, and Mark Gallo, Ph.D., Niagara University

Plasmids are extra chromosomal elements that are normally found in most bacteria. One plasmid, pGlo™, is used in *E. coli* for many experiments, especially as part of the Advanced Placement Biology curriculum. This plasmid contains the green fluorescent protein gene under control of the arabinose promoter, the beta lactamase gene whose product provides beta-lactam antibiotic resistance, an origin of replication, as well as a multiple cloning site. The plasmid is retained in the cell due to selective pressure of the antibiotic. However, very little experimentation has been done on the rate of the loss of plasmids in bacteria. Plasmid loss will be explored when under different selective pressures, namely the additional cost of expression of GFP protein on ability to compete for resources.

RENEWABLE ALIPHATIC-AROMATIC POLYESTERS.

Daniel Verrico, Dr. Massoud J. Miri, *Rochester Institute of Technology*

We are investigating the development of more sustainable polymers that can be used for a variety of applications. While aromatic polyesters are typically thermally and mechanically more stable than aliphatic polyesters, they do not degrade as quickly in the environment. We have synthesized renewable copolyesters based on a combination of aliphatic monomers and monomers with aromatic moieties. Polymerizations were conducted in two stages. First, oligomers were formed by alcoholysis or acidolysis under an inert gas, such as argon. Second, we applied high vacuum to obtain high molecular weight polymer. The polymers' color generally lightened after they were dissolved and crashed in suitable solvents. We analyzed the structures of the polymers by ¹H as well as ¹³C NMR spectroscopy.

S

SEASONAL VARIATION IN RED FOX ACTIVITY

Alanna Richman and Chloe Cottone, SUNY Geneseo

In this study, camera trap images were analyzed to observe the activity of red foxes (*Vulpes vulpes*) and other native species near multiple fox den entrances in the Spencer J. Roemer Arboretum. These cameras have been set up near this den location since the summer of 2017. The game cameras are motion-activated to take pictures

near these den entrances without disturbing the foxes or other visiting species. The aim of this study was to determine (1) which times of the day and night the foxes are most active near the den, and (2) how these activity times change with the seasons. Patterns in the activity of other species active near the fox dens were also described.

SHOTGUNS TO SHARPSHOOTERS: CREATING A DATABASE OF MORE OPTIMIZED AMIRNAS

Samuel Chen, Dr. Xiao-Ning Zhang, *St. Bonaventure University*

Accompanying the recent rapid growth of sequencing technologies, there has been an explosion in the volume of plant genomic data available in online databases. This has inspired research in the function of newly discovered genes. Gene knockout technologies, such as CRISPR/Cas9, is a powerful tool to this end. However, knockout approaches have many limitations. A popular gene silencing method, hairpin (hp) RNA induced RNA interference (RNAi) often causes off-target silencing due to the lack of predictability in the short interfering RNAs (siRNAs) generated. (Xu et al., 2006) Artificial microRNA (amiRNA) mediated RNAi is a newer solution that boasts versatility in choosing target genes and tissues. Previous studies observed a pattern of specifications for making amiRNA that are much more effective and target specific than its predecessors (Li et al., 2013). Based on these specifications, we constructed a database of amiRNA candidates for most nuclear Arabidopsis genes. 533,429 candidate amiRNAs target 27,136 out of 27,445 nuclear Arabidopsis genes representing a 98.87% coverage of the nuclear Arabidopsis genome. This suggests that this method of generating amiRNAs is applicable genome-wide for Arabidopsis genes. Its potential applicability in other plant species has yet to be explored.

SPONTANEOUS CROSS-FOSTERING IN NEONATAL MATERNAL DYADS IN CAPTIVE BELUGA WHALES

Madison Blackwell and Michael Noonan, *Canisius College*

Understanding the prevalence of allomothering is essential when documenting the social nature of any given species. The present report describes instances of shared parenting, and of spontaneous switched mother-calf pairings (calves aligning with incorrect mothers), following the near simultaneous births of five beluga calves in a seaquarium setting. No detrimental effects of these extra-familial associations were detected. The frequency with which such allomothering arrangements occur deserves further investigation, both in the wild and in additional managed-care settings.

STRUCTURAL VARIATION OF MYELIN BASIC PROTEIN IN THE WHITE-FOOTED MOUSE AND ITS IMPLICATION IN NEUROPROTECTION.

Hannah Lamont*, Alexander Ille*, Stacy Amico-Ruvio, *D'Youville College*

*Co-first authors

Myelin basic protein (MBP) is one of the major protein constituents of myelin sheath. MBP serves to sustain myelin membrane structure, enabling the conductivity and insulation necessary for neural signalling. The efficacy of myelin sheath is contingent on a complex interaction of MBP with myelin-associated lipids. This interaction is dependent upon the structural integrity of MBP. Several neurological disorders have been linked to MBP abnormality, further demonstrating its functional significance in the nervous system. The white-footed mouse (*Peromyscus leucopus*) exhibits profound neuroprotective characteristics, is asymptomatic to various disease-states, and has a lifespan twice that of the house mouse (*Mus musculus*). In light of this, we used *M. musculus* MBP as a reference to identify a previously unannotated analog of MBP in *P. leucopus*. Through genetic and downstream proteomic data analysis, we found that variation of MBP is present between the two species. Our results show differences within the open reading frame of the transcripts accompanied by corresponding differences in protein structure prediction. These data introduce the potential of MBP variation

as one of many causal variables contributing to the unique presentation of enhanced neuroprotection and longevity in *P. leucopus*.

STUDIES TOWARD THE TOTAL SYNTHESIS OF NOVEL CROSS-MEMBRANE FLUOROMETRIC PROBES.

LauraAnne Hirschler, Ana Cartaya, Tyler Zimmermann, Danielle Raymond, and Dr. Christina Goudreau Collison, *Rochester Institute of Technology*

Developing an accessible mechanism through which therapeutic molecules traverse cell membranes is critical to drug design and delivery pathways. Possessing both hydrophilic and hydrophobic regions, fluorescent cross-membrane probes have the potential to straddle phase partitions in order to better study these mechanisms. Our research focus is on the synthesis of novel cross-membrane probes that are fluorescently active. The probe's function is to monitor physiochemical changes on both sides of a phospholipid/cholesterol-based model membrane through ratioing the signals. Enhanced methods of drug delivery systems can be further investigated through the interaction between the model cells and the amphiphilic fluorophores based on collected data regarding these interactions

SYNTHESIS AND CHARACTERIZATION OF NOVEL ORGANOSILICON COMPLEXES BEARING THE 8-HYDROXYQUINOLINE N-OXIDE LIGAND.

