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Abstract Booklet

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Abdeljebbar, Douaa*, Haven Rand*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Acrylamide's effects on chromosome loss in Saccharomyces cerevisiae*.- Humans often consume acrylamide, a known carcinogen, through the inhalation of cigarette smoke and the consumption of starchy foods cooked at high temperatures. Aneuploidy, the loss of one or more chromosomes, can result in the uncontrolled growth and genetic instability which are hallmarks of cancer cells. We hypothesized that acrylamide might promote nondisjunction in *Saccharomyces cerevisiae*, a eukaryotic model organism. We investigated the influence of acrylamide on chromosome loss in a disome strain of *S. cerevisiae* which contains two copies of Chromosome VII. Colonies of this strain are red due to the accumulation of AIR (aminoimidazole ribotide), an intermediate in the adenine biosynthesis pathway. Colonies which lose one copy of Chromosome VII are white. Remarkably, we found acrylamide decreased chromosome loss in the disome strain. In addition, we noted that the disome colonies grown on acrylamide developed a pale pink hue instead of the bright red color characteristic of robust AIR production. The accumulation of reactive oxygen species (ROS) in *S. cerevisiae* leads to the depletion of reduced glutathione, which transports the AIR intermediate to the cell's vacuole. We believe that oxidative stress from the exposure of *S. cerevisiae* to acrylamide might be the cause of the pale pink colony color. We intend to assay for oxidative stress and the levels of ROS-induced gene expression in the presence of acrylamide. (**117**)

Adams, Kaleigh*, Gracie Domingo-Whitfield*, and André Walther Cedar Crest College, Allentown, PA 18104. *A novel method of genotyping yeasts involved in beer production using quantitative PCR and High Resolution Melt Analysis*.- Americans consume vast quantities of beer annually (~6.5 billion gallons in 2021), generating billions in revenue for the American beer industry. All beer production begins with grains that are soaked in water to germinate, then mashed and boiled with hops to add flavor, to generate a sugar solution called wort. The wort is cooled and added into tanks with yeast to undergo fermentation that produces the ethanol and carbon dioxide in the beer. Different species of yeast are used to make different beers (Ales vs Lagers), and each species and strain of yeast can result in vastly different flavor and aroma profiles that are specific to each kind of beer. Contamination of beer batches with incorrect yeast strains from previous beer batches or from the environment can lead in undesirable beer outcomes and cause significant financial losses. To ensure that the correct yeast is used in making specific beers, large-scale American beer producers routinely check for yeast contamination in their tanks, but traditional contamination testing methods are often costly and time-intensive; to address these limitations, our has worked to develop a novel method that uses quantitative PCR (qPCR) linked to High Resolution Melt (HRM) analysis to genetically identify yeast strains. Our methodology involves isolating yeast genomic DNA, followed by qPCR-HRM analysis of loci that contain short tandem repeats. Our initial analyses have identified target loci that exhibit promising differentiation capabilities between different beer yeast species (ales vs lagers), and we have been able to discriminate between different strains within beer species. This novel approach will lead to reduced testing times that translate to faster batch releases, minimized production delays, and reduced financial losses from contaminated batches and should pave the way for improved quality control and streamlined logistics within the expansive American beer industry. (**97**)

Adesola, Opeoluwa*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Characterizing the glycoprotein-receptor interaction of Hantavirus infections*.- Hantaviruses are an emerging RNA virus that can be classified into Old World and New World hantaviruses causing different diseases; Hemorrhagic Fever with Renal Syndrome (HFRS) and Hantavirus Cardiopulmonary Syndrome (HCPS), respectively with mortality rates up to 15% for HFRS or even 50% for HCPS (Ermonval et al., 2016). Entry mechanisms are thought to differ, depending on their classification that is dictated, in part, by their glycoprotein sequence. Previous research has characterized the entry receptor, PCDH-1, for New world hantaviruses but not Old world, and identified that it interacts with the Gn glycoprotein. However, whether both of the hantavirus glycoproteins, Gn and Gc, are important for these virus-receptor interactions has not been well characterized. Hence, to delineate the roles of these glycoproteins in their interactions with PCDH-1, we infected wild type and transient PCDH-1 KO populations of 293T cells with a chimeric pseudovirion model containing wild type and mixed Old World and New World hantavirus glycoproteins expressed on a vesicular stomatitis virus core, and compared infectivity rates. Virus production and infection of transient PCDH-1 knockout populations are underway. We expect that infectivity rates will be significantly reduced in the chimera model containing Old world Gn and New world Gc indicating a synergistic role for Old World Gc in virus entry. Understanding the entry mechanisms of hantaviruses will contribute to new knowledge about this emerging pathogen and provide possible targets for future therapeutic research. (**101**)

Ahmed, Umair*, Jonathan Olaleye*, Alex Corsones*, and Laurie DiRosa Immaculata University, Immaculata, PA 19345. *Resistance training versus aerobic training impact on blood glucose regulation: A critically appraised topic*.- Blood glucose levels (BGL) are vital for assessing metabolic health among individuals living with chronic disease processes, particularly Diabetes Mellitus. Exercise is frequently used as a first-line intervention to help regulate BGL in these populations. However, uncertainty exists on which exercise intervention is superior. The purpose of this Critically Appraised Topic is to compare the effectiveness of Resistance Training (RT) versus Aerobic Training (AT) in regulating BGL among individuals with chronic disease. The literature review included Google Scholar, ProQuest, PubMed, and MEDLINE databases. Studies that were published within the last 10 years, involved adults with chronic diseases or risk factors, and male and female subjects were included. Pediatric populations and studies older than 10 years ago were excluded. Based upon a review of the current literature, RT appears to be superior to AT in regulating BGL in individuals with chronic diseases. While AT was beneficial for cardiovascular health and lipid profile improvements, its effects on BGL were less pronounced compared to RT. Limitations of this review include inconsistencies in training regimens, diets, population ages, comorbidities, and variations in measurements between the studies. Future research should focus on standardization of diet, exercise intervention, intensity levels, and metabolic outcome measures. In addition, the effects of different types of RT and AT should be evaluated to examine which type has the most significant reduction in glycemic control. Clinically, this review suggests that healthcare providers should prioritize RT, in conjunction with AT, as a first-line intervention in treatment of chronic disease. (**46**)

Aiello, Nicholas*, and Joshua Loomis East Stroudsburg University, East Stroudsburg, PA 18301. *Efficacy of phage K on killing Staphylococcus aureus grown in biofilm*.- Bacteria can grow as free-floating, single cells or as part of multicellular communities called biofilms. Biofilms form through bacteria adhering to one another and to a surface by secreting polysaccharides, forming an extracellular matrix. This matrix enhances cellular communication and protects the bacterial community from anti-microbial chemicals, including antibiotics. Biofilms are up to 1,000 times more resistant to antibiotics than planktonic (free-floating) bacteria. The National Institutes of Health (NIH) reports that 65-80% of bacterial infections in humans are due to biofilm formation. *Staphylococcus aureus*, particularly Methicillin-resistant *Staphylococcus aureus* (MRSA) is a leading cause of biofilm-associated infections in both healthcare and community settings. In some healthcare settings, 30-50% of *S. aureus* infections are MRSA. *S. aureus* can develop resistance to other classes of antibiotics, including Vancomycin-resistant *S. aureus* and Multidrug-resistant *S. aureus* strains that are resistant to multiple classes of antibiotics. Resistance rates can be particularly high in hospital settings, where antibiotic usage is intensive. The resistance of *S. aureus* to multiple antibiotics is one of the key drivers behind the need for alternative treatments, like phage therapy. Phage therapy is the use of bacteriophages (viruses that specifically target bacteria) to treat bacterial infections, especially antibiotic-resistant bacterial infections. The goal of the project is to determine if phage K, a bacteriophage specific to *S. aureus*, is effective in killing *S. aureus* in the context of a mixed species biofilm. Phage K was more effective in eliminating planktonically-grown *S. aureus* (in broth) and less effective on *S. aureus* in biofilm. Early data suggests that *S. aureus* within a biofilm is indeed more resistant, however, at high concentrations, Phage K was able to significantly reduce *S. aureus*. Further studies are underway to determine phage K efficacy on mixed species biofilms containing *S. aureus* and *Candida albicans*, both commonly present in biofilm-associated infections. (**104**)

