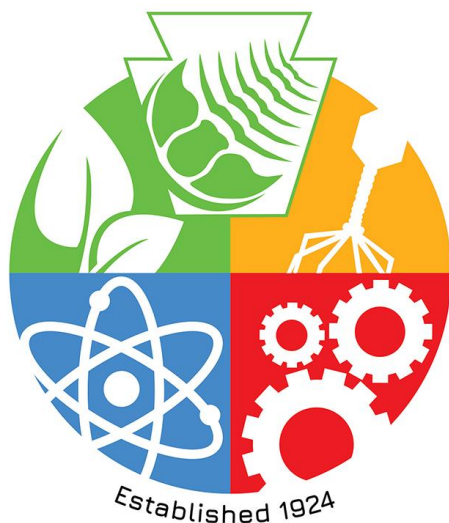


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Abdulrahman, Lieth*, and Ann Yezerki King's College, Wilkes-Barre, PA 18711. *The difference in the course of infection across genetic lines of the confused flour beetle, Tribolium confusum, with the rat tapeworm, Hymenolepis diminuta.*- Many parasites are known to manipulate their hosts in order to increase their chances of completing their lifecycle. The rat tapeworm *Hymenolepis diminuta* is known to cause surface seeking behavior in its intermediate host, Tribolium beetles to encourage the terminal host, rats, to find and eat them, thereby completing its life cycle. Therefore, we hypothesize that the parasite may also encourage migration behavior changes to encourage outbreeding for the parasite. Beetles were infected by a standard protocol and then tested for migration. Both migrated and unmigrated beetles were dissected to assess levels of infection. It was found that environmental conditions greatly changed migration rates. However, under certain conditions we found infected beetles migrate less than their infected counterparts. Our findings indicate that with future adjustments based on this experiment, we might be able to draw stronger conclusions if infections have an effect on beetle migration. (41)

Ali, Anam*, and Amy Hark Muhlenberg College, Allentown, PA 18104. *widerborst and well-rounded: an example to illustrate the relationship of orthologs and paralogs in Drosophila species.*- One of the goals of the Genomics Education Partnership (GEP) is to better understand the evolutionary constraints on networks using the insulin signaling pathway in various *Drosophila* species as a model. In the context of locating an ortholog for *widerborst* (*wdb*) in lesser-studied *Drosophila* species, a strong alignment to another area of the target species' genome was uncovered. This alignment with *wdb*'s protein sequence proved to be part of the coding sequence of the *well-rounded* (*wrd*) gene. *wdb* and *wrd* both encode regulatory B' subunits of protein phosphatase 2A, a member of the insulin signaling pathway. As a result, they have similarities and differences in their structure to help inform their function. Through in silico tools such as the UCSC Genome Browser, NCBI BLAST, and Flybase, we annotated the coding sequences of both genes in *D. kikkawai* and *D. busckii*, which, combined with well-established gene sequence from *D. melanogaster*, provided multiple points over evolutionary time for comparison. It was found that orthologs for *wdb* had greater conservation than orthologs for *wrd*. Additionally, there are areas of each gene that seem to be common between the two, suggesting conserved functional regions. Given the information that we now know about these genes, *wrd* and *wdb* provide a perfect example to build upon in a pedagogical tool. Future work aims to utilize key data taken from this project to create a lesson plan that would increase students' understanding of orthologs and paralogs as they delve into the relationship between *wrd* and *wdb*. (18)

Ambrosino, Marian*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Evaluating fibrosis inhibition in a new murine model of pancreatic cancer.*- Pancreatic ductal adenocarcinoma (PDAC), currently the 14th most common cancer, is expected to be the second leading cause of cancer death by 2030. Limited treatment success can be attributed, in part, to the dense collagen-rich fibrosis of PDAC tumors which limits perfusion and contributes to chemotherapy resistance. Proglumide, a cholecystokinin receptor antagonist, has been shown to attenuate fibrosis within pancreatic tumors and improve treatment. Its effectiveness in metastatic lesions remains unknown and the previously utilized murine pancreatic cancer cell line is poorly metastatic. A new line, MCB/1, has been recently shown to exhibit a high frequency of liver and lung metastases. In the initial stage of testing proglumide efficacy in metastatic disease, we hypothesize proglumide will reduce fibrosis in MCB/1 primary tumors as previously demonstrated in other murine and human PDAC models. To test this, orthotopic injection of MCB/1 cells was performed in immunocompetent C57Bl/6 mice. Mice (25) were randomized into proglumide-treated and control groups, with administration beginning three days post-injection. At three weeks, primary tumors were

isolated and viscera were examined for metastases. Results reveal proglumide treatment had no effect on primary tumor mass, incidence of liver metastasis, or number of lung metastases. However, there was a decrease in the average number of mesenteric metastases in proglumide-treated mice. Histological analysis to quantify collagen in primary tumors using Masson's trichrome staining is in progress. (40)

Antalek, Chloe*, Brad Engle, and Marit Delghandi Wilson College, Chambersburg, PA 17201. *The effects of vitamins, supplements, and other naturopathic therapies on the outcomes of Duchenne muscular dystrophy patients.*- Duchenne muscular dystrophy is a muscle wasting disease caused by mutations to the dystrophin gene. Treatment options such as exon-skipping and gene therapy are available but limited to certain patients depending on age or mutation location. Steroid treatment continues to be used as the standard of care to help slow the progression of the disease. While research correlating various genotype/mutations with Duchenne outcomes is currently being done, research into other factors that may improve outcomes, such as nutritional supplements, is limited. Supplements are a readily available option and can potentially help lessen the inflammation that contributes to devastating outcomes for Duchenne. This study aimed to determine if certain supplements had an impact on the outcomes of ambulation and cardiac and pulmonary function. Data used in this research were obtained from Parent Project Muscular Dystrophy's Duchenne Registry (TDR) version dated 31OCT2023, which collects patient-reported data including a "Nutrition and Supplements" registry module detailing patients' intake of vitamins and supplements. The supplements analyzed in this research were vitamin E, coenzyme Q10, B 50 complex, magnesium, CBD (cannabidiol), vitamin beta carotene, melatonin, calcium, and vitamin D. Data were analyzed to determine if there was a benefit in cardiac function based on the left ventricle ejection fraction determined from an echocardiogram, which is used to measure the amount of oxygen-rich blood pumped out to the body. Histograms and Welch's two factor t-test (statistical software, R) indicated that there was no significant difference in cardiac function by patients taking the supplements (all supplements analyzed had a p-value > 0.05). Analysis on pulmonary function and ambulation status was difficult to effectively accomplish due to limited data. (43)

Armstrong, Alexis*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Development of mouse hepatitis virus chimeric reporter viruses expressing the 3CLpro Pproteases of human coronaviruses HKU1 and OC43 reveals susceptibility to inactivation by natural inhibitors baicalin and baicalein.*- The recent emergence of SARS-CoV-2 in 2019 has highlighted the necessity of antiviral therapeutics for current and future emerging coronaviruses. Recently, the traditional herbal medicines baicalein, baicalin, and andrographolide have shown inhibition against the main protease of SARS-CoV-2. This provides a promising new direction for COVID-19 therapeutics, but it remains unknown whether these three substances inhibit other human coronaviruses. In this study, we describe the development of novel chimeric mouse hepatitis virus (MHV) reporters that express firefly luciferase (FFL) and the 3CLpro proteases of human coronaviruses HKU1 and OC43. These chimeric viruses were used to determine if the phytochemicals baicalein, baicalin, and andrographolide are inhibitory against human coronavirus strains HKU1 and OC43. Our data show that both baicalein and baicalin exhibit inhibition towards the chimeric MHV strains. However, andrographolide induces cytotoxicity and failed to demonstrate selective toxicity towards the viruses. This study reports the development and use of a safe replicating reporter platform to investigate potential coronavirus 3CLpro inhibitors against common-cold human coronavirus strains HKU1 and OC43. (91)

Aryal, Sweta*, Maria Ruccolo, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Comparison of living and dying dividing cricket spermatocytes.*- Meiosis is a fundamental process essential for sexual reproduction, producing haploid cells from diploid

precursors. In meiosis I, homologous chromosomes pair up, and separate in anaphase I, with two chromatids moving toward each pole. In meiosis II, genetic recombination does not occur, and one chromatid moves to each pole during anaphase II. In contrast, mitosis produces genetically identical diploid somatic cells. Chromosomes exhibit diverse types of organization and movements during these cell division processes. Insects are ideal model organisms for unraveling the complexities of coordinating chromosome movements, because male tissues offer a source of populations of both mitotically and meiotically dividing cells that can be readily imaged in living cells. Interestingly, cell division is a process potentially associated with catastrophic error and failures in chromosome segregation—often when errors occur, the best cellular response is to fail in cell division altogether and die. Our goal in this project is to use this system to understand the differences between cells that survive the division process and cells that die during division. In this work, we film living cells, measure a range of events and structures, and compare characteristics of living and dying cells. (47)

Azar, Michael*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Effect of proglumide on expression of type I collagen chains in pancreatic cancer.*- Pancreatic cancer remains one of the deadliest cancers, due in part to its inability to be treated effectively with chemo- and immuno-therapies. These difficulties in treatment arise from the highly fibrotic tumor microenvironment, composed of excessive collagen deposition. Additionally, type I collagen consists primarily of abnormal $\alpha 1$ chain homotrimers, instead of the typically-expressed heterotrimers of $\alpha 1$ and $\alpha 2$ chains observed in normal tissue. Proglumide, a CCK receptor antagonist, has been shown to decrease fibrosis in murine models and improve chemotherapy. Currently, it is not known whether proglumide directly targets the cancer cells or the pancreatic stellate cells attributed with normal matrix production in the pancreas. Previous analyses of the impact of proglumide showed no alterations in COL1A1 ($\alpha 1$) expression in either cell type (RLT-PSC; PANC-1). Given recent literature suggesting COL1A2 ($\alpha 2$) expression is silenced in pancreatic cancer, we sought to examine expression of both chains following proglumide treatment. Initial results in PANC-1 cancer cells show no definitive alteration in COL1A1 expression, but a potential decrease in COL1A2. In stellate cells (RLT-PSC), preliminary analysis over three days of treatment suggests a potential time-dependent increase in COL1A1 and COL1A2 may occur. Additional analyses and an expanded time course will be necessary to confirm these trends. (2)

Azar, Sydney*, and Brian Gray York College of Pennsylvania, York, PA 17405. *Developing a serum-limited growth media for HUVECs.*- Fetal bovine serum (FBS) is commonly used in cell and tissue culture experiments, due to its abundance of cell-growth- and adhesion-encouraging components, but has garnered increasing concern over its ethics and scientific merit. While some immortalized cell lines readily adapt to animal-product-free media formulations on industrial scales, replacement formulations usable at a research scale for many primary cells and attached cell lines are unknown, or are unfeasible without economies of scale. The development of plant-based serum replacement products may circumvent some of these issues, but questions remain about cell growth and viability with plant-derived replacements compared to FBS-supplemented media formulations. Human umbilical vascular endothelial primary cells (HUVECs) grown without additional FBS but with Endothelial Cell Growth Supplement (ECGS) and soy peptone showed growth inhibition and cell morphology was attenuated in comparison to control medium with FBS. The role of ECGS in endothelial cell medium is to support the growth of these attached cells, but it is clear that it is insufficient without the presence of additional serum components. To further promote the development of mostly-animal-product-free media alternatives, it was explored whether the addition of albumin, insulin, and transferrin suffice to encourage growth and support normal endothelial cell morphology and function. Based on this preliminary research, it appears achievable to craft an FBS-limited medium combining ECGS, soy peptones, and

these limited additives to produce growth results similar to those of control media. Further research is needed to determine the effect of removing ECGS from these formulations. (10)

Bajich, Mariana*, Stephanie Bodner*, Naomi Custer*, and M. Logan Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *The Effects of Jazf-1 on the Nervous System of Drosophila melanogaster*.- Jazf-1, juxtaposed with another zinc finger protein, has been linked to the development of the nervous system but how it does this is poorly understood. The study aims to observe the under-expression and over-expression of the Jazf-1 gene in *Drosophila melanogaster* through various pathways in the nervous system. Jazf-1 is conserved in *Homo sapiens* and has been shown to cause endometrial stromal sarcomas and human diseases such as diabetes. To further investigate these pathways, we are investigating gene expression using the Gal4-UAS system. Developed in *Drosophila melanogaster*, UAS is a binary system of gene expression that selectively expresses genes in cell- and developmental stage-specific patterns. Hippo signaling is also relevant in early organism development, with its regulation affecting different tissues and organs. This system is used for genetic labeling and visualization of specific brain regions, allowing us to see differences that manipulating Jazf-1 creates. To examine how Jazf-1 influences gene expression we used a Gal4 driver that was induced in the embryonic stage in all cells and a Gal4 driver that is specific to the nervous system. All embryos were collected within 24 hours of development. Using Real-Time Quantitative Reverse Transcription Polymerase Chain Reaction we will be able to measure the differences in gene expression of select genes. We expect to see a direct correlation between the up and down-regulation of Jazf-1 and genes involved in cell adhesion, Hippo signaling, and the nervous system. The broad impact of this experiment explores the gene Jazf-1, and its effect on *Drosophila melanogaster*, in hopes of future manipulation of this gene for human health and protection against diseases that affect *Homo sapiens*. (17)

Bonser, Hannah*, Alison Edwards, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Examining Replication Protein A and its interactions with proteins Ddc2p, Mec1p, and Tel1p using the budding yeast Saccharomyces cerevisiae*.- Within the United States and many other countries, cancer is one of the primary causes of death. Most treatments we currently have for cancer have unfavorable side effects and are not always effective at destroying or removing this disease. Understanding more about the biochemical and molecular mechanisms of cancer associated proteins using the yeast-two hybrid system within our model organism *Saccharomyces cerevisiae*, or baker's yeast, can help lead to a better understanding of cancer and possibly lead to better treatments. By studying Replication Protein A (RPA) and its interactions with the proteins Mec1p, Tel1p, and Ddc2p we are better able to understand the processes and pathways these proteins are involved in including DNA replication, recombination, and repair. These proteins being studied in yeast all have human homologs including ATR (Mec1), ATRIP (Ddc2), and ATM (Tel1) so the interactions we observe are mirroring interactions that would occur in a human system. These interactions as well as effects of phosphorylation of RPA will give a better picture of what is occurring within the cell's DNA repair pathway and cellular mechanisms of regulation. The main goal of this research is to understand if these protein-protein interactions occur, at what strength do they occur using the ADE2 reporter gene, and if phosphorylation affects their interactions. These discoveries may eventually lead to more targeted and effective treatments for cancer and can bring a better comprehension of the proteins involved in certain cancer related pathways. (31)

Bowers, Connor*, Jeffrey Bardwell, and Brad Engle Wilson College, Chambersburg, PA 17201. *Analyzing the effect of aldosterone on symptoms of vestibular dysfunction in mice*.- Meniere's disease is a debilitating malady, caused by endolymphatic hydrops, a build-up of fluid within the inner ear, which leads to a variety of symptoms including vertigo (dizziness),

tinnitus (ringing in the ear), and hearing loss, which worsen with time. Meniere's has no true cure, causing individuals to rely on medications to alleviate symptoms. This study aims to focus on the impact of aldosterone in leading to symptoms associated with Meniere's disease caused by endolymphatic hydrops. Aldosterone is a hormone that functions to retain fluid within individuals to help maintain homeostasis. Aldosterone in elevated amounts has been shown to lead to endolymphatic hydrops within the ear due to increased fluid retention. Behavioral tests and a behavioral ethogram will be used to examine the hypothesis that increased amounts of aldosterone given for a longer duration will lead to more severe symptoms of vestibular dysfunction than less amounts given for a shorter period. The data was tested for normalcy using histograms and a Shapiro-Wilkes test, and residuals normalcy examined with a quantile-quantile plot. These tests showed that the data was not normal, so either a robust parametric or nonparametric test would be required. Three single variable linear regression models were then used to determine that the amount of aldosterone given predicted the greatest variance on mouse balance with an r-squared value of 0.100, the duration of aldosterone administered had a mid-level impact with an r-squared value of .04, and mouse gender had the least effect on balance with an r-squared value of 0.003. Behavioral data and aldosterone blood level data will continue to be collected and analyzed using regression models throughout the remainder of this experiment. This study will determine if further research into the impact of aldosterone on vestibular dysfunction seen in Meniere's disease patients warrants further investigation. (5)

Brill, Charles*, and Thomas LaDuke East Stroudsburg University, East Stroudsburg, PA 18301. *Effects of human habituation on eastern gray squirrel predator response behaviors.- Sciurus carolinensis* (Eastern gray squirrel) are among the most prevalent urban adapted species, found in areas representing nearly every degree of urbanization. It is known that eastern gray squirrels exhibit variation in responses to visual threats across a gradient of rural-urban habitats, typically exhibiting more relaxed defense responses as the degree of urbanization increases. This relaxation in response is thought to allow eastern grey squirrels to better allocate energy to foraging and reproduction in urban settings allowing them to thrive in such conditions. However, in regards to nonvisual, purely auditory threat cues few studies have been done in regards to how these urban squirrels may alter their behavioral responses. This study seeks to examine the speed of response, duration of defensive behavior, and choice in response across the urban-rural gradient. Eastern grey squirrels across both urban and rural settings will be presented sounds chosen at random from a set of potential encounters. The chosen sounds are divided into four distinct categories, predator, non-predator, artificial, and conspecific warnings. Within each category are sounds representing a variety of possible threats, both avian and terrestrial. Recorded responses will be compared across habitat types at both sound category and individual sound levels. Any variation in responses will be useful in furthering our understanding of how eastern grey squirrels alter their defensive behaviors to thrive in a human dominated ecosystem. (54)

Brown, Megan*, Sherry Poole*, Jenna Waldron*, Dari Goldstein*, Wendi Gavilanes*, Bryce Armstrong*, and Itzick Vatnik Widener University, Chester, PA, 19013. *The effect of exposure to nitrate on freshwater crayfish (Procambarus clarkii).*- Nitrogen, in its various forms, is integral to both natural ecosystems and human activities, particularly in aquatic environments where ammonium (NH₄⁺) and nitrate (NO₃⁻) are dominant forms. However, human activities have disrupted the global nitrogen cycle, leading to elevated nitrate levels in water sources worldwide. This alteration poses significant environmental and health risks, affecting both aquatic organisms and humans. Despite the recognized risks, there remain large gaps in our understanding of the effects elevated nitrate levels have on freshwater organisms, specifically the freshwater crayfish, which are vital components of freshwater ecosystems. We conducted a series of experiments aim to investigating the effects of elevated nitrate concentrations on *Procambarus clarkii* aerobic metabolism, righting

response, hemolymph glucose concentration, and hemocyanin concentration to enhance our understanding of the effects of nitrate pollution on aquatic ecosystems and human health. (114)

Bullek, Autumn*, Sara Delgado, 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 development of wing and eye tissues. For example, Egfr signaling has well-established roles in the patterning of the wing, where it helps specify vein tissues, and the ovary, where it is crucial for establishing the body axes. 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, or constitutively active. We have employed multiple 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 have roles in normal eggshell structure and morphogenesis, rather than 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” to further explore their functions. Characterization of these mutants has revealed expected (previously observed) phenotypes, and in some cases additional eggshell phenotypes not seen with the original knockdown or P-element flies. 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, for example by investigating possible underlying ovarian defects via fluorescence microscopy to look at ovary structure. (109)

Burrell, Alex*, and Sophie Charvet Susquehanna University, Selinsgrove, PA 17870. *Quantifying gene expression in feeding prasinophytes.*- Mixoplankton are unicellular eukaryotes that are an integral component of the carbon cycle within aquatic ecosystems. Accurate delineation of their ecological role remains limited on account of their particular characteristics: the capacity to perform phagotrophic and phototrophic modes of nutrition. Phagotrophy is the strategy used by unicellular organisms to feed on other organisms and phototrophy is the use of photosynthesis to harness sunlight energy and fix CO₂. This flexibility poses a challenge when identifying precisely how mixoplankton interact with the carbon cycle and their aquatic ecosystems, particularly those with the ability to switch between modes of nutrition depending on different environmental factors. Our study focuses on prasinophytes, a group of small mixoplankton among the green algae. Having previously identified a list of “diagnostic” genes potentially indicative of an active feeding lifestyle under low nutrient availability, we now intend to design primers that can be used to study their changes in expression. In our first line of investigation, we are focusing on the Bardet-Biedle syndrome 2 protein (BBS2), involved in primary cilia function, and the light harvesting complex 1 protein 4 (LHCA4), involved in transferring light energy to chlorophyll *a*. Polymerase chain reactions (PCRs) conducted with a first primer set targeting the BBS2 gene, indicated that the BBS2 gene may be amplified from *Cymbomonas tetramitiformis*. Further optimization of primer design and PCR protocol is being explored to improve the efficacy of the amplification for both genes. A final set of primers will be subsequently used for quantitative PCR (qPCR), to monitor the dynamic expression of these target genes under different environmental conditions in *Cymbomonas tetramitiformis* and *Pterosperma* sp. (96)