Kathleen I. Lowry, Bradley M. Kraft, St. John Fisher College; William W. Brennessel, *University of Rochester*

Monoorganosilicon complexes of the form $\text{RSi}(\text{QNO})_2\text{Cl}$ (QNO = 8-oxyquinoline N-oxide; R = Me, tBu, Bn, Ph, p-tolyl) were synthesized and characterized by ^1H , ^{13}C , and ^{29}Si NMR spectroscopy. X-ray crystal structures of $\text{PhSi}(\text{QNO})_2\text{Cl}$, $\text{MeSi}(\text{QNO})_2(\text{OSO}_2\text{CF}_3)$, and multiple solvates of $\text{MeSi}(\text{QNO})_2\text{Cl}$ revealed separated ion pairs with trigonal bipyramidal complex cations in each. In all cases, a single isomer is formed with both N-oxide groups in the axial positions. The similarity of the NMR spectra of $\text{MeSi}(\text{QNO})_2(\text{OSO}_2\text{CF}_3)$ and $\text{MeSi}(\text{QNO})_2\text{Cl}$ in CDCl_3 suggests that separated ion pairs are also present in solution.

SYNTHESIS OF IRIIDIUM(III) COMPLEXES FOR G-QUADRUPLEX-SELECTIVE PROBES

Cory Forsyth, Carly Reed, and Joshua Blose, *The College at Brockport*

This research focuses on synthesizing a library of luminescent iridium(III) complexes that will be tested for their ability to selectively intercalate into G-quadruplex DNA over single-stranded or double-stranded DNA. These luminescent compounds can then act as label-free switch-on fluorescent detecting sensors for important analytes such as metal ions and small molecules, when the G-quadruplex is linked to a DNA aptamer. While the iridium(III) complexes are weakly emissive on their own, when in the presence of a targeted analyte which allows two single strands of DNA to come together forming an aptamer and G-quadruplex structure, the iridium(III) complexes can intercalate and fluorescence is enhanced. The iridium complexes of interest have the general form $[\text{Ir}(\text{C}^{\wedge}\text{N})_2(\text{N}^{\wedge}\text{N})]$. The complexes $[\text{Ir}(\text{ppy})_2(\text{dpq})]\text{PF}_6$ and $[\text{Ir}(\text{pq})_2(\text{dpq})]\text{PF}_6$ have been synthesized, where ppy = 2-phenylpyridine; pq = 2-phenylquinoline; and dpq = dipyridoquinoxaline. Other complexes to be added to the library will also be discussed. After completing synthesis, the binding and luminescent studies will be carried out using fluorescence titration. 1. ACS Appl. Mater. Interfaces 2015, 7, 19060-19067

T

TARGETING THE MEP PATHWAY TO DEVELOP NOVEL ANTIBIOTICS

Miranda Williamson, Kevin Callahan, Anand Sridhar, Maryann Herman, *St. John Fisher College*

Antibiotic resistance is driving an increasing need to find novel antibacterial compounds. The methylerythritol phosphate (MEP) pathway, not found in animals, is an appealing target for new drugs. The most efficient way to inhibit this pathway is believed to be by targeting the first enzyme of the pathway, 1-deoxy-D-xylulose 5 phosphate (DXP) synthase. Preliminary compounds that are believed to inhibit DXP have been synthesized. The goal of this research is to test these inhibitors in an in vitro system with purified DXP synthase and DXP reductoisomerase (DXR).

TESTING ANOCTAMIN FUNCTION IN GASTROINTESTINAL TRANSIT AND VISION IN ZEBRAFISH.

John Purificato, Cody Drought, Jordan Johnson, Alexa Drier, Kelly Anderson, Adam Rich, The College at Brockport

Background: Anoctamin 1 and 2 (Ano1, Ano2) are expressed in the mammalian retina. The retina is required for vision but the role for Ano1 and vision in zebrafish is unknown. Anoctamin 1 is expressed in interstitial cells of Cajal in mice, humans, and zebrafish and is necessary for coordinated motility patterns in mice, but the role in zebrafish is unknown. Ano2 is very similar to Ano1 and we hypothesize that both play a role in zebrafish gastrointestinal transit and motility. GI transit is the movement of intestinal contents through the gastrointestinal tract. GI motility is the contractions of the muscles of the gastrointestinal tract. Aims: The overall goal to determine the function of Ano1 and Ano2 in vision and gastrointestinal motility and to test the possibility that one of these genes can compensate for the other. Methods 1: Zebrafish vision will be tested using an optomotor assay with 7 dpf zebrafish larvae. Assay validation will be tested using blinded 7 dpf larvae. Pharmacological inhibition, and morpholino knockdown, will be used to subtract Ano1 and Ano2 to test their role in vision. Methods 2: The role of Ano1 and Ano2 in GI motility will be examined using a GI transit assay. Movement of intestinal contents will be followed using fluorescence imaging of a non-digestible marker. The specific role for Ano1 and Ano2 in GI transit will be measured pharmacological blockers, as well as morpholino oligonucleotide knockdown of Ano1 and Ano2. Results 1: Wild-type fish show approximately 180-degree body angle in reference to the direction of the moving stripes. Blind fish body angles show no correlation to the direction of the stripes. We will examine vision function after pharmacological inhibition of Ano1 and Ano2. Results 2: We expect that the knockout of Ano1 and Ano2 group will have a reduced GI transit, and increased transit time.

THE AGE OF ADVENTURE: THE UNIVERSITY OF ROCHESTER AND ITS NATURAL HISTORY ENDEAVORS OF THE 1930'S.

Rachel Hammelman, *University of Rochester*

This talk will explore the time between 1926 and 1940 when the university had a close relationship with Ward's Natural Science Establishment along with the creation of its own natural history museum in the Dewey Building. Ward's and the University of Rochester have had a complicated history that spans much longer than just one decade, but these years reveal the shift away from being associated with one another. Money was the driving factor of their separation, as Ward's went through years of financial instability, relying on the university for help. This instability forced Ward's to realize the potential to work as a more commercial company, moving away from the natural history collection business it had been basing its framework on. While tension rose between Ward's and the university, a natural history museum emerged from the work of Edward J. Foyles at the new men's college campus. Much research has been done to find out where the collections in this museum came from and where they went after it closed, with both questions still partially unanswered. We will walk through a timeline of events that led to the university's severing with Ward's as well as the dissolving of the natural history museum, signaling the end of an era in the University of Rochester's history.

THE CONTRIBUTION OF POLLINATION TREATMENT TO POPULATION SPREAD OF AN INVASIVE THISTLE.

