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Abstract Booklet

General Meeting ABSTRACTS

Listed alphabetically by first author's last name.

Acey, Cassandra*, and Steve Ropski Gannon University, Erie, PA 16541. *MTHFR Genetic Variant*.- Methylenetetrahydrofolate reductase (MTHFR) is a gene that codes for MTHFR protein production. MTHFR protein aids the body in processing folate, a natural, water-soluble form of Vitamin B9, and is found naturally in several types of food. People who carry a genetic variant of the MTHFR gene are unable to convert folate to its active form, which is used within the body for important processes, such as DNA and RNA production, healthy red blood cell production, and protein metabolism. These processes are important in the overall function of the human body. Folate plays in important role in breaking down the amino acid, homocysteine. People who have the genetic variant for MTHFR may experience low levels of folate and high levels of homocysteine which can exert harmful effects in the body. There are two common forms of the mutation that can occur on the MTHFR gene that is located on Chromosome 1, C677T and A1298C. Those who are homozygous for one of these variants are more likely to experience health problems related to the genetic variant. There are more people in the United States that have one or two copies of the most common MTHFR variant, than people who do not have an MTHFR variant. It is estimated that about 30-40% of the American population may have a mutation located at C677T on the MTHFR gene. It was found that the A1298C variant was present in 7-14% of North Americans, European, and Australian populations. This is an educational poster that examines the MTHFR gene and variants, the correlation between folate and homocysteine levels, symptoms caused by the MTHFR variants, related health conditions, MTHFR variants and pregnancy, and manageability. (**14**)

Adesola, Opeoluwa*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Extraction of antibiotic producing bacteria from soil sample*.- The war against antimicrobial resistant (AMR) bacteria is at a critical point. Even minor infections that could be treated with antibiotics could become lethal as the bacteria become resistant to already-in-use antibiotics. A strategy for possible control or elimination of AMR is the attempt to discover novel antibiotic-producing bacteria. We extracted antibiotic-producing bacteria from soil in York, Pennsylvania. Isolates were competed against ESKAPE pathogen safe strains; one isolate, 3OA19, created a zone of inhibition against every safe strain tested. We characterized bacterial isolates by performing a Gram stain and sequencing their 16s rRNA genome. Isolate 3OA19 was determined to be Gram-negative and a part of the *Pseudomonas* genus. Disc diffusion assays were used to determine the antibiotic resistance of our isolates. Isolate 3OA19 was resistant to cell wall synthesis antibiotics, suggesting that this could be the function of the antibiotic it produces. Whole genome sequencing was completed and run through the antiSMASH program to determine possible Biosynthetic Gene Clusters (BGC) involved in the production of antibiotics. The BGC pyoverdine is an attractive candidate that we hope to knock out via CRISPR/Cas and assess antibiotic production against ESKAPE safe strains. Taken together, this strategy could identify novel antibiotics that are effective against antibiotic-resistant pathogens. In the long run, we hope to use this information to improve antibiotic production and increase the effectiveness of these antibiotics, progressing the fight against AMR. (**91**)

Ajana-Adegboro, Okiki*, Erica Ward, and Richard Jackson Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Venus flytraps are anesthetized with* *sevoflurane in a dose dependent manner*.- General anesthesia is a state of controlled unconsciousness, yet the mechanisms are not fully understood. Anesthesia affects the body by preventing the passage of nerve impulses, which impairs muscular movement and sensation. Many studies have been done on the effects of anesthetics on animals and humans, but few have investigated the effects on plants. Venus flytrap (*Dionaea muscipulai*) is a unique plant that rapidly responds to touch stimuli. When an insect makes contact with the trigger hairs on the head of the Venus flytrap, an action potential is produced. The action potential activates the motor cells causing the head of the Venus flytrap to close. After the head is closed, enzymes are secreted, and the insect is digested. According to several studies, Venus flytraps are less responsive to physical stimuli when given anesthetics such as diethyl ether. Diethyl ether is an anesthetic that is inhaled but is not commonly used due to flammability. Sevoflurane is a non-flammable alternative but has a shorter half-life in the tissues compared to diethyl ether; this results in a fast induction and recovery time in humans and animals. In this study, the effects of sevoflurane on the Venus flytrap were compared to diethyl ether to determine if sevoflurane anesthetics affect Venus flytraps in the same manner as humans and animals. Venus flytraps were exposed to increasing amounts of sevoflurane. After exposure, trigger hairs were manually stimulated, and response time was recorded. In contrast to humans and animals, sevoflurane had a greater effect on the Venus flytraps response time in a dose dependent manner compared to diethyl ether. These results indicate that mechanism of action and metabolism of sevoflurane in Venus flytrap may be different than animals. (**55**)

Alleman, Alexis*, Deborah Austin, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *A study of musculoskeletal symptoms experienced by Lyme disease patients*.- According to the CDC, Lyme disease is the number one tick-borne vector disease in the United States with approximately 20 to 30 thousand people diagnosed per year. Most cases of Lyme disease go undiagnosed for a period of time because the symptoms are associated with other conditions, such as general aging and arthritis. Early diagnosis is important because treatment is more effective in early stages of the disease; therefore, it is important to develop new tools that can help physicians identify the presence of Lyme disease sooner. The purpose of this study was to observe whether there is a relationship between musculoskeletal symptoms and the pain thresholds of patients diagnosed with Lyme disease. An IRB-approved anonymous survey was distributed by a physician who is known to specialize in treating Lyme disease. Survey results were analyzed to determine what musculoskeletal symptoms were experienced as well as the pain threshold severity. Using NCSS, it was determined that there is insufficient statistical significance to begin developing an evaluation tool for musculoskeletal symptoms and pain thresholds that could be used by physicians as an indicator to test for Lyme disease before ruling out other diagnoses. A much larger data set would need to be collected to determine the potential of an evaluation tool. (**43**)

Aluko, Marvelous*, Erica Ward, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The effect of vaping coil temperature on the viability of oral bacteria*.- Vaping has become popular amongst the teenage and young adult population and has become a public health crisis in just 17 years since it was introduced to US consumers. Vaping-associated lung injuries have been documented and cause lifelong complications for many young people. Recent studies have focused on the chemical composition of vaping liquid as a potential cause of lung injury. Far fewer studies have focused on the potential role of the metal heating element within the vape. Heating elements are responsible for converting vape liquid to inhaled vapor. This study aims to determine if smoking frequency can produce a change in 80/20 nichrome heating element temperature and if the heating element temperature affects the viability of two bacterial species commonly found in the oral microbiome. *Veillonella parvula* is a commensal organism, and *Streptococcus mutans* is an opportunistic organism of dental caries. These species were exposed to e-cigarette vapors at different frequencies in order to simulate regular smoking (20 puffs/hr) and chain-smoking (40 puffs/hr) intervals. The nichrome heating coil submerged under oil produced a higher temperature under chain-smoking conditions compared to regular smoking conditions. *V. parvula* exhibited decreased viability under both regular and chain-smoking conditions, but the viability of the opportunist *S. mutans* was unaffected by e-cigarette vapors at either frequency of exposure. These results indicate that inhalation of nicrome-heated vapors inhibit the growth of commensal *V. parvula* while not effecting the growth of the opportunistic *S. mutans*. These results provide additional support that the high temperatures produced during vaping contribute to the detrimental effects currently associated with vaping. (**50**)

Auker, Linda* Misericordia University, Dallas, PA 18612. *Teaching R to undergraduate ecology students: lessons learned and recommendations*.- As ecological datasets grow in size, there is a need for ecologists to refine their skills in data science and management. While much of this training occurs in graduate programs, an increasing number of graduate opportunities are requiring their applicants to have some background in data skills, particularly in using R, a free and open-source programming environment for statistical analysis and data visualization. Therefore, undergraduates who are trained in using R in the classroom or in independent research may have an advantage in applying for graduate programs in ecology. In this presentation, I will discuss findings from a recently published study in *Ecosphere* and share the experiences I have had in teaching R to an upper-level community ecology course without a lab at a liberal arts university in upstate New York, and contrast this with my colleague’s experience teaching R to her upper-level forest ecology course with a lab at the same university. Each course format had strengths and weaknesses in teaching R. Our shared experience has yielded the following discoveries: 1) R should be taught as a separate skill from statistics; 2) writing assignments take significant preparation time for first-time instructors; 3) there is a tradeoff between teaching R and teaching content. My goal is to share our recommendations and lessons learned with others who are interested in, or experienced with, teaching R to undergraduate students in order to start a discussion. While ecology is the main focus of this presentation, research mentors and students from all science backgrounds are welcome and encouraged to attend. (**70**)

Bailey, Nicole*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Yearly variation in the population density and reproduction of an aquatic invader, Potamopyrgus antipodarum*.- The New Zealand mud snail (*Potamopyrgus antipodarum*) is a world-wide aquatic invader that is known to cause significant ecological harm. Densities of the snail in its invaded range vary from hundreds to hundreds of thousands per square meter. The snail has been established in streams in central PA for over a decade, but the population densities of these snails have not been accurately measured. In the first year of a multi-year study, we sampled five sites in the Spring Creek watershed in Centre County PA in May and July of 2022 to determine the density of these snails using stovepipe sampling technique. We also assessed reproductive effort by dissecting each snail recovered and measuring the length, the brood size, and the proportion of females brooding in each site. Preliminary data suggests that the snails exist in the thousands per square meter at most sites and that there is variation in density and reproductive characteristics over time. The data was limited at one site due to the discovery of a very similar snail, *Fontigens nickliniana*, which has made identification difficult. *Potamopyrgus* appears very well established in Spring Creek. (**83**)

Ball, Mary*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Optimizing the distance between tomato plants to limit aphid infestations through volatile compound*.- Volatile compounds can be used by plants as a defense mechanism against herbivory and infection. Methyl salicylate (MeSA) is a volatile compound that triggers neighboring plants' systemic acquired resistance, repels herbivores, and attracts their natural predators. There has been increasing popularity in evaluating the push-pull method as a form of eco-friendly insecticide. This method relies on repelling predatory insects and attracting their natural enemies. Aphids are detrimental to the health and production of many food crops, such as tomatoes. If the push-pull method were applied to mass production of food crops, such as to tomato plants to limit aphid infestations, it is important to consider the different effects that distance between crops would have on the spread of the infestation. Here we created a model based on the SI model of disease spread and was used to optimize the distance between tomato plants in an agricultural setting to limit aphid infestations using methyl salicylate. It was found that plants should be placed between two and five meters away from each other in order to stop an aphid infestation. This model could be adjusted to other important food crops and common infections or infestations that affect their yield or to include other variables that could be used to limit infections or infestations such as insecticides or herbicides. (**56**)

Barr, Kelly*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Analysis of myelination deficits in a zebrafish developmental hypoxia model*.- Oligodendrocytes are the myelinating cell of the central nervous system, enabling rapid signal transduction in axons via saltatory conduction. During development, oligodendrocyte precursor cells (OPCs) respond to multiple environmental signals and intrinsic timing to initiate myelination. Hypoxic insults during this critical time period disrupts the normal myelination program, causing "maturation arrest" in the CNS. Perinatal hypoxia often results in hypomyelination and neurological deficits in humans. We have developed a novel model for chemical-mediated hypoxia in developing zebrafish as model for oligodendrocyte injury. The oxygen scavenger sodium sulfite is used to reduce dissolved oxygen levels to induce hypoxic conditions. Zebrafish larvae (55 hpf) were exposed to one hour of hypoxia, then returned to normoxic conditions for a 16-hour recovery. Zebrafish larvae RNA was isolated at 72 hpf, and analyzed for myelin gene expression using qPCR. Formation of compact CNS myelin in the spinal cord of hypoxic zebrafish was assessed with fluorescent labeling. Furthermore, this study focused on the role of hypoxia-induced changes in chromatin methylation state. Chromatin samples from 72 hpf zebrafish larvae were prepared following one hour hypoxia and 16 hr recovery. Current analysis of hypoxia-induced changes in Sirt2 activity using chromatin immunoprecipitation (ChIP) assays will assess the role of Sirt2 in our developmental zebrafish model. Sirt2 was recently identified as a critical mediator of oligodendrocyte maturation in mammals. (**36**)

Bart, Alex*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *miR-1307 isoforms, novel population-specific oncomiRs, are associated with survival in African American and European American kidney cancer patients*.- Background: Renal cell carcinoma (RCC) is the most common type of kidney cancer (85%), and has the lowest survival compared to all other urologic cancers. There are three distinct RCC subtypes: clear cell (75%), papillary (15-20%), and chromophobe (5%). African American (AA) RCC patients have worse advanced-stage survival than European Americans (EAs), possibly due to aggressive tumor biology. microRNAs (miRs) and miR isoforms (isomiRs) silence mRNAs by preventing translation, and drive different mRNA expression signatures associated with invasiveness and metastasis. It is unknown if these transcriptomic signatures vary by race in RCC patients. Hypothesis: Population-specific isomiRs are associated with racial differences in RCC survival. Study Design: miR-seq, isomiR-seq, mRNA-seq, and clinical data were downloaded for AA and EA RCC patients in the pan-RCC TCGA discovery cohort (n = 117 AAs, 649 EAs). The PGS miR Expression Workflow, Prism, and cBioPortal were used to determine differentially expressed (DE) miRs, isomiRs, and mRNAs by race ($P < 0.05$). miR and isomiR expression inclusion criteria were ≥3 reads per million (1: low specificity and high sensitivity; 5: high specificity and low sensitivity) and upregulation in AAs. Kaplan-Meier statistics were calculated for overall and disease-free patient survival. Results: miR-1307 was significantly DE in AAs and EAs across two RCC subtypes (ccRCC: $P = 0.021$, pRCC: $P = 0.027$). A total of 7/15 miR-1307 isomiRs met the expression inclusion criteria. High miR-1307-3p|5'- G,3'- x| expression in EAs, and low expression in AAs, was associated with worse disease-free survival in ccRCC (EA $P = 0.012$, AA $P = 0.699$). Conclusion: miR-1307-3p|5'- G,3'- x| may be a novel oncogenic isomiR and biomarker of poor prognosis in ccRCC patients. Clinical targeting via isomiR sponges could decrease expression in EAs while miR-mimics may be utilized to increase expression in AAs, potentially reducing racial disparities in survival. (**74**)

Bath, Sarah*, Daniel Guevin, John Harms, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Development of a cell-based vaccine against pancreatic cancer*.- Aggressive and usually undetected proliferation of pancreatic cancers has prompted extensive research into options for early detection and therapy. We seek to develop a vaccine that will recruit cellular immunity within the tumor-bearing host to target a novel protein expressed by aggressive pancreatic tumors in a mouse model. We have established immortalized syngeneic cells that express a derivative of the Simian virus 40 Large Tumor antigen protein (SV40 T ag) containing a 20 amino acid insertion corresponding to a unique sequence found in the 69 amino acid intron IV encoded segment of the CCK2i4svR pancreatic-cancer associated growth factor receptor. Previous experiments confirmed that immunization of mice with a synthetic peptide corresponding to a 20mer from the insertion sequence did induce generation of peptide-specific CD4+ T cells in C57Bl/6 mice. To test the immunogenicity of the cell-based vaccine, C57Bl/6 mice were injected with the tumor vaccine cells (4A-1) or similar cells (B6/WT-19) that expressed unaltered SV40 T ag to elicit T cell responses against epitopes within the SV40 T ag and the CCK2i4svR sequence. An ELISPOT assay confirmed induction of inconsistent, but detectable CCKCR- and SV40 T ag-specific T cell responses in red cell-depleted splenic lymphocytes by employing target peptides corresponding to a known CD4+ epitope from SV40 T ag, the 20mer from CCK2i4svR, and a control HBV epitope. In the current tumor control study, 4A-1 or B6/WT-19 cells were used to immunize groups of C57Bl/6 mice prior to orthotopic implantation of syngeneic pancreatic tumor cells (Panco2) engineered to co-express express the intron IV-containing variant CCK2i4svR receptor and subsequent proglumide therapy. Preliminary analysis of peritoneal tumors recovered at 4 weeks revealed a significant difference in mass between tumors found in the two groups. Tumor architecture and leukocyte infiltration are being assessed by staining and immunohistochemistry. (**23**)

Biever, Brent*, Maurice Lopez-Soliz*, Ashly Ramos*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The effect of acidification on the mineralization rate of RAS effluent in anaerobic batch reactors for reuse of a naturally-derived hydroponic fertilizer*.- Recirculating aquaculture systems (RAS) require 95-99% less water than alternative fish farming methods and offer intensive, location-independent and season-independent seafood production. Commercial RAS is constrained by the generation of nutrient-dense effluent that requires costly treatment in municipal wastewater treatment plants as direct discharge into natural waterways will result in eutrophication. Previous studies have shown that the effluent contains most necessary plant nutrients and can be used as a hydroponic nutrient solution after treatment to increase plant availability of nutrients through solids mineralization and removal of heterotrophic growth promoting organic matter (OM). Anaerobic treatment (AT) is commonly used to reduce total solids and OM in municipal and agricultural waste treatment, and has provided promising results in developing a hydroponic nutrient solution from RAS effluent. The objective of this study is to determine if acidification would improve solids mineralization and OM removal rates in RAS effluent in continuously mixed anaerobic batch bioreactors by comparing triplicated treatments at a pH of 5.5 and 7.0. Solids mineralization and OM removal rates will be determined by total suspended solids (TSS) and chemical oxygen demand (COD) removal over a 15-day period. It is expected that the lower pH will result in more rapid reduction rates by enhancing the anaerobic hydrolysis and acidification processes. This work will provide foundational data for optimizing effluent valorization techniques in RAS to improve economic and environmental sustainability while providing hydroponics with a naturally-derived nutrient source to reduce reliance on finite mineral fertilizers. (**79**)

Bonser, Hannah*, Alison Edwards *, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining Replication Protein A interactions with the cancer-associated proteins Ddc2p and Mec1p using the budding yeast Saccharomyces cerevisiae*.- Cancer is the second leading cause of death in the United States, with 609,360 deaths in 2022. Characterized by uncontrolled cell division, cancer can arise from DNA mutations that affect proteins involved in cell cycle regulation. One protein that has been identified as helping regulate the cell cycle and in maintaining genomic integrity is Replication Protein A (RPA). RPA is a major eukaryotic single stranded DNA-binding protein that plays an important role in DNA replication, repair, and recombination. When DNA is damaged, RPA may be phosphorylated as a part of the cell's DNA damage response and will then aid in cell cycle regulation. To study the cell cycle, we used the model organism *Saccharomyces cerevisiae* because of the similarities between the yeast cell cycle and the animal cell cycle. Furthermore, *S. cerevisiae* is easily genetically manipulated. Using the homologous proteins in yeast cells, we hypothesized that RPA may physically interact with the cell cycle regulation protein Mec1p (homolog of human ATR) through Ddc2p (homolog of human ATRIP) in a phosphorylation-dependent manner. We used the Yeast Two Hybrid system to find physical interactions between RPA, Mec1p, Ddc2p, and Tel1p (homolog of human ATM). Our data indicate that RPA may directly interact with Ddc2p, but not Mec1p or Tel1p, and that RPA's interaction with Ddc2p may be affected by RPA's phosphorylation state. In addition, Ddc2p may serve as a bridge facilitating an indirect interaction between RPA and Mec1p, but not between RPA and Tel1p. This data suggests that RPA's interactions with other proteins may be regulated by phosphorylation and could play a key role in affecting DNA repair, recombination, or replication processes, as well as cell cycle regulation. A better understanding of these protein-protein interactions could contribute insights for novel treatments for cancers that are caused by defects in cell cycle regulation. (**25**)