Casey, Abigail*, David Foster, Richard Schaeffer, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Berberine: extraction, analysis, and evaluation of antibacterial effectiveness.*- Antibiotic resistance is a concern for medicine today because bacteria are becoming increasingly immune to antimicrobial agents. The overprescription of antibiotics over the last few decades has led to overexposure of bacteria to antibiotic substances, catalyzing their mutation and adaptation. This study seeks to address the growing need for novel antibiotic mechanisms to counter drug resistance utilizing plant extracts with antibiotic potential. *Berberis bealei* was selected as the subject for this study because the plants in the *Berberis* genus are known to produce the compound berberine in high quantities. Berberine is a secondary metabolite that has been identified as the primary active component of these plants, which have been used in traditional Chinese medicine for centuries to treat various ailments including bacterial infections. Extractions were made from branch samples taken from a live plant in south-central Pennsylvania, and they were analyzed with high-performance liquid chromatography (HPLC) and UV-Visual spectroscopy. Using a berberine standard curve, the dry mass percentage of berberine present in the plant was determined to be 1.12%. Preliminary tests with a berberine standard on *S. aureus* and clinically sourced *E. coli* showed that berberine might be effective at preventing growth of *S. aureus* at concentrations as low as 100 ppm and might be able to delay growth of *E. coli* in a dose dependent manner in concentrations ranging from 300 to 400 ppm. (70)

Charvet, Sophie* Susquehanna University, Selinsgrove, PA 17870. *Predation by green algae – regulated by a quest for nutrients?.*- Marine photosynthetic microbes are responsible for half of global primary production but most protist phytoplankton defy the standard plant/animal dichotomy by exploiting both photosynthesis and predation. While mixoplankton likely play a major role in microbial food webs by combining these two trophic modes, their diversity and ecology remain poorly understood. Recent studies indicate that species of prasinophytes, tiny green algae, can selectively consume bacteria, and even seem to increase their feeding when their growth medium contains low amounts of nutrients. This suggests that predation in mixoplankton must be under constant regulation to respond to environmental conditions. To test this, we investigated the transcriptional dynamics behind an observed increase in bacterivory in the prasinophyte *Pterosperma cristatum*. Our results show upregulation of genes involved in essential steps of phagocytosis including prey recognition, adhesion and engulfment, transport and maturation of food vacuoles and digestion. Unexpectedly, genes involved in the photosynthetic electron transfer chain, pigment biosynthesis and carbon fixation were downregulated as feeding increased, implying an abatement of photosynthesis. These results therefore suggest that depletion of inorganic nutrients triggered an alteration of trophic behavior from photosynthesis to phagotrophy in *P. cristatum*. These findings indicate that mixoplankton communities in nutrient-limited oceans can regulate photosynthesis against bacterivory based on nutrient availability. (55)

Christian, Nicole*, Alexander Emam*, Daniel Burden, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Analyzing the effect of E-liquids on oral commensal bacteria.*- The rise in electronic cigarette popularity, especially among adolescents, has prompted research to address the effects of vaping on the lungs. However, the first site exposed to vaping—the oral cavity—has received relatively little attention. Previous studies from our group have shown that E-liquids containing flavoring compounds at high concentrations have significant inhibitory effects on biofilm formation and growth, with cinnamon and menthol being the most detrimental. Herein, the effects of flavored and unflavored E-liquids on the oral commensal species *Streptococcus mutans*, *Streptococcus gordonii*, *Streptococcus intermedius*, and *Streptococcus oralis* were examined. Live/dead staining with confocal microscopy was conducted to determine the overall viability of mixed commensal biofilms following 5% E-liquid exposure. The results demonstrate that E-liquid with cinnamon or menthol flavoring has a bactericidal effect. Hydrophobicity assays were

conducted to test the effects of cinnamon or menthol flavor on the hydrophobicity of these four oral streptococci. While they display a natural hydrophobic tendency, a property that is essential to coaggregation and the formation of biofilms, direct exposure to cinnamon or menthol flavoring significantly increased this tendency. This shift in hydrophobicity may explain previously observed alterations in biofilm structure and may disrupt the homeostasis of oral biofilms. Therefore, vaping has the potential to prompt dysbiosis and alter the status of health and disease in the oral cavity. (68)

Conard, Payton*, Erin Kirschmann, and Eric Sweet Immaculata University, Immaculata, PA 19345. *Developmental profile of locomotor response to novelty and anxiety-like behavior in male and female mice.*- Rodent models of human conditions, such as novelty-seeking or anxiety-like behaviors, can provide valuable information, particularly with regard to how traits emerge developmentally. This project aimed to examine the stability of locomotor exploration of a novel environment and anxiety-like behavior across development in mice, and also to examine the role of biological sex in conservation of those behaviors. The stability of novelty-response and anxiety-like behaviors was assessed in male and female C57BL mice during adolescence and adulthood. Individual mice were exposed to a novel open field (OF) chamber for 90 minutes on four occasions during adolescence and adulthood (postnatal days 25, 27, 60 and 116). Novelty was preserved by changing visual, tactile, and olfactory cues in each exposure. Total distance traveled was recorded (novelty-seeking behavior), as was time in center (anxiety-like behavior). Results suggest that novelty-seeking behaviors in mice are not stable in adolescence but do stabilize in adulthood; total distance traveled was not consistent between p25-27, but was more consistent between p60-116. Interestingly, anxiety-like behaviors in mice were significantly correlated in adolescence, but did not reach statistical significance in adulthood. Additional mice are being tested at each developmental time point, to increase sample sizes. Recent studies have linked the gut microbiome to anxiety-like behaviors in mice, and there may be sex-dependent effects. The role of the gut microbiome as it pertains to developmental stability of novelty-seeking and anxiety-like behaviors in male and female mice has not yet been examined, so a future goal of this project is to investigate this relationship. Fecal samples of individual mice were collected after each OF test to be next-generation sequenced. Analyses will compare microbiome profiles across the four developmental time points and between sexes; and comparisons will also be made between mice with stable behavioral profiles and those with more variable behavioral profiles. (30)

Condon, Sarah*, and Glafera Janet Matanguihan Messiah University, Mechanicsburg, PA 17055. *Evaluation of the growth and agronomic performance of flax varieties (Linum usitatissimum) in South Central Pennsylvania.*- Flax (*Linum usitatissimum* L.) has immense potential in the dietary intervention against chronic diseases. Flaxseed oil contains high levels of omega-3 fatty acids, which can reduce the risk of heart disease. It also has properties that can lower LDL cholesterol and may prevent diabetes and certain types of cancer. This study was conducted to evaluate the agronomic performance of six flax varieties in South-Central Pennsylvania, namely 'CDC Bright', 'CDC Hammond', 'CDC Rowland', 'ND Hammond', 'Omega' and 'York.' Each variety was sown by hand in 3 m x 1.5 m plots in rows of 30 cm apart, with a seeding rate of 50 kg/ha. The plots were laid out in randomized complete block design (RCBD) with four replicates. Plant height, seed capsules per plant, number of seeds per capsule, and seed yield per plant were determined for each variety. Data on plant emergence, plant density, days to flower, days from planting to maturity, and lodging (on a scale of 0-9) were also collected. Throughout the growing season (May to September), weeds were removed manually and pesticides were not applied. Overall, results show that the flax varieties had comparable plot seed yield and agronomic performance. There were no statistically significant differences between variety means (ANOVA, < 0.05) for the following yield parameters: number of bolls (seed capsules) per

plant, number of seeds per boll, and seed yield per plot. The six varieties matured early, with 75% of the seed bolls of each of variety turning golden brown earlier compared with published values in North Dakota. 'Omega' showed lodging in one replicate but all plants recovered after two weeks. None of the flax varieties showed disease. These initial findings show that all six varieties can be grown well in South Central Pennsylvania, with potential to be incorporated in small-scale, sustainable farms. (67)

Conner, Rebecca*, Erica Ward, M. Dana Harriger, and Andrea Nagy Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Using an Ethosomal Solution to Study Transdermal Vitamin D3 Delivery on Dorsal Porcine Ears.*- Oral supplements are available to prevent Vitamin D3 deficiency, but individuals may still not meet the minimum daily requirement of 4000 International Units (IU) for oral medication to be effective. A recently developed ethosomal transmembrane delivery system, which is similar to liposomes but contains ethanol, lets users apply a dermal gel to facilitate faster absorption of a desired drug or active ingredient into the bloodstream. The delivery rate of ethosomes varies in literature due to the concentration of ethanol and permeation enhancers. To mimic human skin diffusion, a porcine ear skin model was utilized to examine if Vitamin D3-containing ethosomes could diffuse through full-thickness porcine dorsal skin and measured the amount of the vitamin that was able to diffuse through. Results from High-Performance Liquid Chromatography (HPLC) suggest ethosomes successfully transfer Vitamin D3 through full-thickness porcine dorsal skin. The results of this study can be used towards the creation of a new form of Vitamin D3 supplementation. (3)

Cruz, Siera*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *The effect of alkylation on mutation frequency and type in yeast.*- Nucleated cells are subject to 10 to 50 DNA double-stranded breaks every day. There are four repair pathways responsible for fixing those breaks, but only one of those four repairs the DNA accurately. We were interested in understanding the relationship between the four double-strand break repair pathways and how a cell determines which to use. To examine this relationship, an alkylating agent was used to indirectly generate double strand breaks in *Saccharomyces cerevisiae*. It was hypothesized that damage-treated yeast would have a higher mutation rate compared to untreated controls. URA3 gene mutations were detected on 5-FOA plates in yeast treated with the DNA-alkylating agent, methyl methanesulfonate (MMS) and untreated control yeast. Yeast treated with MMS had ~4-fold higher *ura3* mutation rates than untreated controls. The result of the mutation rate being higher in MMS-treated yeast than untreated control yeast is expected because inaccurately repaired damage can lead to mutations. Future work will investigate how mutation rates and mutation type vary in the absence of different DNA repair pathways. (37)

Daisey III, Gene*, and Cosima Wiese Misericordia University, Dallas, PA 18612. *Exploring potential causes of increasingly frequent harmful algal blooms in Lake Louise, Franklin Township, Pennsylvania.*- Freshwater lake ecosystems are important ecosystems and provide substantial benefits to human populations. However, harmful algal blooms (HABs) pose a consistent, serious, and increasingly frequent threat to the overall health of freshwater lakes. In recent years, Lake Louise, located in Franklin Township, Pennsylvania, has been experiencing bouts of HABs, degrading the overall health and appearance of the lake, as well as posing concerns for the local community. Despite this concern, there is a lack of clarity as to how to prevent these events from occurring because of the lack of a consensus as to what generally drives HABs in the first place. Field sampling of Lake Louise at 9 locations was conducted monthly throughout 2023. This sampling primarily focused on recording various water quality parameters along with chlorophyll-a readings to represent algae concentrations, and laboratory testing was conducted on samples to measure phosphate levels. Long-term data analysis included regression analyses and correlation

tests to determine if a relationship exists between water quality parameters and algae levels. ANOVA analyses were also conducted to determine if any parameter patterns could be identified based on the month of sampling or the sampling sites. The results showed that no significant relationship could be established between water quality parameters and algae levels across 2023. At the same time, however, the results showed significant differences in nitrate and phosphate readings between the warmer and colder months. Therefore, while no direct relationship could be established, there is a significant change in nitrate and phosphate levels coinciding with observed increases in HAB occurrences in the lake. With this in mind, it is important that future research delves deeper into the potential impacts of nitrate and phosphate levels on HAB frequency in the lake, particularly by establishing more frequent sampling and extending the dataset over multiple years. (100)

Dannenber, Kaitlin*, and Jason Smith York College of Pennsylvania, York, PA 17405. *A study of how plant growth regulators impact plant growth in various succulent species over a ten week period.*- Plant growth regulators (PGRs) are a common tool in greenhouse management and can be utilized to promote desired traits and growth rates in plants such as slowing plant growth to avoid overgrowth prior to sale. It is important for growers to understand the minimum applications necessary to achieve these goals while maintaining cost effective management practices. This experiment examined the effect of various plant growth suppressors on a variety of succulents: *Sedum spathulifolium* 'Silver Roses', *Sedum mexicanum* 'Lemon Coral', *Sedum* 'Fine Gold Leaf', *Sedum hispanicum* 'Spanish Stonecrop', and *Crassula pellucida* subsp. *marginalis* 'Crassula Petite Bicolor'. Foliar spray applications of uniconazole-p (4 ppm-32 ppm), paclobutrazole (5 ppm-40 ppm), and fluprimeidol (4 ppm-32 ppm) were applied to over 600 plants in a replicated greenhouse experiment. Subsequent plant growth was monitored over a ten-week period and compared to untreated controls. Measurements were taken by photographing these plants after 2 weeks, 6 weeks, and 10 weeks and then analyzing growth utilizing ImageJ and Prism10. Our findings resulted in recommendations for growers for the minimum amounts of PGRs needed to suppress growth in each plant species. Minimum effective applications of PGRs included 4ppm of paclobutrazole or fluprimeidole for *Crassula pellucida* subs. *marginalis*, 5ppm of paclobutrazole for *Sedum spathulifolium*, 8ppm of uniconazole-p for *Sedum mexicanum*, 5ppm of paclobutrazole for *Sedum* 'Fine Gold Leaf', and 10ppm of paclobutrazole for *Sedum hispanicum*. These findings provide multiple cost-effective options concerning PGR applications. (113)

Davoudi Kianersi, Hedyeh*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Analysis of chromosome movements in cell division in the milkweed bug Oncopeltus fasciatus.*- There are no comparative analyses of chromosome movements during mitosis, meiosis I, and meiosis II in the same species. In this study we performed an initial characterization of chromosome movement during the three types of cell division in the milkweed bug *Oncopeltus fasciatus*. Milkweed bugs belong to the insect order Hemiptera, and like other Hemipterans have holocentric chromosomes in mitosis. In meiosis, the chromosomes appear to designate a position on the chromosome to act similarly to a monocentric kinetochore. While milkweed bugs have been studied since the first decade of the 20th century, there have been no studies of chromosome movements in living cells of the species. Meiosis I and II spermatocytes were isolated from adult males, while mitotically-dividing cells were obtained by spreading egg contents from cells under halocarbon oil. For each cell observed we measured pole to pole distances in each cell at 20 second time points, instantaneous rates of spindle expansion were measured at all of the time points for each cell. Also, rates of chromosome movement were calculated through anaphase. The preliminary data show that the rate of chromosome movement and spindle movement vary at different time points, including in anaphase, and that rates of chromosome movement in mitosis are faster than those in meiosis I and meiosis II. (48)

Donovan, Angelena*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Synthesis of ionic liquids and their application for electrophilic aromatic substitution reactions.*- This investigation will involve the synthesis of the ionic liquid 1-hexyl-3-methylimidazolium hexafluorophosphate. This ionic liquid will be substituted for the organic solvent methylene chloride and used for electrophilic aromatic substitution of an acetyl group on methoxybenzene in the four position on the aromatic ring. The ionic liquid would stabilize the arenium ion intermediate allowing for a greater product yield. There are many advantages for using these ionic liquids over organic solvents for these reactions. Ionic liquids are recyclable, they can stabilize intermediates, and the product yields are typically higher. Using ionic liquids for organic syntheses would require less energy and would also be a less toxic alternative to typical organic reaction solvents. After the synthesis was completed, the characterization was conducted using FT-infrared (IR) and FT-Nuclear Magnetic Resonance (NMR) spectrophotometers. The IR shows the carbonyl (1700 cm⁻¹), ether (1100 cm⁻¹) and aromatic (18-2000 cm⁻¹) functional groups for the product. The NMR gives the four aromatic hydrogens (7-8 ppm), three methyl hydrogens attached to an oxygen (4 ppm) and three methyl hydrogen attached to a carbonyl (2.5 ppm). (12)

Dotta, Austin*, and Alex Huynh DeSales University, Center Valley, PA 18034. *Uropygial gland size increases isometrically with body size in 35 North American bird species.*- The uropygial gland and the oils it produces have been shown to serve important functions in many bird species including plumage maintenance and chemical communication. Previous species comparisons of uropygial gland size have only been conducted in South American and European birds and have found little to no phylogenetic signal. Here, we document uropygial gland measurements of 34 different passerines, 1 hybrid chickadee population, and 1 piciform in eastern Pennsylvania, most of which are reported for the first time. Uropygial gland size is positively related to overall body size, controlling for phylogenetic relatedness. We show a significant phylogenetic signal of relative uropygial gland size and many of the species with the largest gland sizes belong to the Paridae. Overall, females show a nonsignificant but slight trend of larger relative uropygial gland sizes than males. This effect is stronger in some species than others and can also be seasonally dependent. We found no effect of total eggshell surface area or nest location on relative uropygial gland size. Together our results provide the first documentation of uropygial gland sizes in many of these North American species and provide interesting insight into factors influencing relative gland size including sex, season, and species. (59)

Dotta, Austin*, Taylor DeHaven*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Lampyre lobster hemocyanin is demonstrates no antibacterial activity against ESKAPE relatives.*- 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 pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*). Hemocyanins are proteins that bind and transport oxygen in the hemolymph of crustaceans. The lampyre lobster hemocyanin (LLH) has been shown to be an effective protein carrier and suggested to have antiviral and anti-inflammatory activity. Our study aims to determine whether (LLH) has antibacterial properties. In this study, we tested whether LLH had antiviral activity against both ESKAPE pathogen relatives and other bacteria, including *Enterococcus aerogenes*, *Mycobacterium smegmatis*, *Acinetobacter baylyi*, *Escherichia coli*, *Streptococcus epidermidis*, and *Bacillus subtilis*. No bacterium was inhibited by the range of concentrations used. (90)

Doyle, Aidan J.*, Liam H. Semmler, Evan S. Waite, Vaughn Shirey, and Stephen C. Mason, Jr. Immaculata University, Immaculata, PA 19345. *Comparing beetle (Insecta: Coleoptera) biodiversity at different sites on Hog Island, Maine.*- Healthy ecosystems rely on

the foundation of high biodiversity. Since insects are the most biodiverse animal group in the world, they make ideal study organisms when testing ecological and conservation hypotheses. For this research, we focus on beetle (Insecta: Coleoptera) species richness and abundance to compare different habitats on Hog Island, Bremen, Maine managed by the National Audubon Society. We predict that the site with the most even vegetation community will have different beetle biodiversity than the most uneven vegetation communities. During July 2023, we visited Hog Island for 10 days and sampled five different sites (spruce high elevation, spruce low elevation, spruce blowdown, deciduous mainland, and milkweed field). We set up 4-5 pitfall traps at each site to collect epigeic beetle species. A pairwise comparison for each site was then conducted by using an Analysis of Variance (ANOVA) on beetle abundance. Across our five sites, 182 beetles were collected. The milkweed field had significantly (<0.05) higher beetle abundance than the other four sites. There was no difference between the other four sites when doing a pairwise comparison with beetle abundance. Our original prediction was supported when looking at beetle abundance since the milkweed field had the most even vegetation community. We expect that the milkweed field will also have higher beetle species richness (which will also be presented at PAS). Our research helps to determine the biodiversity on Hog Island. This will directly benefit the National Audubon Society by giving them greater insight into making more effective conservation management decisions for the Island. (82)

Durkee, Hannah*, and Sean Buskirk West Chester University, West Chester, PA 19383. *Investigating the evolution of alcohol tolerance in the ESKAPE pathogens.*- Considering the well-documented development of antibiotic resistance, the potential for evolved tolerance to alcohol-based antiseptics raises concern. Antiseptics are used globally to kill or inhibit the growth of bacteria to prevent infection. The ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter spp.*) are a major cause of healthcare-associated infection and mortality which pose a threat due to the development of multidrug resistance. The main purpose of this study was to determine if these pathogens develop a tolerance to ethanol after repeated exposure and if so, to identify the genes responsible through whole genome sequencing. We accomplished this by determining the concentrations of ethanol that kill 99.9% of bacteria for each pathogen and exposing them to these concentrations for a series of 20 days. We demonstrated that repeated ethanol exposure, killing most but not all cells, results in an increase in ethanol tolerance among the gram-positive ESKAPE pathogens (*S. aureus* and *E. faecium*) in comparison to their respective ancestors. Varying cell mechanisms were involved in ethanol tolerance including transcription activation, ATP synthesis, and cell wall synthesis. The identification of the associated genes contributes to our understanding of bacterial evolution under alcohol exposure and offers insight into potential targets for the development of alternative antimicrobial agents. These findings further reinforce the importance of considering alternative strategies to combat the ESKAPE pathogens and provide a foundation for future research aimed at addressing these challenges. Furthermore, our work highlights the need for deeper investigation into the evolutionary impact of repeated exposure of bacterial pathogens to antimicrobials. (102)