Simran Singh, Suann Yang, Erin Shinski, SUNY Geneseo; Brittany Teller, Penn State University

Invasive species are a major threat to biodiversity, which makes understanding how they spread across the landscape important. In this study we focused on the invasive thistle *Carduus nutans*, and asked how pollination (outcross- or self-pollinated by hand vs. open-pollinated control) influences its dispersal. Initially, we tested the effect of treatment on terminal velocity - the highest velocity that a seed can achieve in still air - of its wind-dispersed seeds. We found that pollination treatment has a significant effect on terminal velocity ($P < 0.0001$). Surprisingly, seed mass didn't contribute to this difference in terminal velocity ($P = 0.1616$). Other factors, such as the size of the plume of these seeds, may instead contribute to differences in terminal velocity. We predict that self-pollinated seeds would travel farther because of slower terminal velocities, and we would not expect these seeds to have any competitive disadvantage in establishment with respect to outcrossed seeds because seed masses were similar across treatments. Furthermore, results of a dispersal model will be included to estimate dispersal rates for different pollination treatments for *C. nutans*. Our findings suggest that some conditions of the invasion process, such as small initial population sizes, can disproportionately promote an invasion.

THE CONTROVERSIAL HISTORY OF THE KINZUA DAM.

Elijah Hall, Kaitlin Stack Whitney, *Rochester Institute of Technology*

The construction of artificial dams can have detrimental effects on river ecosystems, causing direct impacts on wildlife and water quality, in turn impacting community health in surrounding area. Environmental health is increasingly understood to be associated with human health; when environments are drastically altered, the, so too is the inhabitant's lives. Thus, my research examined the causes and consequences of the construction of one such artificial dam and surrounding community, the Kinzua Dam near Warren, Pennsylvania. Using environmental history and policy analysis approaches, I examined the events that led to the passage of the Flood Control Act of 1936 and in turn the Kinzua Dam. The dam has prevented an estimated \$1.2 billion in flood damages since its construction in 1960. However, to obtain the land needed for construction of the Kinzua Dam, 550 individuals from the Seneca Tribe of Indians were forcefully removed from their native land. I then incorporated water quality analysis of the Allegheny River taken by the Environmental Protection Department on the Allegheny Reservation. Blue Green Algae (BGA) levels in the Allegheny Reservoir are currently frequently found to be over the World Health Organizations Caution BGA level of $>100,000/\text{ml}$. These levels are the result of the Kinzua Dam inhibiting the natural current of the Allegheny River. My research is the first to pull together environmental history, policy analysis, and empirical environmental science to begin to understand how the Kinzua Dam is impacting the health of both the watershed and surrounding human community. Incorporating externalities not historically used by economics, such as forced displacement and water quality legacies, the evaluation of Kinzua Dam as a success is less apparent. Additionally, understanding the linkages between artificial dams, water quality, and community health is a critical contribution to the growing field of environmental health research.

THE DEVELOPMENT OF INDEPENDENT SWIMMING IN SEAQUARIUM-BASED JUVENILE BELUGA WHALES.

Emily Began and Michael Noonan, *Canisius College*

The time course over which young animals develop motor and social skills is important in understanding any species' behavior. This study investigated the development of five newborn belugas with particular focus on the behavior shown during instances in which they temporarily swam away from their mothers. Over the course of their first six months of life, the subjects showed marked increases in swimming in non-standard body orientations, exploratory investigations of pool features, and social play with other juveniles. Contact and interactions with other adults were very rare. It is hoped that these findings will establish benchmarks against

which the development of subsequent beluga calves can be assessed. They also may be helpful in interpreting surface observations of juvenile belugas observed in the wild.

THE IMPACT OF HERBIVORES ON METHANE PRODUCTION AND OXIDATION IN WETLANDS.

Briana Burt, *Rochester Institute of Technology*

Wetlands are an extremely important ecosystem, valued at \$140,174/ha/year. Wetlands are also one of the largest biogenic sources of atmospheric CH₄, yet one of the largest uncertainties in the global CH₄ budget. In addition, many natural wetlands have been replaced by created wetlands as required by the Clean Water Act, but they often fail to replace the function of a natural wetland. Artificial wetlands often have lower biodiversity and productivity than their natural counterparts. Management approaches such as herbivore exclusion have been proposed to improve wetland function. Preliminary data at High Acres Nature Area (HANA), shows that excluding herbivores increases plant cover and plant biomass, while reducing CH₄ emissions by approximately 50%. However, it is unknown if changes in CH₄ production or oxidation is driving reduced CH₄ emissions. To determine this, I completed field CH₄ flux measurements along with laboratory soil incubations in caged and uncaged plots at HANA to quantify potential CH₄ production and oxidation rates. My findings support previous findings that CH₄ emissions decrease when herbivores are excluded from in-situ plots. In addition, CH₄ oxidation rates increased and CH₄ production rates increased, leading to a net decrease in net emissions. Overall, my study will increase our understanding of the role of herbivores in wetland CH₄ emissions and the impacts of wetland management techniques used to improve function in created wetlands.

THE IMPACT OF MORROW'S HONEYSUCKLE ON THE NUTRITION AND BODY CONDITION OF BIRDS.

Gretchen Horst, Susan Smith Pagano, *Rochester Institute of Technology*

This study seeks to determine the nutritional quality and impact on avian body condition of an invasive shrub, Morrow's Honeysuckle (*Lonicera morrowii*) at Braddock Bay Bird Observatory. Morrow's Honeysuckle fruit contains the carotenoid rhodoxanthin, which has been linked to aberrant plumage coloration of birds. Twelve Baltimore Orioles (*Icterus galbula*) with aberrant red plumage were sampled for feathers and blood. The reflectance and absorbance of the feathers were measured to characterize the color profile. Since their aberrant coloration confounded normal sexing methods, the birds were sexed molecularly. Morrow's Honeysuckle fruit has two color morphs, red and orange, and samples of each were analyzed for differences in nutritional composition. Pulp from honeysuckle berries was isolated, freeze dried, and analyzed for fat, sugar, fiber, and calorie composition. Fruit enclosure experiments were conducted in the field to determine if birds are eating the fruit and assess preference by birds for berry color morphs. The feather reflectance values of aberrant plumage fell within a range consistent with rhodoxanthin deposition. The fruits were found to be of low quality and the two color morphologies showed little difference in nutritional composition, except the red fruits were higher in total carotenoid content. The field enclosure experiments showed that birds are eating the fruits and demonstrate a slight preference for orange berries. The data suggest that Morrow's Honeysuckle is not an adequate food source for birds and can have adverse effects on their health.

THE IMPACT OF THE INVASIVE HEMLOCK WOOLLY ADELGID ON SOIL STABILITY IN THE HEMLOCK LAKE WATERSHED.