Alkhafaji, Fadi*, Jeremy Burda, and Mahita Kadmiel Allegheny College, Meadville, PA 16335. *Determining the anti-angiogenic properties of CTZ1, a novel drug being investigated for age-related macular degeneration*.- Age-related macular degeneration (AMD) is a multifaceted disease that comes as either wet or dry. If untreated, AMD causes central vision loss. Oxidative stress plays a major role in the pathogenesis of this disease with the dry variant. However, wet AMD, also known as neovascular AMD, has unwanted retinal angiogenesis. Angiogenesis is the process by which new blood vessels arise from previous ones and normally occurs during tissue repair. Excessive angiogenesis as a result of the overproduction of pro-angiogenic factors such as vascular endothelial growth factor (VEGF), causes abnormal and uncontrolled vessel growth that are often weak and may leak into the subretinal pigment epithelial space. A new potential drug, CTZ1, is proposed to exert anti-oxidative and anti-angiogenic properties by using a nicotine analog to disrupt angiogenesis through the acetylcholine-nicotinic receptors. Endothelial tube formation assays using human umbilical vein endothelial cells (HUVEC) were performed to assess the effectiveness of CTZ1 in comparison to Dexamethasone (Dex), a known anti-angiogenic synthetic corticosteroid, as well as in combination with Dex. Preliminary results have shown that CTZ1 is effective in reducing blood vessel formation, similar to Dex, if not slightly better. In comparison to the controls, there is a significant difference, indicating that CTZ1 may potentially work as an anti-angiogenic drug. This study aims to find a novel way of treating AMD, both wet and dry, leading to a potentially less expensive and effective therapeutic for AMD patients who currently require repeated intravitreal injections. (**135**)

Alkhafaji, Mariam*, Hannah Barnett, and Quyen Aoh Gannon University, Erie, PA 16541. *Trans-Golgi network and endosomal adaptors are required for ATP-dependent but not nitrogen-specific growth in Saccharomyces cerevisiae*.- In the yeast *Saccharomyces cerevisiae*, the trafficking of proteins between the cell surface, trans-Golgi network (TGN), endosomes, and vacuoles is regulated by clathrin adaptors. This study investigates the roles of the TGN-endosomal clathrin adaptors in nitrogen-regulated growth. We found that specific combinations of clathrin adaptors are necessary for growth. Given that defects in nitrogen permease trafficking may underlie these growth issues, we explored how different adaptor combinations influence growth across various nitrogen sources. Our results indicate that single deletions of ENT3, ENT5, or APL2 (AP-1 subunit) do not affect growth in either preferred or non-preferred nitrogen sources. However, double deletions of ENT3 and ENT5 (but not APL2 with either ENT3 or ENT5) resulted in reduced growth in both nitrogen conditions. A triple deletion of ENT3, ENT5, and APL2 led to the most significant growth defect under both nitrogen sources. These findings suggest that Ent3 and Ent5 are functionally redundant and complementary to AP-1, with all three being essential for optimal cell growth. Notably, the role of these clathrin adaptors in cell growth does not appear to be directly linked to the regulation of specific nitrogen permeases, implying a broader function in cellular processes that may influence metabolism and cell cycle regulation. To further investigate this, we assessed the impact of adaptor deletions on cellular ATP levels. We observed reduced ATP levels in double and triple mutants, not in single mutants, suggesting a novel role for clathrin adaptors in regulating metabolism, potentially through modulation of signaling pathways that influence cellular energy levels. (**17**)

Allshouse, Tim*, Victoria Abramczuk, and Emily Stowe Bucknell University, Lewisburg, PA 17837. *Isolation and characterization of* *Paracoccus* *sp.* *ME4, a carotenoid producing strain isolated from freshwater*.- The aquatic environment supports the growth of a varied microbial community. These microbes are essential members of the community and support the growth of larger eukaryotic organisms and help maintain the biogeochemical cycles in the environment. While characterizing the microbial community in a pond at the Bucknell University Natural Area we isolated an orange-pigmented bacteria. This strain was designated ME4, subsequent sequencing of the 16SrRNA gene indicated it was a member of the *Paracoccus* genus. Members of *Paracoccus* have been found in diverse ecosystems, but freshwater isolates are not numerous. Additionally, *Paracoccus* species are actively being studied for potential roles in bioremediation, antimicrobial compound production and carotenoid synthesis for commercial purposes. In this poster we present the results of our characterization of the physiological and metabolic capabilities, and genomic characteristics of *Paracoccus* sp. ME4 with particular attention to carotenoid production in response to changes in nutrient availability. (**100**)

Ambrose, Rebecca*, Ashley Batejan*, Lauren Ladik, and Laurie DiRosa Immaculata University, Immaculata, PA 19345. *The coach-athlete relationship and athlete motivation*.- The human experience is based on relationships, and within the athletic field, relationships take place between coaches and parents, coaches and athletes, athletes and athletes, parents and athletes, and more. Specifically, the coach-athlete relationship functions to support the athlete in reaching their full athletic potential. This research explores to what degree the athlete’s perspective of the coach-athlete relationship impacts the motivation of the collegiate athlete. A web- based survey was disseminated by email to student athletes at IU. There were 5 demographic questions and 12 scale-based questions on the how the athlete feels about their coach, their interactions, and performance. A correlational analysis was performed on coach relationship and motivation scores. Scores were also ranked 1-6 to determine if a reciprocal influence on each other was present. The final sample was N=52. Results show that there is a positive, strong correlation (r= 0.85) between the athlete’s perspective of their relationship with their coach and their self-perceived performance levels. When reviewing the ranked responses, results further show athletes do their best because they believe their coach is doing the same, supporting the reciprocal process theory. This study suggests that the perception of a positive coach-athlete relationship may impact student-athlete’s motivation to perform. Therefore, an emphasis on the coach-athlete relationship should be placed and perhaps an educational program for coaches be established. Future research could examine the relationship differences between genders, as well as between individual versus team sports. (**49**)

Ambrosino, Marian*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Quantifying primary tumor fibrosis in a metastatic model of murine pancreatic cancer*.- Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest cancers in the US, often diagnosed at a metastatic stage when the five-year survival rate is just 3.1%. 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 orthotopic pancreatic tumors and improve treatment. Its efficacy in metastatic lesions remains untested. Toward the characterization of a new, more metastatic murine PDAC cell line, MCB/1, mice were injected orthotopically with MCB/1 cells to ensure the primary tumors exhibit proglumide sensitivity comparable to preceding cell lines. We previously reported mice randomized to proglumide-treatment exhibited no change in primary tumor mass compared to control. While incidence of liver and lung metastasis was unchanged, the average number of mesenteric metastases was lower in proglumide-treated mice. Having hypothesized proglumide will reduce fibrosis in MCB/1 primary tumors, we herein report histologic quantification. Paraformaldehyde-fixed tumors were paraffin-embedded and sectioned at one or two depths depending on tumor size. Masson's trichrome staining was performed to differentiate between the collagen matrix and cellular portions. Sections were imaged with a whole-slide scanner and percentage of fibrosis was quantified by Fiji (ImageJ) color thresholding between blue collagen and various red cellular hues. (**190**)

Amesquita, Victor*, and Leena Pattarkine Harrisburg University of Science and Technology, Harrisburg, PA 17101. *3D scaffolds - biopolymer and nanoparticle hydrogels: A systematic study of mechanical and antimicrobial properties*.- In the field of tissue engineering, scaffolds are essential structures designed to promote cellular growth and repair by providing a supportive environment for cell adhesion, proliferation, and differentiation. The development of novel 3D scaffolds using biopolymers and nanoparticle composites offers innovative formulations for fabricating scaffolds with superior mechanical strength, antimicrobial, and water absorption properties. Scaffolds play a crucial role in not only providing a physical framework but also in facilitating biochemical cues that influence cellular behavior, making them vital in regenerative medicine. This study is a systematic investigation of 3 different biomaterials namely alginate, agarose, and gelatin with and without nanomaterial infusion 9graphene oxide, gold nanoparticles and iron oxide nanoparticles. Graphene oxide (GO) nanoparticles are often incorporated into scaffold materials to improve their mechanical strength, biocompatibility, and overall functionality. The unique properties of GO, such as high surface area, electrical conductivity, and In this context, GO serves as a key component in the ACGO composite, where it helps to enhance the physicochemical properties of the scaffold while also influencing biological interactions excellent mechanical strength, allow the scaffold to better support the growth and differentiation of cells, thereby facilitating tissue formation and repair. These properties make GO an ideal candidate for incorporation into scaffolds designed for applications in cartilage regeneration, bone repair, and other tissue engineering applications. Through the incorporation of GO nanoparticles, the ACGO composite scaffold demonstrates improved structural integrity, cellular compatibility, and enhanced bioactivity. The gold nanoparticle infused 3D scaffolds offer antimicrobial properties. These improvements are critical for creating more effective and reliable scaffolds capable of supporting complex tissue regeneration processes. By examining the interaction between the biopolymers and nanoparticles, this work has generated a unique database that is helpful with selection of appropriate scaffold composite for optimized properties for therapeutic applications in tissue engineering. (**84**)