Edwards, Alison*, Hannah Bonser, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Examining the bridging interactions of cancer associated protein Ddc2p with Replication Protein A and Mec1p using the budding yeast Saccharomyces cerevisiae.*- In 2022, there were over 9.7 million deaths caused by cancer worldwide. Cancer, often characterized by its uncontrolled cell division, can arise from a variety of DNA mutations. These mutations may affect proteins involved in cell cycle regulation and can thus facilitate uncontrolled cell division. A protein that helps in the regulation of 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 a major role in DNA replication,

recombination, and repair. RPA may become phosphorylated when DNA is damaged as a part of the cell's DNA damage response. This phosphorylation event may also aid in cell cycle regulation. The model organism, *Saccharomyces cerevisiae*, is used in this study due to the similarities between the yeast and animal cell cycles, as well as the ease with which the yeast cells can be genetically manipulated. Using proteins that are homologous in yeast and human cells, we hypothesize that Ddc2p (homolog of human ATRIP) may act as a bridge between RPA and the cell cycle regulation protein Mec1p (homolog of human ATR) in a phosphorylation-dependent manner. The Yeast Two Hybrid system was used to examine the direct physical interactions between Mec1p, Ddc2p, and RPA to determine whether RPA's phosphorylation state regulates the strength of these interactions. Our results suggest that the Ddc2p interactions with RPA may be modulated by the phosphorylation state of RPA and that this may regulate the RPA, Ddc2p, Mec1p complex formation. By gaining a better understanding of the interactions between proteins we may be able to provide insights for novel cancer treatments. (32)

Eichner, Miranda*, Dhruv Kayastha*, and Nik Tsotakos Penn State University-Harrisburg, Middletown, PA 17057. *Annotation and comparative analysis of the sticks-and-stones homologs in the *Drosophila melanogaster* subgroup: implications for studying human congenital nephrotic syndrome.*- Nephrocytes, through filtration epithelium, play a vital role in the excretory system, which is critical for maintaining homeostasis of fluids in multicellular organisms (Miyaki et al, 2020). The nephrocytes in *Drosophila* display analogous functions, morphological structures, and molecular features, to the podocytes found in the human renal system, making them a model organism for study of glomerular disorders in end-stage renal disease (Helmstädter et al, 2017). In humans, congenital nephrotic syndrome is a glomerulopathy resulting from mutations of the *NPHS1* gene, which encodes the protein nephrin. The *Drosophila melanogaster* homolog, *sticks-and stones*, or *sns*, was named for its mutant form that causes a lack of body wall muscle formation and unfused myoblasts (Bour et al, 2000). The *sns* product is a member of the immunoglobulin superfamily (IgSF) and is important in the formation of multinucleated muscle cells in *Drosophila*. The expression of *sns* also plays a role in the filtration of insect hemolymph through the movement of molecules through a nephrocyte-like diaphragm (Zhuang et al, 2009). The *sns* gene product seems to function in cell adhesion and recognition, believed to play a role in their nephrocyte behavior, as it binds to Kirre to form the nephrocyte diaphragm, a cell junction that distinguishes molecules by size and controls their access to transport channels (Zhuang et al, 2009). Knock down of *sns* results in decreased number of nephrocyte diaphragms on the cell surface. Mutations to *sns* result in mutated nephrocyte diaphragms that do not function properly due to morphological abnormalities (Zhuang, 2009). In the present work, we annotated the *sns* gene in 4 different *Drosophila* species using bioinformatics programs. The annotations of the gene homologs highlight the regions of *sns* that are highly conserved, and the regions of *sns* that are prone to variation. This work will add to the current understanding of the evolution of nephrocyte activity. (33)

Faia, Louis*, James K. Murray Jr., and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Developing a more specific histone deacetylase inhibitor.*- SAHA (Vorinostat) is a histone deacetylase inhibitor (HDai) which is FDA-approved to treat T-cell Lymphoma after the failure of other treatments. Because SAHA inhibits many different histone deacetylases, it comes with side effects including nausea, diarrhea, fatigue, thrombocytopenia, dehydration, and pulmonary embolism. The goal of this project is to test the ability of SAHA-derived potential HDais to increase histone acetylation in yeast. Yeast were treated with SAHA or derivatives previously shown to affect yeast growth and histone acetylation was measured by western blots. Preliminary results suggest that SAHA derivatives that affect yeast growth do not have a significant effect on histone acetylation

levels. This could indicate that they are more specific than SAHA. Further tests are needed to determine what, if any histone deacetylase they are inhibiting. (38)

Fake, Kyle*, Steven Urban, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Impact of agro-wastes: Cocos nucifera (coconut coir), Carya illinoensis (pecan shells), and Oryza sativa (rice husks) on growth timelines, fruition production, and average diameter of Pleurotus ostreatus (oyster mushrooms).*- This experiment investigates how *Pleurotus ostreatus* (oyster mushrooms) would decompose unconventional agricultural waste products into food. It was hypothesized that *Pleurotus ostreatus* would successfully colonize rice husks, coconut coir, and pecan shells, producing edible fruiting bodies faster and greater in mass than traditional, straw-based monocultivation methods. The three experimental groups of the experiment include 100% compositions of the following substrates: *Cocos nucifera* (coconut coir), *Carya illinoensis* (pecan shells), and *Oryza sativa* (rice husks). A 100% composition of a *Triticum aestivum* (wheat straw) control group was benchmarked to measure growth timelines, fruiting mass per kg of substrate, and average fruiting cap diameter. Rice husks reached colonization and total growth timeline faster than all other subjects ($p < 0.05$). Rice husks also resulted in increased fruiting mass compared to coco coir and pecan shells ($p < 0.05$) while showing no difference in fruiting mass compared to straw ($p > 0.05$). There was no statistical relevance observed in the average cap diameter among the groups tested ($p > 0.05$). Since rice husks colonized/produced fruiting bodies faster with no significant differences in quality or quantity, rice husks would be a preferable medium in a commercial setting. In comparison, coco coir and pecan shells are not ideal substrates due to poor fruition ratios and comparable growth timelines to that of straw. Future studies should test other cereal grain husks and nuts for use in oyster mushroom cultivation, observe lignin's impact on oyster mushroom cultivation, and analyze the impact of mixing different substrates. (65)

Ferguson-Richards, Adore*, Zahra Imrani*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Assessing the correlation between pain tolerance and ACTN3 genotype.*- The endurance, strength and speed of slow-twitch and fast-twitch muscle fibers contribute to athletic performance. The *ACTN3* gene, which encodes the sarcomeric protein alpha-actinin-3, is only expressed in fast-twitch muscle fibers. This gene has two alleles: the wild-type R allele and the null X allele, which produces no alpha-actinin-3. Individuals with two copies of the null allele (XX) show decreased athletic performance in sports requiring strength and speed in comparison to those with wild type (RR) and heterozygous (RX) genotypes. However, XX individuals show better performance in sports that require endurance because slow-twitch muscle generates ATP with greater efficiency than fast-twitch. The X allele is overrepresented among certain ethnic groups, likely because the improved energy conversion ability of these individuals has favored survival in nutrient-limited environments. We hypothesized that the increased physical endurance of XX individuals might partly be due to their increased resistance to physical discomfort and pain in comparison to RR and RX individuals. We recruited test subjects in accordance with IRB-approved protocols, determined their *ACTN3* genotypes using buccal DNA extraction coupled with quantitative PCR (qPCR), and measured pain tolerance by completion of a Cold Pressor Test (CPT). We applied the analysis of variance (ANOVA) statistical test to determine correlation between *ACTN3* genotype and pain tolerance. (25)

Flores, Maria*, Torianne Morrow*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Navigating overexpression challenges: mutant MDH production in E. coli.*- The citric acid cycle is an important metabolic pathway in metabolism. Metabolic pathways form complexes of sequential enzymes known as metabolons that benefit from non-covalent association. Malate dehydrogenase (MDH) is one of the enzymes in the citric acid cycle that forms metabolons with other enzymes. MDH uses malate or oxaloacetate as substrates and

NADH or NAD⁺ as cofactors. MDH exists in both cytosolic and mitochondrial isoforms. The enzyme activity of MDH can be post-translationally modified through phosphorylation, an area of interest for this study. To study the activity of these proteins, mutants of MDH were created. These mutants are referred to as phosphomimics, because they replace a Ser or Thr residue with a Glu or Asp residue which mimics the size and negative charge. These mutants are overexpressed in *E. coli*, lysed using sonication and purified using Ni-NTA affinity chromatography. Protein overexpression can be highly dependent on temperature, length of overexpression, and concentration of IPTG. In addition, cell lysis can be additionally problematic in trying to facilitate adequate cell lysing while minimizing protein denaturation and degradation. Following fast-protein liquid chromatography (FPLC), purified fractions are quantitated by Bradford assay and assessed for purity by SDS-PAGE. Purified enzyme is then dialyzed into storage buffer in preparation for determination of activity by enzyme assay. We have initially utilized a His-tagged fusion protein of MDH and green-fluorescent protein (GFP) to easily visualize the progression through overexpression, lysis, and purification steps. Results using wild-type (WT) MDH and four phosphomimics (S8D, S45D, Y56D, and T85D) are expected to have similarly successful outcomes, generating protein for downstream study. We are most interested in how the activity of these phosphomimics will be affected by pH. One hallmark of dysregulated metabolism is altered cellular pH, which may impact the ability of cancer cells to regulate their uncontrolled growth. (46)

Foriska, Isabella*, and **Rajinikanth Mohan** Mercyhurst University, Erie, PA 16546. *Filamentation of novel bacterial and yeast species.*- Investigating the filamentation of bacteria and yeast is a vital field of study that is still evolving and growing to this day. Bacterial and yeast filamentation allows for many benefits for the species that display this trait, including protection from various stressors, such as heat, antibiotics, and even molecular predators, such as immune system cells or bacterivores. However, the exact mechanism of filamentation and what species are capable of exhibiting this trait are still widely unknown. In this study, I sought to discover new species that are capable of exhibiting filamentation by analyzing a variety of representative species from four different phyla of bacteria and a yeast species. Utilizing heat as the primary stressor and gram staining to visualize the microbes, I was able to not only confirm the filamentation abilities of two well-established species, *Bacillus subtilis* and *Pseudomonas aeruginosa*, but I was additionally able to find at least three bacterial species which are not widely known to filament, *Flavobacterium pectinovorum*, *Delftia acidovorans*, and *Serratia marcescens*. These results indicate that the ability to filament under stressful conditions may be much more widespread than previously believed. This implies that this trait may have more benefits allowing for it to evolve in different phyla or carry throughout the line of evolution. Future directions of this study are focused on finding more novel bacterial and yeast species displaying this trait under both heat stress and new stressors, such as salt and antibiotic concentrations. Additionally, another realm to be studied is possible mechanisms behind filamentation. (8)

Foster, Ava*, **Wei-Jin Lin**, and **Lawrence Mylin** Messiah University, Mechanicsburg, PA 17055. *Evaluation of bacteriophage T4-neutralizing antibodies secreted by murine hybridoma clones.*- 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 with 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-neutralizing 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. 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, and culture supernatants from candidate 2F12 consistently showed the strongest inhibition. We have since established clones from each candidate line and reevaluated neutralization. Culture supernatants from clone 3D9-1H7 displayed the strongest inhibition, and this clone was used in a CELLline 1000 unit to produce larger volumes of concentrated antibody supernatants. Characterization of the 3D9-1H7 supernatants will be described. (73)

Franzone, Katherine*, and **Andre Walther** Cedar Crest College, Allentown, PA 18104. *Analyzing the effect of RPA phosphorylation on interactions with DNA repair proteins in Saccharomyces cerevisiae*.- According to the American Cancer Society, in 2024 there will be over 2 million new cancer diagnoses with over 611,000 cancer-related deaths in the United States alone. Current non-specific chemotherapeutic cancer treatments that target actively dividing cells also damage the patient's healthy cells, resulting in unwanted side effects and decreased treatment efficiency. Development of next-generation chemotherapeutic drugs with increased specificity requires an improved understanding of DNA repair pathways. To better understand DNA damage and repair the responses of selected proteins in eukaryotic cells, our project focused on analyzing the interactions of DNA repair proteins in the extensively used model organism baker's yeast, *Saccharomyces cerevisiae*. Specifically, we analyzed the function and role of phosphorylation of Replication Protein A (RPA)—a highly conserved protein involved in DNA replication and repair in both humans and yeast—with the yeast helicases *SRS2* and *SGS1*. To dissect the function of RPA, we examined the sensitivity to DNA damage of previously generated strains that contain various mutations in the yeast RPA homolog, RFA, along with mutated versions of *SGS1* and *SRS2*, using spot assays to look at the survival of yeast on media (YEPE) with various concentrations of the chemotherapeutic agents camptothecin and hydroxyurea. The differences in growth and survival rates of the various strains in the spot assays allowed for preliminary conclusions to be drawn about the effect phosphorylation of RPA in the cellular response to DNA damage. Additionally, we will discuss how these repair proteins are physically interacting depending on the phosphorylation of RPA using a yeast two hybrid system. 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 treatments. (36)

Gallagher, Casey, David Rothblat, and Jaimy Joy* La Salle University, Philadelphia, PA 19141. *Tenofovir disoproxil fumarate induces premature senescence in primary human fibroblasts*.- Human Immunodeficiency Virus (HIV) is an enveloped retrovirus that predominantly targets activated CD4+ T cells. If left untreated, HIV can lead to AIDS (Acquired Immunodeficiency Syndrome), characterized by a severely compromised immune system that increases susceptibility to opportunistic infections and cancer. Combination antiretroviral therapy (cART) has changed HIV from a terminal illness to a manageable chronic condition. There are multiple classes of cART that work to inhibit viral replication by interfering with various stages of the HIV life cycle. While cART effectively inhibits viral replication, it also contributes to age-related comorbidities, such as neurocognitive decline, metabolic disorders, and renal dysfunction, in people living with HIV (PLWH). cART may promote age-related disorders by inducing cellular senescence, which is strongly associated with aging and age-related decline and dysfunction. For example, long-term use of tenofovir

disoproxil fumarate (TDF), a nucleoside reverse transcriptase inhibitor routinely used in the management of HIV, has been previously associated with age-related disease, such as loss in bone mineral density. We sought to investigate whether TDF induces premature senescence in primary human cells and whether this may, in turn, contribute to the accelerated aging phenotype in PLWH. IMR-90 cells, a primary human fibroblast cell line, were treated with high-dose TDF and growth patterns were assessed by measurement of population doubling levels. High dose TDF treatment resulted in premature senescence after one week, as determined by a halt in cell growth and proliferation and an increase in beta-galactosidase positive cells. We also observed an increase in the expression of some senescence associated genes. Collectively, these results suggest that TDF induces premature senescence in primary cells, which may provide a molecular mechanism by which long-term TDF use promotes age-related disease. (39)

Ganzorig, Maral*, and Cecilia Bove York College of Pennsylvania, York, PA 17405. *How ciprofloxacin antibiotic may induce prolonged anxiety-like behavior and gastrointestinal dysfunction in rats.*- Fluoroquinolone antibiotics (FQs) are only recommended for life-threatening infections; however they are still being over-prescribed. FQs may cause Fluoroquinolone Associated Disability (FQAD) which could be long-lasting, if not permanently disabling. FQs may induce Central Nervous System (CNS) symptoms by antagonizing GABAA receptors. Other studies suggested that FQs also act as NMDA receptors agonists. The vagus nerve is under control of both neurotransmitters. Considering that this nerve regulates the gastrointestinal (GI) tract and mood, the goal of this study was to test whether CPX causes anxiety-like behavior in rats and GI dysfunction. Sprague Dawley rats were divided in a control (CTL) and a treatment (CPX) group, which received daily oral administration of 0.9% NaCl and 20 mg/kg of ciprofloxacin respectively for 14 days. To determine whether rodents developed an anxiety-like phenotype, we conducted the Marble Burying Test (MBT), the Elevated Plus Maze test (EPM), and the Open Field Test (OFT) at baseline (day 0), and every 7 days for a total of 4 weeks. At the end of this 4 week period, animals received a dose of phenol red dye, and then were sacrificed. The GI transit was assessed indirectly by measuring fractional dye recovery from the stomach and the small intestine. We compared CTL to CPX animals at each time point, and each group at the different time points. The results of this study suggest that CPX accelerates gastrointestinal transit and causes anxiety-like behavior even two weeks after the end of the treatment. This could be the result of changes in GABAergic and glutamatergic transmission in the CNS. More studies are necessary to confirm the role of the vagus nerve in the observed alterations. (42)

Gaston, Laurel*, and Jeff Erikson Messiah University, Mechanicsburg, PA 17055. *Creating a predictive model for limestone stream health assessment and monitoring through historical macroinvertebrate and water chemistry data.*- Proper limestone stream health assessment is necessary in determining their management and treatment. However, traditional assessments of health such as the Index of Biotic Integrity are based on a sandstone bedrock type, which has a water chemistry set dissimilar to streams with a limestone bedrock type. This different water chemistry in limestone streams can impact macroinvertebrate abundance and diversity, which are the features that traditional sandstone IBIs rely on to assess stream health. Limestone streams regularly have a lower diversity of macroinvertebrates, with a high abundance of a few taxa. This pattern often leads to a poor health assessment of these locations by the standard IBI. Limestone streams also tend to have higher electrical conductivity, alkalinity, and total CaCO₃ hardness. Correlations between water chemistry and IBI metrics and indices for 385 site locations, 121 of which were true (alkalinity \geq 140 mg/L) limestone streams, were investigated to evaluate their statistical significance. This data was collected from the Susquehanna River Basin Commission (SRBC) and historical data from Professor Jeff Erikson of Messiah University.