Jenna Malagisi, Kathryn Amatangelo, *SUNY Brockport*

The objective of this project was to improve the mapping of eastern hemlock (*Tsuga canadensis*) stands around Hemlock Lake, NY, and to highlight areas that are affected by hemlock woolly adelgid (HWA). Pictometry was used to do a preliminary mapping of Hemlock stands around Hemlock Lake, NY. Three to five transects were established on each slope of the sample ravines. Three 10x10 plots were established along each transect to

represent the steep side of the ravine, the shoulder of the ravine, and the forested areas along the ravine. Within each plot the data that was collected included tree density, tree species, DBH, presence or absence of HWA on Hemlock, canopy cover, and plant community composition. The percentage of observed hemlock infected with HWA varied by sample ravine. In the sample ravine furthest North on the western side of the lake, 100 percent of observed Hemlock had visible HWA. Another ravine in the Northwestern region also had a high amount of HWA infected Hemlock with an average of 95% of observed Hemlock infested. The sample ravine that was furthest south on the eastern side of the lake was the least affected by HWA with an average of only 40% of observed Hemlock infected with HWA. Average species richness is highest in the forest plots for all but one of the sample ravines.

THE INFLUENCE OF THE CELLULAR ENVIRONMENT ON Z-DNA FORMATION.

Amanda Hange, Joshua M. Bloise, *SUNY Brockport*

In the cell, chemically diverse solutes known as osmolytes accumulate in response to environmental stresses. To add to the understanding of how the environment inside a cell affects nucleic acid folding and function, we investigated the influence of cosolutes on the transition from B-DNA to Z-DNA in model DNA duplexes. Distinct from the familiar right-handed B-DNA helical conformation, Z-DNA is a left-handed double helical structure with its phosphodiester backbone arranged in a zig-zag pattern that is unique to Z-DNA. Moreover, due to the correlation between Z-DNA formation potential and regions of active transcription, Z-DNA is believed to serve a vital role in the transcription process. Previous literature has shown that divalent metal ions such as Ca^{2+} and Mg^{2+} can promote the formation of Z-DNA in vitro and previous studies from our lab have shown that the presence of osmolytes enhances the formation of Z-DNA, significantly decreasing the in vitro $[\text{Na}^+]$ required for the transition. In our latest experiments, we examined the combination of divalent ions and osmolytes and its influence on the B-Z transition. We utilized circular dichroism (CD) spectroscopy to monitor the B-Z transition in a divalent ion background in the presence and absence of a model osmolyte, PEG 200. Our results thus far suggest that PEG 200 greatly enhances the formation of Z-DNA in the presence of Mg^{2+} as compared with Na^+ alone and significantly decreases the $[\text{Mg}^{2+}]$ required for folding in vitro. Our results with Ca^{2+} thus far suggest that its folding of Z-DNA is similarly enhanced by PEG 200 and that the $[\text{Ca}^{2+}]$ required will be much closer the range of $[\text{Ca}^{2+}]$ observed in vivo.

THE INITIATION AND DEVELOPMENT OF TRICHOMES ON DEVELOPING TOMATO FRUITS

Joseph Dyson, Wells College; Qian Shen, Jocelyn Rose, *Cornell University*

Tomato (*Solanum lycopersicum*) is a major food crop and each plant has tiny hairs called trichomes present on the stem, leaves, flower bud, and fruit. Not much is known about the genetics of tomato trichome initiation and development. To better understand trichome development in tomato fruit, numerous introgression lines (ILs) were observed throughout their development. These ILs are composed of a tomato variety (M82) which includes single introgressed genomic regions from the wild tomato relative, green-fruited species, *Solanum pennellii*. *S. pennellii* has a higher density of trichomes than the domesticated species M82 on all aerial parts. ILs that had higher densities of trichomes when compared to M82 were selected for further analysis. Genes, especially those transcription factors, in these introgressions were screened for high expression in epidermal tissue as these highly expressed genes are strong candidates for controlling trichome initiation and development. To analyze these candidate genes, Virus-Induced Gene Silencing (VIGS) was used to determine if silencing any of the individual genes would yield a phenotype with decreased trichome size or density. Light microscopy was also used to observe the trichomes on leaves and young ovaries in more detail. Stains of the ovaries were produced to more easily view the microscopic trichomes. Understanding more about trichome initiation and development

in tomato fruits can prove to be beneficial for the agricultural success of tomato or improve the fruit's marketability.

THE OBESOGENIC EFFECTS OF BISPHENOLS IN DROSOPHILA MELANOGASTER LARVAE

Allen Murphy, Thomas Pasquale, Edward Freeman, St. John Fisher College

Bisphenol A (BPA) is a common example of an Endocrine Disrupting Chemical (EDC). EDCs can cause an array of issues (metabolic, reproductive, etc.) due to their disruption of the normal homeostatic mechanisms maintained by the endocrine system. Specifically, EDCs can act as agonists or antagonists at membrane and nuclear receptor sites. Humans, agricultural species, and wildlife are increasingly exposed to EDCs from plastics, manufacturing, and environmental pollution. EDCs are also easily stored in adipocytes where they can accumulate throughout an animal's lifetime. Obesogens are EDCs that promote an increased rate of adipogenesis. For example, BPA is suspected of disrupting the normal regulation of the peroxisome proliferator-activated receptor- γ (PPAR γ), which is a key regulator of adipogenesis in vertebrates. BPA may also disrupt normal levels of sex hormones, which can cause an increase in adipogenesis. *Drosophila melanogaster* serves as an inexpensive and easily maintained model for human studies, including those related to obesity and the etiology of this condition. *Drosophila* metabolism has been extensively studied, and a network of interacting pathways is being identified that helps to maintain normal metabolism. The genes that regulate these pathways are also being identified and studied. Because of their rapid life cycle research using *Drosophila* will likely aid in the determination of the mechanism of action of BPA in promoting obesity. In addition, the life cycle of *Drosophila* allows longevity studies to be performed easily and efficiently. In this project, we plan to continue and expand on previous studies conducted in our laboratory. We have evaluated the effects of BPA on the fat content of *Drosophila* larvae and shown that BPA promotes greater fat deposition following exposure from fertilization to the 3rd instar larval stage. Additional doses are being considered and longevity of the treated larvae will be assessed following buoyancy assays. We hypothesize that when *Drosophila* are exposed to BPA the increase in adipogenesis will be associated with a shorter lifespan. In addition, we will also test the transgenerational epigenetic effects of BPA exposure. Transgenerational effects will be determined through the maintenance of multiple generations, following an initial exposure, and their subsequent fat deposition levels as determined by the buoyancy assays. We hypothesize that BPA exposure will impact the F1 and F2 generations, following exposure of a parental generation, through epigenetic mechanisms that promote an increase in fat deposition during embryonic and larval development.