Borowicz, Michael*, Weston Hrin, Angela Vicini, Greg Andraso, Russell Minton, and Michael Ganger Gannon University, Erie, PA 16541. *Young-of-year Lepomis macrochirus (bluegill) and Lepomis gibbosus (pumpkinseed) show significant differences in their gut microbiome and pharyngeal apparatus*.- Fish gut microbiomes are influenced in part by the individual's environment, developmental stage, and diet. *Lepomis macrochirus* (bluegill) and *L. gibbosus* (pumpkinseed) are two closely related fish species that develop a pharyngeal apparatus for processing food items. The diets of adults are known to differ between the two, with pumpkinseed diets composed of more mollusks. Ten size-matched young-of-year (yoy) of each species (37-56 mm total length) were collected from Marina Bay in Presque Isle. For each fish the pharyngeal apparatus was removed, cleared, stained, and used for geometric morphometric analysis of pharyngeal outlines. Intestines were removed, cleaned of digestive material, and used to isolate gut bacterial DNA. The bacterial 16S V4 region was sequenced and analyzed to assess differences between species. Bluegill and pumpkinseed gut microbiomes differed significantly from each other, and bacterial compositional differences correlated with total length were present in both species. Pharyngeals showed changes with total length in both species and were different overall between species suggesting differences in diet. The shape of the pharyngeal apparatus differed between species and showed changes in shape with increasing fish total lengths. Pumpkinseed pharyngeals are more robust and would likely be more useful for crushing mollusks. Our results hint at the interrelatedness of fish gut microbiomes with diet and pharyngeal morphology and suggest that site effects may be minimized in juveniles. (**80**)

Boyce, Katelyn*, and Janet Matanguihan Messiah University, Mechanicsburg, PA 17055. *Preliminary study on hybridization and evaluation of spring varieties of flax (Linum usitatissimum) in South Central PA*.- Flax (*Linum usitatissimum*) shows great potential for reintroduction to south-central Pennsylvania. Flax seed and flax oil are rich in healthy oils that can prevent chronic diseases such as diabetes and cardiovascular disease. While the majority of oilseed flax cultivation in North America occurs in North Dakota and Canada, the growing functional foods market will drive its expansion into new regions. There is therefore a need to determine which high-oil yielding flax varieties can be grown under PA conditions. Two foundational projects were initiated, focusing on a) collecting preliminary data on the performance of flax spring cultivars in Mechanicsburg, PA conditions and b) establishing flax crossing protocols in the greenhouse. In the field, four flax varieties were grown from May – September, 2022. Two varieties ('Omega' and 'AAC Bright') were susceptible to a putative fungal disease due to higher rates of precipitation in PA, while two varieties ('CDC Glas' and 'CDC Rowland') were resistant. In the greenhouse, successful parental crossing rates were established at around 20%, with early spring being the key sowing period. (**97**)

Bratis, Audra*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *A qPCR-based method to differentiate impact and expirated blood spatter using the human oral microbiota*.- Blood stain pattern analysis is a crucial component of crime scene investigation. The two most common patterns are impact spatter, resulting when an outside force strikes an existing pool of blood creating a random dispersion pattern, and expirated spatter occurring when blood is expelled through the mouth or airways. These two patterns are difficult to qualitatively differentiate based on the appearance of the spatter alone; thus, detailed analysis uses additional biochemical methods such as a-amylase screening, saliva trailing, and autopsy analysis to further identify the stain origin. These methods are largely subjective, lack specificity, or are prone to contamination, and thus researchers have turned to methods that use the presence of oral bacteria to identify saliva in blood samples through multiplex end-point PCR. In this study, we further explored the use of unique oral microbiota (*Streptococcus salivarius* and *S. oralis*) to differentiate expirated and impact blood spatter using both end-point PCR and qPCR methods. A multiplex qPCR assay was designed to maximize specificity and sensitivity in the identification of oral bacteria in blood-saliva mixtures. With further optimization, this method may be applied to a simulated crime scene scenario and be run in conjunction with other forensic DNA typing to identify the individuals involved at the crime scene. (**44**)

Braught, Charles*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Ground-Penetrating Radar to Measure Bathymetry and Sediment load of Halfway Dam, PA*.- Ground Penetrating Radar (GPR) can be a powerful method to survey lakes and reservoir for bathymetry, water volume, sub-bottom, and sedimentation deposit. These surveys are performed without adverse impact. Methods for measuring sediment volume in water impoundments have often included invasive techniques such as collecting cores and results are usually rough estimates based on the limited amount of physical data that can realistically be collected. In this study, a GPR was used to map the bathymetry and sediment volumes of Halfway Lake. Halfway lake is located in R.B. Winter State Park, Union County, PA. A 400 MHz transceiver was used to collect 61 radar profiles covering the entirety of the lake. Contour maps of bathymetry were determined to calculate the volume of water. Contour map of Sub-bottom representing the original topography of the lake prior to its construction in 1933 were determined and sediment load were also calculated. Previous studies have estimated the bathymetry with traditional method yet sub-bottom, and water volume were never estimated. In this study, the volume of water and sediment within the lake were successfully calculated. In addition, the rate of sedimentation over the last 100 years were also estimated. Surveys profiles have also shown the channels of Rapid Run and Halfway Run almost filled with sediments. The deepest point was found near the dam with a depth of 2.5 m at the intersection of the two old steams. (**47**)

Brown, Colin*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Implication of <u>Carnobacterium</u> species in the fermentation of indigenous yogurt*.- Yogurt is a delicacy that has captivated tastebuds around the world. The creamy sweet taste that is so distinctive in commercialized yogurt products is caused by fermentation of lactose and other sugars by *Lactobacillus* and *Streptococcus* species. Yogurt could potentially be made with various combinations of lactose-fermenting, lactic acid bacteria, but the extent of using different bacteria outside of the industrial standard has not been well studied. In this experiment, bacteria were isolated from store-bought yogurt and compared to a traditional home-grown indigenous yogurt. Using 16S rRNA sequencing, we isolated several strains of bacteria from both yogurt samples and found that the dominant culturable bacterium in commercial yogurt is, not surprisingly, *Lactobacillus* sp. However, the most common bacterium in indigenous yogurt turned out be *Carnobacterium* sp., a gram-positive lactic acid bacterium, which was previously isolated from animal meat, fish and dairy products but has never been associated with yogurt. Could this novel probiotic bacterium be employed to produce yogurt with a better flavor, consistency and nutritive value that could be used commercially? Further research will explore if this bacterium and other associated isolates are indeed responsible for fermentation and if they could be employed to create better probiotic yogurt varieties. (**108**)

Bruninga-Socolar, Bethanne*, Eric Lonsdorf, Ian Lane, Zachary Portman, and Daniel Cariveau Albright College, Reading, PA 19604. *Making plant-pollinator data collection cheaper for restoration and monitoring*.- Wildflower plantings are a key tool for wild bee conservation, and plant-bee interaction data are frequently used in seed mix design to ensure that plantings provide sufficient resources for a diversity of bees. However, collecting plant-bee interaction data can be prohibitively expensive. Therefore, a crucial question is how does the conservation value of seed mixes vary as a function of the intensity of the data collection effort underpinning their design? We leverage a plant-bee interaction data set to ask how bee richness is expected to change when informed by different scenarios of reduced data collection effort and cost. From the original, large data set, we created reduced data sets by randomly: 1) reducing the number of specimens sampled, 2) reducing the number of sites sampled, 3) reducing the number of sampling days per site, and 4) using data from a single, representative taxon (bumble bees). We ask whether seed mixes designed from these reduced data sets support comparable bee richness to the full data set, and for any reduction in cost. Reductions in the number of specimens sampled and the number of sampling days per site yield seed mixes that support comparable bee richness to the full data set. Reductions in the number of sites yielded seed mixes that support lower bee richness than the full data set. Using only bumble bee interaction data yields seed mixes that support lower bee richness than the full data set, especially when few plants are included in the mixes. We recommend prioritizing broad spatial, temporal, and taxonomic coverage of plant-bee interaction data to guide cost-effective seed mix design. We also provide guidance for practitioners designing programs to monitor bee richness because plant-bee interaction data may be made cheaper by collecting fewer specimens per sampling event or collecting on fewer dates per site. (**59**)

Campbell, J. Michael*, and John Otto Campbell Mercyhurst University, Erie, PA 16546. *Passive acoustic monitoring using artificial intelligence (AI) reveals daily flight activities of roosting Chaetura pelagica (Chimney swifts) at Mercyhurst University in Erie, PA*.- A passive acoustic detection system using a Raspberry Pi device was developed for continuous monitoring of bird species associated with a green roof on a building at the Mercyhurst University campus in Erie, Pennsylvania. The monitoring tool was linked to an Internet-based artificial intelligence (AI) avian vocalization data analysis system powered by the TFLite version of BirdNET, developed by the Cornell Lab of Ornithology. The system could identify bird species that produced vocalizations within several hundred meters of the roof. A discord server was set-up with webhooks to create real-time alerts from the BirdNET-Pi system for remote notifications whenever bird vocalizations were detected on the green roof. The system provided sound recordings and created spectrograms to allow us to verify the identity of bird species reported. It was deployed in mid-July 2022 and successfully identified and detected the diurnal flights and activities of Canada goose (*Branta canadensis*), American crow (*Corvus brachyrhynchos*), American goldfinch (*Spinus tristis*), and Chimney swift (*Chaetura pelagica*) over or near the green roof. The temporal pattern of concentrated Chimney swift detections facilitated an efficient investigation and discovery of a Chimney swift roost located on the university campus. The American goldfinch detections corroborated anecdotal observations that this species may be an agent of seed dispersal for plants that have colonized the green roof. (**69**)

Chen, Tianjie*, Abu Asaduzzaman, and Jose Fuentes Penn State University, University park, PA 16802. *Development of a Python GUI tool to study the atmosphere in the Arctic*.-

Studying the atmosphere of the earth is an important task as it offers insights into weather and climate change, and environmental threats. Atmospheric conditions, especially near arctic circles, are not adequately studied due to difficulties in collecting data. All current arctic atmospheric models are mostly built using Fortran, which is difficult to execute and modify. In this project, a Fortran program for calculating one-dimensional arctic atmospheric models was translated into Python to make the program easier to use and modify. Apart from necessary syntax changes, unused and redundant variables and functions were cut from the program to make it more compact and easier to understand. The translation not only made designing a graphical user interface to make the program more user-friendly possible, but also allow new functionalities to be added to the program, such as format conversion and built-in line and contourf plotting. Despite all these modifications, the output file produced by the Python program maintains the same level of accuracy as the one produced by the Fortran program. However, the nature of Python made the program significantly slower than its Fortran version. In future, we plan to further optimize the program to increase its running speed, add new functions such as the ability to add new elements and three-dimensional modeling, and make the program accessible to users on all platforms. We believe that our Python program will help the atmosphere scientist community to study the atmosphere in the arctic from anywhere at anytime. (**40**)

Cino, Anthony*, Angelique Bauer*, Joseph Colosi, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Nicotine stimulates the expansion of trinucleotide repeats in Saccharomyces cerevisiae*.- Trinucleotide repeat (TNR) tracts are composed of highly repetitive sequences of DNA. TNR expansions occur during DNA replication, when slippage of DNA polymerase causes the formation of a hairpin loop. Expansion events are rare but can be detrimental to human health. Disorders such as Huntington's Disease and Fragile X Syndrome result from the expansion of TNRs. We obtained a strain of *S. cerevisiae* in which TNRs are inserted between the promoter region and open reading frame of the *URA3* gene. Expression of the *URA3* gene in the presence of 5-Fluoroorotic acid (5-FOA) causes the formation of a compound which is lethal to yeast. Expansion of the TNR tract, on the other hand, prevents expression of *URA3* and permits cell survival on 5-FOA. Cigarette smokers are less likely to develop Parkinson's Disease, a complex neurodegenerative disorder. As TNR expansions are implicated in some Parkinson's cases, we postulated that nicotine, an ingredient in tobacco, might stabilize TNR tracts in *S. cerevisiae*. Remarkably, we have found that the addition of nicotine to growth medium has a strong destabilizing effect on TNRs, leading to a high rate of expansions. We demonstrate this effect to be dosage dependent. (**37**)

Collevechio, Sara*, Ainsley Buia*, Raegan Lasczyck, and Valbona Hoxha Lebanon Valley College, Annville, PA 17003. *The role of Tau protein in traumatic brain injury and alcohol sensitivity*.- Tau is a microtubule-associative protein (MAP) critical in neuronal cytoskeleton. Tau proteins have a primary role in maintaining the stability of the microtubules of axons, cell signaling, regulation in genomic stability, and synaptic plasticity. Alterations of the amount of Tau protein, structure, or phosphorylation status lead to a group of disorders called tauopathies. In humans, it has been observed that TBI is associated with tau post injury. *Drosophila* express a form of tau homologous to human tau (*hTau*) called *dTau*. This study investigates the role of tau in post-TBI ethanol sensitivity using two tau deletion mutants (TauMI and TauKO). A hit system was developed to inflict TBI on the *Drosophila*. Using this system, we tested how TBI affects alcohol sensitivity in wild type (CS) and TauMI and TauKO mutants. It was observed that TauMI and TauKO mutants had an increased alcohol sensitivity when compared to the wild type regardless of gender. With TBI, there was no observable difference in ethanol sensitivity between TauKO mutants and wild type. Our results indicate an essential role of Tau in ethanol sensitivity, and further suggest that TBI effects on ethanol sensitivity could be mediated through Tau. (**24**)

Crowell, David*, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Influence of microbiomes between humans and pet cockatiels*.- Microbiomes are communities of microorganisms that live in a specific habitat. Recently, interest in human microbiomes has increased due to evidence that our microbiome affects our health. Microbiomes are unique to the individual; however, individuals can influence each other's microbiomes. For example, the presence of older siblings has shown an increase in the diversity of infant microbiomes, in addition, people in households with dogs share more microbes with their own canine pets than other dogs. However, there is less information known about microbial transfer between humans and more exotic pet species. This project is designed to test whether or not there is microbial transfer between humans and a pet cockatiel, and whether the amount and length of contact influences the amount of microbial transfer. To do this, samples were taken from the mouth and hands of human participants that have varying degrees of contact with the bird, and samples from the mouth and feet of the bird were taken. Bacteria grown from the samples will be tested to see if amount and length of contact influences the amount of microbial transfer. We will use biochemical differential tests to determine the species of sampled bacteria; if necessary, DNA barcoding of the isolated microbes will be performed. Lastly, Jaccard's similarity coeffiecent will be used to measure the similarity between the microbiomes of each human and the bird. (**94**)

Curtiss, Katherine*, and John Campbell Mercyhurst University, Erie, PA 16546. *Evidence of the presence of <u>Neotyphodium lolii</u> in Northwestern Pennsylvania*.- *Neotyphodium lolii* is an endophytic fungus that lives in *Lolium perenne* (perennial Ryegrass), forming a mutual relationship. It occurs primarily in New Zealand and Australia; however, the fungus has been found in Europe and was discovered in Ohio in the summer of 2021. This fungus causes Ryegrass Staggers in ruminating animals, specifically in cows, sheep, and goats, resulting in staggering behavior with little to no control of the legs. The animals become infected with *Neotyphodium lolii* by eating the base of the plant, where most of the fungus is located. This research attempts to determine whether *Neotyphodium lolii* is present in the ryegrass on a farm in Northwestern Pennsylvania after two ewes presented typical symptoms in the spring and summer of 2022. *Lolium perenne* was collected in three different locations where the two ewes began to show symptoms. The samples were stained using 10% KOH and 5% ink vinegar, then observed. The results of the staining showed 60% of sample 1 had the presence of fungus, while sample 2 had 10% and sample 3 had 0%. The results concluded that there was endophytic fungus present in sample 1, with both samples 2 and 3 being inconclusive. However, the correlation between the symptoms observed in the sheep and the Ohio 2021 outbreak, may indicate that the two are connected. Further research is needed to accurately conclude whether the endophytic fungus present in sample 1 was the disease-causing *Neotyphodium lolii*. (**101**)

Delgado, Juliana*, Kendall Heiney*, Andre Walther, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Using the oleaginous fungus Cryptococcus neoformans as a source of lipids for the production of biodiesel fuel*.- While the transition to electric motors is actively under way in cars and trucks, the unique challenges of air, rail, and sea travel are likely to require continued use of combustion engines for the foreseeable future. While the use of fossil fuels in combustion engines is a major source of greenhouse gas emissions, the use of biodiesel created from renewable resources can provide a relatively clean and carbon neutral option for combustion engines. With the intent of developing a method of producing biodiesel at an industrial level, an interdisciplinary approach sought to optimize the multiple stages of biodiesel production from the growth of the oleaginous yeast species *Cryptococcus neoformans* to the chemical conversion of fatty acids to the methyl ester components of the biodiesel product. *C. neoformans* is a particularly attractive system because it is capable of producing high levels of lipids and it has characterized extensively because it is associated with human disease in immunocompromised individuals. This yeast's genome has been sequenced and extensive genetic engineering tools have been developed to allow for genetic manipulation leading to the identification of mutant versions of *C. neoformans* defective in sugar capsule formation that are avirulent. Our lab has focused on characterizing the growth rate of *C. neoformans* wild-type and capsule-deficient mutant strains in hopes of identifying optimal strains for lipid production. We have also begun to isolate lipids from lyophilized batches of yeast, followed by hydrothermal liquefaction, saponification, and esterification to extract and isolate the lipids of the sample to produce the final biodiesel product. Our results indicate that certain mutations in capsule production can impact the growth rate of the strains and can also impact lipid production, suggesting that an optimized strains of *C. neoformans* can be used as a source of a clean burning, renewable, and carbon neutral biodiesel. (**84**)

DeMelfi, Nickerson*, Sarah Stanski*, Cayla Stiles*, and Lisa Kadlec Wilkes University, Wilkes-Barre, PA 18766. *Characterization of novel Drosophila Egf receptor signaling targets with roles in eggshell structure and morphology*.- Signaling by the *Drosophila* epidermal growth factor receptor (Egfr) plays a critical role in many aspects of development, including oogenesis, embryogenesis, and proper development of wing and eye tissues. For example, during wing development, Egfr signaling helps specify vein tissues, and in the ovary Egfr signaling is known to establish the body axes during oogenesis. Our lab has previously identified potential novel downstream transcriptional targets of the Egf receptor using the *Drosophila* ovary as a model system. Our initial work compared gene expression in fly ovaries where the activity of the Egfr pathway was reduced, normal (wild-type), or constitutively active. We have employed a number of approaches to further investigate the expression, biological function, and mechanism of action of putative genes of interest, focusing primarily on genes of previously unknown function. A small-scale functional screen taking advantage of UAS-RNAi transgenic flies to knock down gene expression, as well as available P-element insertion mutants, was used to investigate the possible functions of a group of our novel Egfr-responsive genes. A number of these genes were observed to play roles in normal eggshell structure and morphogenesis, rather than in patterning. Gene mutant/knockdown phenotypes include decreased chorionic integrity, shortened eggs, and various dorsal appendage malformations, as well as decreased fertility. We are using the CRISPR-Cas9 system to create mutations in some of these "morphogenesis genes." Mutants analyzed so far have for the most part recapitulated our previously observed phenotypes, and in at least one case resulted in the observation of an additional phenotype in our null mutant that was not seen in the original P-element insertion line. We are continuing to evaluate our most recently created CRISPR mutants, and will be using our CRISPR lines for further study and characterization of our genes of interest. (**38**)

Dotta, Austin*, Alex Huynh, Caitlin McNamara, Mercille Nguyen, Johnathan Kratzenmoyer, and Francesca Sagarese V DeSales University, Center Valley, PA 18034.