Arhin, Annabel*, Isabella Foriska, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Genetic screen for salt tolerance identifies Sigma Factor A as a critical transcriptional regulator of salinity stress*.- Sigma factors are special dissociable protein subunits that direct core RNA polymerase (RNAP) to the appropriate start site for transcription, a process allowing for the formation of mRNA and subsequently, synthesis of proteins. These subunits, thus, are required for bacterial gene expression. In *Bacillus subtilis*, sigma factor A and sigma factor B are the two major sigma factors that regulate normal function and health of the bacteria, and it is understood that sigma factor A is a housekeeping sigma factor and sigma factor B, an alternative sigma factor activated upon general stress. The specific interactions amongst these two regarding gene expression, however, are not as well understood. In this study, through genetic screen, we discovered sigma factor A as a gene necessary for salt tolerance of *Bacillus subtilis*. Using Western Blot analysis, we discovered that the sigma factor A mutant lacked the antioxidant enzyme, superoxide dismutase (sodA), whereas the sigma factor B mutant exhibited higher levels of sodA, suggesting potential antagonistic or competitional behavior between the two sigma factors. The dependence of sodA gene expression on sig A will be confirmed using quantitative PCR. Genetic complementation will be performed to test if introduction of a functional sigA can restore salt tolerance in the mutant. The discovery of a housekeeping sigma factor as necessary for salt tolerance provides a novel insight into the mechanism of stress tolerance in bacteria. (**95**)

Aryal, Sweta*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Chromosome segregation dynamics in meiosis I, meiosis II, and mitosis in the cells of house crickets (<u>Acheta</u> <u>domesticus</u>)*.- The aims and chromosome behaviors in cell division differ in mitosis and meiosis. In meiosis I chromosome number is reduced from diploid to haploid by separating homologous chromosomes, while in meiosis II ploidy is maintained and sister chromatids separate. In mitosis, the chromosomes are copied and distributed to daughter cells, maintaining a diploid chromosome number. There have been no comparative analyses of chromosome dynamics across mitosis, meiosis I, and meiosis II within a single species. We use live-cell imaging of house cricket (*Acheta domesticus*) spermatocytes to characterize chromosome movement in mitosis, meiosis I, and meiosis II, providing insights into their unique dynamics. In this analysis, we have determined how chromosome position changes from metaphase to anaphase in all three division types. We have also determined that chromosomes move to the spindle poles at the same rates in anaphase I and anaphase II but move at double the meiotic rate of movement in mitotic anaphase. (**187**)

Asper, Callie*, Kira Koutsouftikis*, and Diane Bridge Elizabethtown College, Elizabethtown, PA 17022. *Exploring the role of the microbiome in ferroptotic processes of <u>Hydra</u> <u>vulgaris</u>*.- The microbiome's influence on an organism's metabolism, neurology, digestion, and immunity heightens its potential contribution to medical advancements. Ferroptosis, an iron-dependent form of regulated cell death, is also instrumental in metabolic research and study of disease. Established research demonstrates bacteria's influence on iron availability and lipid peroxidation. However, the relationship between the *Hydra vulgaris* microbiome and its impact on ferroptosis has yet to be studied. This study examined the diversity of the *Hydra vulgaris* bacterial microbiome by creating and analyzing bacterial cultures of the *Hydra*. The *Hydra* were also stripped of their native bacteria to yield "germ-free" organisms. Germ-free *Hydra* and *Hydra* that still had their original microbiome were treated with ferroptosis inducer Diethyl Maleate (DEM) to observe significant differences in *Hydra* death between treatment groups. *Hydra* death is a potential indicator of ferroptosis induction. The germ-free *Hydra* group yielded a significantly higher amount of death. This result necessitates further trials of introducing other ferroptosis inducers, such as RAS-selective lethal 3 (RSL3) for comparison of different ferroptosis inducer effects in both treatment groups. Additionally, the varying bacterial species of the *Hydra vulgaris* microbiome should be sequenced. Classifying bacterial species existent in the *Hydra* microbiome will inform how their specific metabolic processes may promote or inhibit ferroptosis in the *Hydra*. (**93**)

Azar, Michael*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Inhibiting pancreatic tumor fibrosis: Proglumide may not function via collagen downregulation*.- Pancreatic cancer is one of the deadliest cancers, due in part to its resistance to chemo- and immuno-therapies. These difficulties in treatment arise in part from the highly fibrotic tumor microenvironment composed of excessive collagen deposition. Proglumide, a CCK receptor antagonist, has been shown to decrease fibrosis and improve chemotherapy in murine models of pancreatic cancer. Currently, it is not known whether proglumide directly targets the cancer cells or the pancreatic stellate cells attributed with matrix production in normal pancreas. Several studies in our lab have shown relatively unchanged collagen (COL1A1, COL1A2) expression in each cell type upon proglumide treatment; however, these studies were performed in monoculture with limited treatment duration (<72 hrs). Here, we report results testing two hypotheses. First, we hypothesized an extended duration of treatment reflective of in vivo studies may achieve downregulation. Pancreatic cancer (PANC-1) and stellate cells (RLT-PSC) were assessed following 12 days proglumide treatment. No definitive change in COL1A1 and COL1A2 expression was observed, and results paralleled shorter duration treatment. Second, we hypothesized proglumide's effect may be mediated by paracrine or contact-dependent signaling between cell types. In this study, PANC-1 and RLT-PSC cells were cocultured to determine the effect of proglumide on COL1A1 expression. Cocultures did not demonstrate an alteration in COL1A1 expression when treated with proglumide; resulting RNA expression appeared to be an average of the individual expressions of each monoculture. Studies are underway to assess whether proglumide may modulate collagen degradation rather than collagen expression. (**68**)

Baker, Jeanette*, Teagan Thomas, Sydney Grimes, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Abundance of psychrotolerant members of gamma proteobacteria in estuarine beach*.- The bacterial profile of the species living in estuaries vary depending on the unique conditions provided by their environment. In this study we used to serial dilution plating to culture twelve bacteria from an estuary composed of the Delaware River and the Atlantic Ocean then characterized them. Almost all the isolates identified with 16S rRNA sequencing were gamma proteobacteria, some of which were *Psychrobacter* and *Shewanella* species. About half of the isolates were of a yellow or orange pigment, which could possibly be due to the antioxidant function of pigments in an aquatic environment. Most isolates were not salt tolerant, surprisingly, this suggests that they could be a freshwater counterpart. Four of the isolates may be of marine origin as they were halotolerant. All isolates were cold tolerant to some extent, some were extremely cold tolerant and could grow in subzero temperatures. Additionally, many of the isolates were able to grow up to 42°C, this indicates an ability to survive in varying water temperatures as the seasons change throughout the year. Surprisingly, in the preliminary tests no isolates displayed significant motility, which would be expected of bacteria residing in an aquatic environment. The diversity of bacteria living in the same environment is demonstrated by this study along with the implication of individual adaptations each one could have taken up for their survival in this estuarine environment. (**151**)

Bartley, Gracie*, and David Foster Messiah University, Mechanicsburg, PA 17055. *Legacy of charcoal hearths: Impacts on oak forest composition and succession in Pennsylvania*.- The 1800's charcoal-iron industry shaped Pennsylvania oak forests, leaving behind relic hearths that are identifiable by level surfaces, raised edges, and blackened soil. This study investigates how hearths affect the current tree composition and understory vegetation at Camp Tuckahoe in Dillsburg, PA. Eight hearths and equivalent adjacent plots were assessed for tree diameter at breast height (DBH) and understory vegetation cover. Additionally, tree core samples were collected for the largest diameter tree of each species on each plot. Growth rings were counted for cores to assess the effect of hearths on forest succession and provide a broad timeline for the post-charcoal development of this forest. Results showed significantly greater tree basal area off-hearth compared to on-hearth, with no significant difference in tree density and understory vegetation cover. These findings revealed areas that require further investigation to better understand hearth effects on growth and regeneration in three particular tree species: *Nyssa sylvatica* (black gum), *Quercus montana* (chestnut oak), and *Quercus coccinea* (scarlet oak). (**72**)

Beam, Alayna*, and Matthew Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Investigating how Jazf-1 acts as a functional bridge between histone modifying complexes and nuclear hormone receptors*.- In humans, Jazf-1 mutations are associated with Endometrial Stromal Sarcomas (ESS), and some alleles cause an increase in Type 2 Diabetes. Jazf-1 is thought to regulate gene expression through interactions with NuA4/TIP60, a histone modifying complex, and the nuclear hormone receptor NR2C2. Because Jazf-1 is highly conserved between *Homo sapiens* and *Drosophila melanogaster*, we propose studying Jazf-1 using the fruit fly model to better understand its larger role in gene regulation. Specifically, we are investigating Jazf-1's interactions with multiple nuclear hormone receptors homologous to NR2C2 in humans. These include Hr78, which has previously been shown to interact with Jazf-1, and Hr51 and Svp which are predicted to have relatively strong interactions with Jazf-1. For this, we will use a yeast-two hybrid system to test the full Jazf-1 gene and truncated Jazf-1 domains against the nuclear hormone receptors. This will allow us to determine if additional nuclear hormone receptors interact with Jazf-1 and further, which domains of Jazf-1 interact with Hr78 and possibly the additional nuclear hormone receptors. By gaining insight into the functionality and interactions of Jazf-1 domains, we can investigate if and how Jazf-1 might act as a functional bridge between the NuA4/TIP60 complex and nuclear hormone receptors. Overall, this study will provide a better understanding of Jazf-1 as it relates to regulation between histone modifying complexes and nuclear hormone receptors, and by extension how this regulation may influence human disease. (**112**)