THE RELATIONSHIP OF FECAL CORTISOL LEVELS, PERSONALITY TRAITS AND SOCIAL BONDS IN FREE-RANGING JUVENILE RHESUS MACAQUES.

Katharine C. Burke, Carol M. Berman, *University at Buffalo*

The social buffering hypothesis posits that social support can reduce the effects of social and environmental stressors among a variety of species. Supportive evidence is available for wild and free-ranging adult primates, but less is known about whether and how juvenile relationships buffer stress (Seyfarth et al. 2014). In addition, it is unknown how juvenile personality traits may be related to stress levels. We tested the prediction that free-ranging juvenile rhesus macaques (*Macaca mulatta*) with strong social bonds, i.e., those that scored high in social network measures related to proximity, grooming, and social play, and particular personality traits (playfulness, lack of aggressiveness) would display lower basal stress levels. We examined 42 juvenile (18-35 months of age) rhesus macaques living in a single, naturally formed and species-typical social group on Cayo Santiago, Puerto Rico. We collected behavioral data (total 644h, 11h per subject) and fecal samples (mean=7.63 \pm 4.2 samples per juvenile) over 5 months. The behavioral data were used to calculate individual scores for several social network measures, and were entered into a principal components analysis to derive

individual loadings on personality components. Fecal samples were analyzed for concentrations of cortisol metabolites (fCM) using a previously validated enzyme immunoassay for macaques (e.g. Heistermann et al. 2006). We used a generalized linear mixed-model approach to examine the relationship between mean fCM levels, social network variables and personality components. The results showed evidence for both buffering effects and stressful effects related to strong social relationships and personality. Consistent with the social buffering hypothesis, males with high levels of passive contact eigenvector centrality [$t(14)=-3.28$, $p=0.00$] and proximity degree [$t(14)=-3.26$, $p=0.00$] displayed relatively low fCM levels. Conversely, males that scored high on personality traits related to behavioral stress indicators and aggression given displayed relatively high fCM levels [$t(14)=2.64$, $p=0.02$]. In addition, females that scored high on personality components related to playfulness had relatively low fCM levels [$t(7)=-2.10$, $p=0.04$]. However, contrary to predictions, males with high levels of degree groom duration displayed significantly higher mean fCM concentrations [$t(14)=2.78$, $p=0.01$]. Moreover, females with high levels of groom duration betweenness [$t(7)=2.63$, $p=0.03$] and proximity degree [$t(7)=4.57$, $p=0.00$] displayed relatively high fCM levels. These results suggest that strong social relationships can be both a source of stress and mechanism for attenuating it, depending on the type of interaction and the juvenile's sex.

THE RESPONSE OF DIFFERENT DAPHNIA PULICARIA GENOTYPES TO ALGAL BLOOMS CAUSED BY FERTILIZERS

Lillian Denecke, Michael Chislock, SUNY Brockport

Fertilizers from agriculture affect aquatic systems by providing an excess of phosphorus and nitrogen that triggers algal growth and leads to algal blooms. The zooplankton *Daphnia pulicaria* grazes on algae and can combat the effects of algal blooms. *D. pulicaria* have been observed to evolve to tolerate cyanobacteria, and this project explores the responses of *D. pulicaria* that are sensitive to cyanobacteria, and *D. pulicaria* that are tolerant to cyanobacteria to algae in a fertilized aquatic system. The experiment was carried out by introducing tolerant *D. pulicaria* and sensitive *D. pulicaria* randomly to 24 limnocorrals that contain fertilizer and lack fertilizer. The chlorophyll content and amount of *D. pulicaria* per given volume was then analyzed. It was observed that the cyanobacteria-tolerant *D. pulicaria* more rapidly reduced algae in the fertilized treatment. However, grazing by both sets of genotypes resulted in a similar reduction in algal biomass after 48 days. In contrast, effects of both sets of *D. pulicaria* genotypes were similar in the unfertilized enclosures, with marginally lower algal biomass in the cyanobacterial-sensitive vs. tolerant treatment.

THE ROLE OF THE NON-HOMOLOGOUS END JOINING GENE, KU80, IN MITOCHONDRIAL GENOME STABILITY IN BUDDING YEAST.

Brooke Scott, Rey Sia, *SUNY Brockport*

Mitochondria are essential organelles in eukaryotes. They are often referred to as the powerhouse of the cell because mitochondria manufacture ATP, which is required for the successful completion of many cellular processes. Mitochondria have individual genomes, separate from the nuclear DNA, which encode proteins required for respiration. In humans, mutations in the mitochondrial DNA (mtDNA) result in the loss of mitochondrial function which lead to neuromuscular and neurodegenerative disorders. The focus of this study is to determine the role of the nuclear gene KU80 in maintaining mtDNA stability in the budding yeast, *Saccharomyces cerevisiae*. The product of the KU80 gene is the protein, Ku80p. Ku80p, in humans, is encoded by the XRCC5 gene. Ku80p along with Ku70p forms a heterodimeric protein complex, which binds to DNA double-strand break ends and is required for the non-homologous end joining (NHEJ) pathway of DNA repair. The lab is interested in determining whether loss of the KU80 gene plays a role in mitochondrial genome stability. Mitochondrial genome instability can arise via spontaneous point mutations or deletion events. Assays were performed to measure the spontaneous respiration loss rate between wild type and *ku80-Δ* mutant strains.

Spontaneous respiration loss was shown to increase in ku80- Δ mutants compared to that of the wild type. Strains were constructed to determine the role of KU80 in spontaneous direct repeat-mediated deletion (DRMD) events within the mitochondrial genome as well as the nuclear genome. The rate of DRMD events in the mitochondrial and nuclear genomes has so far shown a decrease in the ku80- Δ strain compared to the wild type. Our data suggests that Ku80p plays a role in maintaining the integrity of the mitochondrial genome in budding yeast.

THE SENSITIVITY OF CEPHEID BLUE LOOPS IN THE H-R DIAGRAM TO MIXING LENGTH PARAMETERS

Nicholas Proietti, Samantha Carey, Shashi Kanbur, *SUNY Oswego*; Earl Bellinger, *Aarhus University, Denmark*

Cepheid variable stars are a class of variable stars that pulsate radially due to internal physics, with regular cycles of variations in luminosity within an identifiable stable period and amplitude. When Cepheids reach a particular stage in their life history, the blue loop region of the Hertzsprung-Russell (HR) Diagram, stellar pulsations commence. The full length and existence of these blue loops are heavily dependent to the mass, metallicity and helium abundance of the star. As a consequence, they play a crucial role in comparing theories of stellar pulsation and stellar evolution. In this work, we use MESA, a modern, leading-edge stellar evolution code that solves the differential equations describing stellar structure, to trace the evolution of a Cepheid-like star through the blue-loop stage in the HR diagram. We then examine the sensitivity of the blue loops on this HR diagram to parameters governing the description of convection in MESA. We discuss our results, possible implications and avenues for future research.