Avian predation of insects on corn (Zea mays): effects of general herbivore induced plant volatiles and weather conditions.- Avian species were long thought to be anosmic, or at most have a very limited sense of smell. However, recent studies have begun suggesting that odor may play an important role in many areas of avian life, including foraging and navigation. It has been shown that insectivorous birds can interact in a tritrophic fashion with plants and their herbivores by cuing in on herbivore-induced plant volatiles (HIPVs), important signaling compounds released by plants in response to herbivorous damage. This phenomenon has been observed in a number of plant species, including complex HIPV blends in corn (*Zea mays*). However, simpler single-compound HIPVs have also been shown to be attractive to birds in other host plant species. Here we test if two single-compound general HIPVs, methyl jasmonate and methyl salicylate, attract avian predators to insect prey on corn plants using clay caterpillar models. We observed appreciable levels of bird attacks on our models across 10 experimental sites. However, we did not observe any difference between HIPV and control treatments. Interestingly, we did find that several weather variables, including wind speed and temperature, were significant or near significant predictors of avian predation activity respectively. Together with previous studies, our results add to a nuanced picture of how birds may be using HIPVs to locate insect prey. Additionally, we discuss the potential for birds to act as a natural form of biocontrol in agricultural settings and discuss this possibility in terms of physical location and weather effects (**88**)

Dougherty, Alice*, Eric Snyder, Vaughn Shirey, and Stephen C. Mason, Jr. Immaculata University, Immaculata, PA 19345. *Digitizing the lost biological collections at Hog Island Audubon Camp, Maine*.- Anthropogenic climate change, pollution, and habitat loss are leading drivers of global extinction rates. Due to this, we may not even be aware of the biological complexities of the natural world we are losing. These complexities can often be found, and sometimes can *only* be found, with collected specimens. Thus, digitizing research collections is the most effective method to better understand historic and current species distributions before they disappear. However, only 30% of the US's natural history collections have been digitized. National Audubon Society's Hog Island, located in Bremen, Maine, possesses a valuable research and teaching collection that houses over 600 biological specimens that have not been previously digitized. We spent two weeks on Hog Island to capture each specimen's occurrence data (i.e., date and locality information) with the goal of uploading these data to the Global Biodiversity Information Facility (GBIF). We found their biological research collection contains a total of 623 specimens: 294 vertebrates, 126 plants, 102 fungi, and 51 insects, represented by approximately 352 species. The majority of specimens were collected in Maine and Michigan, USA, with some specimens collected from Canada. Most specimens (32%) were collected between 1960-69 with the earliest specimens collected in the 1800s, which consisted of 5 different warbler species. Eventually, these data will be uploaded to GBIF for data scientists to use to test macro and micro scale hypotheses. We plan to go back to Hog Island and capture more meta-data information (e.g., bird wing length) that will further increase the amount of biological data that will be freely accessible. (**92**)

Flint, Evan*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *The underappreciated role of biotic factors in controlling potentially harmful algal blooms in the Hudson-Raritan Bay*.- Despite widespread distribution of harmful algal blooms (HABs) and new and improved methods for detecting and quantifying them, no unifying ecological explanation has been found. Improved understanding depends upon local, ecological studies that include analysis of phytoplankton species data in relation to both abiotic and biotic parameters. Ecological network analysis was used to detect co-occurrence patterns among abiotic and biotic parameters in a long-term monitoring dataset (i.e., 2010-2021) from the eutrophic Hudson-Raritan Estuary (HRE) between the states of New York and New Jersey. The regular co-occurrence of potentially harmful bloom-forming species with companion species observed through microscopy was supported by the results of ecological network analysis, which showed that there were far more associations between HAB species and biotic parameters (~95%) than abiotic parameters (~5%). Temperature was the environmental variable that was most associated with HAB species throughout the estuary. The numerous network associations of HAB species with one another and with diatoms, dinoflagellates, and zooplankton highlight the complexity of planktonic food webs and interactions. Results also suggest that some taxa may play a central role in structuring the HRE plankton communities. These findings demonstrate that biotic associations play an underappreciated role in plankton structure and the value of examining the ecology of HAB species within the breadth of their biological communities. While network analysis does not fully explain and confirm complex associations among species, it does provide fresh insights and testable hypotheses to strengthen understanding and improve prediction. Although this method is excellent for understanding large volumes of data, its foundation is correlative analysis which tells us little about the nature of the relationship between variables. The next step will be to use random forest analysis to better understand bloom dynamics of *Heterosigma akashiwo*, the species that blooms most frequently in this system. (**1**)

Flores, Maria*, Kaitlyn Strocio*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Gamma proteobacteria are the dominant culturable endophytes in the stems and flowers of the ghost plant, Monotropa uniflora*.- *Monotropa uniflora*, commonly referred to as the ghost plant or Indian pipe is an albino, parasitic plant that feeds on the roots of mycorrhizal fungi colonizing the roots of trees such as the American beech. These plants are ephemeral with short life cycles and typically survive summer months. In order to explore the inner lives of these mysterious plants, we collected their stems and flowers, surface-sterilized them and isolated endophytic bacteria using serial dilution plating. We identified eleven distinct bacterial isolates, mostly belonging to the class Gamma Proteobacteria including several species of fluorescent *Pseudomonas*, *Rouxiella rahnella*, and *Ewingella* species. Interestingly, nearly all isolates were nitrate-reducing and glucose-fermenting and not surprisingly, the flower isolates had distinct metabolic preferences including sugar metabolism, compared to the stem isolates. Given that non-photosynthetic plants like *Monotropa* rely on parasitism for survival, they may possibly rely on microbial partners for vital metabolic services. This study provides a window into the unexplored world of microbial inhabitants of parasitic plants. (**106**)

Foriska, Isabella*, Collin Olson, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Cactus roots harbor an endophytic growth promoting Pseudomonas species*.- The prickly pear cactus, *Opuntia* sp., is a xerophytic desert plant which is distributed in various parts of the United States. Previous studies of the *Opuntia* rhizosphere revealed that the roots were colonized primarily by fungi, with few bacteria being present. In this study, we isolated below-ground microbiota of an Eastern Prickly Pear cactus found in the wild using serial dilution plating and identified them using 16S rRNA sequencing. Of the sixteen culturable bacterial isolates, we found that the four endophytes were exclusively gram negative, with a fluorescent *Pseudomonas* sp. (strain IF1) found as most abundant. The rhizosphere immediately surrounding the roots were colonized by a higher diversity of bacteria, with most of them being gram negative. The bacteria in the surrounding sand were mostly gram positive, including *Bacillus* sp. These results indicate that the cactus roots actively select and colonize specific taxa of bacteria. The bacteria in the three environments were found to be biochemically distinct. Inclusion of the *Pseudomonas* strain IF1 dramatically improved the growth of two different cacti species based on the number of *de novo* padlet sprouts. Thus, wild cacti and endophytic *Pseudomonas* could benefit from a mutualistic interaction. (**78**)

Franges, Jared*, Alexis Armstrong*, Morgan Thomas, Christopher Stobart, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Baicalin shows antiviral activity in against HCoV-OC43 and HCoV-HKU1 nsp5 protease*.- To date, there are seven known human coronaviruses (HCoVs) that cause disease. HCoV-HKU1, HCoV-OC43, HCoV-NL63, and HCoV-229E each cause the common cold. In the past twenty years, SARS-CoV 1, MERS-CoV, and SARS-CoV 2 have emerged into the human population and can cause severe lower respiratory symptoms and death. Treatments for these emerging viruses have been very limited until recently with the arrival of the COVID-19 pandemic. One of the drug targets for CoVs is the nsp5 protease (3CLpro, Mpro). It has been shown that components of Traditional Chinese medicine used to treat acute respiratory infections have antiviral activity against the SARS-CoV 2 3CLpro. It has not been tested whether these components have antiviral activity against the human coronaviruses that cause the common cold. In this study, we are testing the antiviral activity of one of these compounds, baicalin on the 3CLpro of HCoV-OC43 and HCoV-HKU1. We used chimeric CoVs that express the nsp5 protease from either HCoV-OC43 or HCoV-HKU1 in place of the mouse hepatitis virus (MHV) nsp5 to test for antiviral activity. Results from this study show that baicalin has antiviral activity against the proteases during cotreatment, but not pre-treatment or post-treatment. Our study combined with previous studies suggest the antiviral activity of baicalin against multiple coronaviruses. (**49**)

Franzone, Katherine*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Analyzing the effect of RPA phosphorylation on genetic and physical interactions with DNA repair proteins in Saccharomyces cerevisiae*.- In 2023, there will be over 1.9 million new cancer cases diagnosed and over 609,000 people may die from cancer-related causes in the United States alone. Current chemotherapeutic cancer treatments are non-specific, resulting in unwanted side effects and decreasing the efficiency of the treatment. Addressing this problem requires a better understanding of the impacts of the DNA repair pathways that are linked to recognizing DNA damage and preventing the accumulation of mutations that lead to cancer. Our project focuses on analyzing the genetic and physical interactions of DNA repair proteins in the baker's yeast, *Saccharomyces cerevisiae*, which has been used extensively as a model for understanding DNA repair pathways in human cells. Specifically, we will be analyzing the impact of phosphorylation of Replication Protein A (RPA)—a highly conserved protein involved in DNA replication and repair in both humans and yeast—on interactions with the yeast helicases *SRS2* and *SGS1*. Our lab has previously generated strains that contain various mutations in the yeast RPA homolog, RFA, along *SGS1* and *SRS2*, and we examined the sensitivity of these yeast strains to DNA damage using spot assays to analyze the survival of yeast on media (YEPD) with various concentrations of the chemotherapeutic agents camptothecin and hydroxyurea. The differences in survival rates of the various strains suggest that there is a genetic interaction between these proteins that is dependent on RPA phosphorylation and the type of DNA damage. We are further exploring how these repair proteins could be working together by creating and using a yeast two hybrid system with these proteins of interest to examine if they are physically interacting. A clearer picture of RPA's role in DNA repair and its interactions with other genes will allow for a better understanding of the underlying causes of cancer and more specific chemotherapeutic drugs. (**71**)

Glenn, Madeline*, Gabrielle Seagreaves*, Joseph Colosi, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Comparison of bacterial species in three diverse Lehigh Valley landscapes*.- The biomass of bacteria on Earth exceeds that of animals. One gram of soil contains an average of 40 million bacteria. Some soil bacteria perform mutualistic functions such as providing nitrogen to plants, while the functions of many bacteria are unknown. The Lehigh Valley is home to diverse landscapes. We hypothesized that different soil environments would host distinct microbiomes. We sampled soil from an ungroomed meadow on the DeSales University campus, a regularly maintained lawn on DeSales University campus, and a Northern hardwood forest next to the Saucon Valley Rail Trail. We extracted genomic DNA from the samples using a commercial kit. We prepared a sequencing library by amplifying the samples' V3 and V4 regions of the 16S rRNA gene, then ligating indices and flow cell adapters for massive parallel sequencing (next generation sequencing). We report here on the comparative microbiomes of a meadow, lawn and woodland within Center Valley, PA. (**96**)

Greenberg, Samantha*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Investigating differentially expressed genes, functional immunobiology differences, and survival in African Americans and European Americans with distinct renal cell carcinoma subtypes*.- Background: Renal cell carcinoma (RCC) is the most common type of kidney cancer (85%). Clear cell RCC (ccRCC) is the most common subtype (80%) and has an increased immune signature. African Americans (AAs) have lower ccRCC survival rates than European Americans (EAs). A gene expression profile distinguishes ccA and ccB (lower survival and more aggressive tumor biology) ccRCC subtypes. AAs exhibit higher ccB frequencies, but this has not been correlated with differences in survival and tumor biology. Checkpoint inhibitor immunotherapy (CII) is a recent FDA approved treatment for RCC, but response is unpredictable and may explain racial survival disparities. Experimental Design: Clinico-demographic and mRNA expression data were downloaded from The Cancer Genome Atlas using Broad GDAC Firehose. Prediction Analysis of Microarray in R was used to classify ccRCC subtypes. GraphPad Prism performed Kaplan-Meier survival analysis. Partek Genomics Suite and cBioPortal were used to find differentially expressed genes (DEGs) among 3 CII genes (*PDCD1*, *CD274*, *CTLA-4*), 554 cancer immunotherapy resistance and response (CIRR) genes, and novel immunobiology genes. CIRR gene expressions were correlated with survival. Gene Set Enrichment Analysis was performed to find enriched immunological pathways. Results: Within ccB patients, AAs showed significantly better 5-year disease-specific survival. In ccA patients, AAs had lower median expression of *CD274*, but higher expression of *PDCD1* and *CTLA-4*. ccB patients showed reverse trends. Six and 15 DE CIRR genes were found by race between ccA and ccB patients, respectively. Six of these 21 DEGs were significantly correlated with survival differences. 138 novel DE immunobiology genes were found within ccA patients by race, including *LAMA5*, and 172 in ccB patients, including *GPNMB*. Different immunological pathways were significantly enriched by race within subtypes. Conclusion: ccRCC subtype, race, and immunobiology gene expression should be used in combination as prognostic risk factors and to drive new precise treatment options. (**75**)

Guillen-Hernandez, Nicholas*, and Matthew Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *In vivo silencing of SWRI and NuA4 complex members in embryo and larval stages of Drosophila melanogaster*.- The developmental life cycle is maintained through gene regulation and is crucial to the survival of an organism. Throughout the stages of life, histone modifying complexes can regulate multiple genes at critical timepoints. The purpose of this project is to take members of the SWRI and NuA4 histone modifying complexes and silence their expression in *Drosophila melanogaster* some members of these complexes are identical where others are found exclusively in only one complex. To achieve silencing, expression was targeted using RNAi knockdown controlled the Gal4-UAS system under a ubiquitous expressed promoter. Control of the induction was activated by a temperature sensitive Gal80 repressor that is active at 18℃ and inactive at 25℃. Therefore, we can keep the RNAi system off at 18℃ and turn it on at 25℃. We observed lethal timepoints appear to occur at two distinct stages, one in the embryo and one in the larval stage. However, depending on the gene silenced, we see instances of earlier lethality in some samples indicating when regulation is critical for each complex. Preliminary data suggest that members of one complex may be needed for progression through the embryo stage, while another complex is responsible for progression in the larvae stage. Furthermore, these findings are important because they give insight into how the important role of the individual members of each histone modifying complex function. In addition, some of these members have been linked to important diseases in humans. (**27**)

Harlow, Gracie*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Stream chemistry and New Zealand mud snail density and reproduction*.- New Zealand mud snails (NZMS), *Potamopyrgus antipodarum*, are a highly invasive aquatic gastropod that have become established in multiple drainages in Pennsylvania. While data exists on physical and chemical factors that influence their abundance, few studies have focused on NZMS in the Eastern US. This study measured the pH, conductivity, the concentrations of magnesium and calcium ions, and nutrient runoff in the Spring Creek watershed in Centre County PA in May and July of 2022 and related those variables to NZMS density and reproduction. To conduct the research, water samples were taken from Spring Creek and its tributaries at five sites and tested using LaMotte water testing kits, a LaMotte SMART colorimeter, and Vernier electrodes. NZMS density and reproductive effort in the form of proportion of snails brooding and average brood size were recorded. Preliminary results show significant positive correlations between NZMS density and concentrations of nitrate and calcium in Spring Creek. These results are consistent with the expectations that calcium can be a limiting nutrient for mollusks and nitrogen can influence algal growth which is a primary food source. Relationships between other variables and density did not yield consistent trends. (**93**)

Hart, Joel*, Abigail Casey, and David Foster Messiah University, Mechanicsburg, PA 17055. *Exploration of antibiotic mechanism for Berberis spp. extracts and berberine*.- Antibiotic resistance is a major concern for medicine today because bacteria are becoming increasingly immune to antimicrobial agents. This study seeks to address the growing need for novel antibiotic mechanisms to counter drug resistance through the utilization of plant extracts with antibiotic potential. *Berberis bealei* and *B. thunbergi* were the subjects of study because of the berberine content within the genus. Berberine has been identified as the primary active component of these plants, which have been used in traditional Chinese medicine. Stem and root materials were ground into shavings or powder, and extractions were performed with either ethanol, glass-distilled water, or methanol. The extracted plant solutions were then placed onto agar plates coated with a clinical strain of *E. coli* and the zones of inhibition were measured. High-performance liquid chromatography (HPLC) was conducted on *B. bealei* extracts to determine the dry mass percentage of berberine present in the plant, when compared to standard of pure berberine. The effectiveness of extracts on clinically sourced *E. coli*. and the berberine content of the extracts were evaluated. Moving forward the *Berberis* plant extracts will be tested on *E. coli* that have been transformed to be resistant to streptomycin, gentamicin, and ampicillin. (**100**)

Henry, Caitlyn*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Forskolin-mediated cAMP activation upregulates AKAP95 and TNF-α expression despite NF-κB downregulation in LPS-treated Schwann cells*.- Schwann cells have been found to play a critical role in the inflammatory response to nerve injury and neurodegenerative disease. During nerve injury, Schwann cells secrete tumor necrosis factor alpha (TNF-α) and other inflammatory cytokines through nuclear factor kappa B (NF-κB)-dependent mechanisms. This recruits immune cells to the lesion site so that myelin debris can be cleared. After that, Schwann cells acquire a proliferative phenotype via neuronal mitogens and an unknown molecule that activates the cAMP pathway. Although cAMP is known to suppress inflammation through A kinase-anchoring protein 95 (AKAP95)-mediated inhibition of the NF-κB pathway, not much is known regarding the exact mechanism by which it does so. Cells can be treated with lipopolysaccharide (LPS), a bacterial endotoxin, and forskolin, an artificial plant extract, to activate the NF-κB and cAMP pathways, respectively. It was hypothesized that cells treated with LPS and forskolin would express less NF-κB and TNF-α and more AKAP95 than cells treated with LPS only. Immortalized rat RT4-D6P2T cells were treated with different doses of LPS, with or without 2 µM of forskolin, for three hours. Immunoblotting followed by densitometry (expressed as percent control ± SEM) revealed that cells treated with forskolin and 0.1, 1, or 10 µg/mL of LPS had downregulated NF-κB expression (85 ± 30.2%, 78 ± 7.9%, and 63 ± 19.9%, respectively) but upregulated TNF-α expression (188 ± 99.1%, 130 ± 8.1%, and 177 ± 30.0%, respectively) compared to the control. It was also found that cells treated with forskolin and 1 µg/mL of LPS had upregulated AKAP95 expression (212%) compared to the control. These findings suggest that TNF-α expression in LPS-treated Schwann cells may be upregulated due to cAMP-AKAP95-dependent, rather than NF-κB-dependent, mechanisms. Therefore, a better understanding of these pathways may reveal a novel therapeutic target for the treatment of nerve injury and inflammation. (**48**)

Hill, Kara*, Sydnie Rager, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Psychrophilic and chitinolytic fluorescent Pseudomonas species are endomycic inhabitants of a clavarioid coral mushroom*.- Fungi and bacteria are exceptionally diverse groups of microbes but virtually nothing is known about the microbes colonizing the common clavarioid coral fungi. We retrieved a coral mushroom from the Allegheny National Forest in Pennsylvania and isolated three strains of bacteria from inside the fungus using serial dilution plating. Using 16S ribosomal RNA sequencing, we identified these bacteria as two distinct *Pseudomonas* species, belonging to the phylum Proteobacteria, as well as *Chryseobacterium*, belonging to Bacteroidetes. Gram staining ascertained the identity of the three bacteria as gram negative rods. Biochemical tests revealed that all the three strains contained proteolytic enzymes (gelatinase, caseinase) and were able to utilize citric acid as an organic nutrient and all preferred lower temperatures for growth. Both the *Pseudomonas* species were genetically distinct, but biochemically identical in all aspects tested. Both *Pseudomonas* strains were fluorescent and were capable of solubilizing complex phosphate. The *Chrysobacterium* could not utilize any of the nine sugars tested and the *Pseudomonas* strains had very limited sugar preference, surprisingly only oxidizing glucose. Intriguingly, only the *Chryseobacterium* was able to digest starch, and only the *Pseudomonas* species were able to digest glucose, the breakdown product of starch, suggesting a possible mutualistic interaction between the bacteria. Intriguingly, both Pseudomonas species were psychrophilic with one of them growing at temperatures as low as -2°C. Finally, one of the *Pseudomonas* species was found to be chitinolytic suggesting the potential to digest the chitin cell wall of the mushroom. Taken together, these results lead to a working hypothesis that the bacteria colonizing the fungus may be commensal in nature with the capacity to becoming opportunistic pathogens towards the end of the mushroom life cycle. (**8**)