Behney, Maddisyn*, Tyani Orta, and Robert Carey Lebanon Valley College, Annville, PA 17003. *Investigation of expansins in early diverging land plant lineages*.- This study aimed to further investigate the evolutionary history and conservation of expansins within bryophytes. The expansin gene superfamilies of *Marchantia polymorpha*, *Anthoceros agrestis*, and *Ceratodon purpureus* were assembled. These superfamilies were of similar size to other land plants. However, *M. polymorpha* appears to lack the EXPB family, despite EXPBs being present in all other land plants that have been investigated. Like *Physcomitrella patens*, the bryophytes investigated here lack EXLAs and EXLBs, indicating that EXLs likely evolved within the spermatophytes. Bayesian phylogenic analysis reveals four *M. polymorpha* EXPA clades that group sister to known moss clades. *C. purpureus* EXPA and EXPB families were similar to the previously described families within *P. patens*. *A. agrestis* EXPB genes consistently group with the moss EXPBs. In contrast, some *A. agrestis* EXPAs group with angiosperm EXPAs, while others group with bryophytes. SeqLogo analysis revealed that *A. agrestis* and *P. patens* EXPB gene sequences share conserved motifs with angiosperm EXPBs. Distance analysis reveals *M. polymorpha* has more EXPA diversity than other bryophytes. This analysis also revealed that bryophyte EXPBs are highly conserved. Through these analyses, we have determined that there are two possible explanations for the absence of EXPBs in *M. polymorpha*: 1) EXPBs are ancestral to all bryophyte lineages but have been lost in liverworts, or 2) EXPBs arose in the common ancestor of mosses, hornworts, and angiosperms, postdating the divergence of liverworts. Because the exact phylogenetic relationships between bryophyte lineages remain unclear, favoring one of the hypotheses for the lack of EXPBs within *M. polymorpha* is challenging. However, if bryophytes are monophyletic, then hypothesis 1 is most likely. If hypothesis 1 is correct, this would suggest that the common ancestor of bryophytes and angiosperms had at least 2 EXPA genes and 1 EXPB gene. (**57**)

Beiler, Joshua* Penn State University, State College, PA 16803. *Impact of PCSK9 inhibitors versus statins alone on clinical outcomes in patients with elevated Lp(a): A retrospective cohort study*.- Elevated lipoprotein(a) [Lp(a)] significantly increases the risk for cardiovascular disease and mortality; however, targeted management strategies are currently unclear. Statins effectively lower LDL cholesterol but have limited efficacy in reducing Lp(a) and may increase Lp(a) levels. Proprotein convertase subtilisin/kexin type 9 inhibitors (PCSK9i) reduce both LDL cholesterol and Lp(a), but it remains uncertain whether this translates to improved mortality in patients with elevated Lp(a). This retrospective cohort study utilized the TriNetX research database to investigate whether treatment of patients with elevated Lp(a) with PCSK9 inhibitors impacts 5-year all-cause mortality compared to treatment with statins alone. Two cohorts, each consisting of 3,140 patients with elevated Lp(a), were identified using CPT codes and propensity score matched by sex, LDL cholesterol, and HDL cholesterol levels. Mean age of both cohorts was 60.3 ± 11.6 years (52% female, 48% male). Baseline lipid profiles were comparable between groups (LDL 114 mg/dL; HDL 53 mg/dL). The 5-year all-cause mortality rate was 2.006% in patients receiving PCSK9i, significantly lower than the 3.025% observed in patients on statins alone (2.006% vs. 3.025%; Risk Ratio: 0.663; 95% CI: 0.484–0.908; p = 0.0099). These findings suggest a clinically meaningful mortality benefit associated with PCSK9i use in patients with elevated Lp(a). Given the limited therapeutic options currently available specifically targeting Lp(a), these findings demonstrate the potential clinical significance of PCSK9 inhibitors in these high risk patients. Further prospective randomized trials are needed to confirm causality and determine the optimal management strategy for patients with elevated Lp(a). (**139**)

Belanger, Julie* King's College, Wilkes-Barre, PA 18711. *Unexpected particle formation when adding DMSO or ethanol solutions to biological membranes*.- It is common practice to dissolve hydrophobic molecules in DMSO or ethanol for introduction to biological bilayer membranes (cells, viruses, etc) in vitro. This step is needed to ensure that the hydrophobic compound partitions into the hydrophobic layer of the membrane being studied. However, when hydrophobic compounds are dissolved in DMSO or ethanol and added to water, unexpected dispersions can form. A model compound, N-phenyl-1-naphthylamine (NPN) - a hydrophobic fluorescent probe know to partition into the membrane bilayer- can make these metastable dispersions. This is also referred to as the “Ouzo” effect, where the added solvent presumably acts as a hydrotrope. To our knowledge, this has not been characterized in systems where the solute is a solid. The cloudy dispersions that form have initial particle sizes of 400 nm (radius) and are stable for days without any added surfactants. More details on our findings and their possible implications will be discussed. (**87**)

Berry, Sophia*, and Jane Cavender Elizabethtown College, Elizabethtown, PA 17022. *CD44 isoform dynamics: Unveiling its role in SV40 T-antigen induced transformation of human diploid fibroblasts*.- Approximately 20% of cancers are induced by viral oncoproteins and greater than 90% of all cancer-related deaths are due to metastasis. In virally transformed cells numerous CD44 isoforms are expressed and contribute to metastasis and cellular proliferation. CD44, a transmembrane protein, binds hyaluronic acid in the extracellular environment and transmits signals to MAPKinase, PI3K/AKT, and JAK/STAT pathways. CD44 standard (CD44s) is the wild-type isoform; however, alternative splicing of mRNA coding sequences in the variable domain creates CD44 variants. Post-translational modifications include glycosaminoglycan (GAG) attachment and N- and O-linked glycosylation. CD44 can be hypo- or hyperglycosylated impacting its activation state and ability to bind hyaluronic acid. This project investigated the role of CD44 in the viral transformation of human diploid fibroblasts (HDFT) by SV40 T-antigen. To determine if CD44 plays a role in the transformed growth characteristics we evaluated the isoform expression, protein levels, and glycosylation state of the receptor using immortalized human diploid fibroblast (HDFs) and HDFT cells. Isoform and protein expression levels were assessed with RTPCR and immunoblotting, respectively. Glycosylation levels were compared by treating lysates with glycosidases followed by immunoblotting. The data shows no difference in alternative splicing and the predominant isoform was CD44s although variants are detected in both immortal and transformed lines. Protein migration after de-glycosylation indicates that the 5 N-glycosylation sites contain sugar residues, and experiments are ongoing to assess the O-glycosylation differences. Surprisingly, data consistently showed an inverse relationship between T-antigen and CD44 protein expression level; however, RTPCR did not detect a decrease at the transcription stage. We propose that T-antigen expression may alter the isoform or glycosylated state of CD44 altering its activity and recognition by the antibody.

Continued experiments will allow us to determine if CD44 contributes to SV40 transformation and possibly tumorigenesis of other virally induced cancers. (**182**)

Bitner, Amber*, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Presumptive color test for the detection of xylazine*.- Xylazine is an emerging public health concern because it is a compound found in mixtures with illicit drugs such as heroin and methamphetamine. The long-term goal of this research is to find a presumptive color test method that accurately identifies xylazine. By identifying which color tests can be used to detect xylazine-specific functional groups and reviewing the limited literature, a more concise process can be developed. We propose that the Chen-Kao Test and Young's Test can be used to distinguish xylazine from other amine drugs via the analysis of resulting precipitates with microscopy and Raman spectroscopy. It was found with Young's test that all resulting precipitates and supernatants appeared similar in color, making it hard to differentiate between the amine drugs used. However, Chen Kao yields visually different spot plate reactions with xylazine HCl, lidocaine, ephedrine HCl, pseudoephedrine, and diphenhydramine. UV-Vis spectroscopy yielded a spectrum of absorbances that differed between each amine drug tested with Chen Kao reagents. In addition to the amine drugs tested, the controlled substances ketamine, methylenedioxymethamphetamine (MDMA), and methamphetamine were examined. Raman spectroscopy was used to characterize crystals formed with lidocaine, pseudoephedrine, xylazine, ketamine, MDMA, and methamphetamine to yield distinguishable spectra. With this research, a solid foundation of data is established that involves the testing of xylazine with various presumptive tests. With this work, laboratories can implement more effective presumptive testing methods for xylazine, aiding in its identification and differentiation from other amine drugs and controlled substances. (**50**)