THE SYNTHESIS OF TROCHELIOPHOROLIDE A: REDESIGNING AND CONSTRUCTING NEW FRAGMENTS.

Zexuan Jia, Diksha Biswa, Christina Goudreau, *Rochester Institute of Technology*

Trocheliophorolide A is a natural product found in soft corals in the Gulf of Aqaba in the Red Sea. This compound is of interest due to its antibacterial resistance to *S. aureus*, *B. subtilis* and *A. salina*. Structurally, this compound is unique given its unsaturated side chain moiety which is uncommon in natural butenolide molecules. Our synthetic route focuses on reproducing the side chain and coupling it with a beta-lactone ring, thus synthesizing this compound in a highly convergent manner. The success of this project is beneficial to society because access to a greater amount of this compound could advance its efficacy as a therapeutic without harming the natural resources. This presentation will address the total synthesis of two pieces necessary for the final synthesis of trocheliophorolide A starting from commercially available (S)-ethyl lactate and 3-methyl-2-buten-1-ol.

THE ULTRASTRUCTURE OF AMAZON YELLOW-SPOTTED RIVER TURTLE EGG SHELL AND SHELL MEMBRANE.

Gigi Niu and Poongodi Geetha-Loganathan, *SUNY Oswego*

The eggshell is essential for the developing embryo of an oviparous species as it provides mechanical stability, acts as a calcium reserve, transfer of heat, moisture and respiratory gasses. Amazon Yellow-Spotted River Turtle (*Podocnemis unifilis*) is an endangered species, and they have relatively rigid eggshells compared to other turtle species. Description on the characteristics of the embryo development or eggshells of *P. unifilis* is limited in literature. The aim of this study is to describe the ultrastructure of eggshell and shell membrane of *P. unifilis* using the Scanning Electron Microscope (SEM). Egg shells of *Podocnemis unifilis* consists of rigid outer calcareous layer covered with a smooth cuticular layer. The shell units of the calcareous layer composed of aragonite crystals and are anchored in its surface with basal knobs. The base of the shell units are smaller compared to the upper ends leaving a pyramid shaped pore cavities between the units. Below the shell units is a multilayered shell membrane consisting of outer membrane testacea made up of thick and dense mat of fibers, inner membrane testacea with interwoven thin fibers and an innermost smooth inner boundary layer that is continuous with extra-embryonic membrane of the embryo.

THE WARD PROJECT

Robert Minckley, Melissa Mead, *University of Rochester*

Today's talk introduces a project available through the website wardproject.org. Soon after the University of Rochester was founded in 1850, it became closely associated with Henry A. Ward and his business enterprise of collecting, trading and selling biological and geological specimens to natural history museums worldwide. In the late-1800's the third largest natural history museum in the United States was at the University of Rochester. This museum housed material purchased almost entirely from Ward's Natural Science Establishment (today called Ward Science). The Ward Project's aim is to make the specimens associated with the museum, and the extensive collection of papers associated with the Ward's Natural Science Establishment broadly available to the public, historians, biologists, and institutions worldwide. The website focuses on the period from 1860-1906, and is intended to facilitate research into the important contributions that Rochester made to the development of natural history museums, natural history education, and the conservation movement.

THERMAL PROPERTIES OF SUSTAINABLE POLYMERS

William Charbonneau, Dr. Massoud J. Miri, *Rochester Institute of Technology*

The applications of polymers depend largely on their thermal properties. Polymers, whose glass transition temperatures above room temperature or an application temperature are glass-like or brittle, whereas polymers above their glass transition temperature are flexible or stretchable. In addition, semi-crystalline polymers have a melting transition as well. Polymers, such as polylactic acid, are renewable and biodegradable, but have too high a glass transition temperature and heat deformation temperature compared to commodity polymers, such as polyethylene. We applied Differential Scanning Calorimetry (DSC) to determine glass transition temperatures and, where applicable, melting temperatures of different sustainable polymers synthesized in our research group. In addition, we used Thermal Gravimetric Analysis (TGA) to determine the purity, thermal stability and residuals of the polymers.

THREE YEARS OF INVASIVE CATTAIL REMOVAL IN A PEATLAND OF CONSERVATION SIGNIFICANCE IN OSWEGO COUNTY, NY.

Justin Searles, Sarita Charap, Joseph McCarthy, Bianca Fernandez, Koty Kurtz, Nathan Mckean, Faith Page, and C. Eric Hellquist, *SUNY Oswego*

Peatlands are unusual wetlands that often provide habitat for rare species. In coastal plain peatlands along the south shore of Lake Ontario, endangered bog buckmoth (*Hemileuca* sp.1: Saturniidae) populations have decreased in recent years. In one of their most important localities, expansion by cattail (*Typha angustifolia*) is jeopardizing the habitat and growth of the bog buckmoth's primary food source, the bog buckbean (*Menyanthes trifoliata*). Since 2016, we have been manually removing cattails by cutting stems below the water line to determine if this method would be an effective, low impact management strategy for slowing the spread of invasive cattails. As of this fall, there are 3x fewer cattails in cut plots than in uncut control plots. With regard to seasonal management, cutting in the spring results in less biomass and inflorescence production than waiting to remove cattails in the fall. Living biomass has been ca. 4 g/m² in spring harvest plots and ca. 8-16g/m² in fall harvest plots. Cutting cattails and removing the biomass from the peatland mat has essentially eliminated dead biomass in experimental plots compared to the control plots. The elimination of dead biomass in experimental plots is an important step to maintain conditions that will support the growth of bog buckbean that would otherwise be covered with dense cattail thatch. Controlling cattail thatch and thus promoting bog buckbean growth should help maintain the tenuous populations of the bog buckmoth in central New York.