Hoitt, Julianna*, and Daniel Strombom Lafayette College, Easton, PA 18042. *Identifying critical thresholds for crown of thorns starfish concentration in reefs*.- Since 1962, the Crown of Thorns Starfish species, *Acanthaster solaris*, has been observed to be overpopulated in certain regions of the Great Barrier Reef, so much so these regions of coral reefs were in danger. Before overpopulation, crown of thorns starfish species peacefully coexisted in the Great Barrier Reef region of Queensland, Australia. With only a few starfish per hectare, they feed on fast growing coral which maintains their growth. This allows slow-growing corals to have room to expand. But there can quickly be too many starfish. Official outbreak status is approximately 15 starfish per hectare, and at this point they have the potential to destroy 90% of the reef cover. This is damaging to the entire ecosystem because of the importance of coral reefs. Though this has been occurring for years, scientists have struggled to determine exact growth rates of the starfish populations and the reasoning for outbreaks remains undetermined. Using mathematical optimization, the population size that should be monitored the closest was determined. A classic optimization model was used to determine the most volatile number by identifying an equation that models the consumption of fast-growing coral and another that models consumption of slow-growing corals. Combining these two equations by subtracting the slow-growing coral consumption from fast-growing corals, we get the optimization equation that models the general well-being of the reef. When this optimization equation is analyzed, we found that approximately six crown of thorns starfish is the most volatile amount per hectare, and this is where focus should be. This result may allow conservationists to allocate resources most effectively to save reefs from further destruction. It will shift focus from areas of the reef that are beyond salvation; where assistance will only lead to short term help, to reefs that can be saved in the long run. (**2**)

Horne, David* Gannon University, Erie, PA 16541. *Erie's total solar eclipse 2024: education and engagement in the shadow of the moon*.- A total solar eclipse will occur in Erie, PA on April 8th 2024 at 3:16PM, the city of Erie will not bear witness to another until 2099. On April 8th the people of Erie and the surrounding area will see the sun obscured during a totality of 3 min 42s. A total solar eclipse is an awe inspiring event that everyone should witness in their lifetime and accordingly garners a great deal of attention from people of all ages and walks of life. As educators we need to be prepared to answer a great deal of questions from both students and the public alike. In this age of freely available information we need to be ready to combat the enormous amount of misinformation that will be circulating. As coordinator of Gannon University's eclipse outreach efforts, I will present our plan to engage local schools and other institutions and our plan to provide information and resources on how to observe the total eclipse safely and enjoyably. I will also discuss methods of informing and educating students and the local community on the science and observing methods associated with a total eclipse. I will also address how we intend to involve Gannon students in our outreach program and the pivotal role they will play in disseminating information to their peers, area schools and the community at large. (**16**)

Horne, David*, and Lily Zheng Gannon University, Erie, PA 16541. *Flat physics in the laboratory: generation and study of flow patterns in a 2-D Soap Film*.- The behavior of vortices and turbulence in a Two-Dimensional flowing fluid have been a subject of a great deal of practical and theoretical study in physics, behaviors which heavily influence the fields of oceanography and meteorology. Two-Dimensional fluids behave differently to 3-D fluids as the energy in a 2-D vortex becomes heavily affected by a fluid's viscosity and rate of heat dissipation. Vortex patterns in two-Dimensions undergo what are termed 'Inverse energy cascades' in which turbulence features progress from small to large scales. These effects are difficult to generate and observe without the very specific conditions designed to produce 2-D flowing films. The Gannon University Fluid Dynamics laboratory has designed and constructed a machine capable of generating such flowing 2-D films. This equipment produces stable and highly resilient soap films which can run for durations of many hours at a variety of flow rates, allowing for study of 2-D flow patterns and vortices in real time. By introducing custom 3-D printed obstructions to a flowing film our apparatus can generate a variety of wake patterns of differing size and morphology. We then use high frame rate photography and video recorded at visual and 546.1nm wavelengths to capture the behavior of vortices and their interaction with obstructions and other vortices. Images and video are analyzed using custom IDL programs to quantify shape, size and patterns of vortices within the film. This data is used to create predictive models of 2-D turbulence. We present new results of 2-D flow patterns and vortices generated in flowing soap films from our laboratory apparatus. We will show vortex interactions in 2-D and the effects of obstructions placed in the film using high resolution imagery. We also discuss our efforts to create computational models of these effects based on our image analysis. (**66**)

Jaber, Khoula *, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Testing the model: exploration of a predictive mathematical model for antibiotic resistance in bacteria*.- Antibiotic resistance has been a growing public health crisis made evident by the emergence of antibiotic resistant strains in clinical cases and environmental isolates. Overuse of antibiotics and their persistence in the environment provide a constant selective pressure that encourages the growth or resistant strains. The degree to which extended exposure leads to sustained resistance against antibiotics is a question that can be explored via mathematical modeling. Many models have been developed to predict the resistance emergence, specifically utilizing derivative models over time to represent the rate of emergence of resistant isolates. The purpose of this project was to test the predictive power of published mathematical models by Ibargüen-Mondragon et. al, 2014. by simulating environmental exposure of a type-strain of *Escherichia coli* to the antimicrobial, triclosan. Using a 96-well plate design, we selected random individuals in a larger population of growth and monitored their growth in the presence and absence of triclosan. After confirming the predictive capabilities of the model, we broadened the scope of the study to explore both Gram positive and Gram negative bacterial species and additional antibiotics. The ultimate goal of this project is to attain realistic modeling procedures using power series functions to depict change more accurately in bacterial growth over time. (**107**)

Jaber, Khoula*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Enterobacteriaceae species and antibiotic resistance: enhanced expression of efflux pump genes*.- The emergence of antibiotic resistant bacterial strains has been driven by antibiotic overuse worldwide and is a growing concern in clinical settings where the primary goal is to reduce infection. Derived resistance occurs through random mutations in the bacteria genomes that subsequently alter antibiotic binding sites on target proteins and/or change influx and efflux regulation in cells. Triclosan is an antimicrobial that was commonly used in over-the-counter products (e. g hand soaps, hand sanitizers, and toothpaste) prior to its FDA ban in 2017. Research has demonstrated that since its initial use in the 1970's, triclosan has been accumulating in the environment due to its non-biodegradable nature; thus, there is a concern regarding these reservoirs serving as constant selective pools for antibiotic resistance. A previously noted mutation involved in triclosan resistance is the FabI G93V/S mutation, which alters the triclosan binding site on the FabI reductase enzyme in lipid biosynthesis. However, varying levels of resistance in these bacteria strains indicate additional means for bacterial survival. This project investigates overexpression of the AcrAB-TolC multi-drug efflux pimp as a mechanism for resistance sources in two Enterobacteriaceae species, *Escherichia coli* and *Enterobacter cloacae*. RT-qPCR data revealed that over expression of both the *acrA* and *acrB* genes occurred in both completely resistant and partially resistant triclosan strains of *En. cloacae*. Overexpression of these genes seems to be constitutive as the introduction of triclosan to cultures prior to RNA isolation did not lead to enhanced gene overexpression when compared to cultures grown in its absence. Further research aims to explore overexpression of the AcrAB operon from plasmids introduced in *E. coli* and to determine whether over expression of the efflux pump components is sufficient to impact resistance to triclosan. (**52**)

Jahraus, Tyler*, and David Foster Messiah University, Mechanicsburg, PA 17055. *Tissue culture propagation of Virginia bluebells, <u>Mertensia virginica</u>*.- *Mertensia virginica*, more commonly known as Virginia bluebells, is a spring ephemeral plant in the Boraginaceae family with bell-shaped, sky-blue flowers native to eastern North America. As of yet, it has resisted almost all attempts to initiate in tissue culture. To rectify this, we are using novel hormone combinations of various synthetic auxins and cytokinins at various levels as well as experimenting with etiolated leaf tissue. Plants were obtained from Spring Haven Perennials and planted outdoors spring 2021. In Fall 2022 the source plants were moved into a Percival Environmental Chamber and cold stratified in potting media at 4ºC until they began emerging late Winter 2023. Etiolated leaf tissue was harvested, sterilized using 10% bleach and Tween-20 for three (3) minutes and introduced to MS salts plus micronutrients culture media with synthetic auxin indole-3-butyric acid (IBA) at 1 and 2.6 ppm both of which induced substantial rooting and callus formation. Additional samples were cultured with 1 ppm synthetic auxin thidiazuron (TDZ) and the synthetic cytokinin 2,4-dichlorophenoxyacetic acid (2-4-D) as well as a 1 ppm TDZ and IBA combination, neither of which has initiated rooting. Since IBA alone was successful, the next step is to initiate rooting with IBA before transferring to a separate cytokinin-rich media to initiate shoot growth. (**57**)

Jahraus, Tyler*, and David Foster Messiah University, Mechanicsburg, PA 17055. *Aquaponics for education and research using a novel biodigester employing terrestrial earthworms <u>Eisenia fetida</u> in water*.- Vertical farming, controlled environment agriculture, hydroponics, and aquaculture are fast emerging areas of food production due to their gains in productivity per unit energy invested over conventional agriculture and fishing. However, a great need exists for those who can manage such systems and minimize waste within them. Herein I detail a novel aerobic biodigester employing terrestrial earthworms (*Eisenia fetida*) continuously immersed in water. I give examples of the use of this biodigester in various educational, research, and production systems from elementary school through university in the United States as well as other countries in cooperation with Intag corperation. Specific details of nutrient use efficiency and waste conversion/reduction as well as increased growth rates will are provided for various crops including leafy greens, tomatoes, bananas and woody plants including cocoa. (**4**)

Jerome, Evan*, Michael Shin, and Erik Lindquist Messiah University, Mechanicsburg, PA 17055. *Testing for the presence of Batrachochytrium dendrobatidis and B. salamandrivorans in a local population of Eurycea longicauda*.- Amphibian species around the world are threatened by the fungal disease chytridiomycosis, which is caused by two closely related fungi, *B. dendrobatidis* (*Bd*) and *B. salamandrivorans* (*Bsal*). Due to its infectious and deadly nature, chytridiomycosis is known as the most devastating disease to infect vertebrates in recorded history. *Bd* is the fungus, of the two that cause chytridiomycosis, that is more widespread, in every continent amphibians are found in, and the bigger problem currently. *Bsal* is the fungus that is newer and has not dispersed as far, as it has not made it to continents like North America yet. While *Bd* continues to be the more widespread fungus, making the continued monitoring of *Bd* important, the main concern currently is *Bsal*, partly due to the threat of *Bsal* making it to North America. One of the reasons the concern is so high for *Bsal* making it to North America is because North America holds some of the biggest hotspots of salamanders in the world. This study aims to test a local population of *Eurycea longicauda* (long-tailed salamander), a salamander native to Eastern North America. The salamanders will be specifically tested for the presence of *Bd* and *Bsal* to assess what threats face local salamander populations, and to continue to help the monitoring of *Bd* and *Bsal* worldwide. In the fall of 2022, 28 salamanders were sampled from Messiah Universities campus and swabbed for both *Bd* and *Bsal*. The swabs were placed in vials with ethanol and stored in a refrigerator until DNA extraction and qPCR can be performed in the spring of 2023. (**5**)

Jones, Sydney*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Comparative study of genetic mutations observed in independently isolated triclosan-resistant strains of Cronobacter muytjensii*.- Antibiotic resistance is a growing concern for infectious disease treatment in clinical settings. The bacterium, *Cronobacter muytjensii,* is responsible for meningitis, enterocolitis, and bloodstream infections in newborns and infants via contaminated formula. Previous work in our lab demonstrated that triclosan exposure selects for bacteria with resistance to this antimicrobial and concurrently decreases the effectiveness of antibiotics used in other disease treatments. Even though the United States has now banned the use of triclosan in consumer products (e.g., soaps, toothpastes, and plastics), other countries lack such regulation. This continued use of triclosan combined with the ability of triclosan to persist in the environment, makes the compound a constant threat for acquired antibiotic resistance in the medical field. In this study, whole-genome sequencing was used to identify four point mutations and one deletion in a triclosan resistant strain of *Cronobacter muytjensii*. These genomic changes were further explored in other independently isolated triclosan-resistant strains using a PCR-based RFLP method to identify common routes of antibiotic resistance. Further characterization of these mutations will use gene cloning and mutagenesis for the overexpression of each of these alterations in *Escherichia coli* to better understand how each individual change contributes to overall antibiotic resistance. (**20**)

Joyce, Isabella*, and Austen Barnett DeSales University, Center Valley, PA 18034. *Interrogating the role of retinal determination genes in the eyeless arachnid, Archegozetes longisetosus*.- The retinal determination gene network (RDGN) is a network of interacting genes collectively utilized for specification of eyes in arthropods. A recent genome sequence of the tropical soil-dwelling arachnid, *Archegozetes longisetosus,* revealed that this species retains orthologs of all RDGN genes. This is paradoxical, as these arachnids have secondarily lost their eyes. Additionally, an RNA-Seq analysis revealed that these RDGN genes are expressed during embryonic development. While the roles of RDGN genes in other eyeless arthropods have been previously studied, the role of the RDGN genes in *A. longisetosus* is not well understood. To elucidate the evolutionary pressures maintaining these RDGN genes in the genome of *A. longisetosus*, we performed *in situ* hybridizations targeting its RDGN orthologs throughout embryonic development. Our results suggest novel and alternative roles for these RDGN orthologs, specifically in the formation of the embryonic head and limbs. These results reveal how developmental genes that were previously used in one context can be recruited into other developmental processes, a phenomenon known as developmental co-option. (**15**)

Kelly, Olivia*, Samantha Geci, Natalie Carris, Jillian Sullivan, James Colvin, Athena Martinez, Varvara Liashenko, Emily Misko, and Prasad Dalvi Gannon University, Erie, PA 16541. *The impact of diabetes mellitus pathology and treatment on development of neurological and psychiatric disorders*.- Diabetes mellitus (DM) is a chronic condition resulting from insulin deficiency or systemic insulin resistance. In this disorder, either the pancreatic β-cells are unable to produce enough insulin, or the secreted insulin is ineffective to overcome the peripheral or central insulin resistance. Over time, glucose metabolism becomes dysregulated resulting in overt DM that is characterized by hyperglycemia and chronic systemic inflammation. This research review discussed the connections and possible correlations between DM and several different psychiatric and neurological diseases, including Parkinson's disease (PD), major depressive disorder (MDD), and Alzheimer's disease (AD). Disease severity in patients, similarities in pathophysiology, and common therapeutics in these disease conditions have been discussed. Specifically, the effects of a common hallmark pathology, systemic inflammation, is under focus as a potential underlying cause of each of these diseases; treatment for the resulting inflammation has also been discussed as a contributor to developing pathologies. Review of biological pathways and molecular events associated with these diseases allow for further investigation into developing a connection between each of these conditions. While no claims of causation can be made, DM does show significant correlations and associations with other diseases such as PD, MDD, and AD. Each of these conditions show some overlapping risk factors, biological pathways, mechanisms, and therapeutic approaches with DM. Interestingly, depending on the factor, DM can influence progression of these psychiatric and neurological disorders, and vice versa, these psychiatric and neurological disorders can also affect DM development. (**22**)

Kelshaw, Charles*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Establishing baseline conditions prior to dam removal in Bushkill Creek, PA*.- The proposed removal of four small dams in Easton, PA along the Bushkill Creek, a tributary of the Delaware River, has provided a valuable opportunity for baseline monitoring and establishment of reference conditions using historical information. One important principle in ecological restoration practice is to develop reference models for planning and communicating a shared vision of project targets. Given that we are in the site assessment phase of the Bushkill Creek restoration project, the objective of this research was to build a long-term (2009-2023) pre-removal monitoring dataset for water quality, macroinvertebrates, freshwater mussels, and fish. Monthly monitoring data were collected from sites approximately 35 m upstream and downstream of dams and free-flowing reference sites located approximately 5 km upstream of all dams. Dissolved oxygen concentrations and macroinvertebrate biodiversity are significantly reduced at sites upstream and downstream of dams relative to reference locations. Although multiple areas along the Bushkill Creek were deemed appropriate habitat for mussels based on substrate and flow conditions, no mussels were detected in Bushkill Creek using timed surveys (i.e., a total of ~50 person-hours). This finding is not surprising given that mussels attach their larvae to fish hosts to complete their reproductive cycle and that Bushkill Creek has 7 consecutive dams, which act as physical obstacles restricting the dispersal and distribution of fish hosts. Bushkill Creek is historically high in fish species richness, which include many native species such as Eastern Brook Trout (*Salvelinus fontinalis*) and Slimy Sculpin (*Cottus cognatus*). These native fish have been almost entirely replaced by stocked exotic game fish that can survive in fragmented areas such as the Brown Trout (*Salmo trutta*) and Rainbow Trout (*Oncorhynchus mykiss*). These data imply that removal of the dams would lead to improvements in water quality, biotic integrity, and resilience in lower Bushkill Creek. (**77**)

Kent, Tristan*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *circRNA expression in differentiating SH-SY5Y cells*.- Circular RNAs (circRNAs) are a recently discovered form of genetic material whose roles in cellular function, development, and differentiation are still undergoing investigation. CircRNAs have a cyclic structure, are very stable, are often found in high quantities, and can regulate gene expression by acting as a microRNA sponge or by disrupting the process of RNA binding proteins. Circular RNAs are known to have various functional roles, including in a variety of cancers. One human cancer cell line in which the roles of circRNA are largely unknown is the SH-SY5Y cell line, which is derived from human neuroblastoma and can be differentiated into neuron-like cells through treatment with retinoic acid. The purpose of this study was to quantify and compare levels of several circular RNAs, including circFAT3, in differentiated and undifferentiated SH-SY5Y cells, using NEFM (neurofilament) as a positive control. The obtained results from quantitative PCR (qPCR) showed that NEFM was highly expressed in retinoic acid treated SH-SY5Y cells, while circFAT3 was downregulated along with its host mRNA. This supports a proposed role for circFat3 in regulating cellular proliferation, but runs counter to previous data suggesting that circFat3 may be upregulated during neuronal differentiation. (**19**)

Kimmel, Peyton*, Caitlyn Henry, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Creatine upregulates the expression of anchoring proteins and creatine kinase in S16 Schwann cells*.- Neuronal development and regeneration after injury in the peripheral nervous system is coordinated by Schwann cells, whose signaling networks are dependent on ATP. Creatine is a component of high-energy phosphate storage involved in regulating cellular ATP. Although the role of creatine is established in the muscular system, not much is known about its effects on Schwann cells. Schwann cell proliferation is facilitated in vitro by the addition of heregulin (H), a neuronal mitogen and forskolin (F), an activator of the cyclic AMP/protein kinase A (PKA) pathway. Anchoring of PKA in the cell is accomplished by A-Kinase anchoring proteins (AKAPs), that scaffold signaling complexes. Preliminary studies have shown that incubation of Schwann cells with creatine at a concentration of 2μM, and 20μM stimulated significant proliferation. Based on these findings, it was hypothesized, that treating Schwann cells with creatine and forskolin will up-regulate the expression of AKAPs, creatine kinase (CRK) and cyclin D3. Immortalized S16 Schwann cells were treated with no mitogens (control, N2), H (12.5ng/mL), F (2μM), H+F and creatine at 2 and 20 μM concentration, for various time points. Densitometry results from Western blots reveal that cells treated with 2μM creatine and F for 6 hours expressed a robust increase in AKAP 149 (214.3%) and CRK (716.9%) with a moderate change in AKAP95 (98.04%) and cyclin D3 (83.43%) when compared to other conditions. However, addition of 20 μM creatine with F elicited a synergistic response in the expression of both AKAP149 (278.29%) and CRK (5448.7%) when compared to unstimulated cells (H: 30.67%, H+F: 71.77%). Concomitantly, addition of F and 20 μM creatine also changed the expression of AKAP95 (101.08%) and cyclin D3 (115.38%).These results suggest that creatine augments the expression of AKAP 149 and CRK expression while simultaneously influencing AKAP95 and cyclin D3 proteins to orchestrate Schwann cell growth. (**13**)