Final results utilizing Microsoft Excel and Minitab showed a consistent non-statistical significance in correlation between conductivity, alkalinity, and total CaCO₃ hardness for % Tolerant Organisms, % Chironomidae, PADEP Tolerance Values, and % TV \geq 7 metrics and indices across limestone streams when compared to all streams. Therefore, their removal in a true limestone stream IBI may be beneficial. Continued research in Spring 2024 will seek to assess predictive model accuracy to new field data. (111)

Gibbs, Evan*, **Jessica Nolan**, and **Jason Smith** York College of Pennsylvania, York, PA 17405. *A recursive matlab model for nitrate in a decoupled aquaponics system.*- Recently, aquaponics has been at the forefront of sustainability efforts, combining both aquaculture and hydroponics to effectively use the waste of fish to grow plants. The design of such systems has prompted the development of specific fish diets to also be more sustainable, with some including the reuse of food waste from humans. This study focused on developing a mathematical model for predicting nitrate concentrations among the two components of a self-designed, decoupled aquaponics system, where nitrate concentrations were primarily influenced by the protein composition of a sustainably-sourced fish food diet consisting of food waste from a college cafeteria. A recursive, piecewise model was created to predict nitrate concentrations in a system of Blue Tilapia (*Oreochromis aureus*) and Hybrid Winterbor F1 Kale (*Brassica oleracea var. Sabellica*). To test this model's accuracy, six individual decoupled aquaponics systems were run, with diets composed of either 25% or 40% protein. Our model predicted that when the protein content of the food was increased to 40%, there would be at least 90% higher levels of nitrate in the fish tank by the end of 9 weeks, resulting in a longer-lived presence of nitrate in the plant component of our systems. An experiment, carried out to validate the model, confirmed a sizable difference in the level of nitrate concentrations in the fish tanks. However, the systems highlighted an over-prediction by our model for the plant-uptake rate of nitrate when water was transferred to our plant components. This study highlights a promising model that can be further refined for increased accuracy and can be generalized to have strong application in both commercial and hobbyist aquaponics. (101)

Glenn, Madeline*, **Gabrielle Seagreaves***, and **Lara Goudsouzian** DeSales University, Center Valley, PA 18034. *Assessing changes in pond fungal communities after chemical treatment.*- Ponds are important repositories of biodiversity that can house many endangered and rare aquatic taxa. They provide refuge for terrestrial and aquatic wildlife in heavily modified landscapes such as campuses or neighborhoods. In these settings, chemical treatments are often applied to pond water to reduce the growth of plants and algae. The effects of these treatments on fungal communities within the ponds are largely unknown. We collected soil samples from two such environments: a university campus pond treated with herbicides and anti-algal agents, and an untreated pond in an adjacent nature preserve. We extracted genomic DNA and submitted the samples to a commercial facility for amplification and paired-end sequencing of the ITS2 region of the fungal genome. We performed sequence analysis using the DADA2 ITS pipeline. The three most abundant genera in the treated pond were *Pyrenochaetopsis*, *Penicillium*, and *Coniochaeta*, and the three most abundant in the control pond were *Fusarium*, *Discosia*, and *Cladorrhinum*. Of note is the presence of the genus *Talaromyces* in the treated pond, a pathogenic mold endemic to southeast Asia which causes disease in rodents and humans. We conclude that both ponds contain similarly diverse fungal communities, but with scant overlap of genera between the two. (6)

Greene, Hallee*, and **M. Logan Johnson** University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Better understanding of protein interactions with jazf-1.*- Endometrial stromal sarcomas, (ESS's), are rare uterine malignancies that occur in women. Gene fusions are one of the main causes for these sarcomas with a JAZF1/SUZ12 fusion being the most

common. Less frequently, *jazf-1* gene fusion with other genes results in ESS's, but these always include the N-terminus of *jazf-1*. This experiment aims to further define protein interactions with *jazf-1*. The yeast two-hybrid system brings two proteins of interest together to test for direct interactions in an *in vivo* setting. Previous yeast two-hybrid interactions have uncovered interactions with *jazf-1* between *hr78* and *drm* in *Drosophila melanogaster*. Therefore, we have generated a series of segments with *jazf-1* to test against *hr78* and *drm* in a yeast two-hybrid system. Using this approach should allow us to define what regions contribute to protein-protein interactions with *jazf-1* and known interacting proteins. Furthermore, should better define the N-terminal region of *jazf-1* that contributes to ESS formation. (85)

Grove, Austin*, and Daniela Zarnescu Messiah University, Mechanicsburg, PA 17055. *Testing the effect of phosphoglycerate kinase 1 activation with terazosin in a Drosophila model of amyotrophic lateral sclerosis.*- Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease which affects motor neurons and results in paralysis and eventual death. ALS has no cure and the treatments for it offer no substantial alteration in the disease progression. It is characterized by a delocalization of the DNA/RNA binding protein, TDP-43, into the cytoplasm. Approximately 31,000 patients live with ALS in the United States, and about 5,000 people are diagnosed with this disease yearly. 50% of individuals diagnosed with ALS live three years or more after diagnosis, 25% live five or more years, and only 10% live more than ten years. Mechanistically, mitochondrial dysfunction, increased oxidative stress, and decreased ATP production are linked to ALS pathology. Previous findings from the Zarnescu lab showed that increasing glycolytic flux either genetically or with a high carbohydrate diet neurons is protective in *Drosophila* models of ALS. This makes targeting cellular bioenergetic pathways a promising strategy for therapy. Specifically, the glycolytic enzyme phosphoglycerate kinase 1 (PGK1) was downregulated in astrocytes of mice with ALS. PGK expression is reduced in fibroblasts of ALS patients, and glycolytic ATP production is reduced in patient derived i-motor neurons. In zebrafish, increased activation of PGK with terazosin improved motor behavior phenotypes. I hypothesize that terazosin mediated activation of PGK1 rescues the motor deficit phenotype in *Drosophila* models of ALS as it does for zebrafish. To test my hypothesis, I administered terazosin in *Drosophila* models of ALS in three different concentrations, 1, 10 and 20 μ M in media. The effects of the drug were measured using locomotor behavior and survival assays in flies expressing wild-type TDP-43 (TDP-43WT) or disease associated mutant TDP-43 (TDP-43G298S) in motor neurons, compared to w1118 genetic background controls. Preliminary experiments showed that using terazosin to activate PGK improves locomotor function but has no significant effect on survival in *Drosophila* models of ALS based on TDP-43 overexpression. These data suggest that increasing glycolysis may be a viable strategy in mitigating aspects of motor neuron dysfunction in ALS. (26)

Hauk, Tyler*, Natasha Sherinsky, and Tanya Hawley Matlaga Susquehanna University, Selinsgrove, PA 17870. *Impacts of water availability on Plethodon cinereus.*- Throughout the past several decades, we have seen a continuous increase in global surface temperatures. In response, some habitats are drier, and these abiotic changes have resulted in shifting distributions for species across a variety of taxonomic groups. We examined the effects of water availability on *Plethodon cinereus*, the Eastern Red-Backed Salamander, a species that breathes exclusively through its skin and requires damp conditions to survive. This species has two main color morphs, the red-striped and lead phases, with lead phase individuals documented to have increased tolerance for higher temperatures and limited water availability. Our study asks how salamander growth and behavior differ in low and high-water availability treatments in artificial mesocosms in the lab. We measured the growth rate over three months and quantified time to movement in behavioral tests. In low water availability conditions, growth rate and reaction times were reduced, with a larger impact for

the red-striped morphs. Our results suggest that the lead phase morph has a greater tolerance for low water availability than the red-striped morph. In contrast, in the higher water availability mesocosms, the red-striped individuals grew at a faster rate than the lead phase. Our study contributes to our understanding of how *Plethodon cinereus* will respond to modified abiotic environments with climate warming. (83)

Hill, Kara*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Diisononyl phthalate exposure induces a unique phenotype for multiple *Bacillus* isolates.*- Phthalates are synthetic chemicals used in the softening of plastics and as a solvent in personal care products, but these compounds can act as endocrine disruptors and chronic exposure can injure the liver, lungs, kidneys and the reproductive system, particularly in infants and adolescents. Although much is being researched about the direct impact on human health, studies on the impact of phthalates on the human microbiome and normal flora microbes are surprisingly scant. Phthalates may be inhaled into the lungs, ingested into the gut or absorbed through the skin therefore this project tests the effects of the DINP ester (diisononyl phthalate) on bacteria that would normally inhabit these environments. This included a screening of 48 different bacterial species with various concentrations of DINP. This selection includes *Streptococcus*, *Lactobacillus*, *Bacillus*, *Escherichia coli*, *Micrococcus* and *Staphylococcus aureus*. While most bacteria appeared unaffected, remarkably, multiple *Bacillus* isolates displayed a cell death phenotype, reminiscent of viral plaques. The effects of phthalates on bacteria was also displayed through biochemical and tolerance tests and showed little to no replicable inhibition to growth or function so far. Gram staining was performed and may provide insight to a stress response seen from bacteria due to the high concentrations of phthalates. Future directions include SDS-PAGE in order to detect possibly differentially expressed proteins and biochemical tests to determine if the bacteria are metabolically affected by DINP. (57)

Hofmann, Olivia*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Gene expression analysis of *Phytophthora infestans* auxiliary activity 17 (AA17) family genes PITG_04949 and PITG_13520.*- The infectious oomycete *Phytophthora infestans* is the causal agent of potato late blight, a disease that leads to annual crop losses estimated to be between 3-10 billion USD worldwide. During infection, *P. infestans* secretes proteins known as effectors, which facilitate host penetration and colonization. Some of these effectors belong to a large group of enzymes referred to as carbohydrate-active enzymes (CAZymes), many of which play an important role in the pathogenicity of *P. infestans* by breaking down cell wall polysaccharides in the host plant. *Phytophthora infestans* genes PITG_04949 and PITG_13520, which belong to the recently discovered auxiliary activity 17 (AA17) family of CAZymes, encode copper-bound lytic polysaccharide monooxygenases, a class of CAZymes that degrade pectin. However, the actual role of these genes in pathogenesis, if any, has not been fully investigated. In this study, PITG_04949 and PITG_13520 were cloned and sequenced, and their expression profiles during infection were analyzed using quantitative PCR (qPCR). Overall, gene expression of PITG_04949 and PITG_13520 was significantly upregulated during infection when compared to vegetative mycelium tissue. Additionally, expression of both genes was highest at 36 hours post inoculation (hpi), with PITG_04949 experiencing a 52,000-fold increase in expression at 36 hpi, suggesting a potential role in pathogenesis. This study lays the foundation for future research on the enzymes encoded by PITG_04949 and PITG_13520 and their potential role in pathogenicity. (7)

Hu, Jinrong*, Daniel Strömbom, Swati Pandey, and Elizabeth Batchelar Lafayette College, Easton, PA 18042. *Optimal resource allocation to combat spotted lanternfly infestations.*- The spotted lanternfly is an emerging global insect pest that is threatening both economic and environmental interests and have proven difficult to deal with in regions where

it is invasive. Recently, a study introduced a modeling framework for generalizing empirical efficacy control studies and its main result is a generalized population growth formula that is useful for determining the proportion of lanternfly present that has to be treated with a given set of controls to induce population decline. However, in its current form it cannot be used to address the more relevant question of how to best deploy a given set of controls with given efficacies for maximum impact on the population. Here we introduce a generalization of this published formula and show that it can be used to address this optimality question in some cases. More specifically, we show that when the effect of applied controls increases linearly with control effort the optimal strategy is to exhaust each control sequentially in order of effectiveness. Then we consider the case where the effect of the applied controls exhibits a more realistic diminishing returns type response with effort and derive control 'switching times' in terms of the model parameters using a heuristic argument. Given that funds and other resources available to combat the lanternfly are limited, we should try our best to use them in the most effective way and our work represents a step in this direction. (52)

Jacob, Austin*, and Bridgette Hagerty York College of Pennsylvania, York, PA 17405. *Assessment of ranavirus in Eastern box turtle (*Terrapene carolina carolina*) samples from West Shore Wildlife Center.*- Wildlife diseases such as ranavirus often go unnoticed in wild populations; however, they can be detected when animals are brought into rehabilitation centers. Globally, ranavirus has resulted in serious mortality events and is implicated in declines in amphibian and reptile populations. Illnesses such as this can greatly impact the survival of Eastern box turtles (*Terrapene carolina carolina*). The primary objective of this study was to test the prevalence of ranavirus in box turtles admitted to the West Shore Wildlife Center (WSWC). In 2023 WSWC admitted a total of 48 turtles. This sample can provide a look into the health of box turtles in south central Pennsylvania. Box turtles are impacted by several diseases with similar symptoms including herpesvirus, adenovirus, and ranavirus. Genomic DNA was extracted from oral and cloacal swabs collected from 16 box turtles. A conserved section of the major capsid protein gene (FV3) was amplified using standard PCR and dye-based quantitative PCR was used. Quantitative PCR can be beneficial to detect pathogens and quantify viral load. Presence of FV3 in the samples conflicted between the standard PCR and qPCR methods of detection despite follow up tests. Multiple samples were found to be positive using standard PCR but viral DNA was not detected with qPCR. Ranavirus had a prevalence rate of 18.8% based on standard PCR, but was not detected with qPCR. Ranavirus DNA presence was difficult to verify, but refinement of these procedures will continue. It is likely that ranavirus is not the primary illness impacting box turtles in York County. Improving diagnostic tests such as this would allow West Shore Wildlife Center to distinguish easily among common diseases and improve their treatment of box turtles and other ectothermic patients. (97)

Jahraus, Tyler*, Richard Gouge*, and David K. Foster Messiah University, Mechanicsburg, PA 17055. *Migwéch: Science, language, and relationship in the ethnobotany of the Forest County Potawatomi.*- Ethnobotany requires science, language, and relationship. This is never more apparent than in understanding, rediscovering, and helping revive the ethnobotany traditions of the Forest County Potawatomi in Northern Wisconsin. Through this endeavor, we provide examples of understanding the pharmacology of specific compounds, the proper linguistic way to address the plants, and the importance of both personal and cultural relationships with traditional knowledge keepers and current practitioners. The Native American contributions to the fields of botany and medicinal botany have previously been sectioned to a realm of skepticism and temperament, however with an increase an interest in novel pharmacological pathways, especially when related to antibiotic resistance and over the counter remedies, has allowed this knowledge to be recognized and aloud to thrive. The traditions of the Forest County Potawatomi medicine men and native healers with regards to their relationships to the plants around them provide a crucial

resource for the modern world to reconnect with what has been lost in a purely allopathic worldview of medicine and medicinal botany. Through a relationship with the plants and the people who cultivate them, we learn much about the world around us and its occupants. (64)

Jones, Bryan*, and **David Foster** Messiah University, Mechanicsburg, PA 17055.

Environmental and seasonal variations of postmortem necrophagous insect communities on Rattus norvegicus.- Forensic entomology focuses on the activity of Necrophagous insects on decaying remains, with blowflies being the most common insects found at crime scenes. One major problem with forensic research in this field is that it is not done through multiple trials in different environments or seasons. Therefore, the solution for this study includes using frozen rats as cadavers, due to their low cost and large numbers. Rats were placed in multiple environments over the fall season, and insect communities were observed to see how response time, maggot development, and insect diversity varied with environments and as average temperature decreased. Results showed that terrestrial environments had a different effect than wet environments because it affected the temperature of the cadaver, which affects the growth of the volatile organic compounds that attract insects. Decreasing temperature also correlated with less insect diversity and slower development of maggot masses. Although our study showed positive results, there are other variables to account for, such as time of day, maggot species, and precision in measuring mass and temperature, so adjustments will have to be made for future research. Overall, this study proved effective in using dead rats as cadavers in forensic research to observe different environments simultaneously and over long periods of time. (50)

Kang, Genelia* Northwest Pennsylvania Collegiate Academy, Erie, PA 16508. *Super giant basal cell carcinoma: A comprehensive systematic review*.- Introduction: Basal cell carcinoma (BCC) is a common skin malignancy. Super giant basal cell carcinoma (SGBCC), defined as a lesion greater than 20 cm in diameter, is a rare oncological entity, with few descriptions of its characteristics, risk factors, and outcomes. We completed a systematic literature review to better understand this entity. Methods: A systematic literature search for the years 1972-2023 was conducted with PubMed, Google Scholar, Medline Ultimate, and Cumulative Index to Nursing and Allied Health Literature databases. All abstracts, studies, and citations were reviewed. The final analysis included peer-reviewed English language articles involving human subjects with lesions greater than 20 cm in diameter. We identified 20 case reports for our analysis. The sample size was too small to conduct extensive statistical analysis. Results: Most cases were reported in North America and Europe. Males outnumbered females approximately 2:1. The mean age at diagnosis was 61 years. The lesion was located on trunk in 16 out of 20 cases. In 13 patients, the lesion had been present for more than 10 years and 7 cases reported metastasis. Several reports documented low socioeconomic status and poor mental health as risk factors. Regarding treatment, eleven patients underwent surgery, six patients underwent radiation, and four patients were treated with immunotherapy (Vismodegib). Conclusion: Although basal cell carcinoma (BCC) is known to have a favorable prognosis, SGBCC is highly aggressive with ability to metastasize. Our review reveals SGBCC has been present for more than 10 years duration and is more commonly diagnosed in males in their sixth decade. Additional risk factors include low socioeconomic status and poor mental health. In the absence of identifiable specific histologic factors, we believe self-neglect is the likely etiology of the large size. Treatment options may be multimodal with a combination of surgery, radiation therapy or immunotherapy (Vismodegib). (44)

Katzenmoyer, Jonathan P.*, and **Francis Mayville** DeSales University, Center Valley, PA 18034. *Extraction and analysis of the antioxidant resveratrol from various dried fruit*.- The objective of this study was to extract, isolate, and analyze the antioxidant resveratrol from various dried fruits. The dried fruit that we used contained no additives or preservatives.

Resveratrol was quantified to compare the amount of this antioxidant found in the different fruits. Soxhlet extractor techniques were implemented to extract resveratrol from each dried fruit sample. The concentration of the antioxidant was quantified using ultraviolet spectroscopy at a wavelength of 310 nm. The purity of the extracted resveratrol was determined using Gas Chromatography-Mass Spectrometry (GC-MS). The antioxidant properties were measured using a Ferric Reducing Antioxidant Power Assay (FRAP) and compared to known antioxidants through the formation and detection of reactive oxygen species using visible spectroscopy in a 96-well plate reader. The analysis of the data collected from this study would suggest which type of fruit contained the most resveratrol. (11)

Kremer, Alena*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Screening for novel antibiotic producing bacteria.*- Antibiotics have been a highly researched topic as they are becoming a necessity in the medical field as bacterial strains become more resistant to treatment. Most known antibiotics have been isolated from the soil bacterium, *Streptomyces* and an increase in antibiotic resistance has become a major challenge in the medical field. Testing diverse bacteria from different sources to isolate potentially novel antibiotics may help overcome the issue of antibiotic resistance, especially as new strains of infectious bacteria emerge. We tested a collection of bacteria from a variety of sources against four commensal or potentially pathogenic bacteria commonly associated with humans to find signs of growth inhibition. Our results show specific *Bacillus* and *Pseudomonas* species that inhibited the growth of target bacteria, suggesting that the bacteria can be novel antibiotic-producing sources. In the future, I will continue testing bacteria against the selected target bacteria to find additional instances of antibiosis and work on identifying some of the compounds that could be tapped as potential antibiotics. (94)

Kuzmiak, Faith*, and Wendy Boehmler York College of Pennsylvania, York, PA 17405. *Expression pattern of Canavan Disease-associated ASPA gene during development of zebrafish (*Danio rerio*).*- Canavan Disease (CD) is a rare, rapidly-progressing neurological disorder that begins in infancy and is typically fatal by age 10. CD is the result of a mutated ASPA gene, which codes for the enzyme aspartoacylase. Murine models have served as the primary model system for CD research and while they have been effective, there are limitations to these models, such as the difficulty in conducting prenatal screenings and the costly nature of high-throughput drug screening. These limitations could be addressed by utilizing a zebrafish model system to gain a better understanding of the early stages and progression of CD. The objective of this research is to assess the spatiotemporal expression patterns of the CD-associated ASPA gene in zebrafish embryos. To accomplish this, the temporal expression was assessed first by conducting reverse transcriptase polymerase chain reaction (RT-PCR) at four major developmental timepoints (24 hours post fertilization (hpf), 48 hpf, 72 hpf, 5 days post fertilization (dpf)). Results indicated expression of the ASPA gene at all four critical timepoints. Whole mount *in situ* hybridization (WISH) is currently underway to assess the spatial expression of the ASPA gene. Understanding the spatiotemporal expression of the ASPA gene in zebrafish and investigating this model system in the context of Canavan Disease will lay the foundation for future mechanistic and therapeutic studies. (34)

Leidig, Charles, Drew MacDonald, Justin Kerby II, and Ian Cost* Albright College, Reading, PA 19604. *Role-playing medical cases in Human Anatomy and Physiology courses with undergraduate students using principles from Dungeons and Dragons.*- Imagination and assuming roles is a typical method of play for human beings throughout their lives. We encourage this in younger students, whether through dress-up type play or playing board and party games. After a certain age, this use of role assumption and imagination tends to be relegated to specific courses and situations such as theater classes and drama clubs in

educational settings. However, role-playing in a classroom setting is a valuable educational tool that enables students to use information that they have learned in a practical way. In our Human Anatomy and Physiology courses at Albright College we introduce undergraduate students to complex medical cases and we employ principles of play found in Dungeons and Dragons style role-playing games. This style of play is easy for students to learn and, with popular games like Baldur's Gate also currently highlighting this style of play, students are able to quickly dive into their roles as surgeons, nurses, and paramedics to use their knowledge of anatomy and physiology to recognize, diagnose, and treat patients during content assessments. This style of knowledge assessment creates less stress than traditional laboratory practicals and simulates a working environment that students interested in healthcare will likely be experiencing in some form shortly after graduation. Less stress and simulation of a working environment are popular with students. Grades of students appear to be trending upward after the implementation of this system, though more data is still required. (84)

Liashenko, Varvara*, Molly Sawyer*, Emily Misko, Praveer Singh, Dominic Pearson, Gabrielle Hollenbeck, He Liu, and Prasad Dalvi Gannon University, Erie, PA 16541.