Bocaj, Gabriel*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *How effective is sunscreen at preventing UV-mediated DNA damage?*- Ultraviolet (UV) radiation causes multiple types of DNA damage including extra bonds between bases, loss of bases, and even strand breaks. Damage like this in skin cells exposed to UV light can lead to cell death and eventually cancer. While cells can repair much of the UV-mediated DNA damage through the nucleotide excision repair pathway, it is recommended to add the extra protection of sunscreen on exposed skin when one goes outside. Different sunscreens absorb or block UV light differently, either by reflecting or absorbing UV radiation. We were interested in whether different sunscreens were equally effective at preventing UV-mediated DNA damage. To this end, we tested whether three different SPF 30 sunscreens (Banana Boat Sport Ultra, Coppertone Sport 4-In-1, and Sand Cloud Mineral Sunscreen) would equally reduce the death of yeast *Saccharomyces cerevisiae* exposed to UV radiation. We hypothesized that all three sunscreens would work equally well to prevent cell death. Consistent with our hypothesis, we found that all three sunscreens were equally effective at protecting *S. cerevisiae* from UV-mediated cell death when a film of the sunscreen was placed between the UV source and the cells. Future work will investigate the mechanism by which the sunscreens protect yeast from UV radiation. (**123**)

Bonnet, Ashley*, and Akeisha Belgrave Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Exploring Myxococcus xanthus as a sustainable approach for iron bioremediation*.- Iron pollution is a significant environmental challenge that contributes to negative impacts on marine life and plant life within an ecosystem, resulting in reduced biodiversity. Some examples of iron pollution are acid mine drainage, agricultural runoff, and waterway contamination. Current remediation methods such as limestone treatments and filtration, are often costly and generate secondary waste. This study focuses on exploring *Myxococcus xanthus*, a soil dwelling bacterium, as a potential bioremediation tool due to its ability to sequester and store iron using specialized biochemical systems, including siderophore production and encapsuling-mediated iron storage. The research aims to evaluate the efficiency of *M. xanthus* in iron uptake under different conditions, including varying iron concentrations. Preliminary findings indicate that *M. xanthus* effectively tolerates iron and grows similarly within iron rich environments compared iron deficient environments. However, there is a potential inhibitory effect observed in the presence of Fe^{3+}. Laboratory experiments will monitor iron sequestration at environmentally relevant concentrations (25 micromolar - 100 micromolar) over 72 hours using a Ferrozine assay to quantify iron levels. This study will provide insights into the feasibility of *M. xanthus* as a low cost, sustainable alternative for mitigating iron pollution in contaminated environments. (**175**)

Bonser, Hannah*, Alison Edwards, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining the interactions between Replication Protein A and associated proteins Mec1p, Tel1p, and Ddc2p using Saccharomyces cerevisiae and the yeast-two hybrid system*.- Although cancer related deaths continue to decline with new technologies paving the way to better treatments, the number of cancer incidences continues to grow in the United States. This rise in many common types of cancer points to a need for more research and a better understanding of how cancer arises. One of the ways that research can support this goal is through understanding the proteins involved in the DNA replication, repair, and recombination pathways and how they interact with each other at a basic level. Using the yeast-two hybrid system and *Saccharomyces cerevisiae* as a model organism, this research aims to better understand Replication Protein A (RPA) and how it interacts with proteins Mec1p, Tel1p, and Ddc2p. Examining how these proteins interact in yeast can provide insights into how they may interact in humans since each of these proteins have human homologs. The primary objective of this study is to determine if RPA interacts with Mec1p, Tel1p, and Ddc2 and on which of the three subunits of RPA they interact with as well as determining if phosphorylation of RPA's second subunit effects its interactions. Using the yeast-two hybrid system with the ADE2 reporter gene, plating interactions and growth curves can be used to measure the strength of these protein-protein interactions. With this study a better comprehension and fuller picture can be understood about how DNA replication, repair, and recombination pathways operate. A more extensive understanding of these pathways can lead to better treatments for diseases that target them like cancer. (**69**)

Bortz, Jordyn*, and Frank Varriale King's College, Wilkes-Barre, PA 18711. *Jaw dropping mechanics: Preliminary insights from a simplified analysis of shark jaw properties*.- Sharks play a key role as apex predators in many marine ecosystems. This study examined the lever arm mechanics of over 40 shark species from various families, ranging from the small Cuban dogfish (*Squalus cubensis*) to the largest living carnivorous shark, the great white (*Carcharodon carcharias*), and the second-largest living shark, the filter feeding basking shark (*Cetorhinus maximus*). The objective was to identify patterns in lever arm properties across shark species by quantifying the moment arm as a percentage of total output lever. To do this, 3D models of lower left or right jaws were obtained from an online repository and measured at standardized anatomical landmarks to calculate moment arm values. I hypothesize that sharks with shell-crushing feeding habits should exhibit the highest percentages, fat eating species will fall within an intermediate range, and filter-feeding sharks would display the lowest values. These findings indicate that simplified lever arm parameters that can be easily collected from data sets limited to only the Meckel's cartilage can be a proxy for ecological roles. (**155**)

Brochu, Jackie*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *A general framework for modeling biological control of the spotted lanternfly and similar invasive pests*.- The spotted lanternfly is an emerging global invasive insect pest. In its native regions, populations are regulated by natural enemies, but in invaded areas it appears to lack effective natural enemies, necessitating human intervention. To date, most management efforts in the U.S. have focused on non-biological control measures such as insecticides, bark injections, and host plant removal. However, the lanternfly continues to spread, leading to suggestions that biological control may be necessary. Unfortunately, studies have shown that some initially promising biological control agents, such as egg parasites and entomopathogens may not be highly effective, at least on their own. Recently, various animals in the U.S. have been observed preying on the lanternfly, including social birds. A recent modeling study has also established conditions under which social birds could collectively contribute to the biological control of invasive lanternfly populations. Specifically, this study provides a framework for modeling the emergence of collective biological control by social animals that are sensitive to the lanternfly's potential toxicity. However, some of the other recently observed lanternfly predators are not social, and some are not sensitive to its potential toxicity. Here, we introduce a generalized version of the collective biological control model that incorporates all possible combinations of sociality and toxicity sensitivity. We establish conditions under which each type of predator can lead to robust biological control, establish how the social learning process proceeds for each, and quantify the relative speed and effectiveness of control across predator types. Together, these models provide a framework for studying the emergence of biological control by agents with any degree of sociality and toxicity sensitivity, including interactions between different types. Given that predators with diverse characteristics have been observed killing lanternflies, understanding how to facilitate their emergence and interactions could inform management strategies for the lanternfly and similar invasive pests. (**140**)

Broom, Michael*, Carla Garzon, and Jaclyn Fiola Delaware Valley University, Doylestown, PA 18901. *Using Hemp (Cannabis sativa) for the Phytoremediation of Lead and Arsenic in Former Orchard Soils on Delaware Valley University's Campus*.- Historic pesticide applications in orchards have led to the accumulation of lead (Pb) and arsenic (As) in soils, posing potential environmental and health risks. This study aimed to evaluate the feasibility of using hemp (*Cannabis sativa*) for phytoremediation of Pb and As in former orchard soils at Delaware Valley University. The first phase involved a soil survey of multiple locations on campus to determine contamination levels. While most sites had Pb and As concentrations below the U.S. Environmental Protection Agency (EPA) safety thresholds, elevated levels were found in some areas, justifying further remediation efforts. The most contaminated site was selected for a hemp phytoremediation experiment, where hemp plants were grown to assess their ability to uptake Pb and As from the soil. After a full growing season the summer of 2024, the plants were harvested and analyzed to determine metal accumulation in different plant tissues. The results showed successful uptake of both contaminants, with higher concentrations in the roots (Pb: 9.95 mg/kg, As: 2.32 mg/kg) compared to the stems (Pb: 1.97 mg/kg, As: 0.76 mg/kg) and leaves (Pb: 1.71 mg/kg, As: 0.45 mg/kg). This pattern suggests that Pb and As are largely retained in the root system with limited translocation to aboveground biomass of the hemp plants. Our findings indicate that hemp can play a role in the remediation of Pb- and As-contaminated soils and could still have potential use of the aboveground biomass. Hemp's fast growth and biomass potential make it a promising candidate for phytoremediation, particularly in marginally contaminated sites where traditional soil removal is impractical. (**166**)