Krall, Colleen*, Sheana Ramcharan*, Michael Foulk, Jack Williams, and Luis Cabo-Perez Mercyhurst University, Erie, PA 16546. *Changes in microbial populations and volatile organic compounds in an isolated decomposing tissue sample*.- Estimation of the *postmortem interval* (PMI) constitutes a critical component of forensic criminal investigations. Most current forensic anthropology methods attempt to estimate PMI from visual assessments of broad overall decomposition stages, often based on research examining full bodies at outdoor “body farm” facilities. While valuable, those observational designs do not control for most influencing variables, thus being highly dependent on local environmental conditions and factors. This limitation is further compounded by the scarcity of those facilities, which allow for observation of decomposition at a very limited set of locations and environmental regimes. To address some of these limitations, an increasing number of studies seek to improve and add to these methods by incorporating information on the relationship between macroscopic decomposition changes and those observed on microbiological, geochemical, or biomolecular markers and processes during the decomposition process. We utilize an experimental design based on the analysis of isolated muscle tissue samples in a controlled, hypoxic laboratory environment, to compare the evolution of both the microbial community composition and the VOCs released as decomposition byproducts across time. Aside from additional insight into both the microbial communities and molecular pathways involved in the decomposition process, we discuss some promising avenues and similar potential research designs to explore some related issues, including buried body detection, cadaver dog training, and estimation of PMI. Preliminary findings of this design relate to the quantification and sequencing of DNA from soil samples, as well as to the collection and characterization of VOCs along the decomposition process. (**29**)

Kroznuskie, Alexandra*, Phoenix Marr-Jones*, Kayleigh LeDouaron*, Alexis Armstrong, Morgan Thomas, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Isolation of antibiotics producing bacteria from soil*.- Antibiotic resistance is a major health concern due to misuse or improper use of antibiotics in the past. Many of these antibiotic resistant infections are caused by the ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*). Our study aims to identify novel antibiotics produced by bacteria from soil. Many bacteria in the soil naturally produce antibiotics. We have collected soil samples from several different locations around the Lehigh Valley and isolated bacterial colonies from those soil samples at either 25°C or 30°C to select for nonpathogenic bacteria. Once isolated, we tested the bacterial isolates for antibiotic production using microbes that are closely related to the ESKAPE pathogens. We have found multiple isolates that limit growth of the ESKAPE relatives and are characterizing them. Using ethyl acetate, we extracted the antibiotic as the organic component of the isolates. Ongoing work will determine whether the antibiotics that are produced are novel. (**85**)

Kulp, Noah*, Nicholas Griffith, and Dr. David Osgood Albright College, Reading, PA 19604. *Comparing the effects of multiple disturbances on deer browsing impacts of understory plant communities within Eastern deciduous forests*.- Our study aimed to evaluate impacts of deer over-browsing, in combination with other disturbances, on the forest understory vegetation community. This study was conducted in two different parks near Reading, Pennsylvania, that have different histories of deer management. The parks are also exposed to anthropogenic stressors such as timbering and frequent landscaping, combined with various outdoor recreational activities. The magnitude of these various stressors differs within the park and sampling locations were situated to coincide with this variation allowing us to compare deer browsing stress with other stressors. We used a deer scat survey in both parks to evaluate the frequency of deer visits to each study location, and then different locations within each park. Quadrat sampling (0.25 m2) (n = 12 per site) was used to identify the plant species and percent cover. The composite Floristic Quality Index was then used to assess the understory habitat integrity of each . The differences in the FQI were affected more by species type (non-native or native) than species richness and individual coefficient rankings. in the average FQI value between the disturbed and control locations at Nolde Forest, indicating timbering had relatively low impact on the understory plant community, indicating other disturbances having a greater influence on the FQI. Despite deer grazing activity being different, the understory habitat structure did not statistically differ between the parks. which is likely due to the *variety* of disturbance present within both parks causing differences in the understory vegetation communities of both locations. (**58**)

Kumar, Nidhi *, Jared Franges, Brennan Gerancher, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Cloning and expression of potential innate immune targets of coronavirus nsp5 protease*.- Innate immunity is the first line of defense against viruses. When an RNA virus enters the host cell, it can be detected by RIG-I-like receptors in the host cell cytoplasm. The receptors will then signal to the nucleus to induce antiviral genes. To successfully replicate, viruses must either avoid being detected or block the induction of the antiviral genes. We know that Coronaviruses are detected by the host cell but that the antiviral genes are not induced. One of the ways viruses can evade the detection pathway is use viral proteases to cleave the proteins in the signaling cascade. We use the model coronavirus mouse hepatis virus (MHV) for these studies. We hypothesize that the MHV main protease, nsp5, is cleaving host proteins to block the induction of antiviral genes. We have performed *in silico* protease digests of proteins within these signaling pathways and identified 5 candidate proteins that could be cleaved by MHV nsp5. We have cloned 3 of these genes from mouse cells and tagged them with Flag. This will allow us to easily detect cleavage products. Ongoing work will then determine whether these proteins are cleaved by the virus protease and the outcome of that cleavage on innate immune signaling and virus replication. (**86**)

Lapp, Sean*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Assessing the metastatic potential of a murine pancreatic cancer cell line and the effect of anti-fibrotic* *treatment on disseminated disease*.- The prognosis of pancreatic adenocarcinoma is especially devastating when diagnosed in the metastatic stage, with only 3% of patients surviving 5 years. Its lethality is partly attributed to a densely fibrotic tumor microenvironment that limits chemotherapeutic delivery. It is hypothesized that reducing this fibrosis would increase infiltration of therapies into the tumor and improve efficacy. Proglumide, a CCK receptor antagonist, has been shown to reduce fibrosis in murine primary tumors of pancreatic cancer; however, its effect on metastases is unknown. To test the hypothesis that proglumide will also decrease fibrosis in disseminated disease, a reliably metastatic model is essential. We tested the metastatic potential and primary tumor growth of a newly acquired murine pancreatic cancer cell line, MCB/1, by injecting the cells into syngeneic, immunocompetent C57Bl/6 mice using four different injection routes: orthotopic, intrasplenic, intravenous, and subcutaneous. With high frequency, the mice developed numerous metastases in the liver and lungs following intrasplenic and intravenous injection, respectively. Next, 18 mice underwent intrasplenic injection of MCB/1 and were randomized to either normal or proglumide-treated water for 3-4 weeks. In parallel, orthotopic injections were administered to 7 mice to also confirm the effect of proglumide on primary tumors. Proglumide was associated with no significant change in number of liver metastases or primary tumor mass. Quantification of fibrosis by Masson's trichome staining is ongoing in both primary and metastatic lesions. (**31**)

Large, Ashley*, Reagan O'Donnell*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Using quantitative PCR with high resolution melt analysis for rapid genotyping of brewery yeasts*.- In 2021, 149 billion barrels of beer were brewed in the United States. Beer is made by taking a grain (usually wheat) and putting it through a process of milling, mashing, lautering, boiling, whirlpooling, cooling, fermenting, maturing and filtering. The most popular styles of beer are ales and lagers that differ in their production process and most importantly in the type of yeasts used in the fermentation step of beer production. Ale yeasts (*Saccharomyces cerevisiae*) are top-fermenting yeasts that need warm temperatures during the fermentation process that yield fruity and aromatic beers, while lager yeasts (*Saccharomyces pastorianus*) are cool temperature, bottom-fermenting yeasts that yield crisp and refreshing beers. The difference between these two processes, as well as the incredible variety of lager and ale yeast strains that yield different flavor profiles is an important factor to know for the overall process. Our lab is focused on developing a rapid technique for genotyping beer yeasts during the brewing process. Our technique is based on isolating genomic DNA from various strains of beer yeasts, then using Quantitative PCR (qPCR) to amplify specific Short Tandem Repeated sequences (STRs) from the genome, followed by a High Resolution Melt (HRM) analysis to identify specific genotypic markers associated with individual yeast strains. We have used this technique to genetically characterize a number of commercially available beer yeast strains and have been able to distinguish between lager and ale species, and will show that we are also able to distinguish within different strains of lager or ale yeasts. Developing a rapid test that can differentiate between strains of yeast will greatly help breweries ensure that yeast strains are not mixed or contaminated during the brewing process which may result in beers that contain unpleasant or incorrect flavors. (**35**)

Lasczyck, Raegan*, Gina Natale*, and Valbona Hoxha Lebanon Valley College, Annville, PA 17003. *The effect of Dunc-13 during acute alcohol use post-traumatic brain injury*.- Traumatic brain injury (TBI) refers to a blow or jolt to the head that damages the brain, resulting in impaired function. Several studies have reported that a significant number of individuals with TBI eventually drink alcohol at or above the levels of consumption prior to the injury. However, the brain has been shown to be less tolerant to alcohol after TBI. This increased sensitivity to alcohol means alcohol's effects on neuronal activity and neurotransmitter release may be more severe. This is especially concerning in cases of mild TBI, in which individuals often go about their days as normal. Some research suggests alcohol tolerance may be a result of ethanol binding to the presynaptic protein Mammalian UNC13-1 (Munc-13-1), reducing the neurons' ability to communicate. They also suggest that reducing Dunc13 (a homologue of unc13) in *Drosophila* promotes tolerance to alcohol. In this study, we utilized the fruit flies, *Drosophila melanogaster* to investigate if *dunc13* loss-of-function mutants are still tolerant to alcohol following TBI. After subjecting flies to mild TBI, we exposed them to 80% ethanol and then measured the time to sedation. We also recorded the mortality rate of flies 24 hours after ethanol exposure. Our results indicate that dunc13 flies do not maintain their tolerance to alcohol following a brain injury. Hence, the protective effects of Dunc13 to alcohol dissipate post injury. Our results suggest that TBI may induce ethanol sensitivity through molecular mechanisms which are independent of Dunc13. (**46**)

Lay, Nancy*, Joy Karnas, and Lawrence Quarino Cedar Crest College, Allentown, PA 18104. *Crime scene saliva: distinguishing human vs canine contributors*.- Body fluids, such as saliva, are often found in criminal investigations, and their identification provides crucial context to crime scene reconstruction and can be used to corroborate witness or victim statements. In addition, non-human biological material is forensically relevant due to canine bite-related cases, the transfer of pet or wildlife biological material, and crimes involving animals. In cases involving bitemarks, morphological analysis may not be able to reliably differentiate human from canine bitemarks; thus, methods for saliva identification rely on the detection of amylase, an enzyme involved in digestion. Assays for amylase are typically protein-based and can lead to false negatives when these tests are unable to detect a degraded enzyme. Despite the advantage of DNA being more stable than proteins, no DNA-based method currently exists to differentiate canine saliva from human saliva. *AMY1* and *AMY2* are the genes that code for salivary amylase and pancreatic amylase, respectively. Both gene sequences are found in humans and canines (with an 83% sequence identity) and both species express pancreatic amylase; however, only humans express salivary amylase. This project targeted unique regions of the *AMY1* and *AMY2* gene sequences in order to create a qPCR-based assay to differentiate between canine and human saliva. A multiplex approach took advantage of differences in the amplicon sizes of the PCR products to further enhance the efficiency of this assay. Future research will explore multiple dog breeds and mixed human/canine samples to determine the broad application of this assay to a variety of crime scenes. (**42**)

Lazar, Michael*, Jacquelyn Maddox, and Akeisha Belgrave Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Bioremediation of acid mine drainage using <u>Pleurotus ostreatus</u> (oyster mushroom) mycelium*.- Acid Mine Drainage (AMD) is an unfortunate byproduct of the anthracite mining industry, and a large source of environmental pollution in Pennsylvania. AMD is formed when rocks containing iron(II) sulfide are brought to the surface by mining where upon reaction with water and oxygen form sulfuric acid and dissolves heavy metals such as iron. One of the most common treatments is limestone to neutralize the acidity but does not address the iron content or precipitates. This study investigated an alternative treatment method to reduce iron content in AMD. The capacity of the basidiomycete fungi *Pleurotus ostreatus* (oyster mushroom) to bioabsorb iron and remediate AMD waters was investigated. *P. ostreatus* was cultured in burlap sacks and placed in a stream mesocosm tank with AMD water for 3 weeks. AMD-derived water treated with 100mg dehydrated *P. ostreatus* powder produced a 21.4% reduction in dissolved iron concentration during a 30-minute treatment. Additionally, qualitative testing was performed to determine the ability of *P. ostreatus* to influence biofilm production, a marker in the remediation of polluted waters. Experimental tanks with live mycelium sacks far exceeded the biofilm growth of positive controls. Bioremediation of AMD using *P. ostreatus* mycelium treatment is a novel, cost-effective, and promising approach to reduce the high concentrations of dissolved metals associated with AMD and promote biofilm formation. (**63**)

Lebish, Madison *, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Predator-prey relationships within natural, restored, and created vernal pools*.- The fact that several vernal pool restoration and creation attempts in eastern Pennsylvania and New Jersey have been paired with conservation of natural pools in the same area provided a valuable research opportunity to compare amphibian habitat quality, including predator and prey composition and abundance, between project sites and natural, reference pools. We used a total of five natural, four restored, and six created pools distributed over four sites in eastern Pennsylvania and Warren County, NJ. To measure desired outcomes, we used successful reproduction and metamorphosis of two vernal pool indicator species, the wood frog and spotted salamander. Although many previous studies indicate that restored and created pools rarely replace function lost in the destruction of natural pools, success of vernal pool indicator species was not necessarily related to pool type in this study. Results indicated that pool depth, volume, and hydroperiod were among the best predictors of success, regardless of pool type. Mean predator abundance was eight times higher in pools with longer hydroperiods. We documented a 96% decrease in wood frog survival rates in a semi-permanent, natural pool following a 41% decrease in overhead canopy cover and an increase in green frog abundance. At the same time, wood frog reproductive success increased in nearby restored pools with lower predator abundance. Pools with the highest mean survival rates for the two indicator species combined were short- or long-cycle pools (i.e., hydroperiod of 12-35 weeks) with low predator abundance (i.e., <1 organism L-1) and greater proportions of arthropod prey relative to other food items. (**76**)

Lepouski, Kelly*, Brad Engle, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *Effects of combination treatments of epigenetic inhibitors (belinostat and 5-azacytidine) on human glioblastoma cells*.- Many cancers, including glioblastoma (GB), are difficult to treat, have low survival rates and high recurrence rates, and develop resistance to conventional treatments. Genetic and epigenetic factors play a role in these undesired outcomes. Recent research has identified epigenetic factors, including DNA methylation, histone modification and small noncoding RNAs (miRNAs), that are altered in many cancers. Some of these changes in the cancer epigenome can be reversed with epigenetic inhibitors, such as histone deacetylase inhibitors (HDACi) and DNA methyltransferase inhibitors (DNMTi) leading to new therapeutic approaches. The use of single inhibitors has shown limited clinical success; however, combination therapies have shown more positive results. This study tested the cytotoxicity of belinostat (an HDACi) and 5-azacytidine (a DNMTi) alone and in combination on human glioblastoma cells. Glioblastoma cells were plated in 96-well plates containing 10,000 cells per well, and the % cell viability was determined using an MTT assay. Dose response curves were generated (0 to 10 μM concentrations) using six different treatment conditions: no treatment, media, DMSO, HDACi alone, DNMTi alone, and HDACi and DNMTi combined. Belinostat and 5-azacitidine were both shown to be cytotoxic to GB cells in a dose-dependent manner. Belinostat was more effective than 5-azacitidine. A synergistic effect was also observed when the drugs were used in combination. Combination therapy using both belinostat and 5-azacytidine could represent a promising treatment for glioblastoma in the future. (**73**)

Levri, Joseph*, and Richard Bell Penn State University-Altoona, Altoona, PA 16601. *Production of nano-structured materials for use in hydrogen fuel cells*.- The purpose of this project is to develop a new gas diffusion/catalyst layer for hydrogen fuel cells. Hydrogen and oxygen gases enter different ends of a hydrogen fuel cell. Hydrogen gas enters the anode and passes through the gas diffusion layer to the catalyst where it is split into protons and electrons. Protons permeate through a proton exchange membrane to a second catalyst layer while the electrons pass back through the electrically conductive diffusion layer out of the cell to an external circuit and then back to the cathode side of the fuel cell passing through the diffusion layer on that side. Oxygen enters the cathode side of the fuel cell and diffuses to the catalyst layer. The oxygen molecule splits into individual oxygen atoms and combines with the electrons and protons to produce water, the only emission product. The current gas diffusion layer is composed of porous, conductive carbon cloth in which the platinum catalyst is applied to the surface of the cloth. Replacing the carbon cloth with a structured metal nanowire mesh is expected to improve the efficiency of the fuel cell in two ways: increase the electrical conductivity at lower pressures and prevent the contamination of the catalyst layer by carbon monoxide. To form the desired nano-structured mesh, an aluminum plate is anodized by placing it in a polyprotic acid solution and passing a current through the sample. This process causes a porous aluminum oxide (alumina) structure to form. By varying the purity of the aluminum and changing the acid during the anodization process, various structures can be formed. The porous alumina then serves as a template that is filled with a material(s) of choice using electrodeposition. After deposition the alumina is dissolved leaving behind the metal nano-structure to be used as the diffusion/catalyst layer. (**21**)

Lin, Wei-Jin (Michael)*, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Generation of bacteriophage T4-neutralizing antibodies using monoclonal technology*.- Induction of host antibodies that block infection by binding to pathogen surface structures is a goal of current vaccines. Past Messiah University Microbiology courses included experiences wherein students blocked bacteriophage T4 infection of *Escherichia coli* B cells using polyclonal T4-specific goat antiserum, which is no longer commercially available. We are generating mouse monoclonal T4-neutralizing antibodies to use in course laboratory experiences. Balb/c mice were immunized twice over a two week period with ~ 1.6 – 3.5 x 1010 pfu of T4r+ phage from which endotoxin (lipopolysaccharide) had been depleted by gentle organic extraction. Serum was prepared from blood collected by cheek vein puncture and assessed for T4-neutalizing activity in a 96-well plate scale-screening assay. Briefly, small amounts of T4 (with or without pre-exposure to antibody) and *E. coli* B were combined in each well. Ongoing infection by T4 limited the density of bacterial growth in a well when measured at 6 – 8 hours. The presence of neutralizing antibody prevented infection, instead allowing the bacteria to grow to saturation. Serially diluted serum samples were compared to determine relative neutralizing titers. To produce hybridomas, cryopreserved B-lymphocytes isolated from the spleens of T4-immunized BALB-C mice were fused to P3X63Ag8.653 cells using polyethylene glycol. Hybrids were distributed in 96 well plates and selected in HAT medium. After two weeks, supernatants were tested for T4-neutralization in the plate-based screening assay (which utilized an antibiotic resistant clone of *E. coli* B). The increased optical densities of four wells (1C9, 2F11, 2F12, and 3D9) suggested the presence of hybridomas secreting T4-neutralizing antibodies. These candidates were expanded and retested. Culture supernatants from candidate 2F12 consistently showed inhibition in multiple the screenings. Positive candidates were preserved by freezing (-80°C). A CELLine1000 bioreactor was seeded with cells of candidate 2F12 to produce concentrated monoclonal antibody culture supernatants. (**6**)