Review on diabetes and obesity treatments.- Diabetes mellitus (DM), once a relatively contained health concern, is now rapidly spreading globally, and becoming an alarming pandemic. DM is a chronic condition in which glucose homeostasis is impaired due to either the pancreatic β -cells being unable to produce enough insulin that leads to type 1 DM, or the secreted insulin being ineffective because of peripheral or central insulin resistance that leads to type 2 DM. The mortality rates associated with DM are also rising worldwide. As the diabetes pandemic continues to escalate, it becomes increasingly crucial to pinpoint the underlying causes driving its growth so that effective measures can be taken to prevent its progression. One of the leading causes of the development of type 2 DM is obesity, which is defined as excessive or abnormal accumulation of fat or adipose tissue in the body that can impair glucose homeostasis. As such, more than 90% of patients with diabetes are either overweight or obese, and therefore, it is imperative to understand how to treat obesity and diabetes in these patients either through lifestyle modification or medication. Numerous pharmaceutical and surgical approaches are currently available for the treatment of obesity and diabetes. A review of these treatment options, the underlying mechanisms, potential complications, and the overall outcomes of these treatments warrants further investigation for proper management of these conditions. (13)

Lippitt, Kade*, Madeline Glenn*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *The mycobiome of four distinct bog environments.*- Bogs are specialized, oligotrophic ecosystems created by the repeated growth and death of certain plant communities, including peat moss which forms a thick layer of organic debris at the water's bottom. The Tannersville Cranberry Bog (named for the cranberries at its center), a peat bog in northeastern Pennsylvania, was formed approximately 10,000 years ago as a result of glacial melting and movement. Sphagnum moss (peat) which accumulates in peat bogs fosters anaerobic, acidic conditions which slow decay. Animals and plants that die in bogs are often well preserved at the deeper depths, as evidenced by an abundance of fossils found in such bogs. Fungi are a diverse clade of eukaryotes found in all soil environments. They fill numerous ecological niches, including decomposition of organic matter and nutrient cycling. The impact of bog conditions on these soil microbial communities and their ability to metabolize detritus is unknown. To characterize the mycobiome of the Tannersville Cranberry Bog, soil was sampled at a depth of 15cm from four sites: the center of the bog, a foot trail directly adjacent to the bog, 5m from the trail, and 10m from the trail. Samples were sent to a commercial facility for massive parallel sequencing (next generation sequencing) of the ITS2 region, and sequencing files were analyzed by the DADA2 ITS pipeline. We report here on the composition of fungal communities in relation to their proximity to the bog. (75)

Lopez-Soliz, Maurice*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Assessing the effect of gravity and coagulant aided thickening methods on the nutrient profile of RAS effluent for potential reuse in hydroponic production.*- Recirculating aquaculture systems (RAS) provide sustainable intensive seafood production in non-coastal regions through extensive waste treatment processes that can achieve >99% system water reuse. This treatment results in the consistent production of an effluent requiring costly treatment prior to discharge to avoid pollution. This effluent contains plant essential nutrients that can be made available through microbial mineralization and organic matter (OM) removal, enabling suitability for reuse as a hydroponic crop fertilizer instead of being discharged. However, the low nutrient concentrations in comparison to commercial fertilizers limits widespread applicability. Sludge thickening is a technique utilized in wastewater treatment where coagulation and flocculation of OM promote the aggregation of small particles into a sludge that can be separated from the supernatant and undergo downstream treatment. Chemical salts such as aluminum sulfate octadecahydrate and iron (III) chloride anhydrous have been utilized in previous RAS effluent studies to optimize the sludge thickening process. The objective of this research is to analyze the nutrient and total suspended solids (TSS) accumulation of RAS effluent sludge after a 90 mg/L salt addition. Sludge was thickened using the ASTM Coagulation-Flocculation Jar Test and was compared to a gravity settling treatment as a control. Additionally, the effect of 15 minute and 1 minute settling times on sludge thickening was assessed. Preliminary results indicate that sludge thickened with either salt with a 1 minute settling time produced a sludge higher in TSS content than the gravity control with a 15 minute settling time. This research aims to establish fundamental data for enhancing effluent valorization techniques in RAS, thereby advancing both economic and environmental sustainability. Furthermore, it aims to provide hydroponics with a naturally-derived nutrient source by utilizing sludge thickening as a pre-treatment to microbial mineralization therefore reducing reliance on finite mineral fertilizers. (77)

Madera, Jack*, Liam Rivard, David Rothblat, and Jaimy Joy La Salle University, Philadelphia, PA 19141. *Rilpivirine treatment alters growth patterns and delays the onset of senescence in primary human fibroblasts.*- More than 1.2 million people were reported to be living with Human Immunodeficiency Virus (HIV) in the United States in 2021. HIV preferentially targets and kills activated CD4+ T cells and, to a lesser extent, monocytes. Combination antiretroviral therapy (cART) successfully inhibits viral replication but requires lifelong adherence. Paradoxically, long-term use of cART is associated with early onset of aging-related chronic conditions in people living with HIV (PLWH). This accelerated aging phenotype is partly driven by cellular senescence, a stable cell cycle arrest in which cells undergo distinct phenotypic alterations. Senescence is associated with organismal aging due to the senescence associated secretory phenotype (SASP), a collection of autocrine and paracrine pro-inflammatory cytokines, chemokines, and soluble factors secreted by senescent cells. Various stressors, such as oxidative stress, chronic inflammation, and mitochondrial dysfunction, can lead a cell into senescence under normal conditions. In the case of HIV infection, senescence may be induced via the virus itself, inflammation, or even cART. Thus, while cART can effectively inhibit viral replication, it may also contribute to the accelerated aging phenotype by promoting senescence. To better understand the potential relationship between cART and cellular aging, primary fibroblasts were treated with rilpivirine, a second generation non-nucleoside reverse transcriptase inhibitor (NNRTI), and cell growth patterns were assessed. Cells treated with rilpivirine had slower population doubling levels compared to untreated cells. After ~60 days in culture, a higher proportion of untreated cells were senescent, as determined by beta-galactosidase positivity, compared with Rilpivirine-treated. Senescence-associated gene expression was comparable between Rilpivirine-treated and control cells, supporting the conclusion that Rilpivirine delays the onset of senescence in primary human fibroblasts. (23)

Mathur, Vinayak* Cabrini University, Radnor, PA 19087. *Distribution of prophages in the Streptococcus bacteria genus and their role in increasing host pathogenicity.*-

Bacteriophages are a category of viruses that only infect bacteria. Virulent phages cause the cell to produce new phages and lyse, while temperate phages remain in a latent state following phage lysogeny and integration of genetic material into the host genome as prophages. This integration enhances the genetic diversity of the host species, and the new genetic material may offer advantageous traits to aid the host's survival and adaptation to new environments. Streptococcus bacteria are pathogens that infect both humans and animals, causing invasive infections and a diverse set of diseases. We hypothesized that strains of Streptococcus that have prophages present in their genome are linked to increased pathogenicity or antibiotic resistance. We used PhageWeb to identify prophages found within the 819 strains of Streptococcus genus from GenBank and the distribution of prophages across different species within the genus. With the Progressive Mauve software, we compared the sequences of identified prophages to determine similarities and relationships between the different prophages. Ultimately, based on information from gene ontology databases, we found that different prophages were associated with various virulence factors, adherence factors, and antibiotic resistance genes in their respective bacteria. Bacterial strains containing these prophages may have increased pathogenicity and the embedded genes could have a role in bacterial survivability in different environments. This genetic variation and these prophage characteristics shed light on the evolutionary dynamics of these bacteria species and can be applied to phage therapy. (22)

Metzger, Bradlee*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Cultivating Lactuca sativa (Bibb lettuce) using various fertilization methods in controlled environment agriculture.*- With the global population rising and arable land decreasing, food security is a significant concern. A way to combat the scarcity of land is by using controlled environment agriculture (CEA) methods such as hydroponics (soilless growing) and aquaponics (a combination of aquaculture and hydroponics) which provide location-independent and season-independent growing. Recent literature has captured the individual analysis of hydroponic fertilizer or aquaponic culture water on plant nutrient uptake, but it is unknown the potential benefits of a hybrid system that utilizes nutrient-rich effluent supplemented with hydroponic fertilizer. Integrating fish culture water with hydroponics has the potential to limit reliance on finite synthetically derived fertilizers and reduce pollution from aquaculture. This study investigated how fertilization sources impacted the growth of Bibb lettuce (*Lactuca sativa*) as determined by wet weight and chlorophyll content. Bibb lettuce seedlings were transplanted into nutrient film technology (NFT) racks that each received nutrients from a different source for three weeks. At five weeks, the lettuce was harvested. Wet weights were obtained for each rack of plants and chlorophyll content was analyzed in five random plants from each system. Preliminary results show lettuce obtaining nutrients solely from aquaponics effluent had significantly lower wet weights ($n=3$, $p<0.05$) while the hybrid system performed comparably to the standard hydroponics system ($n=3$, $p>0.05$). Upcoming analysis of chlorophyll content will allow conclusions to be drawn relating to the health of the plants across these systems. Additional research will be needed to track how the system maturity, including beneficial bacteria populations and nutrient management, impacts the availability of nutrients for plant uptake. (79)

Michael, Mary*, Randy Cassell, and Erik Lindquist Messiah University, Mechanicsburg, PA 17055. *Dietary analysis of Plethodon wehrlei: a cryptic species of lungless salamander in Pennsylvania.*- This study examines and analyzes the diet of Wehrle's salamander, *Plethodon wehrlei*, a species of terrestrial lungless salamander found in the eastern United States. Though Plethodontidae is the largest family of salamanders, there has been a significant lack of literature on the diet of the relatively cryptic species

of *Plethodon* in the eastern United States. Salamanders are important indicator species and constitute a large amount of the vertebrate biomass in eastern deciduous forests. Understanding their dietary habits allows for a more comprehensive analysis of ecosystem function and health. During the 2023 fall season, in Pennsylvania's Allegheny Plateau, *Plethodon wehrlei* specimens were collected and preserved so as to examine their diet. Gut content was obtained by dissection and then identified under a stereomicroscope. 15 *Plethodon wehrlei* samples were collected from an Elk County site. Additionally, in order to increase the sample size of *Plethodon wehrlei*, 16 specimens from Pennsylvania were obtained from the Carnegie Museum of Natural History's Section of Amphibians and Reptiles. Of these 16 specimens, gut content were sought. Our results revealed a diverse array of prey items and seasonality. *Plethodon wehrlei* were found to mostly consume Hymenoptera (ants, bees, and wasps), Diptera larva (immature flies), and Collembola (springtails). (61)

Micklus, Morgan*, Anthony Teo*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Mouthwash and the oral microbiome*.- The oral microbiome refers to the community of organisms which inhabit the oral cavity, and is highly variable from person to person. The bacteria and fungal species which compose the microbiome enter the mouth through eating/drinking, respiration, and contact with other organisms. 25% of adults in the United States report using mouthwash, an oral rinse used to clean teeth and gums, consistently. While the oral microbiome is one of the most explored and established fields within metagenomics, little research exists regarding the use of different mouthwashes and their effects on oral microorganisms. Studies using probiotic mouthwash, which is mouthwash containing live bacteria, have shown an increase in commensal bacteria and reduced counts of pathogenic bacteria, but the effects of probiotic oral treatments on the oral microbiome have not been studied. In the study, we examined the effects of commercially available probiotic oral rinses on oral microbiome diversity. We assessed our individual baseline biome diversities before any treatments were applied, then repeated the analysis after the use of probiotic mouthwash. Here we report the results of our metagenomic analysis of the use of probiotic mouthwash treatments on oral bacterial and fungal populations. (76)

Minton, Russell* Gannon University, Erie, PA 16541. *Freshwater snails introduced over small ranges form novel gut bacteria associations reflecting their environment*.- Host organism gut microbiomes can be separated into two components: a core microbiome adapted to the host; and a facultative portion that is environment dependent. This is especially true in alien species that form novel associations with bacteria from environments they are introduced in. I aimed to describe the gut bacterial communities and the environmental factors influencing them in the 'native exotic' snail *Elimia comalensis*, a species native to central Texas that has spread over a range of 280 km. The range of *E. comalensis* was initially described as limited to the Guadalupe and San Antonio River drainages along the Edwards Plateau; by 1969 the species was present from Del Rio in the west to Salado in the east. The spread of *E. comalensis* relied on human intervention, with movement likely accompanying intentional *Gambusia* introductions across the state from source populations in the Guadalupe drainage. Gut microbiomes were studied from five snails per site by generating bacterial 16S rDNA V3/V4 sequences using PCR and Illumina chemistry. Proteobacteria was the most abundant bacterial phylum in all samples, and Rhodobacteraceae was the most abundant family. Bacterial Shannon diversity and Pielou's evenness did not significantly differ across collection sites. Analyses of UniFrac distances suggested significant differences in bacterial communities in all pairwise site comparisons except Comal/San Marcos. Four sites possessed at least one bacterial phylum that could serve as a diagnostic bioindicator for that location. Multivariate regression suggested that bacterial community structure in snails from each site was a function of water chemistry, and

BIO-ENV analysis suggested different water variables affected bacterial presence/absence versus relative abundance. My data suggested that species like *E. comalensis* form gut microbiomes that reflect the environments they are introduced in to, even when those habitats are relatively close geographically. (108)

Morton, Delaney*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Unveiling aquifer heterogeneity: ground penetrating radar as a pioneering tool for preferential flow visualization.*- Ground Penetrating Radar (GPR) represents an innovative approach to exploring the complex nature of aquifers, a task typically considered outside its conventional domain. This research pioneers the utilization of GPR as a non-intrusive and cost-effective method for identifying preferential flow paths within aquifers, a task traditionally tackled through labor-intensive and expensive drilling techniques or via other geophysical methods such as electrical, seismic, electromagnetic methods. The study was carried out at a shallow aquifer in the Center for Environmental Education and Research (CEER). Despite the presence of observation wells and established soil composition profiles, detecting preferential flow routes remained challenging. To address this, GPR surveys, coupled with auger soil sampling for water moisture analysis, were employed as a novel approach. Using a 400 MHz antenna, 52 transects were conducted across a 21m x 31m grid area, with individual GPR profiles spaced one meter apart. RADAN 7 software was used for data processing to produce 2D profiles and 3D models. Auger samples were used to determine water content through an oven-dry method. Two-dimensional GPR profiles indicated strong reflections slightly above the expected water table depth, suggesting that the reflection occurred within a partially saturated layer rather than at full saturation. This observation was corroborated by the water content analysis. The results demonstrate that GPR signals delineate a partially saturated subsurface layer, likely representing the upper extent of a capillary fringe. The three-dimensional GPR model provided a comprehensive view of the aquifer's heterogeneity, highlighting groundwater pathways that were not uniform throughout the study site. This study underscores the effectiveness of GPR as a valuable tool for characterizing aquifer heterogeneity, offering efficient groundwater flow visualization. (78)

Murray, Mackenzie*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Caseinase production in bacteria specimens, the search for novel sources.*- Hydrolytic enzymes play an invaluable role in bacterial biochemical functions, through catalyzing the breakdown of proteins, carbohydrates, nucleic acids, lipids, and other biochemicals. This project looks at caseinase, a hydrolytic enzyme with broad industrial applications, from the milk industry to leather production. There is limited research that focuses on bacterium that produce caseinase. In this study, I sought to test a wide range of bacteria to find novel bacteria not formerly documented regarding caseinase production. After plating bacteria on tryptic soy agar plates containing 2% skim milk and monitoring them for multiple days, over 130 isolates displayed caseinase activity, some of which were novel. While not all of the samples have been sequenced, preliminary analysis indicates that there is a wide variety of species present in the collection, some of which have limited publications about. This study will serve as a way to broaden the current repertoire of known bacteria that produce hydrolytic enzymes and widen the pool of bacterial sources for scientific experimentation in a wide range of industries. (56)

Neto, Isabella*, Kelly Reid, Kimeal Parham, and Richard Kliman Cedar Crest College, Allentown, PA 18104. *Minimal genetic variation in DNA sequences of spotted lanternflies, Lycorma delicatula.*- *Lycorma delicatula* is an invasive species that poses an economic threat to a plethora of U.S. agricultural industries such as plants, crops and forestry. Commonly known as the spotted lanternfly, this species has raised significant concerns in the northeastern U.S. Native to China, this species infests many plants, but the preferred plant is *Ailanthus altissima* (tree of heaven). Over time, as the lanternflies continue to infest

agriculture, other species can be impacted due to the weakening of their energy source. After being detected in Pennsylvania in 2014, the spotted lanternfly is seen reproducing annually, with a life cycle that begins in mid-spring and ends during the winter. Based on their small number of generations in the U.S. and possibly small founder population, the species may exhibit little genetic variation. This can be analyzed by sequencing nuclear genes in several individuals. Our data for three genes (*tua2*, *b2tub*, and *Hsp70c*) indicate that there is little variation within *Lycorma delicatula* in western New Jersey and eastern Pennsylvania. (49)

O'Connor, Corinne*, and Jenny Hayden Cedar Crest College, Allentown, PA 18104. *Effects of lysine acetylation on DNA repair in Mycobacterium smegmatis*.- This research focuses on how lysine acetylation affects the DNA repair pathway in *Mycobacterium smegmatis*. Lysine acetylation is a post-translational modification that affects protein activity. Deacetylases take acetyl groups off of lysine residues while acetyltransferases put acetyl groups onto lysine residues. The Ku protein, which has been shown to be active in DNA repair, is regulated by lysine acetylation. Non-homologous end joining is a DNA repair process that does not require a repair template, and most bacteria do not perform this function. By plating the bacteria on media with phleomycin, which causes double stranded breaks, we are testing the efficiency and fidelity of non-homologous end joining DNA repair. UV radiation exposure is also used in this project to induce DNA damage to understand different DNA repair pathways. Mutant *M. smegmatis* strains lacking deacetylases or acetyltransferases are used to understand the role of lysine acetylation in DNA repair. Our hypothesis is that a mutant strain without deacetylases ($\Delta deAc$) will perform non-homologous end joining less efficiently than wild-type *M. smegmatis*. *M. smegmatis* is used as model for *Mycobacterium tuberculosis*, the bacteria that causes tuberculosis disease. Tuberculosis is a disease that has caused significant health complications globally, with over 1 million people dying from this disease annually. This study will help us better understand *Mycobacteria's* ability to deal with stress and how to prevent the spread of the global health crisis of tuberculosis. (105)

O'Donnell, Reagan*, Lauren Heiland, and André Walther Cedar Crest College, Allentown, PA 18104. *Applying quantitative PCR with high-resolution melt analysis for rapid genotyping of brewery yeasts*.- The global beer market was worth around USD 610.34 billion in 2021 and is estimated to grow to about USD 814.54 billion by 2028. The brewing of beer involves several steps: malting, mashing, boiling, cooling; resulting in a sugary liquid (wort), followed by fermenting, conditioning, and packaging. The fermentation process combines specific strains of brewing yeasts with the wort in tanks that exclude oxygen, and after a period of 2-8 weeks, the resulting liquid is beer. Different yeast species are used in the production of different kinds of beers such as ales or lagers, resulting in different beer properties and flavor profiles. Ales are fermented with top fermenting yeast (*Saccharomyces cerevisiae*) that grow at warmer temperatures and that result in fruitier beers. Lagers are brewed with bottom-fermenting yeast (*Saccharomyces pastorianus*) that thrive at cooler temperatures and result in more crisp and less bitter beers. With each species of Ale and Lager yeast there exist many different yeast strains that vary only slightly, yet can produce different taste profiles. Our lab is focused on creating a rapid genotype test for identification of different brewery yeasts. Our technique is based on isolating genomic DNA from various brewery yeast strains, then using a quantitative PCR (qPCR) to amplify specific Short Tandem Repeats (STRs) from the genomic sequence, followed by a High-Resolution Melt (HRM) analysis to identify certain distinguishable genetic markers on the individual yeast strain's genomic DNA. We have used this technique to distinguish between ale and lager commercial beer yeast strains and have been able to distinguish among various lager and ale strains, therefore both interspecies and intraspecies identification. Developing a rapid genotype test that can distinguish brewery yeast strains from each other will help beer companies identify and

prevent contamination in growing beer fermentation tanks, which will help breweries save money. (29)

Paul, Sherin*, and Shiqi Zhang East Stroudsburg University, East Stroudsburg, PA 18301. *Exploring The Establishment Of AM Symbiosis In Brachypodium distachyon In Response To Spent Coffee Grounds Fertilizer.*- Coffee is a widely consumed and traded product that produces excessive amounts of spent coffee grounds as a by-product. Anecdotal suggestions have been made to incorporate spent coffee grounds in local gardens as a sustainable method due to its high primary nutrient content and antimicrobial properties on pathogenic microbes. However, the effects on arbuscular mycorrhizal fungi symbiosis have not been explored. This study aims to investigate the effects of direct applications of spent coffee grounds, both caffeinated and decaffeinated, on AM fungi symbiosis in *Brachypodium distachyon* under growth chamber conditions. Using wild-type *B.distachyon* seeds inoculated and grown under growth chamber conditions for 5 weeks in caffeinated, decaffeinated and non-coffee ground treatments, this study intends to i) determine the percentage of AM fungi colonization of roots, ii) evaluate plant nutrient uptake by chlorophyll analysis, and iii) assess the impact of spent coffee grounds on soil properties by the calculation of the pH and moisture of the growing substrates. (107)