Brown, Nya*, and Cecilia Bove York College of Pennsylvania, York, PA 17405. *CRISPR/Cas9 knockout of a fragin biosynthetic gene in Pseudomonas laurylsulfativorans*.- Antibiotic resistance is a rapidly growing global crisis that has claimed the lives of 1.27 million people worldwide as of 2019 (CDC 2025). This has led to the need to investigate novel antibiotics, some of which can be discovered using bacteria isolated from the soil. This study investigates a soil microorganism, DB7-22WB, and its potential as an antibiotic producer with activity against the ESKAPE pathogens, a group of multidrug-resistant bacteria. This soil isolate was identified to be *Pseudomonas laurylsulfativorans* with 98.41% identity and tested for antimicrobial activity using competition plates against safe relatives of the ESKAPE pathogens. The presence of zones of inhibition (ZOIs) indicated that the isolate produced an antibiotic effective against all of the tested safe relatives. A genomic analysis through Anti-SMASH 2.0 identified a secondary metabolite in the biosynthetic gene cluster (BGC) known as the fragin pathway. Previous literature demonstrated that this pathway is linked to the production of antimicrobial compounds in other *Pseudomonas* species. A hypothetical protein-encoding gene within the BGC, CTG62_17 was selected as a target for CRISPR/Cas9 knockout to evaluate whether this gene is necessary and sufficient for the production of the antibiotic. A specific guide RNA (gRNA) was designed and inserted into a suitable plasmid known as pCasCure-Rif plasmid. Electroporation will be used to introduce the assembled plasmid into *P. laurylsulfativorans* and the relationship between CTG62_17 and antibiotic production will be evaluated by testing the mutated isolate against ESKAPE pathogens using competition plates. If the size of ZOIs decreases or they completely disappear, we will conclude that gene CTG62_17 may play a role in antibiotic production in the fragin biosynthetic pathway. In conclusion, this study explores the role of a novel antimicrobial compound in a bacteria isolated from the soil as a way to combat antibiotic resistance. (**98**)

Bryan, Jamie*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Evaluating ecological restoration progress in Bushkill Creek, PA: results of longitudinal monitoring before and after dam removal and freshwater mussel reintroduction*.- Dams have significantly altered river ecosystems by disrupting natural flow patterns, fragmenting habitats, obstructing fish migration, and degrading water quality. While dam removal is increasingly used as a restoration tool, fewer than 10% of removals have been scientifically evaluated, limiting our understanding of long-term ecological effects. The removal of four run-of-river dams and reintroduction of two species of freshwater mussels in the lower Bushkill Creek, a tributary of the Delaware River located in eastern Pennsylvania, has provided a valuable opportunity to advance scientific understanding of ecosystem response to stream restoration. The project was funded by the Natural Resource Damage Settlement following the 2005 PPL Martins Creek coal ash spill, which severely impacted freshwater mussel populations and other natural resources in the Delaware River and its tributaries. Thus far, our multidisciplinary research has involved the collection of more than 14 consecutive years of ecological monitoring data (e.g., dissolved oxygen, pH, conductivity, macroinvertebrate diversity) at seven sites upstream and downstream of the Bushkill Creek dams and three free-flowing reference sites located approximately 5 km upstream of all dams. Pre-restoration data indicate that water quality and macroinvertebrate assemblages are significantly impaired upstream and downstream of dams relative to reference conditions. Preliminary post-restoration results indicate improved water quality and shifts in macroinvertebrate community composition, with an increase in sensitive taxa at restored sites. Additional monitoring at freshwater mussel reintroduction sites are indicating that substrate stability, sediment grain size, and flow conditions are more conducive to survival and settlement at one of the sites. Continued monitoring of water quality (e.g., dissolved oxygen, biotic indices of water quality, suspended sediment) and habitat conditions (e.g., sediment grain size) at restored sites will allow further assessment of site suitability for the reintroduced mussels. (**71**)

Callaghan, Natalya*, and Leena Pattarkine Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Coral bleaching - An innovative, sensitive, and predictive approach using glutamate dehydrogenase as a biomarker*.- Coral bleaching is a significant consequence from climate change, disrupting the symbiotic relationship of corals and the zooxanthellae. The major environmental stressors are global warming leading to higher sea temperature and ocean acidification due to acid rain pollution. Corals are an important marine species, with any interference impacting many aspects of the trophic cycles. This study highlights the significance of integrating biomarker assays with environmental simulations to predict and therefore mitigate coral bleaching.To assess coral health, a molecular biomarker approach was studied, focusing on the enzyme glutamate dehydrogenase (GDH) as an indicator of stress that would cause bleaching. GDH plays a crucial role in nitrogen metabolism of corals, reflecting any response to thermal and pH stress. To simulate global warming and acid rain pollution, a series of spectroscopic (absorption and emission) experiments are conducted on commercial protein with varying temperature gradient and buffers with varying pH. The data obtained is interpreted as protein conformational changes from the assay conditions mimicking global warming and acid pollution. The spectroscopic assays are repeated using the enzyme extracted from coral tissues. (**150**)

Caporaletti, Luciana, Emma Sokaloski*, and Brandon Mabey* Penn State University-Wilkes-Barre, Dallas, PA 18612. *Beech leaf disease in two Pennsylvania state parks*.- First identified in Ohio in 2012, Beech Leaf Disease (BLD) is a rapidly occurring disease in the American Beech Tree (*Fagus grandifolia*) in the United States. It is caused by an invasive nematode (*Litylenchus crenatae*). This parasite causes chlorosis which affects photosynthesis and consequently the Beech tree's ability to produce carbohydrates. This disease also compromises the tree's immune system, leaving it vulnerable to other pests and pathogens. Symptoms include interveinal darkening, leaf curling, and leaf dieback, leading to tree mortality. Current treatments for a small number of trees in parks or backyards include antiparasitic sprays, however, no economically feasible method for treating forest stands exists. The method of transmission remains unknown. Until that is fully understood, it is important to take precautionary steps to curb the spread of this disease. This includes reporting symptomatic trees to officials and not transporting firewood from one forest to another. After obtaining permits from the Pennsylvania Department of Conservation and Natural Resources (DCNR), we surveyed Beech trees in both Frances Slocum State Park and Promised Land State Park in Pennsylvania. During the summer of 2024 we used these surveys to determine the presence of Beech Leaf Disease in each park. We considered a tree symptomatic if it showed signs of interveinal darkening and leaf curling. We counted 1,394 trees in Promised Land, of which 1,166 were symptomatic. We counted 26 Beech trees in Frances Slocum and none of them were symptomatic. We recognize that this may be an underestimate as some trees may be diseased without showing signs. This baseline data is important for agencies, such as DCNR, the US Forest Service, and the National Park Service to track the spread of this disease across the U.S. It also aids in forest management, as it specifically targets this tree species for conservation. (**162**)

Castaneira, Ryan*, and Nik Tsotakos Penn State University-Harrisburg, Middletown, PA 17057. *Differential expression of long non-coding RNAs associated with macrophage polarization is specific to surfactant protein A isoforms following infection with Klebsiella pneumoniae*.- Surfactant Protein A (SP-A) is a protein important to lung physiology with demonstrated immune modulatory functions in alveolar macrophages, in addition to its eponymous surfactant functions. The associated genomic locus in humans hosts two functional genes, SFTPA1 and SFTPA2, and one pseudogene. To add to the complexity of the system, each of the products of the two functional genes has several variants which have been characterized to differentially regulate lung function mechanics and survival in response to a bacterial infection. Using RNA-seq data previously obtained from a humanized transgenic mouse model, we examined the differentially expressed gene (DEG) profile of long-noncoding RNAs (lncRNAs) in SP-A KO mice as well as mice that carried human SP-A1 (6A2, 6A4) or SP-A2 (1A0, 1A3) 6 hours post infection with *Klebsiella pneumoniae*. In the present study, we compared the change in expression of well-characterized lncRNAs in the different SP-A genotypes and their significance in alveolar macrophage (AM) polarization. Several lncRNAs differentially expressed following exposure to *K. pneumoniae* are preferentially dysregulated in an isoform-specific manner. We explored the association of these lncRNAs to macrophage polarization. Preferential dysregulation influencing AM polarization could explain immune function outcomes associated with the presence of SP-A1 or SP-A2 after acute exposure to *K. pneumoniae*. (**64**)

Chinchilli, Vernon, Rong Zhao*, and Chixiang Chen Penn State University, State College, PA 16803. *A new targeted-federated learning framework for estimating heterogeneity of treatment effects: A robust framework with applications in aging cohorts*.- Leveraging data from multiple study sites offers great opportunities to improve the estimation efficiency of causal estimands. However, it also poses challenges due to population heterogeneity and data privacy constraints. While several advanced methods for causal inference in federated settings have been developed in recent years, most focus on difference-based averaged causal effects and are not directly applicable to multiplicative-scale estimands for a target population. More importantly, existing methods fail to effectively address effect modification. In this study, we introduce a novel federated learning framework to study the heterogeneity of causal effect for a targeted population based on projection-based estimand. This framework integrates information from multiple data sources without sharing raw data, accounting for covariate distribution shifts among sources. Our proposed approach is shown to be doubly robust and can conveniently handle continuous and categorical outcomes. Furthermore, we develop a communication-efficient bootstrap-based selection procedure to detect non-transportable data sources, thereby ensuring robust information aggregation without introducing bias. The superior performance of the proposed estimator over existing methods is demonstrated through extensive simulation studies. Finally, we illustrate the utility of our approach with a real-world application on nationwide Medicare-linked data. (**42**)