Lopez-Soliz, Maurice*, Jordan Mears*, and Bernardo Mesa Cruz Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Preliminary implementation of a multiplex quantitative PCR (qPCR) analysis to detect environmental DNA (eDNA) from chytrid fungus and ranavirus at Michaux State Forest, Pennsylvania*.- Amphibians can experience population decline due to infectious diseases such as chytrid fungus –*Batrachochytrium dendrobatidis* – (Bd) and ranavirus –*Iridoviridae* – (Rv). Environmental DNA (eDNA) techniques, in conjunction with qPCR, detect amphibian species and quantify pathogen DNA in aquatic environments. Our objective was to detect and quantify Bd and Rv eDNA, via a multiplex qPCR analysis, from vernal pools located in the southern end of Michaux State Forest, Pennsylvania. We collected 33 water samples (~500 mL) from 16 pools in the months of April, May, and August (2022). In the lab, we performed vacuum-aided water filtration (409.5 ± 16.5 mL) through a cellulose nitrate membrane (0.2 µm pore size) within 3.5 h of collection. We stored membranes at -80 °C until DNA extraction. We extracted DNA from membranes with the DNeasy PowerSoil® Pro Kit (Qiagen Group) according to manufacturer, except for extended vortexing step (2.5-hour) (Brannelly *et al.* 2019). We used a multiplex qPCR protocol (Standish *et al.* 2018) for DNA quantification of Bd and Rv. Our results indicate a Bd positivity rate of 18.75% (n = 3) in April and 0% for both May and August, whereas Rv displayed 0% in April, 8.3% in May and 20% in August. We observed 647.3 ± 241.5 copies of Bd/dL and 225.5 ± 185.9 copies of Rv/µL. Concentrations of Bd were slightly higher compared to previous results in western Pennsylvania, whereas Rv concentrations were similar or higher than previous findings in other areas. This study is a step forward to refine and broaden biomonitoring approaches for these amphibian diseases, at a landscape scale, in Michaux State Forest. Future efforts should include molecular means (e. g., barcoding) for amphibian species detection to develop a deeper understanding of pathogen/host/disease dynamics in the system. (**3**)

Mamani, Della*, and Steve Ropski Gannon University, Erie, PA 16541. *When a duck nests on your green roof……again!*.- When curious waterfowl discover a green roof, the possibilities are endless and allows ongoing research. Located atop Gannon University's NASH Library and Student Learning Commons is a now 6-year-old green roof. As many know, on May 23rd, 2021, a nesting mallard was discovered during a routine clean out of the plant beds. This mallard was a successful anomaly and would soon be a mother to 6 ducklings and safely removed by researchers and W.I.N. on June 21st. Through video equipment and close observations from the library staff and researchers there was an ability to closely monitor the behaviors of the mallard. While the mallard's subtle but various behaviors were a primary focus, the idea that animals would make use of a green roof as a habitat is significant and not well documented. While at the time we had never seen this before, it occurred again on April 20th, 2022. During the first nesting we were unable to tag the mallard but from gathered photos of the waterfowl's marking, we were able to determine that it was the same mallard as before. This nesting cycle had varying instances including less vocalization, nonresearching individuals walking over the nest, and a different capture method the day after hatching. Even with these different variables, the mallard managed to hatch every egg while during the last cycle only half hatched. This pushes us to research the impact of green roofs even farther and what they mean for the future of waterfowl, animal, plant and human generations. (**61**)

Mason, Jr., Stephen C.*, Vaughn Shirey, Evan S. Waite, Michael R. Gallagher, and Nicholas Skowronkski Immaculata University, Immaculata, PA 19345. *Prescribed fire severity changes ground beetle (Coleoptera: Carabidae) taxonomic and functional community composition*.- Prescribed fire is a conservation management tool that is frequently used to foster biodiversity by attempting to mimic historic wildfire regimes, reduce invasive species, and maintain habitat integrity. Simultaneously, insects that provide essential ecosystem services such as decomposition, nutrient cycling, and pest control, are globally declining. Within the pyroentomology literature there are mixed reports of positive and negative effects that prescribed fires have on insect communities. This is likely due to generalizing prescribed fires and not accounting for fire heterogeneity created by the fire characteristics such as fire severity. To better understand if prescribed fire severity can affect insect communities, we used multispectral reflectance data collected by Sentinel-2 to methodically quantify prescribed fire severity and compared ground beetle (Coleoptera: Carabidae) taxonomic and functional community composition responses between an unburned site and two sites burned with contrasting fire impacts. We found 23 ground beetle species and used 30 morphological, physiological, phenological, and ecological functional traits for each species. We found that our moderate fire severity site had different taxonomic and functional community compositions from both our unburned and high severity site. Surprisingly, we did not find a strong difference in taxonomic or functional ground beetle composition between our unburned and high severity site. Thus, we provide support that prescribed fire severity does affect ground beetle community composition and encourage future pyroentomology studies to account for fire severity which will help guide conservation managers to make more accurate decisions and predictions about prescribed fire effects on biodiversity in our native landscapes. (**67**)

McGarity, Kendall*, and Steven Ropski Gannon University, Erie, PA 16541. *The Yellowstone earthquake of 1959*.- On August 17th, 1959, an earthquake hit near Hebgen Lake in southwest Montana. It is one of the largest earthquakes observed in the United States, and the area surrounding it is still experiencing the effects to this day. The initial earthquake lasted less than 1 minute and triggered a massive landslide that was traveling 100 mph, caused many fault scarps, and damaged roadways. The landslide moved than 80 million tons of rock down into the canyon below, which formed Earthquake Lake. The rocks and debris also covered the popular camping site, Rock Creek campground. The surrounding areas of Hebgen Lake were affected by the earthquake by the lake rising nearly 8 feet (2.4 meters) and caused roads and highways along the shoreline to collapse into the water. In addition to the landslide, a few more effects were cracks and geysers that developed as a result of the earthquake. Although earthquakes can cause extensive damage in the environment, they can also be very important to the hydrothermal systems by helping to remove blockage of minerals in geysers. (**18**)

Mech, Stephen* Albright College, Reading, PA 19604. *Frequency of ticks on Peromyscus variation by year and habitat*.- Ticks are an important vector for several diseases, including Lyme disease. Small mammals serve as an important host for ticks in nature, so monitoring the abundance of ticks on small mammals may provide insights into potential risks to humans. My students and I have been monitoring several populations of white-footed mice

(*Peromyscus leucopus*) in response to habitat management, primarily different timbering regimes, in a small local forest over multiple years. Using these data, I explored the relationship between habitat type and number of ticks on mice across multiple years. My analysis suggests that while there is some variation in number of ticks per mouse in different habitats, there is much more variability in number of ticks per mouse between years. Thus, in this relatively limited area, interannual variation is more important than local habitat variation linked to disturbance. Additionally, the number ticks found on individual mice is correlated with the number of times the mouse is captured but not with the sex of the mouse, suggesting more active mice may be more susceptible to tick infestation. (**68**)

Miller, John*, and Andrew Samuelsen* Albright College, Reading, PA 19604. *Pursuit of understanding the mystery of marcescence in American Beech trees*.- The phenomenon of marcescence occurs across several tree species such as Oak (*Quercus)* and Beech (*Fagus)*, both members of the Fagaceae family. Marcescence is the holding on to leaves throughout the winter instead of dropping them in the fall as most trees do. In this study we attempt to understand why marcescence in American Beech trees (*Fagus grandifolia),* occurs only in the juvenile to middle age trees. We hypothesize that younger Beech trees have a higher leaf nitrogen content and hold their leaves throughout the winter to mulch themselves in the spring. We took leaf samples from twenty different trees grouped in three categories: young, middle age, and old. We also obtained the DBH and canopy density of each tree to determine when the transition to marcescence occurs. We found that the DBH in which the transition of marcescence to non-marcescence occurs is around 30 cm. The leaf nitrogen content will be measured this upcoming summer using an elemental analyzer. (**95**)

Morgan, Abigail*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Analysis of Lck expression and function in cultured rat microglia*.- Microglia are the resident macrophages in the central nervous system (CNS), where they remove foreign material and cellular debris, and initiate neuroinflammatory responses. Microglia are essential for neurodevelopment and contribute to synaptic pruning to increase the efficiency of neuronal transmission. Microglia are also involved in neurogenerative diseases, and migration to the site of injury may play a significant role in disease progression. Previous research has shown that Lck, a Src-kinase family member, is involved in migration signaling pathways in Schwann cells. The purpose of this study was to investigate the role of Lck in microglia, as we determined that Lck expression is significantly higher in microglia than other glial cells. Primary cultures of rat microglia were treated with lipopolysaccharide, a strong activator of immune cells, and fractalkine, a chemokine that attracts immune cells to sites of infection. Lck expression was analyzed following RNA isolation and qPCR. Lck expression was increased after a 24-hour activation by both LPS and fractalkine. A preliminary migration assay showed significant increase in migration when treated with fractalkine and reduced migration when cultures were co-treated with A77, an Lck inhibitor. (**34**)

Mountz, Camryn*, Jeffrey Bardwell, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *Gypsy moths (Lymantria dispar) ovipatory in Michaux State Forest based on tree species and age*.- Gypsy moths (*Lymantria dispar*) are an invasive species that defoliate forests across North America. The USDA estimated that industry, agriculture, and land management stakeholders spend $26 billion annually trying to control invasive species across the country. Gypsy moths complete holometabolous stages with an annual life cycle whose larvae feed on hardwood vegetation, and possess few North American predators or parasites to control their spread. Gypsy moths threaten many native trees along the east coast, causing mass defoliation which decreases tree species biodiversity. Approximately 150 different species of trees have been identified to be susceptible to gypsy moths, the main target being Oak species. This study seeks to observe the relationship between the presence and number of egg mass and tree maturity and species within Michaux State Forest, Franklin County, Pennsylvania. Preliminary results indicate Gypsy moths prefer depositing egg masses on adult Chestnut Oaks. (**99**)

Nemec, Ryleigh*, Whitney Cabrera, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *What's hiding on our lab floor? Student sourcing antibiotic discovery*.- Antibiotic resistance is a growing problem in the world today. According to the CDC, about 2.8 million antibiotic-resistant infections occur in the U.S. every year, resulting in 35,000 deaths. Predictions indicate that the number of infections and deaths will increase unless we find solutions to counter antibiotic resistance. Discovering and developing new antibiotics is essential to fight against antibiotic resistance. Our goal is to find new antibiotics by studying novel environmental microbes and their interactions with each other. We are working alongside an organization known as Tiny Earth, which aims to find antibiotic-producing microbes that can kill drug-resistant bacteria. New antibiotics are desperately needed to slow the impacts of antibiotic-resistant pathogens, and environmental microbes are a promising source for drug development. In the summer of 2021, we isolated organism JH–4 from a laboratory floor at Cedar Crest College. We found that JH–4 was active against Staphylococcus epidermidis on all-culture media. Crude metabolites of JH-4 were found to create zones of inhibition against S. epidermidis, Bacillus cereus, and Mycobacterium smegmatis on both all–culture and tryptic soy agar media. We are currently performing 16S rRNA DNA sequencing to determine if these antimicrobial properties are novel. A minimum inhibitory concentration method will also be employed using the filtered supernatant of JH-4. These next steps will help to gain a further understanding of the antimicrobial properties of JH-4 and the microbe itself. Understanding the antimicrobial characteristics of novel environmental microbes is crucial to lowering antibiotic resistance. (**105**)

Ordoñez Siza, Catalina*, and Quyen Aoh Gannon University, Erie, PA 16541. *Role of SCAMP3 regulating CXCR4 trafficking*.- The CXC-Chemokine Receptor Type 4, CXCR4 is a G-protein coupled receptor that helps regulate cell growth and division, differentiation, and migration. CXCR4 can be overexpressed when its trafficking to the lysosome is decreased. Overexpression of CXCR4 is associated with metastasis in cancer and promotes HIV infection. When bound to its CXCL12, CXCR4 is ubiquitylated and downregulated via endocytosis. At the early endosomes, CXCR4 is ubiquitylated by the ubiquitin ligase ITCH and then sorted into multivesicular bodies by the ubiquitin adaptor proteins Hrs and Tsg101. Degradation of CXCR4 occurs in the lysosomes. This project is interested in whether Secretory Carrier Membrane Protein (SCAMP) 3, which interacts with Hrs and Tsg101, regulates CXCR4 trafficking. RNA interference will be used to knockdown SCAMP3 and CXCR4's localization relative to markers of the early endosome and lysosomes will be monitored through indirect immunofluorescence. Control immunofluorescence assays were performed with pulse chase time of 5, 15, 30, and 60 minutes to examine CXCR4 localization. We have found that CXCR4 accumulates in large compartments, indicative of lysosomes at 60 minutes or later. We are currently working to optimize the assay to accurately measure colocalization with both endosomal and lysosomal markers. (**12**)

Porter, Savannah*, and Christopher Dolanc Mercyhurst University, Erie, PA 16546. *Tree-rings reflect the impact of climate change on high elevation* <u>*Pinus albicaulis*</u> *(whitebark pine) in Northern California*.- Whitebark pine (*Pinus albicaulis*) grows in the highest elevation forests and timberline between southwestern Canada and the western United States typically in windy, cold, and snowy climate zones. Summers are short and cool, including a cool growing season at 55°F to 59°F, with hotter summer days reaching 79°F to 86°F. There are often droughty periods with low rainfall or remaining snowmelt water for several weeks during mid- to late-summer and whitebark pine depends on long-lasting snowpack to access moisture during the growing season. However, California has been experiencing extreme droughts and is expected to get drier with climate change. This study includes tree ring widths of twenty whitebark pine (*Pinus albicaulis)* samples from Heavenly Ski Resort, South Lake Tahoe, California. Samples were cut into cross-sections and were prepared in the laboratory using standard techniques then, cross-dated visually using the list method. Analyzed using the software WinDendro for accurate measurements and other parameters (minimum, maximum, and average density). Preliminary results suggest a reduction in growth for most of the twenty individuals from 1996 to 2011. Average ring width for all twenty samples was 0.3702mm in 1996 and 0.2479mm in 2011. These suggest that that the growth of whitebark pine is slowing down. By comparing these years with climate records, we hope to determine which environmental factors are driving the decline in growth. (**62**)

Raczkowski , Alyssya*, and Linda Auker Misericordia University, Dallas, PA 18612. *The effects of a model invasive epibiont on the anchoring and burrowing rates of freshwater unionids*.- Zebra mussels (*Dreissena polymorpha),* an invasive bivalve from the Caspian Sea, spread into various waterways around the world through ballast water. These mussels may use epibiosis (overgrowth) to ensure their own survivability, at the expense of other living organisms such as freshwater mussels (*Unionidae*). Due to the increased population size and spread of the invasive zebra mussel, freshwater mussel biodiversity and survivability has significantly decreased leading to endangerment and extinction of many freshwater mussel species. Our research aims to focus on the impacts of the abiotic factors in this epibiotic relationship, examining the weight, shape, and density of zebra mussel epibionts, and the effects on anchoring and burrowing rates and survivability of freshwater mussels. Additionally, we will test if the weight of one or more zebra mussels attached affects freshwater mussel's burrowing and anchoring ability when water flow is introduced. We hypothesize that there is a relationship between the quantity and quality of epibionts on freshwater mussels in relation to anchoring and burrowing rates. We used an assorted amount of 3-D printed zebra mussel epibionts, replicating and varying structure, quantity, shape, and weight, to attach on live freshwater mussel shells. Our five experimental groups of unionids varied by the number of attached model epibionts (1-5 per shell). Burrowing and anchoring were assessed by measuring the depth of each unionid shell from the surface of the sand. These data were compared to a control freshwater mussel's depth, containing no epibiont structures. Our results will further build upon limited existing studies that examine the relationship between freshwater mussels and invasive zebra mussels. (**87**)

Rager, Sydnie*, Marcie Hricovec, and Rajinkanth Mohan Mercyhurst University, Erie, PA 16546. *Prevalence of caseinase enzyme in bacteria*.- Caseinase is an enzyme implicated in the digestion of the milk protein, casein as well as other casein-like structural proteins. Caseinase is generally found in fungi as well as milk-spoiling soil bacteria such as *Bacillus* sp., pathogenic bacteria such as *Pseudomonas* sp. where it functions as a virulence factor, and *Streptomyces* sp etc. Less is known about the distribution of the caseinase enzyme in other bacteria. In this study, a screen of caseinase-producing bacteria resulted in the identification of over 50 isolates of caseinase-producing bacteria. Caseinase production was most prominently present in bacteria from food and soil sources. Diverse food samples showed a surprising enrichment of human skin microflora, predominantly *Micrococcus* spp. and *Staphylococcus* spp., whereas caseinase-positive bacteria isolated from soil were mostly *Bacillus* spp. Not surprisingly, fermenting bacteria such as *Streptococcus* sp. isolated from dairy products also contained caseinase. In addition, caseinase was also observed in *Aeromonas* and *Enterobacter* spp. isolated from wet environments reaffirming the presence of caseinase in potential pathogens. Studies are underway to identify caseinase-producing enzymes in these bacteria, as well as taking a closer look into the circumstances in which the enzyme is produced. (**10**)

Reid, Jonathan*, Mackenzie Tewksbury*, Kate Greenwood*, and Brian Gray York College of Pennsylvania, York, PA 17405. *Circular RNA expression in immune cells following chemical stimulation*.- Circular RNA molecules (circRNA) are regulatory structures covalently bonded at the 5′ and 3′ ends. Multiple functions for circRNAs have been identified, including sponging microRNAs, RNA silencing, and acting as biochemical effectors. Previous research has identified multiple circRNAs in infection and autoimmunity disease states, and some are reported in particular immune cell types. hsa_circ_0049224, hsa_circ_005519 and hsa_circ_VMA21 are described in several disease states, while circFSCN1 and hsa_circ_0000279 are identified in dendritic cells. All prior reports are from human patients or *ex vivo* biopsies and tissue samples, and include contaminating cell types, tissue architecture, or isolation procedures that may markedly alter the interpretation of results. This study explores initially whether these circRNAs are found in a single immune cell type, and then within a limited subset of human white blood cells. Jurkat T cells, derived from a T cell lymphoma, and commercially purchased human peripheral blood mononuclear cells were subjected to a range of chemical treatments. These chemical treatments were selected to simulate immune system activation, immunosuppression, as well as how genetic regulation was affected by immune suppression that was concurrent with an active insult. As DMSO was used to reconstitute the modulatory chemicals, it was added as a vehicle control to one set of cells in all experiments. Dexamethasone treatment suppressed cells; and ionomycin and phorbol myristic acid activated immune cells. Treated cells were sampled at 24 and 72 hours post-treatment, and total cellular RNA isolated via Trizol and tRNA and rRNA molecules removed with a Qiagen protocol. cDNA was then made and used for PCR, with GAPDH as the housekeeping control. We found differential expression of the various circRNA targets in Jurkats at 72 hours but not at 24 hours. In primary human cells, we found limited expression of hsa_circ_005519 at 72 hours. (**39**)

Rettger, Jason*, Rajinikanth Mohan, and Kaitlyn Stroscio Mercyhurst University, Erie, PA 16546. *Isolation and characterization of sucretolerant bacteria from honey and high sugar media*.- Sucretolerant bacteria can tolerate the osmotic stress caused by high concentrations of organic solutes such as sugars. These bacteria are implicated in the spoilage of fruit juices, concentrates, cane sugar and other confectionary products. Yeasts and other fungi are commonly associated with sucretolerance, but much less is known about sucretolerance in bacteria. Moreover, the amount of research concerning sucretolerance in bacteria is marginal compared to the study of halotolerance or salt tolerance in bacteria. In this study, thirteen sucretolerant bacteria were isolated from honey and high sugar media that could grow on media up to 30% glucose. Gram staining revealed that most isolated strains were Gram positive. 16s rRNA sequencing of the isolates confirmed that most isolates were *Bacillus* sp. and also revealed novel osmotolerant bacteria including *Brevibacterium* and *Aurantimonas* species. Differential expression revealed the induction of a 15kD protein in response to sugar stress, which appears to be conserved in three related *Bacillus* species. The identification and characterization of this protein could shed light on mechanism of sucretolerance in bacteria. Overall, much less is known about sucretolerance in bacteria compared to fungi as well as halotolerance in bacteria, and this study aims to address the knowledge gap. (**9**)