Pecorelli, Sara*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Analysis of glycoprotein secretion from OKF6/TERT-2 (oral epithelial) cells after E-liquid treatments.*- The use of electronic cigarettes has been shown to be detrimental to oral health. Our lab has shown that the presence of E-liquids in oral epithelial cell cultures with DFK media induce cytotoxicity. When growing OKF6/TERT-2 cells in E-liquid treated media, the pH of the cell supernatant is significantly altered in the presence of cinnamon E-liquid. In addition to changes in pH, changes in the expression/secretion of mucin glycoproteins was speculated to be impacted by E-liquid presence. Mucins are a family of glycoproteins produced by salivary glands and oral epithelial cells that are involved in antimicrobial defense and water retention in the mouth. This project analyzes the impact of cinnamon, menthol, strawberry, and tobacco vape flavors on mucins by comparing the amount of mucins produced and released by oral epithelial cells in each flavor condition to a control sample that has not been exposed to any vape chemicals. Alterations in the levels of released mucins under experimental conditions could indicate a negative impact of E-liquid flavors on oral immune activity and hydration, which offsets the oral homeostasis. Exposure of OKF6/TERT-2 cells to the cinnamon E-liquid causes a decrease in the amount of mucins present in the supernatant, as indicated by SDS-PAGE. Overall, the results of this research further support the speculation that cinnamon E-liquids are one of the most harmful flavors to oral health. The information obtained from this research sparks future ideas regarding the analysis of mucin expression at the level of mRNA with and without cinnamon E-liquid treatment, to obtain further information on the impact of this vape flavor on these proteins. (21)

Perneta, Nicholas*, Victoria Kenney, Olivia Montvydas*, and Joshua B. Slee DeSales University, Center Valley, PA 18034. *Is Iso-Q the missing clue? Evaluating the anti-inflammatory effects of isoquercitrin.*- Heart disease is the leading cause of death in the United States. Atherosclerosis, a condition characterized by the buildup of lipids within blood vessels accompanied by the release of inflammatory cytokines and leukocyte adhesion, is a prominent underlying factor contributing to coronary heart disease. Another related medical concern associated with elevated levels of inflammation is the rejection of implantable medical devices, such as pacemakers and vascular stents. In the pursuit of a natural compound that could attenuate excessive inflammation, bovine aortic endothelial cells (BAOECs) and THP-1 cells were used as model cell lines. Isoquercitrin, a naturally occurring compound found in a range of fruits and vegetables, has shown promise in mitigating

inflammation, addressing metabolic disturbances, and modulating inflammatory pathways and cytokine responses. To investigate the hypothesis that isoquercitrin can alleviate inflammation in BAOECs, both a TNF- α assay and a wound healing experiment were conducted. Findings suggest that isoquercitrin does not exert any significant anti-inflammatory effect on cells subjected to TNF- α -induced inflammation. Furthermore, isoquercitrin does not enhance wound healing in BOAECs. THP-1 adhesion assays on polyurethane films were conducted with isoquercitrin to determine the impact of isoquercitrin on biocompatibility. There was no noticeable decrease in adhesion by THP-1 cells after treatment, indicating that isoquercitrin does not have an impact on the biomaterial rejection of a common polymer used in medical devices. Overall, isoquercitrin was not found to have any anti-inflammatory effects in the cell models evaluated herein, suggesting that it may not be suitable as an anti-inflammatory supplement. (24)

Pilaitis, Julia*, and **Daniel Strömbom** Lafayette College, Easton, PA 18042. *Quantifying the initiation and spread of fashion trends on TikTok.*- In the last decade, trends, especially in fashion, have seen significantly shorter lifespans with platforms like TikTok playing a pivotal role in their rapid adoption and discard. Here, we collect data from TikTok Creative Center for 10 trends over a 3-year period and quantify and provide preliminary modeling for the initiation and spread of these fashion trends. We find that the average trend grows for 5.6 ± 1.34 months and then declines and we show that the initial phase can be well estimated by an exponential function. Then we use the data to fit the initial phase of a FitzHugh-Nagumo-like model and find that the average proportion of views threshold is 0.0038 and the average peak value is 0.13. Understanding the initiation and spread of trends may be useful for fashion companies to forecast and assess trends and exploring analogies between neuron-firing and the spread of fashion trends may facilitate this. (51)

Ramsey, Ruby*, and **John Harms** Messiah University, Mechanicsburg, PA 17055. *Assessing the efficacy of anti-fibrotic treatment on pancreatic cancer metastases.*- Pancreatic cancer is expected to become the second leading cause of cancer death by 2030 and currently has an overall 5-year survival rate of only 11%. The majority of pancreatic adenocarcinomas are identified during the metastatic stages, when surgical resection is no longer possible. Response to chemotherapy is also extremely poor, due in part to the uniquely high level of fibrosis, comprising 50-80% of tumor volume. Reducing this fibrosis in the tumor microenvironment may increase vasculature and perfusion, allowing therapeutic agents to better penetrate and combat the tumor. Our lab has previously shown that proglumide, a CCK receptor antagonist, significantly decreases fibrosis in primary tumors of pancreatic cancer. We hypothesize the effect of proglumide will have similar efficacy in tumor metastases. To study this, we utilized a murine pancreatic cancer cell line, MCB/1, injecting those cells into immunocompetent C57Bl/6 mice via intrasplenic injection. This injection route was previously shown by our lab to regularly produce metastases in the liver and less often, the lungs. Mice were randomized between normal or proglumide-treated drinking water for 3-4 weeks. At necropsy, liver metastases were dissected, fixed, and paraffin-embedded for histological sectioning. A mean of 14 liver metastases were obtained per mouse. While proglumide could potentially block the mitogenic effect of gastrin signaling and thereby decrease the size and detectability of metastases, no significant difference in the incidence or number of metastases was observed. Masson's trichrome staining and quantitative imaging are ongoing to assess fibrosis in individual metastases. (19)

Reese, Allyson*, **Sherri Buerdell**, and **Deborah Austin** Wilson College, Chambersburg, PA 17201. *Inhibition of Streptococcus equi growth by five types of equine bedding.*- *Streptococcus equi* causes strangles, one of the most infectious domestic equid diseases, that affects horses, donkeys, mules, and ponies. Five types of equine bedding were tested including *Pinus echinata* (southern yellow pine), *Linum usitatissimum* (flax), *Juniperus*

virginiana (eastern red cedar), *Hordeum vulgare* (barley straw), and shredded newspaper. *S. equi* is vectored to equines through bedding, contaminated equipment, and through direct contact with an infected equine. Although most equines recover from strangles, some may die from asphyxiation due to swelling around the trachea. The focus of this research was on whether specific types of equine bedding would inhibit the growth of *S. equi*. Mueller-Hinton agar plates were inoculated with *S. equi*. Seven wells were made in each plate and small particles of each bedding were placed in individual wells. One well remained empty as a negative control, one well contained sterile deionized water as a negative control, and one penicillin disk was placed in the center of each plate as a positive control. Plates were incubated at 37°C for 24 hours and examined, and if zones of inhibition were present, they were measured. Using one-way ANOVA followed by Tukey's post-hoc test, it was determined that southern yellow pine ($p=0.000024$) and eastern red cedar ($p=0.000007$) were statistically significant in their ability to inhibit *S. equi* over the other three bedding types. The spread of *S. equi* could be reduced in equine facilities by using southern yellow pine, eastern red cedar, or a combination of both bedding types. (98)

Reid, Heidi*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Exploring the prevalence and variation of the enzyme laccase within bacteria.*- Laccases are a common oxidoreductase enzyme utilized by prokaryotes and eukaryotes for both oxidation and degradation reactions. In vivo, laccases can catalyze the degradation and detoxification of pollutants and contaminants, as well as provide essential protective functions. For example, laccase enzymes found in bacteria can protect against hydrogen peroxide and ultraviolet radiation. Laccases have a variety of applications including bioremediation, which involves the use of microbes to remove pollutants and contaminants from the environment. While bacterial laccases have been found to be more stable than fungal laccases at high thermal temperatures and varied pH, they are also difficult to produce in large quantities at a reasonable cost. Furthermore, these enzymes often require expensive mediators because of their low redox potential. It is important to understand the extent of these factors in order to find ways to improve their usage and possible benefits in the future. In this study, new sources of laccases were sought and explored. This was done by screening a large collection of bacteria on media containing 2,6-dimethoxyphenol (DMP) to identify laccase activity. The screening process aimed to discover new sources of laccases that could potentially offer improved characteristics than the currently available enzymes. The discovery of new sources of laccase may offer a solution to the limitations stated above, which would allow for a greater usage of this enzyme in academic and industrial settings. (103)

Rettger, Jason*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Unraveling the interplay between osmotic and oxidative stress: insights from saccharide-adapted bacteria via superoxide dismutase induction.*- Investigations into the homeostatically interruptive role of reactive oxygen species hold promising insight into food spoilage as well as healthcare concerns. Superoxide radicals are well understood to damage biological molecules, including DNA and proteins, which can be fatal for organisms at any level of life. The cause-and-effect relationship between cellular osmotic stress leading to oxidative stress, specifically from saccharides, is less characterized in literature. This study initially sought out broad saccharotolerant microbes, those who could survive in saccharide/sugar rich environments; and potentially spoil confectionary products. Upon identifying model prokaryote *Bacillus subtilis* as saccharotolerant, further molecular tests were employed to investigate the mechanisms behind such osmotic stress. Using protein characterization, Western Blotting, and genetic analysis via gene knockout, our study has found a reliance on superoxide dismutase (SOD) for saccharide stress tolerance in *B. subtilis*. Other osmotic stressors, like highly saline environments, also show an expression and reliance of SOD. Based on the nature and role of SOD in oxidative radical scavenging and reduction, further tests into known oxidative compounds have also produced these results. Moving forward,

quantification of SOD expression will be conducted in qPCR and enzyme assay tests to support our findings. The understanding of superoxide dismutase for defense of reactive oxygen species produced by osmotic or traditional oxidative stressors at the prokaryotic level could provide insight into survivability mechanisms of resistant bacteria that particularly spoil sugary foods. In addition, hashing out the mechanisms of osmotic and oxidative stress related protein induction in prokaryotes holds promise in eukaryotes and human physiology due to the similarities in function of superoxide dismutases. (9)

Richert, Caleb*, and David Foster Messiah University, Mechanicsburg, PA 17055.

Improving analysis of a Pennsylvanian hardwood forest fire using ArcGIS Pro in 3D.- ArcGIS is a powerful and effective tool in land and forest management for collecting spatial data over large areas not easily collected in the field, including geological, soil, and boundary data. In March of 2021, an unprescribed fire burned 141 acres of mixed hardwood forest at Camp Tuckahoe in Dillsburg, Pennsylvania. In Fall of 2021 and 2023, researchers at Messiah University performed 55 m transect studies using 5m interval quadrats, estimating the percentage cover of species in 1 x 1m and 2 x 2m plots below and above DBH. We hypothesized that hardwood percent cover would increase in 2023. We found evidence to reject most of our null hypotheses and concluded that prescribed burns can be an effective management tool for reducing understory overshadowing by red maple *Acer rubrum* and mountain laurel *Kalmia latifolia*. Additionally, we supplemented quadrat sampling with raster data selection in ArcGIS Pro to extract soil and geological data to examine fire impact in different local environments. GIS was also used to display fire boundaries in 3D to examine total acreage and extent of the fire. This study emphasizes the importance of collecting baseline data in critical ecological areas for the examination of environmental disturbances. GIS should be further utilized for the creation of 3D and 4D models tracking zonal change through time. (62)

Rossiter, Taylor*, and Meda Higa York College of Pennsylvania, York, PA 17405.

Investigating a stenothricin-like pathway: uncovering the antibiotic potential of the soil bacteria Paenarthrobacter nicotinovorans using CRISPR Cas9 gene editing.- The antimicrobial resistance crisis is one of the greatest concerns among the scientific and healthcare communities. Common infection-causing bacteria (known as the ESKAPE pathogens) are becoming increasingly untreatable using established antibiotics. Therefore, there is a need for the discovery of novel antibiotics or new ways to increase antibiotic efficiency to try and solve this crisis. To achieve this, we isolated a bacterial sample from soil and plated it against different ESKAPE pathogen safe relatives to screen for antibiotic zones of inhibition. This isolate demonstrated antagonistic activity against several ESKAPE pathogen safe strains, including *B. subtilis*, *P. aeruginosa*, and *S. epidermidis*. Whole genome sequencing identified the isolate (3TR12_21) as *Paenarthrobacter nicotinovorans*. A stenothricin-like biosynthetic gene cluster was also identified through the secondary metabolite identification/analysis software, antiSMASH. This study aims to characterize the antibiotic produced by *P. nicotinovorans* using a specialized CRISPR transcription inhibition system using a catalytically inactive Cas9 enzyme. We plan to knock out several genes in the stenothricin-like biosynthetic pathway, Sten K, Sten M, Sten L, Sten F, and determine whether this disrupts the antibiotic producing activity of the isolate. Taken together, these results could ultimately lead to the identification of the antibiotics the isolate is producing, and potentially the identification of a novel antibiotic that could be used against ESKAPE pathogens. (71)

Salo, Shannon*, and Brian Gray York College of Pennsylvania, York, PA 17405.

Determining the role of FODMAPs molecules in the production of short-chain fatty acids in the human gut microbiome.- Functional gastrointestinal disorders (FGID) have been increasing in prevalence over the past 10 years, with irritable bowel syndrome (IBS) one of

the most diagnosed FGIDs. One treatment option, the low-FODMAP diet, has been found to limit several symptoms in some patients with IBS. FODMAPs (fermentable oligo-, di-, and monosaccharides and polyols) are a group of short-chain carbohydrate molecules which are readily digested by gut bacteria. Low-FODMAP diets cause abundance and diversity changes within the gut microbiome due to the shift in available carbohydrates, although results of multiple studies present conflicting data on which genera appear to fluctuate. Short-chain fatty acids (SCFAs) are frequent metabolic endpoints for numerous gut bacteria, and different mixes of SCFAs provoke a variety of organismal responses via neuroendocrine signaling in the gut. Very few studies have looked at the direct relationship between FODMAP availability and secondary metabolite outputs from gut microbes. To understand how individual FODMAPs molecules affect SCFA production in human gut bacteria, anaerobic media were supplemented with one of several FODMAPs and were then used to grow three different bacterial species associated with different IBS outcomes. SCFA production in these media were then analyzed via high-performance liquid chromatography to determine the SCFA production profiles. The results of this study will help make connections between SCFA levels and FODMAPs molecules, as well as provide a starting point for future human-based studies of the SCFA-FODMAPs-microbe interaction. (72)

Saxe, Nathaniel*, and Jeff Erikson Messiah University, Mechanicsburg, PA 17055. *Non-Biting Midges (Chironomidae) as bioindicators of specific pollutants.*- It is known that the mouth structures of Chironomidae become deformed in presence of inorganic and organic pollutants. Potential diagnostic patterns of these deformities have been unexplored. We collected local Chironomids and exposed them to increasing concentrations of inorganic metals in a laboratory setting. Metals utilized include nickel, copper, lead, and cadmium and exposures were based on the LC50, half of LC50, one-fourth LC50, and one-eighth LC50, in addition to a control treatment. In total, there were five treatments and five replicates per metal. Exposure began around the second instar and individuals were removed before pupation. After exposure, individuals were decapitated, and head capsules were removed and mounted on microscope slides. Deformity regions and rates were recorded and analyzed for statistical significance. It was found that copper had a significantly lower deformity rate and nickel had a significantly higher deformity rate. Among the nickel concentrations, there was a significantly high deformity rate in the 39.8 mg/L treatment. Further deformity patterns were found but were not statistically significant. Additional replicates may solidify these findings, which have practical applications in rapid field assessments of water quality and identification of pollutant sources. (74)

Semmler, Liam*, Aidan Doyle, Vaughn Shirey, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Exploring the differences in plant communities across Hog Island, Maine.*- Plant communities provide critical ecosystem services to biodiversity across the planet. Learning how to determine different plant communities from the macroscale to the microscale is essential to understanding other species' distribution, patterns, and functional roles. By using foundational ecological metrics such as species richness and abundance we can start to compare differences between plant communities and habitats more effectively. For this research, we identified various habitats based on plant diversity metrics across Hog Island, Bremen, Maine, managed by the National Audubon Society. In July 2023, vegetation data was collected over ten days on Hog Island across five separate sites (spruce high-elevation, spruce low-elevation, spruce blowdown, deciduous mainland, and milkweed field). A 1x1m quadrat was used to collect plant species richness and abundance around insect pitfall traps for each site. We then conducted a one-way analysis of variance (ANOVA) for the plant abundance and a Shannon Evenness Index (SEI) across all five sites to attain the differences between the sites. There were significant differences ($p < 0.05$) in plant abundance between our spruce low-elevation site and three

other sites: spruce blowdown, deciduous mainland, and milkweed field. Additionally, for the SEI, we found significant differences between the milkweed field and three other sites: spruce high-elevation, spruce blowdown, and deciduous mainland. By knowing the vegetation abundance and evenness of different sites, the information can be used to help the National Audubon Society make better predictions about how other organisms (e.g., insects, birds) utilize these sites. (87)

Sentz, Abby*, Sherri Buerdsell, and Brad Engle Wilson College, Chambersburg, PA 17201. *Sarcoptic mange susceptibility in juveniles and adult red fox (*Vulpes vulpes*) by camera trapping.*- Sarcoptic mange (*Sarcoptes scabiei*) is a highly contagious parasitic disease commonly found in over 100 mammal species worldwide. In North America, sarcoptic mange has been reported in fox species, coyotes, wolves, black bears, porcupines, rabbits, squirrels, and raccoons. It is essential to monitor this parasitic disease in the red fox (*Vulpes vulpes*) population due to the high transmission rate of the *S. scabiei* mite. Red fox individuals were evaluated using camera trapping to determine the relative incidence of sarcoptic mange in juvenile and adult red foxes. Motion-sensitive cameras were placed in six Adams County, PA locations for two months to determine the four most active sites for data collection. These sites were along farmland, national parks, creeks, and forests. The photos were then assessed for coat condition to determine if the red fox individual had sarcoptic mange. No symptoms of mange were observed in any fox individuals recorded. Chi-square analysis indicated that activity levels differed between seasons, with the highest activity occurring in the fall (spring: 8.63%, summer: 32.99%, fall: 49.75%, and winter: 8.63%). More fox activity occurred in areas that were close to humans (86.29%). (99)

Settle, Caitlin*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Screening to identify new amylase enzymes.*- Hydrolytic enzymes are essential to break down various organic and inorganic chemicals in organisms and industries. Amylase, a hydrolytic exoenzyme, catalyzes the breakdown of starch and has a variety of applications in medicine and industry. While amylase is valuable, research is limited regarding the bacterial species capable of amylase production and the different conditions in which they can function. In this study, we sought to find novel bacteria with amylase activity in various environments and conditions. Using isolated bacterial cultures and performing starch hydrolysis tests, we found that the amylase activity was most prominent in the phylum Bacillota. *Bacillus* species were most enriched in our samples as amylase positive bacteria, followed by *Curtobacterium* and *Pseudomonas*. Amylase-positive bacteria were most enriched in fermented products, fruit, high salt, and high sugar environments. These results indicate that amylases with possibly different properties can be isolated from diverse bacteria. These findings are significant for understanding the conditions in which amylase is functional and discovering potential applications for amylase in industry. (93)

Sheppard, Jordan*, and Sophie Charvet Susquehanna University, Selinsgrove, PA 17870. *Optimizing protocols to study prasinophyte bacterivory.*- Marine phytoplankton are a diverse community of microorganisms credited with most of the world's oxygen production and carbon dioxide absorption due to their photosynthetic activity. However, most of them are mixoplankton, combining both photosynthesis and predation, but we have no way of telling which trophic mode they use at any given time in their natural environments. Their predatory activity, and its associated release of CO₂, might have unexpected impacts on the global carbon cycle. In order to better understand the ecological impact of mixoplankton, their predatory behavior must be studied. Prasinophytes are small flagellates belonging to the chlorophyta, close relatives of land plants, and were long thought to simply be phytoplankton due to their ability to photosynthesize. However, recent work has shown that they are also bacterivorous, meaning they can feed on bacteria, although the mechanisms behind this behavior are not fully understood. Past methods have used bacteria labeled with DTAF or

the live stain CellTracker Green (CTG) to track bacterivory, but both methods are flawed when it comes to studying small flagellates like prasinophytes. We posit that using bacterial prey that express their own fluorescence will prove a less biased tracker for bacterivory in small mixoplankton. Using a GFP-bearing plasmid to transform marine bacterial communities, we will obtain constitutively fluorescent bacteria through the expression of said GFP gene. We believe that GFP-expressing prey will improve visualization of the engulfment and digestion of bacteria by mixoplankton when compared to CellTracker Green (CTG). Optimizing the protocols to study feeding in prasinophyte cultures will allow us to develop more hypothesis-driven experiments to improve our understanding of the cellular mechanisms and the genetic controls behind their predatory behavior. From this, surmising their impact on the carbon cycle may prove more feasible. (81)