Christopher, Eurnett*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Freshwater mussel restoration following dam removal in Bushkill Creek, Pennsylvania*.- The removal of four run-of-river dams and reintroduction of freshwater mussels in the lower Bushkill Creek, a tributary of the Delaware River located in eastern Pennsylvania, has provided a valuable opportunity to advance scientific understanding of ecosystem response to stream restoration. The overall objective of the restoration project is to re-establish connectivity, rehabilitate water quality, and reintroduce a viable population of freshwater mussels, considered keystone species, in the creek. Following dam removal in June 2024, a total of 2500 individual mussels of two species (i.e., *Utterbackiana implicata* and *Sagittunio nasuta*) were reintroduced to two sections of the Bushkill Creek. Approximately 15% of the mussels were fixed with Passive Integrated Transponder tags (i.e., Biomark HDX12 PIT) or Hallprint tags (i.e., externally visible individual ID tags) to enable study of mussel life history traits (i.e., survival, growth, movement), population growth, and demographic data that will inform management decisions. The specific goal of my research is to create a baseline for long-term monitoring of two reintroduced mussels by quantifying post-release survival, density, and settlement. Recovery rates dropped from 99.6% (site 1, 2.0 km from confluence with Delaware River) and 99.2% (site 2, 6.0 km from confluence) in July to 1.1% and 0.0% respectively by October. Preliminary results indicate some downstream movement of mussels at site 1 and that survival and settlement are better at site 2, which has greater depth, lower water velocity, and finer sediment grain size. Mussel restoration is more or less experimental, and low recovery rates are not uncommon to reintroductions of propagated mussels. Our project represents both a method of stream health assessment and an opportunity for learning that will inform future reintroductions. (**70**)

Cook, Anna*, Kylee Crayne, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *High throughput screening of bacteria for prevalence of UV fluorescence*.- Some bacteria like *Pseudomonas* species produce fluorescent compounds that glow under UV light. Some of these compounds referred to as siderophores are released by bacteria to harvest iron from the medium and others are released by bacterial pathogens like

Pseudomonas aeruginosa as toxins. The genus *Pseudomonas* contains over 200 species and it is unclear which lineages of *Pseudomonas* contain fluorescent species or strains. It is also virtually unknown if genera other than *Pseudomonas* can be UV fluorescent. To test this, in this study, we screened a collection of nearly 500 bacteria in King's B (KB) medium to assess the prevalence of UV fluorescence in various bacteria, since the peptone component of King's B medium can stimulate production of UV fluorescent compounds. I inoculated bacteria in 96 well plates containing KB broth and documented UV fluorescence after 2-7 days. We found nearly 17% of the bacteria exhibited UV fluorescence and all the bacteria that were sequenced (nearly half), using 16S rRNA sequencing were exclusively *Pseudomonas* species. Phylogenetic analysis will be performed to evaluate if UV fluorescence evolved in specific lineages. Upon completion of this ongoing experiment, the screen could also reveal if UV fluorescent compounds are produced by genera other than *Pseudomonas* species. Finally, the inhibition of the fluorescence in these bacteria by iron supplementation will be tested to determine which of these compounds are possible iron-harvesting siderophores. Thus, this study will help us understand the distribution and significance of UV fluorescent compounds in the bacterial kingdom. (**94**)

Corbeill, Nathan*. *Measuring the rate of photosynthesis using a floating leaf assay with Spinacia oleracea*.- Photosynthesis is the process by which a plant creates glucose and oxygen from carbon dioxide and water using energy from light through a series of reactions. These reactions take place in the thylakoid membrane and stroma of the chloroplast. The products of the light reaction, including ATP and NADPH, are used in the dark reaction (commonly known as the Calvin cycle) to convert carbon dioxide into glucose. Thus, the rate of photosynthesis is dependent on the availability of carbon dioxide, water, light, and other factors. My project aimed to evaluate the rate of photosynthesis while varying the levels of carbon dioxide available for the plant to use. By using sodium bicarbonate as a substitute for atmospheric carbon dioxide and measuring oxygen production, we can determine the rate of photosynthesis. As carbon dioxide levels increase, will the rate of photosynthesis also increase? This question was investigated using a floating leaf assay while varying the concentrations of sodium bicarbonate in a solution. Leaf disks were obtained from common spinach (*Spinacia oleracea*), then put in a low-pressure environment to replace the air in the spongy mesophyll layers with sodium bicarbonate solution causing the samples to sink. As the leaf disks photosynthesize creating oxygen, bubbles formed on the leaves causing them to float. By counting the number of disks floating and graphing the 1/T50 time, a rate of photosynthesis was calculated for each concentration of sodium bicarbonate. Results show optimal photosynthesis at around 0.045 M solution with rates seeming to plateau at higher concentrations. This raises the question of other possible limiting factors, such as light intensity or temperature, inviting further research. (**14**)

Costantini, Kathryn*, and Clinton Jones Mercyhurst University, Erie, PA 16546. *Quantification of polyphenols in different tea samples using a Folin-Ciocalteu Assay*.- In this research, a Folin-Ciocalteu assay is utilized to quantify the amount of polyphenols in different tea samples. Tea contains a variety of polyphenols, which are compounds with one or more hydroxyl residues attached to an aromatic ring. Gallic acid acts as the standard with which the phenolic content in tea samples is compared. A standard curve was created using gallic acid for the quantification of polyphenols. Different Asian teas are brewed using traditional brewing methods from China, Japan, and India. Tea samples are diluted and replace standard gallic acid in experimental samples with F-C reagent and sodium carbonate. The donation of electrons from phenolic residues in gallic acid and polyphenols in tea elicit a color change of the F-C solution from yellow to blue, which can be analyzed spectroscopically at 765 nm. Absorbance values obtained for tea samples are compared to those in the standard curve to quantify polyphenols in various tea samples. Polyphenols act as antioxidants, so a measure of phenolic content in tea samples acts as a measure of antioxidant capacity. Data obtained in this research will demonstrate potential differences in antioxidant capacity between different types of tea and possible fluctuations of phenolic content based on the brewing method used. (**24**)

Crookston, Justin*, and M. Logan Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Modeling endometrial stromal sarcomas using JAZF1 gene fusions*.- Endometrial Stromal Sarcomas (ESSs) are a group of rare uterine cancers that have limited research and typically lead to hysterectomies in affected individuals (Puliyath & Nair, 2012). Although their molecular mechanisms remain unclear, the leading cause of (ESSs) in humans are JAZF1 gene fusions. To better understand JAZF1 fusions, we are focusing on conserved genes found between *H. sapiens* and *D. melanogaster* provide an opportunity to establish a disease model for ESS. To achieve this, we will attempt to construct two different fusion proteins: JAZF1/SUZ12 and JAZF1/PCL, the PHF1 homology in *Drosophila*. We amplified the region of JAZF1, Su(Z)12 and Pcl responsible for disease in humans. Using Gibson Assembly, the fusion constructs will be cloned into an *E. coli* with a pENTR plasmid. Once cloned, the fusion genes will be shuttled to a plasmid where expression is controlled using a UAS system containing transposable elements to allow integration into the *D. melanogaster* genome. By establishing recombinant fusion genes, we will now be able to analyze and express target tissue in *D. melanogaster*. Our lab and others have demonstrated that JAZF1 acts as a key regulator in eye development. Using the eye tissue, we can better understand the impact of the fusion gene on JAZF1's normal function without being lethal to the organism. Additionally, the flexibility of these genetic tools will allow us to compare JAZF1 fusion genes in different contexts to gain insight into how they alter normal gene expression-providing better understand how JAZF1 gene fusions alter basic cellular functions. This will provide further insight into understanding the mechanisms behind insight into Endometrial Stromal Sarcomas mutations. (**113**)

Curtiss, Katherine*, and Christopher Dolanc Mercyhurst University, Erie, PA 16546. *Mortality and ecological succession of an ash-dominated forest impacted by the emerald ash borer: an eight-year study*.- The emerald ash borer (*Agrilus planipennis*) is an invasive species of beetle that has caused widespread damage and mortality to ash (*Fraxinus* spp.) trees throughout the United States and Canada. Native to Asia, the beetle has no real predator in North America, nor has the ash species developed any resistance to their attacks like the trees found in their native range. This allows the beetles to invade an area with a swift and severe outcome. In this study, we looked at an impacted stand of an ash-dominated forest located in Asbury Woods, Erie PA in order to gather more information on ash regeneration and the ecological succession of the forest. The first data was collected in 2016 before the invasion occurred, and every year since. The results show a rise in mortality in mature ash trees after the beetles were detected, with 76.69% of the original ash population dying by 2024. An increase of 86.27% in smaller ash trees due to epicormic sprouts and saplings were also noted from 2016 to 2024, with 2016 having a total of 51 smaller ash trees with a DBH bigger than 2.5 cm and less than 10 cm, and 2024 having 95 ash saplings within the same category. This increase in ash saplings and epicormic sprouts could lead to a cyclical relationship with the ash species and the beetle, with the ash recovering enough to replenish the seed bank before the beetles reenter the area and eventually kill them. The data also indicates a rise in density to the understory due to the changes in canopy cover. No evident increase or decrease in species diversity was noted within the study, though due to the site still undergoing changes this could differ in the future. (**73**)