TOWARDS THE ELUCIDATION OF NOVEL VIRAL FACTORS THAT HIJACK HOST UBIQUITINATION PATHWAYS

Madison Muehl, Josh Lapham, and Dr. Geoffrey Lippa, , *Alfred University*

In order for eukaryotic cells to function, the synthesis of enzymes and other proteins must occur; but in order to maintain a balance within the cell, proteins must also be degraded. Ubiquitin protein complexes “tag” these target proteins for degradation, while another protein complex known as the proteasome breaks down the “tagged” proteins. One class of Cullin-RING ligase (CRL) complexes, comprised of Cullin 5, ElonginB, and ElonginC proteins, has the ability to execute this ubiquitination process. However, some viruses can express proteins which control CRL ubiquitination by either augmenting or cutting off host ubiquitination function. For example, HIV expresses a viral infectivity factor (Vif) which inhibits the DNA editing activity of human enzyme APOBEC3G by transporting it to the CRL complex for ubiquitination and degradation. With supporting evidence in the literature, we are inclined to believe other viruses use a similar mechanism of action. Utilizing the Virus Pathogen Resource (ViPR), PubMed BLAST, and homology modeling we were able to identify three other viral proteins that contain sequence and structural motifs similar to Vif, which may allow for interaction with the CRL complex. These proteins include NS5A (Human Hepatitis C Virus), NS1 (West Nile Virus), and Z-protein (Lassa mammarenavirus). After expressing and isolating these proteins using E. coli expression vectors, we can determine how these viral proteins interact within the context of Cullin 5, Elongin B, and Elongin C host proteins. Understanding these binding interactions will reveal more about viral control over the host ubiquitination process, ultimately providing insight into future anti-viral therapeutics.

TRANSCRIPTOMICS OF THE OPHIOPLOCUS ESMARKI BRITTLE STAR.

Alexandria Shumway, Hyla Sweet, *Rochester Institute of Technology*

The development of the brittle star *Ophioplocus esmarki* was characterized and RNA was isolated from the vitellaria and juvenile stages. Echinoderms have an early nervous system at the larval stage, and a separate nervous system at the juvenile stage. Through transcriptomics, candidate neural genes will be analyzed within the embryo, larva, and juvenile. Sequencing libraries were prepared using the TruSeq RNA library preparation protocol. The samples were sequenced with Illumina v3 chemistry using the multiplex paired-end sequencing protocol. The sequencing was performed on an Illumina HiSeq 2500 with 100-bp paired-end reads. A transcriptome database was generated from this RNA and was quality checked through Trinity, FASTQC, and Trimmomatic tools. The brittle star reads were then matched up with corresponding genes through Blastx and has several genes shared with *Amphiura filiformis*, *Ophionotus victoriae*, *Patiria miniata*, and *Lytechinus variegatus* species. The eggNOG-mapper tool was also used to identify IDs for gene ontology and further analysis.

TREATING CANCER WITH PHYSICS: NANOPARTICLE BREAKTHROUGH

Jared J. Bouldin, Carolina C. Ilie, *SUNY Oswego*

Since the first creation of nanoparticles in 1960, and their first uses in medicine during the 70s, scientists have been developing new ways to use nanoparticles for treatments and imaging of cancer patients. Today over a dozen different types of nanoparticles, from magnetic nanoparticles to nanocomposites, are being tested. Superparamagnetic iron oxide nanoparticles, for example, are being used in various methods for treating cancer such as targeted drug delivery and imaging. These advancements in particle types, theranostic methods, and electromagnetic properties may bring about a new way to combat cancer in the near future.

U

USING DRONES TO MONITOR HARMFUL ALGAL BLOOMS.

William White, Josh Andrews, Ileana Dumitru Ph.D., Peter Spacher Ph.D., John Halfman, Ph.D, Lisa Cleckner, Ph.D., *Hobart and William Smith Colleges*

Harmful Algal Blooms (HABs) occurrence has increased in recent decades. Traditional monitoring programs are expensive and time consuming. The use of UAS (Unmanned Aerial Systems) assures high-resolution space and time monitoring for HABs, and is economical for small bodies of water. By using UAS (Matrice100 and Phantom3) we obtained aerial photographs of eight Finger Lakes which span the oligotrophic to eutrophic spectrum of algal productivity. Water samples were collected/analyzed simultaneously. The Green/Blue (G/B) ratio extracted from the aerial photos was proportional to chlorophyll-a abundance. The algal pigments are characterized by unique light absorbance and reflectance features, and spectral images obtained from two up-down visible spectrometers revealed a prominent feature ~790 nm which correlates to the concentration of algae in the water.

USING MICRO ALGAE TO REMEDIATE AGRICULTURAL EFFLUENTS FROM WESTERN NY AND EXPLORING HARVESTED BIOMASS FOR BIOFUEL POTENTIAL.

Daniel Anini Baah, Dr. Jeffery Lodge, *Rochester Institute of Technology*

Western New York hosts numerous Agro-industries which contribute massively to the US economy. Among these are Dairy and biogas, Poultry, Cheese, Tofu and Greek Yogurt plants whose activities also discharge effluents high in pollutants like NH₃, PO₄, NO₃, and Fe which adversely affect aquatic systems and watershed if untreated. As WWTPs remain highly restrictive these high grade effluents, Microalgae Treatment Technology provides a sustainable alternative to treating Agricultural waste waters onsite. The study analyzed and treated effluents from selected production plants within NY State with different algal strains. Free suspended Algae was applied to treat food based effluents in both bioreactor and open pond settings. All pollutant levels exceeded USEPA limits. *Botryococcus* sp and *Chlorella* sp averagely reduced 99% of NO₃ from Synergy's Dairy and biodigester effluents within 5 days residence time (RT) as most algae species removed 75% phosphorus within 5 days RT. *Nostoc* sp removed 98% NO₃ from Kreher farm's Egg wash effluents but moderately removed PO₄ within 6 days RT while *Anabena* and *Chlorella* sp impressively removed 90% PO₄ and over 90% NO₃ within an average of 3 and 12 days RT respectively. Tofu, Cheese and Greek Yogurt whey all achieved bio-remediation targets in relatively shorter residence time. Biomass harvested through centrifuge showed high bands for triglycerides and Free Fatty Acids (FFA) although ultrasonication disruption technique did not impact lipids, glucose and methane yields in anyway. *Chlorella* sp showed an avg 27% sugar yield compared coffee and other algae biomass which yielded only avg 10% sugars. Single and double extraction from Biomass increased Biomethane potential (BMP) by 1 and 5 folds respectively to 10ml meth/gVS and 25ml meth/g VS. Microalgae have then proven to reduce pollutants in agricultural effluents while producing high quality biomass for bio-energy purposes.