Rogers, Karina*, Rabab Alamairy, Sarah Dubrul, Keaton Bryson, Gary Vanderlaan , Davide Piovesan , and Matt Gacura Gannon University, Erie, PA 16541. *The creation and testing of fungal based biomaterials for multipurpose use*.- The growing environmental crisis and the instability of the global economy demonstrate the need for development in green industry and renewable materials, as they are crucial to providing a long-term solution. Fungal-based biomaterials have been a topic of interest, serving as both a cost-effective industrial material and as a continuous food surplus for low-income communities. This project aims to repurpose waste generated by local Erie businesses into growth substrates for fungi. Edible fungi such as *Pleurotus ostreatus* (oyster mushroom), *Trametes Versicolor* (turkey tail mushroom*), Lentinula edodes (*shitake mushroom), and *Hericium erinaceus* (lion's man mushroom) are widely accessible white-rot mushrooms, that can decay wood and other high in cellulose substrates. The fungal biomass cultivated in their growth is resilient and versatile composite brick-like material, that can be sold for construction or insulation purposes. Fungal bricks were created and tested during the spring semester of 2023. *P. ostreatus* and *T. versicolor* were the initial fungi selected to inoculate materials for the creation of bricks. Both species *of fungi are* fast colonizers of substrates enriched in ligno-cellulose, which allow for the rapid production of material. Several substrates, sterilized in an autoclave, were inoculated to determine the most suitable for growing a strong biomaterial. The materials chosen for this are recycled paper, brewer spent barley grain, sawdust, and coffee grounds. All waste products were taken from local businesses around Gannon University, Erie PA. The fungi have been grown on these substrates (in varying combinations) at room temperature for 1 to 2 months, to allow for the maximum amount of biomass to be produced. After the production of fungal bricks, they were deactivated (growth stopped) using heating/drying. The mechanical properties of the materials will be tested at various temperature using an MTI-10k. (**104**)

Rosander, Kara*, Deborah Austin, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *Comparative study of the effect of precipitation on microplastics in the Conococheague Creek*.- Water pollution is a significant global issue. It is estimated that 14,000 people die each day from water pollution worldwide. Pollutants can enter the air, soil, or water and change their physical, chemical, and biological characteristics, which can cause harm to humans and aquatic life. Microplastics are plastic particles that are less than 0.5 mm and these can enter water sources, specifically the creek by surface water runoff after heavy rain, wastewater (treated and untreated), industrial effluent, degraded plastic waste, and atmospheric deposition. Microplastics pollute the environment and waterways because they take up to thousands of years to chemically degrade. In the environment, they can act as vectors for harmful containments like heavy metals, pharmaceuticals, and bacteria. The small size of microplastics allows them to easily be ingested. The Conococheague Creek is the source of drinking water for Chambersburg. This study investigated whether the introduction of microplastics into the Conococheague Creek is correlated with precipitation. Two sites along the Conococheague Creek were selected-one upstream from Wilson College and one downstream. Although the results show no statistical significance between precipitation and microplastic concentration, a significant difference was identified between fibers and both films and fragments ($p < 0.025$). (**102**)

Rose, Emily*, and Monique Rogals Marywood University, Scranton, PA 18509. *Optimization of protein miraculin for use as a sweetener in soft drinks*.- Non-nutritive sweeteners (NNSs) have been linked to health risks, largely because they alter gut flora. Despite this, the use of NNSs is rising. Soft drink companies are using NNSs to reduce the sugar content of their products while retaining the expected level of sweetness. A better option might be to use a biomolecule with a routine digestive route that activates the sweet taste receptor much more intensely than sugar so that energy released by digesting it is minimal. Miraculin, a 24kDa glycoprotein, is a “sweet-tasting” protein which, in a low pH environment, activates the sweet receptor hundreds of times more intensely than table sugar. It would be a natural addition to soft drinks, which already have a low pH. However, soft drinks need to be shelf-stable at room temperature for months at a time and WT miraculin has too short a half-life. Traditionally the tongue is pre-coated with miraculin before eating sour foods, a step that would likely not appeal to many consumers. Both problems may benefit from a detailed model of the miraculin-sweet receptor interaction. More than a decade ago, a 10ns molecular dynamics simulation (MD) of a homology model of miraculin was run. MD of protein dynamics, multiprotein complexes, and computation in general have improved drastically. Additionally, it was modelled on a low-identity template without glycans. There is now a better, experimentally determined, template candidate available and it matches well with an AlphaFold generated structure. There are also experimental structures of the, quite similar, savory taste receptor now available for docking simulations. This model can be modified to identify mutants with better protein stability and different binding properties. The predictions made using the MD can be verified using in vitro experiments. Transition to *Pichai pastoris* for additional testing should be straightforward. (**45**)

Runyan, Rose*, Sherri Buerdsell, Deborah Austin, Kimberly R. Todd, Nucharin Songsasen, and Hila Shamon Wilson College, Chambersburg, PA 17201. *Development of a method for rapid boldness scoring of individual swift fox (Vulpes velox) during pen husbandry visits and assessment of its application across varying populations*.- The swift fox (*Vulpes velox*) is a canid species that inhabits the northern Great Plains region of the United States and Canada and faces continuous threats to population expansion and growth. Subsequently, the Fort Belknap Department of Fish and Wildlife and Smithsonian Institution launched a five-year reintroduction plan in 2020 to translocate individuals from established populations in Colorado and Wyoming to the Fort Belknap Reservation in northern Montana. The aim is to create a self-sustaining population that will expand and connect with fragmented northern and contiguous southern populations across the species’ range. During this time, research is being conducted to understand how bold personality affects individual fitness with implications for population-level dynamics. This study aims to create a method for evaluating individual swift fox boldness levels prior to release in the form of a survey that may be completed by technicians in the field. The survey was created based on behavioral observations of videographic data collected during the 2021 translocation, provided by the Smithsonian, and utilizes Likert scale and multiple-choice style questions for easy scoring. However, because the videographic data processed focused solely on a Wyoming release cohort, concern arose for the applicability of this survey across source populations. Therefore, the second part of this study utilizes videographic data from both

Colorado- and Wyoming- sourced foxes to compare activity budgets between source populations. Contrary to the initial hypothesis, data analysis has revealed significant differences in the activity budgets between these two populations, which may have implications to their fitness post-release. This study will provide a broad-based methodological tool to assist ongoing research in swift fox recovery. (**65**)

Samuels, Andrew*, Erin Renwick, and Michael Ganger Gannon University, Erie, PA 16541. *Soil bacteria affect rhizoid development in the fern Ceratopteris richardii: initial investigations of the patterns and potential mechanisms*.- Soil bacteria, specifically the plant growth-promoting rhizobacteria (PGPR), have been shown to engage in molecular communication with plants and have major effects on plant growth and disease resistance. Our understanding of these relationships is seed-plant specific and concerns interactions between plant roots and PGPR. Such relationships likely developed when plants first colonized land, well before the development of roots, where the rhizoid-producing gametophyte stage was more prominent. Seedless vascular plants, like the fern *Ceratopteris richardii*, have both a root-producing sporophyte stage and a rhizoid-producing gametophyte stage, and thus can offer a unique perspective on these relationships. *C. richardii* gametophytes may be either male or hermaphrodite. The hermaphrodite-secreted hormone, antheridiogen, influences individuals to develop as male, while in its absence, individuals develop as hermaphrodite. The Gram-negative soil bacterium *Pseudomonas nitroreducens*, isolated from the roots of the fern *Onoclea sensibilis*, has been shown to increase the percentage of hermaphrodites in culture and also dramatically increase the length of rhizoids in both males and hermaphrodites. Experiments were performed to determine whether other soil bacteria could affect rhizoid development and to infer potential mechanisms. The rhizoid effect was common among other Gram-negative bacteria (including species like *Escherishia coli* K12) and even fungi, but much less common among Gram-positive bacteria. Gametophytes grown from older spores showed reduced growth rates compared to gametophytes grown from younger spores. However, this effect was not evident when the older spores were grown with bacteria that promote rhizoid growth. Finally, the Gram-negative bacteria affecting rhizoid development also appear to increase the proportion of hermaphrodites, suggesting that the rhizoid and sex-determination effect may be due to a common mechanism. (**81**)

Shaw, Andrew*, and J. Michael Campbell Mercyhurst University, Erie, PA 16546. *Analysis of biodiversity within freshwater mussel populations inhabiting Conneaut Creek, Erie PA*.- Research of Conneaut Creek's freshwater mussel populations begun back in 2016 was continued in September, and November of 2022. The large numbers of shells of recently dead mussels have prompted us to explore mussel mortality evident at two sampling sites on Conneaut Creek between 4 and 9 km upstream from where the stream enters Ohio. The goal of this ongoing research is to try to unravel what is causing some species to experience more mortality than others. Shells of previously deceased specimens were collected with the aim of evaluating the age-structure of the most affected species. The death assemblage contained nine different species with dominant taxa including *Eurynia dilatata, Lampsilis siliquoidea, Lasmigona costata, and Vilosa iris. Eurynia dilatata* (Spike) had the highest number of deceased individuals. There are several different possible causes of death including but not limited to mismanagement of wastewater, predation, non-point source pollution, and displacement from the channel during high water storm events. *Eurynia dilatata* (Spike) had the highest number of casualties within the death assemblage. Storm water events are suspected to have been responsible for the significantly high amount of dead Spike mussels. As we continue to analyze the death assemblage, we will begin to gain a better understanding of population trends and explore different hypotheses. (**103**)

Smith, Laila*, Oanh Nguyen*, and Matthew Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Brain morphology and gene expression changes of Drosophila melanogaster in the brain and nervous system resulting from misregulation of Jazf-1*.- Jazf-1 is an important regulator of genes expression in both *Homo sapiens* and *Drosophila melanogaster*. In *Drosophila*, it has been suggested that Jazf-1 is important in the regulation of the nervous system. However, the precise role it plays in the nervous system is currently unknown. To better understand how Jazf-1 regulates the nervous system, this study uses two different approaches. One of these, focusing on morphology, and the other, gene expression changes. Both approaches use an upstream activation sequence (UAS) to either induce overexpression of Jazf-1 or a RNAi knockdown of Jazf-1. In the first approach, specific nervous system drivers activate the UAS system and GFP. Therefore, targeted neurons are misregulating Jazf-1 while simultaneously being marked by GFP. This allows a comparison of structural differences among the GFP expressing cells. The second approach uses the GAL4-UAS system to misregulate Jazf-1 and quantitative RT-PCR to find expression differences. Preliminary data suggested a change in gene expression in the nervous system when Jazf-1 is manipulated. Therefore, using a pan-neuronal driver in the GAL4-UAS system, we are exploring a wider variety of gene expression within the nervous system. With this combined approach, we should be able to determine the role of Jazf-1 in the overall nervous system morphology and gene expression. (**30**)

Spagnola, Lily*, and Audrey Ettinger Cedar Crest College, Allentown, PA 18104. *Influence of social group size and habitat density on the development of Rocio octofasciata (Jack Dempsey) cichlid fish behavior*.- Animal models are essential to behavioral research because they allow us to mimic many of the processes seen in humans. Fish models are particularly useful because they are much simpler than humans, yet still express complex behavioral patterns, as well as having hormonal systems similar to humans. In social animals, adult behavior may depend on early social experience. Here, the social development of the Jack Dempsey cichlid, *Rocio octofasciata*, was observed and manipulated experimentally. Previous work in a range of fish species has shown two possible results of varying population density, with higher densities resulting in either earlier or later development of adult behaviors. Habitat size has also been observed to have an effect on the development of behavior, causing different species to show earlier or later development. To test each of these questions in an additional species, three broods of Jack Dempsey cichlids were divided into groups of different sizes and reared in small or large tanks, resulting in a range of population densities and habitat sizes. Groups were observed to determine the order in which behaviors appear and whether there are differences among type or quantity of behaviors across tanks of different density or size. Behaviors were recorded and tallied several times per week. Initial data shows that fish raised in tanks of higher density developed aggressive behaviors earlier than lower density tanks, and that increased aggression was typically present in larger individuals and in tanks where fish grew more rapidly. Long term observations will allow us to determine whether the earlier development of aggressive behaviors results in different behavioral patterns in adulthood. (**26**)

Steinbicker, Mary*, Chip Krilowicz, and Stephen C. Mason, Jr. Immaculata University, Immaculata, PA 19345. *Dragonflies and damselflies from Franklin Parker Preserve in the New Jersey Pinelands*.- Biodiversity loss can have widespread environmental consequences on ecosystems and human society. Dragonflies and damselflies (Odonata) make optimal study taxa to examine these consequences due to their relative ease of identification and charisma. Additionally, they contribute to vital ecosystem services such as pest control and energy cycling and make ideal bioindicators to determine water quality. In this study, Odonata species richness was documented in Franklin Parker Preserve (FPP) in the New Jersey Pinelands to gather baseline data in this globally rare ecosystem. From 2006 to 2011, sweep nets and photographs were used to document 9 Odonata families represented by 74 species. All specimens were digitized and eventually uploaded to the Global Biodiversity Information Facility (GBIF). Approximately 40% of New Jersey's known Odonata species were represented in roughly 4,047 hectares. Notably, we collected the Southern Spreadwing, (*Lestes australis,* Walker, 1952)*,* which previously has been unrecorded in New Jersey in any peer-reviewed publications. We have established baseline data to help determine any future changes within the Odonata community, such as local species extirpation and/or range expansions. Perhaps most importantly, we provided FPP's conservation managers a reference for the species occurring on their property to help them make more informed land management decisions. We look forward to future studies examining the Odonata at FPP as climate change continues to affect ecosystems at the local and global scale. (**82**)

Steppic, Gabrielle*, Jack Carone, Bailee Werner, Skyler Speciale, and Michael Foulk Mercyhurst University, Erie, PA 16546. *Mapping the chromatin architecture of the larval salivary gland, polytene chromosomes in Bradysia coprophila*.- During larval development of the fungus gnat, *Bradysia coprophila*, the entire genome is replicated multiple times with no intervening mitosis and the copies remain synapsed together to form giant polytene chromosomes. Superimposed on this process, several isolated origins of replication fire several more times, producing localized areas of DNA amplification above the polytene level. Transcription of the genes at these loci produces DNA puffs. One such DNA puff, on chromosome 2 at locus 9A (II/9A), has been extensively characterized. Recently, the *Bradysia* genome was sequenced and assembled, and several new polytene chromosome amplicons were identified. In this work we will attempt to characterize the chromatin architecture in the polytene chromosomes using the Assay for Transposase Accessible Chromatin followed by sequencing (ATAC-seq). Pre-amplification, amplification and post-amplification stage salivary glands will be collected from larvae and intact nuclei will be isolated. They will then be incubated with Tn5 transposase loaded with Illumina Sequencing Adapters. Tn5 will cut accessible DNA and simultaneously ligate on Illumina Sequencing Adapters. The tagged DNA will then be sent for Illumina sequencing. The resulting reads will be mapped back to the *Bradysia* genome assembly. The mapped 5' end of the reads will be identified, and their location will identify regions with DNA unassociated with proteins and will reveal the chromatin architecture. We will use the results to assess the chromatin architecture during amplification of the II/9A and compare that to the newly identified amplification loci. We tested several conditions to maximize the isolation of salivary gland nuclei. Additionally, we will present preliminary analyses of the ATAC-seq results. (**28**)

Sterantino, Olivia*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Species status assessment and seed bank analysis of the federally endangered northeastern bulrush (Scirpus ancistrochaetus)*.- Vernal pools are seasonal depressional wetlands that provide habitat for distinctive plants and animals. Despite being considered keystone resources to be prioritized in conservation efforts, most research has focused on vernal pool obligate animal species and ignored obligate plants. Pennsylvania has five state-rare plants that are dependent on vernal pool habitat, including the northeastern bulrush, *Scirpus ancistrochaetus*. Multiple factors of the northeastern bulrushes' life history and reproduction are unknown, including its germination requirements, dispersal method, and apparent reliance on asexual reproduction via rhizome. Although studies suggest that this species flowers regularly and sets seed each season, genetic diversity of the plant is low. Answers to these questions, as well as updated field status information, are necessary for full-scale conservation of the endangered species. Therefore, the goals of this study were to collect updated monitoring information on known populations of the northeastern bulrush in Pennsylvania and New York and to investigate the plant's life history and reproductive strategy. Over the summer of 2022, fifteen historic sites, last visited between 1993 and 2015, were monitored. Two of the fifteen sites were found to support northeastern bulrush, and both occurred on private property in Bath, PA. At these two sites, an analysis of the seedbank was conducted to determine where the majority of achenes fall within the pool and how this correlates to germination rates. Results of the seed bank analysis suggest that achenes are viable but most abundant directly below the parent plant, suggesting that reduced genetic diversity may be related to issues with dispersal rather than seed viability. (**54**)

Suter, Gavin*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *A test of the enemy release hypothesis using the invasive New Zealand mud snail*.- New Zealand Mud Snails (NZMS), *Potamopyrgus antipodarum*, are an invasive species that are found widespread throughout the world and can cause large-scale ecological damage. One of the most prominent hypotheses to explain why this invader does so well outside their native range is the enemy release hypothesis, which states that invasive species are able to outcompete native species due to the absence of natural parasites and predators in the invaded environment. The purpose of this study was to examine populations of NZMS and native snails from multiple locations in the mid-Atlantic region for infection by parasites and compare the rates of infection. Our hypothesis was that NZMS would be less parasitized than native snail species. We collected 1,605 NZMS and 346 native snails from 3 sites in the Musconetcong River, NJ, and 1 site in the Boardman River, MI. The results of the study yielded one instance of digenetic trematode infection found in an *Elimia livescens* in the Musconetcong River. However, a different kind of parasite/symbiote was also found. A total of 15 out of the 1,605 NZMS collected were infected with a mix of *Chaetogaster limnaei vaughini*, an endoparasitic Annelid, and *Chaetogaster limnaei limnaei*, an ectosymbiotic Annelid; a total of 107 native snails out of the 346 collected were infected by the same mix of *Chaetogaster limnaei* species. The infection rates of the NZMS and native snails were 0.935% and 30.9% respectively. These results suggest that the enemy release hypothesis is supported for *Potamopyrgus antipodarum*. It should also be noted this is the first recorded case that we know of, where *Chaetogaster limnaei* infects *Potamopyrgus antipodarum*. (**90**)

Taiwo, Oluwatomilola*, and Leena Pattarkine Harrisburg University of Science and Technology, Harrisburg, PA 17101. *A novel, minimally invasive, paper-based biomarker assay for molecular diagnosis of preeclampsia*.- Preeclampsia is a severe (many times fatal) pregnancy condition marked by high blood pressure and proteinuria that can strike at any point throughout the pregnancy or immediately after birth. Although the exact cause of this condition is unknown, there are several symptoms commonly associated with it. At molecular level, PIGF (Placental growth factor) and its ligand Tyrosine kinase have been commonly identified as being associated with the condition, however there is no diagnostic method to estimate these. This study reports development of a (liquid-biopsy) biomarker-based assay of serum samples for molecular diagnostics of the condition in a sensitive way, for an early detection. The novelty of this study is in the paper based diagnostic assay designed as a prototype for a portable and at-home diagnostics. The work reported involves immunoassays using fabricated serum samples, biotinylated antibodies for PIGF, and a paper-based assay developed using functionalized nanoparticles to quantitatively evaluate concentrations of the growth factor (PIGF). The immunoassay allowed quantitative estimation of PIGF within 10-50 ng concentrations. Nanoparticles were functionalized with PIGF and its binding with biotinylated PIGF was colorimetrically followed in the paper-based assay. This assay has the potential to differentiate generic high blood pressure patients from those with preeclampsia using a minimally invasive method diagnostic assay, a technology that is highly desired presently. (**51**)