Smith, Caleb*, and David Foster Messiah University, Mechanicsburg, PA 17055. *Effects of a low-intensity fire on an oak forest in Central Pennsylvania two years post-burn.*- Beneficial effects of low-intensity fires in oak forests are increasingly recognized yet few studies follow such low intensity fires for multiple years after the fire. Such fires alter regeneration, species composition, and can be used to reduce invasive species and increase abundances of fire-tolerant species and decrease abundances of fire-intolerant species. On March 14, 2021, an unprescribed, low-intensity fire burned over 141 acres of deciduous forest at Camp Tuckahoe BSA near Dillsburg, Pennsylvania. Herein I use data from two class projects that sampled the area in September 2021 and September 2023 to look at changes in understory vegetation. Sampling methods include visual estimation of percent cover for species <1.5m tall and <10cm DBH. Dead and live stems were also recorded for woody species >1.5m tall. Student T-tests were used to compare differences between sites inside & outside of the fire boundary. Data demonstrates total shrub cover increased from 23% in 2021 to 48% in 2023, with recovery of *Vaccinium spp.*, *Kalmia latifolia*, *Gaylussacia baccata* and *Quercus montana* being the highest. *Acer rubrum* decreased the most in percent cover and also experienced the only 2 tree (>1.5m tall) mortalities observed. Composition of shrubs & saplings <10cm DBH changed significantly more than trees >10cm DBH, illustrating the fire's low intensity and the regenerative potential of the fire-tolerant species present on the site. Future long-term studies could determine how this disturbance impacted forest composition and if repeated prescribed burns would be necessary to facilitate higher regeneration of species like oaks and huckleberry. (60)

Snavelly, Tyler*, Ashley Darrow*, Stella Phillips*, Laicie Terry*, and Valbona Hoxha Lebanon Valley College, Annville, PA 17003. *Gold-based therapy: Investigating the side effects at the organismal level.*- Cancer is a disease in which an individual's cells grow uncontrollably and killed an estimated 609,850 people in 2023. Currently, cisplatin, is a widely used platinum based chemotherapeutic drug approved by the FDA for cancer treatment. However, cisplatin acts through non-cell cycle-specific cytotoxicity by binding to and breaking DNA strands, leading to various side effects such as neurotoxicity, anemia, seizures, and nephrotoxicity. Moreover, in some cases, cancer cells can develop an acquired resistance to cisplatin, causing genetic changes that make the drug ineffective. In recent years, gold-based compounds have emerged as an alternative to platinum-based drugs. Several studies have reported that gold compounds are a promising anticancer therapy, due to exhibiting anticancer properties through comparatively weaker interactions with cellular DNA, indicating that their cytotoxicity is through DNA-independent mechanisms. However, the side effects of gold-based drugs are not known. In this study, we wanted to investigate the side effects that a gold-based compound, Au (TPA)Spy has. Using *Drosophila melanogaster* as a model organism we tested the side effects of Au (TPA) Spy on *Drosophila* survivorship and motor activity. We used different doses of Au (TPA) Spy and observed the survivorship and climbing assay, a measure of motor activity. Our results show that cisplatin in *Drosophila* can be lethal 9 days after subjects are treated with 400 µg/ml. However,

Drosophila treated with Au (TPA) Spy at the same concentration have normal survivorship (99.5% survival rate). Au (TPA) Spy did not affect motor ability of *Drosophila* either, as measured by the climbing assay. This study is very important in understanding the benefits of using alternative cancer treatments, such as gold-based complexes in decreasing side effects and decreasing the rate of cancer cells present. (14)

Soerens, Evangeline*, and **Lawrence Mylin** Messiah University, Mechanicsburg, PA 17055. *Evaluation of a cell-based vaccine against pancreatic cancer.*- Aggressive and undetected proliferation of pancreatic cancer requires early detection and therapy. We are using mice to develop a vaccine that recruits cellular immunity to target a novel protein expressed by aggressive pancreatic tumors. Highly aggressive pancreatic tumors may express an altered form of the cholecystinin/gastrin receptor that contains extra amino acids in an internal loop (CCK2i4svR). We established immortalized syngeneic cells that express the Simian virus 40 Large Tumor antigen protein (SV40 T ag) bearing a 20 amino acid insertion representing a portion of the extra 69 amino acid intron IV-encoded segment found in the CCK2i4svR receptor. Previous experiments confirmed that immunization of mice with a synthetic peptide corresponding to the same 20mer induced the 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 control cells (B6/WT-19) that expressed unaltered SV40 T ag. An ELISPOT assay confirmed induction of inconsistent, but detectable CCKCR- and SV40 T ag-specific T cell responses by using as targets peptides corresponding to a known CD4+ epitope from SV40 T ag, the 20mer peptide 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 before orthotopic implantation of syngeneic pancreatic tumor cells (Panco2) engineered to co-express the intron IV-containing variant CCK2i4svR receptor and subsequent proglumide therapy. Preliminary analysis of peritoneal tumors recovered after 4 weeks revealed a significant difference in mass between tumors found in the two groups. Tumor architecture and T cell infiltration are being assessed by staining and immunohistochemistry. The current methods have allowed us to detect T cells, and efforts are now underway to determine whether frequencies differ between tumors harvested from the vaccine and control groups. (1)

Sontheimer, Danielle*, and **Amy Parente** Mercyhurst University, Erie, PA 16546. *MDH and metabolic regulation: insights from phosphomimic mutants.*- The citric acid cycle is an important metabolic pathway in fuel metabolism. Metabolic pathways form complexes of sequential enzymes called metabolons in order to proceed more efficiently. One enzyme in the citric acid cycle that is known to form metabolons with many different enzymes is malate dehydrogenase (MDH). MDH exists as two isoforms, mitochondrial and cytosolic, allowing metabolons to form based on the needs of the cell. The enzymatic activity of enzymes can be post translationally modified. There are many forms of post translational modification, but phosphorylation is of interest in this study. Mutants of cytosolic MDH have been created to investigate changes in enzymatic activity. These specific mutants are referred to as phosphomimics, wherein a negatively charged amino acid (such as Glu or Asp) is substituted for Ser or Thr to "mimic" phosphorylation of these residues. Mutant MDH proteins are prepared by overexpression in *E. coli*. MDH enzyme assays are performed to identify if the mutated residue is important for MDH to perform its chemistry. Preliminary results indicate that several phosphomimics have altered enzyme activity, particularly with regard to changes in pH. This has implications in cancer biology, as dysregulated metabolism is well known to alter cellular pH and may impact the ability of mutated cells to regulate their proliferation. (45)

Spagnola, Lily*, **Laura Blanco**, **Jessica Maamari**, and **Audrey Ettinger** Cedar Crest College, Allentown, PA 18104. *Social group size and habitat density influence*

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. In preliminary experiments, 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 in lower density tanks, and increased aggression was typically present in larger individuals and in tanks where fish grew more rapidly. These experiments were repeated using a new tagging technique that allowed for the tracking of individuals, rather than just a group as a whole. Observation of individual fish has allowed us to measure behavioral development more precisely. Future experiments will follow individuals into adulthood to observe long-term effects of early behavioral experiences. (53)

Stevens, Molly*, and Derek Straub Susquehanna University, Selinsgrove, PA 17870. *Indoor Testing of Low-Cost Volatile Organic Compound Sensor: Sensirion SGP-41.*- Volatile organic compounds (VOCs) are organic compounds that undergo evaporation quickly due to their low boiling points. VOCs consist of many different compounds including formaldehyde, benzene, acetone and ethanol. VOCs can cause a myriad of health effects on humans, ranging from eye irritation to cancers, such as leukemia. The particular compound, along with exposure time and concentration, determine the health effects felt by humans. Indoors, there are many sources of VOCs that humans are exposed to daily. Cooking fumes, building materials, perfumes and cleaning products are just a few examples of indoor VOC sources. Due to the potentially harmful nature of VOCs, it would be beneficial to know when and how one is being exposed. However, common VOC detectors cost many thousands of dollars and are not practical for most people. The Sensirion SGP-41 is a low-cost VOC sensor with the purpose of detecting changes in the concentration of total VOCs, without differentiating between individual compounds. In this experiment, the SGP-41 was calibrated in a laboratory setting to determine whether it is properly detecting changes in known total amounts of VOCs indoors. The SGP-41 was shown to be effective in its laboratory calibration, and was then used to make measurements at various indoor locations that, in theory, would emit VOCs. The sensor was deployed in multiple food preparation areas, as well as exposed to smaller point sources. In analyzing data, it was found that the Sensirion SGP-41 was effective at detecting changes in total concentrations of VOCs, and therefore it can serve as an accessible tool to determine when and how one is being exposed to VOCs indoors. (112)

Stonbraker, Madison*, and Matthew Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Insight into how Jazf-1 regulates gene expression in the eye nervous system.*- *Jazf-1* is a human gene that has demonstrated to modify histones that influence the expression of other genes. Since it is highly conserved, we can use *Drosophila melanogaster* to study *Jazf-1* *in vivo* and better understand its role in specific tissues. While it is unknown how *Jazf-1* affects neurons within *Drosophila*, evidence shows it regulates

neurons and eye development in *Drosophila*. Using a UAS-Gal4 system we can specifically upregulate and downregulate Jazf-1 in the eyes. We can also make this system more sensitive by using a *Lobe* (allele which influences eye development. We hypothesize that changing Jazf-1 expression in the developing brain and eyes would influence histone modifications and change specific gene expression. If we need to, we can also do this in a more sensitive system by using an *L2* genetic background. Using a list of 16 potential genes that Jazf-1 regulates in the nervous system of the eye, we would use Quantitative RT-PCR to see if changing Jazf-1 levels will change expression of these genes. This experiment will provide an *in vivo* context of how Jazf-1 changes gene expression and regulates normal tissue development. (16)

Story, Lydia*, Deborah Austin, and Jeffrey Bardwell Wilson College, Chambersburg, PA 17201. *The effectiveness of sulfur-containing compounds on the inhibition of growth of Streptococcus pyogenes.*- This study focused on identifying chemical compounds that can be used as an alternative to traditional antibiotics to treat strep throat infections caused by the Group A Streptococcus strain, *Streptococcus pyogenes*. Antibiotics often cause undesired side effects or are not effective against continually mutating microbes. To potentially combat this, allicin (diallyl thiosulfinate), dimethyl sulfoxide, diallyl disulfide, allyl methyl sulfide, and diallyl sulfide were tested as inhibitory agents. These compounds were evaluated to determine if certain functional group(s) were responsible for the effectiveness against *S. pyogenes*. Antimicrobial activity was assessed by a Kirby-Bauer disk diffusion assay, using each compound in the pure liquid form. Diallyl disulfide, allyl methyl sulfide, and diallyl sulfide, were mixed respectively with dimethyl sulfoxide to observe the effects of these combinations. The antibiotic penicillin was used as a positive control, to ensure the accuracy of the results. Measurements of the diameter of the zones of inhibition were used to determine the antimicrobial effectiveness of the solutions. Statistical significance was determined by one-way ANOVA and post hoc Tukey HSD (confidence level: 95%, alpha value: 0.05) for compounds, mixtures, and compounds v. mixtures, respectively with p-values of <0.00001. Results of the Tukey HSD indicated that the disulfide bond may be necessary for antibacterial properties. Diallyl disulfide (allicin metabolite) was statistically the most effective compound (p-value <0.001), following penicillin (positive control). A mixture of allyl methyl sulfide and dimethyl sulfoxide was also statistically more effective than pure allyl methyl sulfide (p-value <0.001), suggesting an allicin molecule could be formed *in situ*. This research illustrates that compounds with disulfide bonds could serve as candidates for novel antibiotics against gram-positive bacteria. Future studies will need to be performed *in vivo* to ensure the disulfide compounds are safe for human consumption at effective concentrations. (58)

Tabakha, Maya*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Effects of e-liquids on THP-1-derived m1 macrophage phagocytosis.*- The use of e-cigarettes among adolescents has surged over the past decade due to the presumed advantages over traditional tobacco products. While initially believed to carry fewer adverse health consequences, their additive impact raises concerns about the validity of this claim. Notably, it was found that e-liquids can directly affect white blood cells and influence immune function. Unpublished research, reveals an aberrant cellular morphology of THP-1-derived M1 macrophages when polarized in the presence of e-liquids, suggesting an alteration in the immune response. One of the main characteristics of M1 macrophages is their ability to phagocytose foreign bacteria. Therefore, this project aims to conduct additional studies on the phagocytic capacity of M1 macrophages in the presence of e-liquids which we think would be altered. To that end, we are testing THP-1-derived M1 macrophage phagocytosis efficacy on *Escherichia coli* using CFU counting and expect to have enough data by early April. If this immune response against *E. coli* is either increased or diminished, these findings would indicate that vaping has implications on macrophage responses against bacteria,

leading to immune dysfunction. Importantly, *Porphyromonas gingivalis* is the main contributor of periodontal disease (PD), and it is subject to phagocytosis by innate immune cells, such as macrophages. Our group has published a study where THP-1-derived M1 macrophages can phagocytose *P. gingivalis* *in vitro*. Therefore, as a future direction, we plan to investigate the phagocytosis efficacy of *P. gingivalis* in the presence of e-liquids, which we think would be altered as well. Given the correlation between e-cigarette use and periodontal disease, understanding the effects of immunity under these conditions give us further information about the progression of PD which could impact oral health as well as systemic health. (110)

Thompson, Sydney*, and **Mahita Kadmiel** Allegheny College, Meadville, PA 16335. *Measuring the effect of corticosteroids on epithelial integrity of the human corneal epithelial monolayer in the presence and knockdown of the glucocorticoid receptor.*- The integrity of epithelial cells is crucial for stability and structure of the cornea. If this barrier is compromised, external infection can enter the eye and if left untreated, this condition could lead to vision loss. Glucocorticoids are stress hormones known to play a role in inflammation (Kadmiel and Cidlowski, 2013). Glucocorticoids are distributed throughout the body and are produced by the adrenal glands. At high doses or with chronic treatments, active glucocorticoids in the eye can cause vision issues such as increase in intraocular pressure and the risk of cataracts. In this study, we aim to answer how treating corneal cells with dexamethasone (DEX), a synthetic glucocorticoid, will affect cell membrane integrity, specifically, in the absence of the glucocorticoid receptor (GR). To determine the contribution of GR in maintaining epithelial integrity, we are performing experiments where human corneal epithelial tissue (HCET) cells are transfected with small interference RNA (siRNA) targeting nr3c1 (gene encoding GR) or a scrambled gene sequence (non-targeting control, NTC). Transfected cells are seeded into a transwell plate, then treated with DEX (0, 10, 100, and 1000 nM). After 24 hours, trans-epithelial electrode resistance (TEER) will be measured on each well using the voltohmmeter. Our preliminary studies show that, of the four conditions, the NTC with DEX condition had the highest resistance, followed by the GR knockdown with DEX. This indicates that glucocorticoid-mediated epithelial barrier protection is mediated through the glucocorticoid receptor. It is clinically important to investigate and understand the role of glucocorticoid receptor signaling in human ocular cells because of the implications glucocorticoids have on ocular inflammation. (20)

Thurber, Caleb*, and **David Foster** Messiah University, Mechanicsburg, PA 17055. *Comparative growth of Brassica rapa var. chinensis (Pak choi) and Lactuca sativa var. crispa (red salad leaf lettuce) in a hydroponic nutrient solutions with and without addition of aquaponic stimulant solution and fulvic acid in a Nutrient Film Technology (NFT) hydroponics system.*- Hydroponics systems involve plants being grown in nutrient solution. Aquaponics are a form of hydroponics producing the nutrient solution using fish waste broken down by bacteria and worms into usable nutrients for the plants including the biostimulant fulvic acid that putatively increases plant growth. This study compares growth of two species (*Brassica rapa* var. *chinensis* (Pak choi) and *Lactuca sativa* var. *crispa* (red salad leaf lettuce)) in side-by-side trials of hydroponic nutrient solution with either addition of 10% by volume of worm compost tea, aquaponics growth solution, or fulvic acid stimulant solution. Comparisons include plant height, leaf number, and total harvestable mass. It is expected that the hydroponics solution with 1/10 aquaponics solution will produce faster growing and larger plants than the hydroponics solution without added aquaponics solution. (66)

Tomov, Sophie*, **Sabeen Safi***, and **Giancarlo Cuadra** Muhlenberg College, Allentown, PA 18104. *The effects of E-liquids on THP-1 macrophage differentiation and gene expression.*- While E-cigarette usage is continuing to increase in popularity, the notion that it is harmful to its users continues to decline. Several studies show physiological alterations of the epithelium of the mouth and airway, as well as a deficit in immunological function when

exposed to E-liquids. Macrophages in the airway are significantly hindered in their phagocytic efficacy and produce excessive reactive oxygen species. Previous unpublished data by our group has shown that M1 macrophages, when polarized in the presence of E-liquids, display atypical morphology. During monocyte differentiation to M1 macrophages, the genes *MHC class II*, *CD11b*, *CD80*, *CD64*, *CD32*, and *iNOS* are all expected to be upregulated to allow for T cell activation, migration, and antibody recognition. Inspired by the atypical morphology of M1 cells post-polarization in the presence of E-liquids, this study aims to determine if the changes observed may be attributed to alterations in gene expression. To test this, M0 cells will be polarized to M1 in the presence of various E-liquids. RNA will then be collected and reverse transcribed to cDNA. The expression of *MHC class II*, *CD11b*, *CD80*, *CD64*, *CD32* and *iNOS* will be evaluated by qPCR and compared to the expression profiles of both M0 and untreated M1 macrophages. We predict that the selected genes will be underexpressed in M1 cells polarized in the presence of E-liquids in comparison to their control. This would indicate that the presence of E-liquids during polarization hinders the upregulation of *MHC class II*, *CD11b*, *CD80*, *CD64*, *CD32*, and *iNOS*. In the past two decades, E-cigarettes have introduced an unprecedented public health crisis, prompting the need for further studies into the effects of E-liquids on human health. Understanding the effects of E-liquids on the immune system and macrophage biology is paramount in beginning to address this issue. (69)

Undieh, Unimakon*, and Michael Shin Messiah University, Mechanicsburg, PA 17055.
Nickel response of irt1 mutants in Arabidopsis thaliana.- Plants are sessile organisms that deal with biotic and abiotic stresses in their environment. Heavy metal ions like nickel, zinc, lead, cadmium, and iron can constitute abiotic stress and are toxic to plants even in minimal concentrations in micromolar ranges. With the rise in industrialization, a need for hardy, genetically modified plants resistant to heavy metal ion toxicity has arisen. In this study, we propose to further investigate the role of iron-regulated transporter 1, *AtIRT1*, in the response to nickel ion toxicity in *Arabidopsis thaliana*. Previous studies (Nishida et al. 2011) indicated that *AtIRT1*, the primary iron uptake transporter in the root, is also involved in nickel uptake and showed that when in iron-deficient conditions, plants accumulate more nickel. Nishida et al. (2011) showed that *irt1-1* and *irt1-2* mutants were hypersensitive to nickel and showed chlorotic lesions when grown in tissue culture in the presence of iron and 25 μ M NiCl₂ compared to wild-type Col-0 plants. We propose to extend the 2011 study of the effect of nickel on wildtype and *irt1* mutants in the presence of iron with a dosage response curve of nickel, not just at a single concentration. We propose to use *irt1* mutants SALK_024525 (*irt1-1*), SALK_054554 (*irt1-2*), and CS869354. To determine if different *irt1* alleles have distinct responses to nickel, *A. thaliana* wildtype, and *irt1* mutants will be grown on doses of nickel ranging from 0 μ M to 120 μ M in 20 μ M increments. (95)