V

VACCINE DESIGN AGAINST COLORECTAL CANCER ANTIGEN CEACAM-1 USING IMMUNOINFORMATICS TOOLS

Aditya Gupta, Andrew Rosato, *Rochester Institute of Technology*

Carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) is a membrane glycoprotein that mediates intercellular interactions influencing cellular growth, immune cell activation, apoptosis, and tumor suppression.⁸ Due to its multi-faceted role as an immune checkpoint inhibitor and tumor marker, CEACAM1 has recently emerged as an attractive target for cancer immunotherapy. Since CEACAM1 is highly expressed in several different types of cancers, a multi-epitope peptide cancer vaccine targeting CEACAM1 might have

antitumor effects by directly attacking cancer cells. However, such a vaccine has not been developed. In the present study, a computational approach was used to design a multi-epitope vaccine that contains several regions of CEACAM1 (usually 9 – 15 mers). These epitopes recognized by CD8+ and CD4+ T cells were determined by various online servers, which apply different algorithms. The CD8+ and CD4+ epitopes were linked together by AAY motifs to enhance epitope presentation and EAAAK linker was introduced to N and C terminals of the vaccine for efficient separation. A 3D model of the vaccine was generated by homology modeling and docked favorably to the major histocompatibility complex (MHC) class I and II allele structures. Analysis of docking structures by Ramachandran plots revealed 94% residues in energetically favorable regions. Stability of the docking structure was further supported by the presence of multiple hydrophobic patches and hydrogen bonds.

VARIABILITY IN DOM COMPOSITION AND CARBON METABOLISM IN CREATED WETLANDS.

Benjamin Hamilton, Carmody McCalley, Christy Tyler, *Rochester Institute of Technology*

Wetlands are valuable ecosystems that provide ecosystem services such as carbon cycling. Carbon cycling is influenced by the composition of dissolved organic matter (DOM), which is in turn shaped by wetland characteristics, such as plant communities, hydrology, and past land use. Because of the ecological value of wetlands, the Clean Water Act mandates that new wetlands be created to replace natural wetlands. This project examined DOM composition and carbon metabolism in three created wetlands that differed substantially in hydrology, plant community composition and past land use to identify key characteristics that drive DOM chemistry and C cycling in these systems. The DOM was analyzed using NMR spectroscopy. The results of these analyses were compared to the plant communities, hydrology and rates of anaerobic carbon metabolism of each site. Results suggest that there are differences in DOM composition between each of the wetlands as well as seasonally and these differences result in shifts in C cycling.

VESICULAR STOMATITIS VIRUS MATRIX PROTEIN FUNCTIONS OF INHIBITING NF-KB ACTIVATION AND INHIBITING INTERFERON RESPONSE ARE INDEPENDENT.

Amanda N. Weiss, Kaitlin A. Marquis, and Maureen C. Ferran, *Rochester Institute of Technology*

Upon infection of the cell, the vesicular stomatitis virus (VSV) matrix (M) protein is responsible for inhibiting host gene expression at the transcriptional, RNA export, and translational levels. This block in host gene expression favors viral replication because it prevents activation of the antiviral response, including the production of interferon beta (IFN- β). Our previous studies have shown that the methionine at position 51 of the M protein is crucial for inhibiting host transcription and IFN- β expression. We have also shown that the M protein prevents activation of NF- κ B, a host transcription factor that is essential for induction of the IFN- β gene. However, that work left uncertainty as to whether suppression of IFN- β production and inhibition of NF- κ B activation were necessarily linked or independent. This project aimed to determine whether these functions are, in fact, separable. We utilized VSV strains 22-20, which has a mutation in M at position 52, an otherwise well-conserved position, and 22-25, which is 22-20's corresponding wild type strain. Immunofluorescence experiments in L929 cells showed that infection by 22-20 was associated with NF- κ B activation, whereas infection by 22-25 showed NF- κ B remaining largely cytoplasmic, thus inactive. We have also shown that little to no IFN- β mRNA or protein is produced in 22-20 or 22-25 infected cells, indicating that suppression of the interferon response is functionally retained in both virus strains. Single step growth curve experiments demonstrated that these viruses replicate to similar levels during infection. Taken together, our results suggest that position 52 of the M protein is essential for M-mediated inhibition NF- κ B activation, but not for IFN suppression. As such, these two M protein functions are separable.

VISUALIZING SMALL PROTEINS OF MYCOBACTERIUM SMEGMATIS AND M.TUBERCULOSIS WITH WESTERN BLOTTING.

Katherine Cotten, Jill Canestrari, Matt Champion, Keith Derbyshire, Todd Gray, *SUNY Geneseo*

Small proteins are difficult to detect and often overlooked in mycobacteria, as well as other bacteria. A protein is considered to be small if it is around 5 to 50 amino acids long. However, most genetic sequence databases do not accept submissions of sequences less than 200 nucleotides. We have used two ways to identify small proteins: ribosome profiling and “specialized” mass spectrometry. Ribosome profiling, along with RNA sequencing (RNA-seq), allows us to identify small open reading frames (sORFs) by showing where the ribosome translates small proteins encoded in mRNAs. We have also used data from modified mass spectrometry to retain and identify, rather than discard and ignore, peptide signatures consistent with an encoded small protein. However, without independent validation, many people remain skeptical as to whether these small proteins are actually being expressed. We used these data to predict the transcriptional start site and the translational start codon of the small protein. We have amplified 15 of these predicted sORFs and cloned them into a vector that contains an epitope tag, which allows us to visualize these proteins by Western Blot. Small proteins that we detect by Western Blot will validate expression of these small proteins in mycobacteria. Following validation, the small proteins may be studied biochemically or by introducing mutations in the sORF. Additionally, validating this subset of small proteins by Western Blot will provide an estimate of the accuracy of our RNA-seq and mass spectrometry methods for identifying sORFs. With this knowledge, small proteins can be confidently identified and annotated, providing a more accurate genome annotation for mycobacteria.

W

WHEN IS THE OAK TWIG PRUNER (ANELAPHUS PARALLELUS) INFECTED WITH WOLBACHIA SP.?

Luciana Cursino, Sarah Bresette and William Brown, *Keuka College*

We found the endosymbiotic bacteria, *Wolbachia* sp., in adult oak twig pruners (Cerambycidae; *Anelaphus parallelus*), a wood-boring beetle, collected from red oaks (*Quercus rubra*). We intend to determine when *Wolbachia* sp. infects the beetle. Current working hypotheses include: 1) Eggs are bacteria-free and larvae acquire bacteria as they consume woody tissue; 2) Eggs are bacteria-free and larvae acquire *Wolbachia* sp. if they are attacked by parasitic wasps that contain the bacteria; 3) Eggs already contain *Wolbachia* bacteria that remain in beetles throughout their life cycle; 4) Eggs are laid with *Wolbachia* sp. and chemicals released by the host plant hinder the infection. To address the first hypothesis, DNA was extracted from larval tissue and the *wsp* gene marker was amplified by endpoint PCR to identify the presence of *Wolbachia* sp. None of the seven larval samples tested were positive for *Wolbachia* sp. Our next goal is to increase the sample size of larvae examined and then explore the remaining hypotheses by testing for the presence of *Wolbachia* sp. in beetle eggs and adult parasitic wasps.