Tian, Zizhong*, and Shouhao Zhou Penn State University, University park, PA 16802. *Comparison and extension of interrater agreement statistics under the two-rater dichotomous-response case with correlated decisions*.- Introduction Measurement of the interrater agreement (IRA) is critical for psychological research and social sciences. To assess the extent of agreement above the level attributed to chance, many methods have been proposed including the famous *Cohen's kappa*. As the most popular IRA statistic in many disciplines, however, *Cohen's kappa* may exhibit some paradoxical performance under special data patterns. Additionally, existing comparative studies of IRA statistics are limited by the scope of included IRA methods and overly simplified simulation settings. Overall, it lacks guidance on appropriate choices of IRA methods in applied social research. Methods We propose a novel simulation framework for IRA methods under two-rater dichotomous-response cases. It accounts for the underlying rater characteristics and potential rater correlations and enables a "true" IRA measure as the benchmark for quantitative assessment. We also conduct a comprehensive literature review, which identifies 10 important IRA measures for comparison. Using extensive simulations, we evaluate the performances of the considered IRA measures, and further develop an extension that relaxes the implicit rater homogeneity assumption in *Gwet's AC1* method to improve IRA quantification. Results The simulation assessment shows that *Gwet's AC1* performs the best in estimating the "true" IRA, especially under extreme outcome prevalence. However, when the two raters have different marginal rates, *Gwet's AC1* tends to have a large bias. The new method, named extended *AC1*, shows comparable performance as *Gwet's AC1* in general cases but is more robust than the original *AC1* in the case of high discrepancies in raters' marginal voting distributions. Discussion This study includes the largest list of IRA methods for comparison. The generalized data-generating framework can better mimic the realistic rating processes and reveal the distinctions among different IRA methods. The simulation results and the proposed extension provide useful guidance on choosing proper IRA statistics under different practical conditions. (**11**)

Till, Sarah*, Rebekah Hollenbeck, and Steven Ropski Gannon University, Erie, PA 16541. *A census of the bat population of Gannon University, Erie, PA*.- For the past twelve summers, a census of the bat population has occurred on the Gannon University campus in Erie, PA. The numbers for the first three years held relatively steady, but the data for the past eight years indicates a dramatic decline. White Nose Syndrome was first reported in 2006 in a cave in New York. The disease has killed an estimated 7 million bats in the eastern United States since then and has spread throughout Pennsylvania and into northeastern Ohio. This fungal infection has killed 95% of bats in some caves and may result in the listing of three bat species as endangered in Pennsylvania, including *Myotis lucifugus* the predominant bat on the Gannon campus. This study will compare yearly data by building, time of year, building side and species composition to determine how White Nose Syndrome has affected the Gannon campus bats. A decrease in numbers may be partially responsible for an increase in West Nile Virus in the area. The results will also be used to place bat houses at appropriate locations to encourage bat presence on campus. A compilation of ongoing results of the study reveals a rapid decline of the bat population in Erie Pennsylvania between the summer of 2012 and the summer of 2013, which has yet to bounce back. The conclusion of our study at this time is that bat presence, including, but not limited to that of *Myotis lucifugus*, have been negatively affected by the presence of White Nose Syndrome. (**64**)

Townsley, Taylor*, Kelly Orlando, and Jiangyue Zhang Immaculata University, Immaculata, PA 19345. *DNA barcoding and spectroscopic analysis of the medicinal supplement Serenoa repens*.- Medicinal plants have been used for centuries to provide a better quality of life for individuals; today, numerous medicinal plants are incorporated into dietary supplements. The FDA regulates dietary supplements under a different set of rules than those that cover prescription entities, meaning they do not have to include as much information as is necessary for those drug products. When taking supplements, most people want to know what exactly the contents are and at what concentration. The plant *Serenoa repens,* also referred to as saw palmetto or dwarf palm plant, is used as an herbal supplement in the aid of prostate health, especially for benign prostatic hyperplasia (BPH). Labels on supplement bottles state that there is only pure *S. repens* in each capsule. Our hypothesis is that some brands of supplements may not contain *S. repens*, or may contain more than just the stated plant species. To determine the presence of *S. repens* material in the supplement, we used DNA barcoding with plant-specific primers to test three different *S. repens* brand herbal supplements. In addition, the structure of extracts from these same three brands were compared to finasteride, a drug used to treat BPH, through various spectroscopic techniques, including MS, IR and NMR. The observation of spectroscopic peaks will allow identification of functional groups, which can be used to compare the strength of each supplement corresponding with that collected spectra. This experiment should help solidify that the key ingredient in each supplement is what it is claiming on nutritional labels, including filler materials. (**33**)

Truong, Amy*, Carly Clayman, Piel Sarah, and Kilbaugh Todd University of Pennsylvania, Philadelphia, PA 19104. *Sodium fluoroacetate shows trends of dose- and age-dependent effects on citrate synthase and aconitase enzymes in zebrafish (Danio rerio)*.- Sodium fluoroacetate (SF), is a toxic substance occurring naturally in plants that is absorbed by the oral and inhalation routes. The toxin, exhibiting a structural similarity to acetyl co-enzyme A, works through irreversibly binding to aconitase and preventing conversion of citrate to isocitrate. Accumulation of citrate drives a negative feedback loop that inhibits glycolysis and cellular respiration. Zebrafish (Danio rerio) subjects of embryonic, larval, and adult stages were exposed to 0.1 mM to 1 mM SF doses to assess mitochondrial content, which was evaluated with citrate synthase (CS) western blots. Aconitase activity was assessed with an enzymatic assay. 1 day-post-fertilization (dpf) embryos exposed to 1 mM SF for 3 hours show a trend of increased CS, while the 2 dpf embryos show an opposing trend of decreased CS. When exposure time was increased to 24 hours, 1-2 dpf embryonic subjects exhibit a trend of decreased CS. In adult brain samples, there was a U-shaped dose response, with a trend of decreased CS at 0.5mM SF and increased CS at 1.0mM SF. There was a significant increase in aconitase activity with exposure to 0.5mM SF, compared to controls when assessing exposure of embryos (1-2dpf), larvae (4-5dpf), and adults. When comparing subjects within the 0.5mM SF exposure group, adults showed greater aconitase compared to embryos and larvae. The varied doses and ages of SF exposure provide insight into understanding the mechanisms of SF's mitochondrial toxicity. Increased aconitase activity and a trend of reduced citrate synthase levels in embryos, larvae, and adults exposed to 0.5mM SF suggests a potential compensatory response to SF. Further studies will examine CS and aconitase across SF doses in embryos and larvae, and hearts of SF-exposed adults will be assessed to further evaluate SF's impact on mitochondria. (**41**)

Tulio, Dominic *, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Finding the amino acids within members of the Candida glabrata PMU gene family that confer phosphatase activity*.- Phosphate is an essential nutrient that the opportunistic human fungal pathogen, *Candida glabrata*, uses in various cellular processes. These single-celled organisms need to be able to cleave phosphates from organic molecules in their environment and take them into the cell. *C. glabrata* has a three-gene family consisting of *CgPMU1*, *CgPMU2*, and *CgPMU3*; while all three encode enzymes with phosphatase activity against some phosphate-containing compounds, *CgPMU2* encodes an enzyme that is upregulated when the cell is starved of phosphate and is able to cleave phosphate off of a wide range of organic compounds in the external environment (Orkwis et al., 2010). The proteins expressed by this three-gene family are approximately 75% identical in amino acid sequence. Orlando *et al*. determined that the novel amino acid changes that conferred broad-range phosphatase activity on CgPmu2 protein were generally found toward the C-terminal end of the protein (Orlando et al., 2015). In that paper, they identified a number of individual amino acids that conferred increased phosphatase activity on CgPmu2, but when they combined all of their identified point mutations into the *CgPMU1* gene, they were not able to fully replicate the strong, broad-range phosphatase activity of the full-length CgPmu2. Therefore, we used the predicted structures of CgPmu1 and CgPmu2 to identify additional CgPmu2-specific amino acids that were likely to help confer this broad-based phosphatase activity, and combined those point mutations with the ones identified in the 2015 paper. We plan to measure their phosphatase activity to determine if our identified amino acids were able to confer the broad-based activity found in full-length CgPmu2. Since *C. glabrata* is listed in the "High" group in the WHO Fungal Priority Pathogens list, understanding the biochemical pathways that control the uptake of an essential nutrient in *C. glabrata* may help make possible future development of antifungal treatments. (**7**)

Wallace, Ryder*, Jeffrey Bardwell, and Brad Engle Wilson College, Chambersburg, PA 17201. *Multifactor analysis of the spread of deer tick (Ixodes scapularis) borne diseases in Pennsylvania*.- Deer ticks (*Ixodes scapularis*, Class Arachnida) are ectoparasites found throughout the eastern and midwestern regions of the United States and responsible for 95% of vector-borne diseases in the country. *I. scapularis* prefer feeding on the white-tailed deer (*Odocoileus virginianus*) and the white-footed mouse (*Peromyscus leucopus*) but sometimes parasitize humans. *I. scapularis* carry an array of diseases such as Lyme Disease, Babesiosis, and Anaplasmosis. This study uses Lyme Disease data to generate historical and future linear regression models, which can then be used to identify future trends for Babesiosis and Anaplasmosis in Pennsylvania. Unlike Lyme Disease, these two diseases are both prevalent in New England and currently spreading south. Using county-level data, this study aims to understand the conditions that could lead to the spread of Babesiosis and Anaplasmosis across three Pennsylvania counties: Northumberland, Snyder, and Union. Independent variables include *I. scapularis* populations, human populations, temperature levels, precipitation levels, and currently reported locations for all three diseases in Pennsylvania. The dependent variable is normalized disease presence (frequency of collected potential disease vectored ticks / county population). Using R library packages dplyr, magrittr, stats, and tidyr, a linear regression model shows statistical significance for population (t-statistic: 2.348, p-value = 0.0312) and intercept (t-statistic: -2.347, p-value = 0.0313) for Union County. This predictive model can be used to create a county-level choropleth map to document twenty-year historic trends of Lyme Disease and forecast future prevalence of Babesiosis and Anaplasmosis in Northumberland, Snyder, and Union counties. This model creation can be used by other researchers; civilians; and people at risk of Lyme Disease, Anaplasmosis, or Babesiosis to warn about potential locations susceptible to the spread of these diseases. (**98**)

Wilcox, Mackenzie*, Caitlyn Henry, Peyton Kimmel, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Creatine reduces the effect of LPS-treated immortalized Schwann cells*.- In the peripheral nervous system, Schwann cells wrap around axons, forming the myelin sheath, which protects nerves. Schwann cell growth is regulated by the cAMP pathway, which can be activated by using forskolin. When neurons are injured, Schwann cells change their phenotype to begin dividing to allow remyelination of the neuron. However, the pathways regulating remyelination are not well known. *In vitro*, Schwann cells can be exposed to lipopolysaccharides (LPS) to simulate a local inflammatory environment, mimicking that of when neurons are injured. Preliminary observations have shown that creatine stimulates Schwann cell proliferation. Based upon these observations, it was hypothesized that the addition of creatine to Schwann cells treated with lipopolysaccharides would have higher rates of growth compared to cells incubated without creatine. Schwann cells were incubated at a density of 35,000 cells/well in a 96 well plate and treated with control media (N2) and forskolin (F). The mitogen-stimulated cells were then incubated with creatine (2μM or 20μM) and LPS (500ng, 1μg, or 10μg) for 6 hours. Cell proliferation was calculated by measuring the optical density, using the MTT viability assay, and then expressed as percent control. Schwann cells elicited increased cell growth with addition of 20μM creatine (109.4806±0.037091%) and 10μg LPS (119.3351±0.043758%) to mitogen-stimulated cells in comparison to control (80.25637±0.105338%). However, 0.5μg LPS treatment revealed a decrease in proliferation (67.0876±0.057415). Meanwhile, Schwann cells elicited increased cell growth with the addition of 20μM creatine to 1μg LPS (127.6176±0.050237) and 10μg LPS (112.2529±0.078845) treated cells. Based upon these observations, it was concluded that Schwann cell recovery was dose-dependent upon creatine and treatment with LPS caused a dose-dependent decrease in cell growth. Continuing this research will determine if these effects remain the same when Schwann cells are treated at 12 and 24 hours, which will provide insight on long-term recovery after injury. (**17**)

Wineburg, Morgan*, Kathryn Sarachan, and Brad Engle Wilson College, Chambersburg, PA 17201. *Effects of the beta blocker propranolol on human glioblastoma migration and cytotoxicity*.- Approximately 250,000 people in the world are diagnosed with glioblastoma annually and 200,000 die from the disease. It is the deadliest form of brain cancer, with the average age of incidence peaking at 75-84 years. One important factor in the clinical outcomes of cancer is migration. Glioblastoma has a high rate of migration causing the cancer to become metastatic quickly. Studies have shown that beta blockers, specifically propranolol, can attenuate the migration of various pancreatic and cervical cancer cells. This study will assess the ability of propranolol to arrest migration in glioblastoma cell cultures. The experimental groups were treated with 150, 200, and 250 μM propranolol, respectively. Cell cultures were incubated at 37 °C for three hours to allow for cell adhesion to the inserts then treated with propranolol for 24 hours. Each treatment was replicated twelve times. A cell migration assay was used to quantify the degree to which treated and untreated glioblastoma cells penetrate the 8.0μm barrier. Propranolol significantly (p=0.00445) inhibited the migration of glioblastoma cells irrespective of treatment groups. In addition, an MTT assay was done to assess propranolol-induced cytotoxicity at concentrations of 100, 150, 200, 250, and 300 μM. Propranolol significantly (p=0.00626) reduced cell viability in all treatment groups. Cytotoxicity increased among the groups as propranolol concentration increased (p=0.0004). (**72**)

Winters, Declan*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Population and genetic consequences of habitat fragmentation in wood frogs (<u>Lithobates sylvaticus</u>)*.- Habitat fragmentation and the associated reduction in connectivity between habitat patches are commonly cited causes of genetic differentiation and reduced exchange of genetic material in animal populations. Connectivity of upland forests is particularly important for vernal pool-breeding amphibians, such as the North American wood frog (*Lithobates sylvaticus*), because they have site-specific habitat requirements and a high rate of natal pool fidelity. Previous studies in Jacobsburg State Park, PA have investigated the effect of road proximity on the upland movement of wood frogs by comparing results between a fragmented site, which is <100 m from two roads, and an unfragmented site where the nearest road is greater than 1000 m away. Wood frogs were significantly more abundant in traps further away from roads at the fragmented site, indicating that the presence of roads may be reducing the amount of upland habitat utilized by adult wood frogs. The objective of this research was to build on this former study by comparing genetic diversity as a measure of gene flow in wood frog populations between the isolated and fragmented sites. Microsatellite DNA markers were used to determine the population structure between the vernal pools at each site and the genetic diversity of each wood frog subpopulation at four vernal pools in Jacobsburg Park. Results demonstrate that population genetic diversity was high and similar to other studies of wood frog populations. There was a comparable degree of population differentiation between the fragmented and isolated sites, suggesting high connectivity among populations. A future direction will be to study the sex-biased dispersal (SBD) of the wood frog since gene flow may be asymmetrical if one sex is more likely to disperse to nearby pools than the other. (**60**)

Wolfgang, Jessica*, Vaughn Shirey, and Stephen C. Mason, Jr. Immaculata University, Immaculata, PA 19345. *Post fire effects on plant vigor in the New Jersey Pinelands National Reserve*.- Fires are becoming more frequent and severe due to global climate change. Former studies have supported Plant Vigor, in which fires have the ability to increase plant growth rate compared to adjacent unburned habitats. In the NJ Pinelands National Reserve (PNR), wildfires occur at some of the highest frequencies in the country. To combat these wildfires, prescribed fires are often implemented, thus, it makes an ideal opportunity to test if plant vigor is also occurring in the PNR. We predicted that oaks (*Quercus* spp.) and heaths (Ericaceae) would grow faster at our wildfire and two prescribed fire sites compared to our unburned sites. At each site, approximately 20 oak and 20 heath leaves were collected between May and September of 2018. Each leaf was photographed to determine its area using computer vision training through “makesense.ai.” We then plotted the average leaf area for each site through time to observe the growth rate. Using 1,830 leaves (prescribed: 835, wildfire: 278, control: 717), we found that heaths grew fastest to slowest at our wildfire, prescribed fire, and unburned sites, respectively, throughout the season. For the oaks, we found the opposite pattern. However, the average oak leaf area at the wildfire site was highest at the beginning of the season compared to our other sites. The growing patterns between heaths and oaks after fires may represent different growing strategies between the two taxa. It is possible that oaks have a higher resilience after fires than heaths because they immediately grew to their maximum leaf size less than a month after the wildfire, while heaths used the entire season to gain maximum leaf area. Studying plant vigor gives us greater insight into community resistance and resilience and provides future opportunities to study further effects. (**89**)

Wolfinger, Madison*, Khushali Vyas, and André Walther Cedar Crest College, Allentown, PA 18104. *Optimizing a PCR-based technique to examine telomerase regulation in Saccharomyces cerevisiae*.- After DNA replication, organisms must address the end-replication problem that prevents DNA from replicating chromosomal ends, resulting in a loss of important DNA after each cell division. To overcome this, cells attach non-coding DNA sequences to the ends of chromosomes called telomeres that can be partially shortened with each division. Telomeres are synthesized by a ribonucleoprotein called telomerase that can synthesize DNA from an RNA template. In most normal somatic cells, telomerase expression is inactive, but in cancer cells telomerase expression is often upregulated, allowing telomeres to maintain their length, supporting the formation of tumors. *Saccharomyces cerevisiae* is a yeast that is used as a model for function and regulation of human telomeres. In order to understand telomeric function and regulation, it must be measured. There are many methodologies and techniques that allow for the visualization of telomeres, Southern and Western blotting for example. These methods, though, can be difficult and more expensive. A much easier and efficient way to visualize telomeres would be to develop a PCR-based protocol. To understand how telomerase is activated and telomere synthesis we examined telomere length in yeast strains with or without different genetic mutations. Following the genomic DNA isolation and PCR, gel electrophoresis was used to analyze the telomeres. We will present data suggesting that a PCR-based protocol allows us to measure the regulation of telomere length in yeast. Understanding how normal cells regulate telomere synthesis will provide insights into how malignant cells activate telomerase, providing potential targets to kill cancer. (**32**)

Wood, Britney*, and Chris Kavanau East Stroudsburg University, East Stroudsburg, PA 18301. *Use of circular arrays of Kohonen self-organizing maps for reference-free rotational alignment of photographs*.- One of the ongoing problems of machine vision and digital photography is finding a technology to bring rotationally unaligned images into reference-free rotational alignment, in order to eliminate blur and for signal to reinforce and noise to cancel out. We circumvented the dependence of user- or computer-generated external or internal reference images used by other so-called “reference-free” techniques. Alignment is performed using an unsupervised Kohonen self-organizing map configured on a circular ring of artificial neurons. Although alternative alignment protocols often depend on ad hoc parameters, the technology described here instead achieves the minimization of one objectively calculated target function by varying only one free parameter. These Kohonen self-organizing maps preserve the topological properties of the input images, the relative angular orientations of the dataset images are obtained directly from the array's circular coordinate system by noting each mapped dataset image's respective circumferential coordinate placement around the circular array. The process was completed, and the outcome revealed camera images that were aligned almost perfectly. (**53**)