Updegrave, Madelyn*, and Jenny Hayden Cedar Crest College, Allentown, PA 18104.
Uncovering antibiotic-producing bacteria in soil samples.- Antibiotic resistance is a growing problem globally. Almost 5 million deaths were associated with antimicrobial resistance (AR) internationally in 2019. Genetic changes in pathogens are the cause of AR, but overuse of antimicrobials does accelerate the pathogens' genomic changes. Cases of AR are only expected to keep rising in the future, and we must find a solution to this growing public health threat. One important solution is to discover and develop new antibiotics by studying microbes, which lets us see how they inhibit the growth of each other. Doing research with Tiny Earth has given us a chance to achieve those goals. Tiny Earth (TE) is a network of students and instructors that do research on soil bacteria to discover and study new antibiotics. TE logs any bacteria that are pathogen-inhibiting in a database and students can share those same bacteria to their chemistry hub for further genomic and metabolic testing. After that testing, the antibiotic compounds can then be chemically identified to combat the AR situation. In this study, I discovered one bacterial isolate, named MU4, which was found

in a soil sample from Northampton, Pennsylvania. When streaked on top of *Staphylococcus epidermidis*, MU4 creates a zone of inhibition on both 1/10 tryptic soy agar (TSA) and full-strength TSA. MU4 is a Gram-negative rod. Crude metabolites of MU4 grown on full-strength TSA and 1/10 TSA were tested against *Staphylococcus epidermidis*, *Staphylococcus saprophyticus*, and *Enterobacter aerogenes*. Future research includes genetic identification of MU4. Research is one of the key components of understanding bacteria and antibiotic resistance. Future researchers in Tiny Earth could happen upon a new antibiotic or discover a specific AR gene, which could help slow or even stop this public health crisis. Using that information, we can discover and develop new antibiotics. (106)

Valerio Peralta, Yadeyli*, and Jessica Nolan York College of Pennsylvania, York, PA 17405. *Comparing two different methods to estimate turtle abundance in Lake Marburg (Hanover, PA).*- Water from Lake Marburg (Hanover, PA) is utilized by the Glatfelter Paper Company during manufacturing. The constant usage of the lake water often results in water level fluctuations, which have the potential to impact aquatic basking turtles living within the lake. In Lake Marburg some of the most common species found are painted turtles (*Chrysemys picta*), red-eared sliders (*Trachemys scripta elegans*), and red-bellied turtles (*Pseudemys rubriventris*). Red-bellied turtles are of particular interest as they are threatened in PA. We studied turtles from Hidden Cove and Black Rock Cove during summer 2023. Our objective was to examine the abundance of the turtles within the coves using two methods. We captured turtles using traditional basking traps and also monitored them using trail cameras attached to established basking platforms. Our population estimate of the three species in Lake Marburg showed that painted turtles are the most abundant turtle species in the two coves while red eared sliders were the least abundant. Surprisingly, there was not a correlation between the number of turtles captured in traditional traps and the number observed using trail cameras in the same cove. There may be several reasons for the lack of correlation. First, differences between the species may be due to potential competition for the optimal basking locations. Red-bellied turtles and red-eared sliders were seen more often on the larger basking platforms while painted turtles were seen on the smaller basking traps. Secondly, differences may also be due to drastic fluctuation in water levels that reduced the number of basking locations available in the lake. Water depth is an important characteristic for turtles' habitat and basking behavior. Further research on other ways water depth impacts turtles can help formulate effective conservation plans for red-bellied turtles. (88)

Wardlaw, Ashley*, Madison Dalton, Morgan Bryant, and Ann Yezerksi King's College, Wilkes-Barre, PA 18711. *The effects of atorvastatin on fish physiology.*- Pharmaceuticals are finding their way into the environment and contaminating all bodies of water including freshwater ecosystems and drinking water. One of the top pharmaceutical drugs reportedly found in freshwater ecosystems is Atorvastatin. Atorvastatin is a cholesterol-lowering drug that is known to have side effects that cause muscle weakness. We chose largemouth bass (*Micropterus salmoides*) to reflect the damage that pharmaceuticals could be doing to aquatic wildlife. Fish are good bioindicators because they can live in various bodies of water and are sensitive to changes in their environment, especially since they are known to be able to uptake chemicals through their gills. We placed 102 juvenile largemouth bass, in three different conditions: control (no drug), low (22.2 ng/L) and high (222.0 ng/L) concentrations of Atorvastatin based on current levels of the drug in various waterways. After exposure, the bass was euthanized and evaluated for muscle physiology standard protocols for measuring threshold, force of muscle contraction, timing of a muscle twitch and result EMGs. Despite conflicts with some unaccounted-for variables, corrected data did suggest some physiological changes. (89)

Washco, Lauren*, and Amy Hark Muhlenberg College, Allentown, PA 18104. *Regulation of CBF1 and SVALKA during acute cold stress in Arabidopsis thaliana.*- Epigenetic regulation in

eukaryotes is a complex process involving multiple mechanisms to aid in the initiation of transcription. The plant *Arabidopsis thaliana* utilizes epigenetic and other factors to regulate genes necessary for acute cold acclimation. *CBF1* is a transcription factor activated in response to cold stress that in turn activates the *COR* (cold-regulated) genes that ultimately promote freezing tolerance. *GCN5*, a histone acetyltransferase, has been implicated in influencing *CBF1* and *COR* gene expression. Through qPCR, we are able to measure the expression of *CBF1* in *Arabidopsis* plants harboring different T-DNA loss-of-function mutations in the *GCN5* locus. This allowed us to extend the understanding of the role *GCN5* plays in *CBF1* expression. In addition to *GCN5*, *SVALKKA*, a long noncoding RNA, also regulates *CBF1* transcription. *SVALKKA* suppresses the transcription of *CBF1* to regulate the intensity of the cold stress response. We are also investigating the possible regulation of *SVALKKA* by *GCN5*. Through a semi-quantitative gel-based assay, our preliminary findings indicate decreased *SVALKKA* expression in *Arabidopsis* homozygous for *gcn5-1* during the first four hours of cold exposure. While the mechanism is unknown, these initial findings suggest the possibility of *GCN5* to not only regulate *CBF1* but *SVALKKA* as well. (15)

Weaver, Jackson*, and Sean Buskirk West Chester University, West Chester, PA 19383. *Repeated exposure to ethanol selects for mutants with reduced ethanol sensitivity in Staphylococcus aureus.*- While the development of antibiotic resistance in bacteria has been well characterized, remarkably little is known of whether bacteria develop reduced sensitivity to surface disinfectants, such as alcohol. As a member of the normal skin microbiota and cause of many healthcare-acquired infections, *Staphylococcus aureus* is frequently exposed to alcohol through the use of hand sanitizers and disinfection protocols. Here, we utilized adaptive laboratory evolution to directly investigate the evolution of *S. aureus* following repeated exposure to alcohol. We initiated 12 independent populations of *S. aureus*, founded from 4 diverse strains (1 community-associated, 3 hospital-acquired). Each population was exposed to 50% (v/v) ethanol for 15 seconds before rescue in growth media, repeated for 21 cycles. To test the ethanol sensitivities of each evolved population, alcohol sensitivity assays were conducted using an Opentrons OT-2 liquid handling robot. We find that all strains exhibit reduced ethanol sensitivity compared to their respective ancestor, demonstrating that alcohol tolerance is an evolvable trait in *S. aureus*. Further, we find that the community-associated strain was more sensitive to alcohol than the healthcare-acquired strains, suggesting that ethanol resistance is already evolving in clinical strains of *S. aureus*. To test the limitations of the evolved tolerance to ethanol, future work will investigate the survivability of the evolved populations in higher concentrations of ethanol (55-60%), as well as isopropanol. Overall, our findings suggest that the continued use of alcohol-based disinfectants may lower their efficacy by selecting for bacterial mutants with reduced alcohol sensitivity. (86)

Wilcox, Mackenzie*, Caitlyn Henry, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Lipopolysaccharide alters cell viability and location of NF- κ B and TNF- α in cAMP-stimulated RT4-D6P2T Schwannoma.*- Schwann cells (SC), the primary glial cell of the peripheral nervous system, produce the myelin sheath that insulates and protects the axon. Neuronal damage stimulates SCs to divide and secrete pro-inflammatory cytokines, such as TNF- α , through the NF- κ B pathway. Preliminary studies have shown that treating cAMP-activated SCs with lipopolysaccharides (LPS), downregulates the expression of NF- κ B and AKAP95, an important anchoring protein of the cAMP/protein kinase A pathway. As a result, it was hypothesized that activating the cAMP pathway in LPS-treated Schwann cells would alter cell viability, promote translocation of NF- κ B into the nucleus, and cause an interaction between NF- κ B and AKAP95. To test the hypotheses, SCs were treated with control media (N2), or forskolin (F), and LPS at various concentrations and durations (n=3). Using the CellTiter-Glo viability assay, it was found that treating SCs with 10 μ g/mL of LPS with F decreased cell viability for all time points. To determine the location of NF- κ B and

AKAP95, SCs were treated with N2 or F and various concentrations of LPS for 1 hour, and visualized using fluorescently tagged antibodies. Qualitative observations indicated that NF- κ B was present in both the cytoplasm and the nucleus for all treatments. Quantification of colocalization using Pearson's Correlation coefficients (PCC) with ZenBlue software, revealed a strong interaction for NF- κ B and AKAP95 in all conditions, except for cells treated with F + 0.1 μ g/mL LPS. Cells treated with 0, 1, or 10 μ g/mL LPS with F had lower PCC (0.8822 \pm 0.0813, 0.4971 \pm 0.0501, and 0.7555 \pm 0.0209, respectively) in comparison to cells incubated in control media (0.9306 \pm 0.0221, 0.8718 \pm 0.0743, and 0.7878 \pm 0.0088, respectively). However, cells treated with 1 μ g/mL LPS+F (0.8434 \pm 0.0730) had a higher PCC than those incubated in control media (0.7475 \pm 0.0830). These results suggest that the interaction of NF- κ B and AKAP95 in cAMP-activated cells is dependent upon LPS dose even though cAMP decreases viability. (4)

Wilde, Nicholas*, Mackenzie Wilcox, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *The Effect of LPS on Phosphorylation of AKT Signaling in Schwann Cells.*- Schwann cells (SC), the principal myelinating cells of the peripheral nervous system, play a vital role in neuronal repair following peripheral nerve injury. The damaged axon stimulates Schwann cells to initiate an inflammatory response which allows immune cells to the site of injury to clear the myelin debris so that neuronal growth could be facilitated. Although extensive studies have explored the field of neuronal repair, the exact mechanisms by which Schwann cells assist in axonal regeneration are unknown. Previous studies have shown that pathways involving cAMP, the universal second messenger, and the cell survival signal protein kinase B (AKT) are known to be involved in SC growth. To understand the role of cAMP and AKT pathways in neuronal cell injury, RT4-D6P2T rat SCs were cultured in control media (N2), or the cAMP activator forskolin (F), and treated with different doses of the bacterial endotoxin, lipopolysaccharide (LPS) and incubated for 3, 6, or 12 hours. Western analysis of phosphorylated-AKT (p-AKT) in forskolin treated cells revealed an upregulation of protein expression in cells incubated for 3 hours with 0.1 μ g LPS (1.91% \pm 1.057) to 1 μ g LPS (2.02% \pm 1.524) to 10 μ g LPS (4.27% \pm 3.903) compared to N2 and F (0.77% \pm 0.374). For 6-hour treatments, an upregulation was seen at 0.1 μ g LPS (1.14% \pm 0.599) to 1 μ g LPS (3.09% \pm 0.204) but had a decrease in expression at 10 μ g LPS (1.67 \pm 0.904) compared to N2 and F (1.01 \pm 0.364). At 12-hours, upregulation was only seen in 1 μ g LPS (11.76% \pm 10.630), while both 0.1 μ g LPS (1.31% \pm 0.683), and 10 μ g LPS (1.22% \pm 0.315) had similar values when compared to N2 and F (2.04% \pm 1.834). For 24-hour treatments, an upregulation was seen across all treatments as the dosage of LPS + F increased with N2 + F (0.297% \pm 0.021), 0.1 μ g LPS (0.409% \pm 0.183), 1 μ g LPS (1.482% \pm 0.978) and 10 μ g LPS (2.028% \pm 13.410). These findings suggest that, during nerve injury, the cAMP pathway may be activated to upregulate p-AKT in SCs. A better understanding of how AKT and cAMP pathways interact may reveal a potential target for treatment of nerve injury and inflammation. (27)

Witkofsky, Victor*, Sarah Marston*, Callie Asper*, and Diane Bridge Elizabethtown College, Elizabethtown, PA 17022. *Investigating ferroptosis in the model invertebrate species *Hydra oligactis* and *Hydra vulgaris*.*- Ferroptosis is a form of regulated, iron-dependent cell death caused by accumulation of lipid peroxides. Defective regulation of this process is implicated in neurodegenerative diseases, cancer, and inflammation. Ferroptosis occurs in diverse animals but has not been documented in *Hydra*, an invertebrate genus used for studies of stem cell biology and aging. To investigate whether ferroptosis occurs in *Hydra*, we treated *Hydra oligactis* and *Hydra vulgaris* with the ferroptosis-inducing and ferroptosis-inhibiting compounds. The inducers diethyl maleate and erastin induce ferroptosis by reducing availability of glutathione within the cell, which leads to inactivation of the phospholipid peroxidase glutathione peroxidase 4. The inducer RAS-selective lethal 3 induces ferroptosis by directly inactivating glutathione peroxidase 4. In *Hydra oligactis* and

vulgaris DEM, erastin, and RSL3 caused thickening of the external epithelial layer, tentacle shortening, the appearance of rounded cells detached from the body, and death. To confirm that the effects of the inducers resulted from ferroptosis, ferroptosis inhibitors were used to counter the effects of the ferroptosis inducers. Inhibitors used were liproxstatin-1 and ferrostatin-1, which suppresses lipid peroxidation; β -mercaptoethanol, which would be expected to increase intracellular glutathione availability; and the iron chelator deferoxamine. Surprisingly, ferroptosis inhibitors tested did not counter the effects of the ferroptosis inducers used. To determine whether the ferroptosis inducer RSL3 causes the lipid peroxidation characteristic of ferroptosis, we stained *Hydra oligactis* and *Hydra vulgaris* treated with RSL3 with Bodipy C11 (581/591). Staining provided no evidence of lipid peroxidation. Our results raise the question of whether *Hydra* are unusually resistant to ferroptosis or undergo a type of ferroptosis with unusual properties. (104)

Wolfgang, Jessica R.*, Francesca C. Giardini*, Vaughn Shirey, and Stephen C. Mason, Jr. Immaculata University, Immaculata, PA 19345. *Testing the plant vigor hypothesis after wildfire in the New Jersey Pinelands National Reserve.*- The Plant Vigor Hypothesis states that rapidly growing plants, particularly after a disturbance, are less structurally and chemically defended, and therefore will be more susceptible to phytotroph attack. Last year, we supported that oak leaves (*Quercus* spp.) at our wildfire site were growing more rapidly than oak leaves at our unburned site in NJ Pinelands National Reserve. This year, we wanted to determine if the leaves at the wildfire or unburned sites would have more plant pathogen and insect herbivore (phytotroph) damage. We predict that the leaves at our wildfire site will have more pathogen and insect herbivore damage since they grew more rapidly. To test this, we counted the number of pathogen and insect herbivore damage (e.g., leaf miners, gall makers) on 120 oak leaves from each of our study sites (n=240). We then conducted a paired t-test to compare the phytotrophic damage on the leaves from both study sites. Our preliminary results show that pathogen damage was actually higher at the unburned site ($p = <0.001$) than at our burned site. There was no difference for insect herbivory between the two sites ($p = 0.30$). Based on these preliminary results, our prediction for the Plant Vigor Hypothesis was rejected for both plant pathogens and insect herbivory. The wildfire likely decreased most of the plant pathogens and insect herbivores that would have caused the damage to the leaves we were analyzing, and they could not immediately recolonize the burned site to take advantage of the potentially undefended leaves. In contrast, the plant pathogens and insect herbivores at the unburned site were never negatively affected. We plan to continue analyzing more oak leaves for phytotrophic damage and will be testing if the leaves in the burned site are less structurally and chemically defended. (80)

Wolfinger, Madison*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Understanding how RPA phosphorylation affects the telomere synthesis pathway.*- The complete and accurate DNA replication of chromosomes, along with active DNA damage repair pathways, are required to ensure the integrity of human chromosomes. Defects in DNA replication, DNA repair, or chromosomal end maintenance can lead to cancer in human cells. During DNA replication, organisms need to address the end-replication problem that prevents DNA from replicating chromosomal ends, resulting in a loss of important DNA after each cell division. To combat this, cells attach telomeres to the ends of their chromosomes. Telomeres are non-coding DNA sequences that can be partially shortened with each division without negatively impacting chromosomal function. Telomeres are synthesized by a ribonucleoprotein called telomerase that synthesizes DNA from an RNA template. In most normal somatic cells, telomerase expression is inactive and regulated. In malignant cancer cells, however, telomerase expression is upregulated, allowing telomeres to maintain their length, supporting tumor formation. *Saccharomyces cerevisiae* is a yeast that is used as a model for function and regulation of human telomeres. Many proteins affect the function of

telomerase, including the single-stranded DNA binding protein Replication Protein A (RPA). RPA plays important roles in DNA and telomere maintenance. Phosphorylation of RPA can change its function, which may affect telomere synthesis. To understand RPA phosphorylation and telomere synthesis, we examined telomere length in different *S. cerevisiae* strains with or without genetic mutations. Following genomic DNA isolation and PCR, gel electrophoresis was used to analyze the telomeres. We will present data suggesting RPA phosphorylation may regulate the length of telomeres lengths in yeast. Understanding how normal cells regulate telomere synthesis will provide insights into how malignant cells activate telomerase, providing potential targets to kill cancer. (28)

Yendluri, Saiananya*, Marissa Hooks, Taylor Besch, and Mahita Kadmiel Allegheny College, Meadville, PA 16335. *Effect of Glucocorticoids on Zonula Occludens 1 (ZO-1) expression in human retinal pigmented epithelial cells.*- Glucocorticoids (GC) are natural steroid hormones produced by the adrenal glands, crucial for their anti-inflammatory functions. Corticosteroids, synthetic versions, are used to treat specific types of blindness like diabetic retinopathy and macular edema. Dexamethasone (Dex), a corticosteroid, is recognized for its ability to modulate tight junction proteins in epithelial cells. Our research aims to elucidate how GC signaling impacts the integrity of retinal epithelial cells. We conducted wound healing assays using Human Retinal Pigmented Epithelial Cells (ARPE-19). ARPE-19 cells were treated with Dex (0 & 1000nM) for 24 hours, followed by wound healing assays. Brightfield images were captured at 0, 8, and 24 hours, and ImageJ software was employed to quantify wound closure. Immunofluorescence (IF) and Western blotting (WB) techniques were utilized to assess the expression of zona occludens 1 (ZO1) - a tight junction protein, and the glucocorticoid receptor (GR), the primary receptor for GCs, in cells at the leading and outer edges of the wound. Our results indicated that Dex treatment inhibited wound healing, with Dex-treated cells closing only 69.7% of the wound compared to 78.8% in the control ($p < 0.05$). IF analysis did not reveal significant differences in ZO1 levels. However, WB results demonstrated a decrease in ZO1 expression in cells at the outer edge of the scratch (Control 0.35 a.u. & Dex 0.13 a.u.; $p < 0.01$) and an increase in ZO1 expression in cells at the leading edge (Control 0.10 a.u. & Dex 0.26 a.u.; $p < 0.02$) following Dex treatment, suggesting cell-specific effects of GCs. Overall, our study suggests that Dex exerts differential effects on ZO1 expression in ARPE-19 cells, indicating the cell-specific actions of GCs. This research contributes to a better understanding of factors influencing retinal pigmented epithelial integrity and may have implications for therapeutic approaches. (35)

Zilinski, Cora*, Benjamin Ziegler*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Polydatin shows no antiviral activity toward the Human Coronavirus 3C-like Proteases of HCoV-OC43 or HCoV-HKU-1.*- With the emergence of three novel coronaviruses (Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), Middle East Respiratory CoV (MERS-CoV) and SARS-CoV 2) within less than 20 years, highlights the need for broad acting antivirals that can be used in case of another coronavirus emergence. Polydatin is glucoside derivative of resveratrol which can be extracted from the plant *Polygonum cuspidatum*. Polydatin and resveratrol have antioxidant and anti-inflammatory properties and have been shown to have antiviral activity. The antiviral activity of these compounds has been shown to target and inhibit the active site of viral proteases. Specifically, polydatin has been shown to have potent inhibitory activity against the coronavirus 3C-like proteases (3CLpro) from SARS-CoV 2 and MERS-CoV and some inhibitory activity against the papain-like protease (PLP). Additionally, it may have antiviral activity against HCoV-OC43. However, it is unclear whether polydatin targets 3CLpro other human coronaviruses including ones that cause the common cold. Using chimeric reporter mouse hepatitis virus (MHV), that express the 3CLpro of either HCoV-HKU1 or HCoV-OC43 in place of the MHV protease, we tested for virus inhibition by polydatin. We demonstrate

that polydatin has no significant cytotoxicity at the concentrations tested. Additionally, when cells are treated with polydatin at the time of infection, there was no decrease in viral replication measured by luciferase activity. This work provides insights into the efficacy of polydatin as an antiviral and demonstrates the need to test multiple CoVs to determine the broad efficacy of antiviral compounds. (92)