Delayo, Nicholas*, Patricia Strazdus, and Andrea Nerozzi Wyoming Seminary Upper School, Kingston, PA 18704. *Cellobiase activity in oyster mushrooms*.- Waste plant materials are a potential source of sugar for the production of ethanol, an important biofuel. Cellulases are integral to this process because they break down cellulose and release glucose, which can then be used in fermentation by yeast to produce ethanol. Consequently, it is important to identify microbial sources of cellulases. This study investigates how the age of oyster mushrooms (*Pleurotus ostreatus*) affects the activity of cellobiase. This experiment followed three phases: the evaluation of enzyme concentration on product formation using commercially available cellobiase, the measurement of cellobiase activity in differing mushroom parts (stem, gills, and flesh), and the assessment of enzyme activity in oyster mushrooms grown over a 15 day time period. The protocol includes preparation of a mushroom extract and quantification of the amount of product and reaction rate, as measured by hydrolysis of the artificial substrate p-nitrophenyl-α-D-glucopyranoside via spectrophotometry (410 nm). Mushroom stem extracts, which exhibited the highest cellobiase activity of all mushroom parts, were used to assess the effect of mushroom age on cellobiase activity. The results indicate that the growth cycle of the oyster mushroom affects the timing of cellobiase activity, with the maximum activity observed 11 days after activation. (**54**)

Delgado, Juliana*, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Rapid quantification of edible cannabinoid products by chemiluminescence and FRAP assay*.- Edible cannabis products have been booming in popularity, with the compound's most common cannabinoids, tetrahydrocannabinol (THC) and cannabidiol (CBD), found in tinctures, candies, and beverages. In 2014, a Colorado study found cannabis edibles made up 40% of the $700 million in cannabis sales. Two years later, another study reported 93% of young adults in the area had consumed cannabis edibles at least once. This increased prevalence and demand have emphasized the need for reliable quantification techniques for cannabinoids in edible products to contribute to a company's quality assurance efforts. The ferric reducing antioxidant power (FRAP) assay and chemiluminescent reactions using N-bromosuccinimide (NBS) with sodium hypochlorite have been explored as two new rapid quantification techniques. Despite the antioxidant properties in cannabidiol (CBD), the FRAP assay was not found to react with CBD, Δ^8-THC, nor Δ^9-THC. Chemiluminescent detection using NBS as the oxidative agent has been confirmed to quantify cannabinoids in simple matrices over 0.318 μM - 31.8 μM. This study explores alternate solvent systems for the oxidative reaction to eliminate the need for an additional extraction of cannabinoids from more complex matrices: oil and candy products. The success of a chemiluminescent assay in quantifying cannabinoids in a broad range of cannabis products will assert an overall more cost and time-efficient method for manufacturing laboratories. (**51**)

Demaree, Kate*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Fire as an ecosystem management tool: Does burn season affect plant composition?*- One characteristic that defines grassland ecosystems is regular disturbance. Natural wildfires maintain the open structure of grasslands by preventing encroachment of woody plants and promoting diversity of native grasses and forbs. Therefore, grassland restoration often involves prescribed burns as a tool to maintain biodiversity, prevent woody species encroachment, and replenish soil nutrients, but less is known about how the timing of burning influences succession, diversity, and dominant species. The objective of this long-term monitoring study is to work with Jacobsburg State Park (Nazareth, PA) to compare differences in vegetation composition between five meadow units burned during the growing season and five burned during the dormant season. We hypothesize that dormant-season burns will promote grass dominance, while growing-season burns will encourage forb dominance. Using a stratified random sampling design in fall 2023 and 2024, plant species coverage was determined using 1m2 quadrats along transect lines in each burn unit ($N \geq 10$ per year). Currently, *Solidago spp*., *Andropogon gerardi*, and *Panicum virgatum* are dominant across all burn units, and preliminary analysis suggests that burn season does not yet have a significant effect on plant diversity or group dominance. However, data collected over the past year establishes a baseline for continued burning and monitoring that will inform adaptive management practices for grassland restoration in Jacobsburg State Park. (**158**)

DeNucci, Christine Kate*, Dhara Javia, and David Glick King's College, Wilkes-Barre, PA 18711. *Powering small devices using electricity generated from the mud through Geobacter and Shewanella within microbial fuel cells (MFCs), known as mudwatts*.- Globally, human population has increased and human activities that rely on non-renewable energy sources, can have a negative effect on the world. Therefore, the Microbial Fuel Cells (MFCs) were invented, a type of bio electrochemical system that is designed to convert organic matter into electricity and uses specific microorganisms like *Geobacter sulfurreducens* and *Shewanella oneidensis*. It was discovered that MFCs could generate electricity output with the addition of food sources and chemical mediators. A study on wastewater treatment and other applications using MFCs has shown to be beneficial, as they are clean and effective technologies. In our research study, we mostly focused on using MudWatts, a smaller version of the Microbial Fuel Cells (MFCs), which can also generate electricity by utilizing various food sources and chemical mediators. The goal was to enhance energy production by determining which compounds, such as polyacrylate, acetate, buffers such as HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), and TRIS ((Hydroxymethyl) aminomethane), work best for optimizing energy production. Throughout the experiment, different food sources and chemical mediators were tested within the MudWatts and we found that the combination of iron, HEPES, acetate, towel papers, and sponges (IHATS) produced significant energy output, but with cellulose - polyacrylate, iron, TRIS, acetate, towel papers, and sponges (ITATS), resulting in even greater energy output. Additionally, we found that only orange peel with cellulose - polyacrylate ITATS could produce over 200 microwatts of power. These findings suggests that a small clock could be powered using this method and could theoretically power other small devices in the future, including pacemakers, Kindles, and glucose monitors. Overall, Mudwatts are affordable, sustainable, and have potential applications in both healthcare and environmental - related fields. (**176**)

Devine, Natalie*, Katherine Johnson*, and André Walther Cedar Crest College, Allentown, PA 18104. *Identification of proteins that interact with Replication Protein A in a phosphylation dependent manner using the Yeast Two-Hybrid system in Saccharomyces cerevisiae*.- Cancer which is the second leading cause of death in the United States, can be caused by mutations in the genome that inactivate or modify genes required for proper regulation of cell cycle regulation and responses to cellular stress. Maintenance of genomic integrity requires the proper function of pathways involved in DNA replication, DNA repair, cell cycle regulation, homologous recombination, and telomere maintenance. An important protein involved in all of these processes is the highly conserved, single stranded DNA binding protein Replication Protein A (RPA) RPA, that has previously been shown to interact with a large number of other proteins involved in maintaining genomic integrity. RPA is composed of three subunits, and the second subunit (RFA2) is phosphorylated in a cell cycle dependent manner and in response to DNA damaging agents. We hypothesized that RPA phosphorylation can control its physical interactions with cancer proteins. To test this, we used the Yeast Two-Hybrid system (Y2H), which is an assay using *Saccharomyces cerevisiae* with reporter genes that can identify protein-protein interaction partners. We screened through a yeast cDNA library to identify proteins that interact with RPA and found that approximately a third of RPA's interactions seem to be regulated by phosphorylation, suggesting that RPA phosphorylation may play an important role in regulating DNA repair and cell cycle pathways by modulating physical interactions. We have been systematically isolating and using DNA sequencing to identify candidate proteins that interact with RPA in a phosphorylation dependent manner and will be sharing those results. Once the proteins are identified, this will help us learn more about RPA's interactions with cancer-related proteins and may provide insights into new treatments for cancers caused by abnormal protein-protein interactions. (**59**)

Donelson, Hayley*, and David Matlaga Susquehanna University, Selinsgrove, PA 17870. *Efficacy of anthelmintics on parasite load in horses in Central Pennsylvania*.- Nematodes are a type of helminth that live in the environment and can become parasitic to animals, especially grazing animals such as horses. Anthelmintics have been used to reduce parasite load of livestock due to potentially life-threatening clinical manifestations that can occur with a high parasite load. Resistance of internal parasitic nematodes to anthelmintic treatments has been a growing concern in livestock for quite some time. However, research on this topic is inconclusive. This study aimed to examine whether nematodes such as strongyles are becoming resistant to anthelmintic treatments. Fecal samples were taken from 37 horses before treatment with anthelmintics by a veterinarian. Samples were collected in vet sleeves and stored in a refrigerator until counted. The fecal egg count (FEC) was done using the McMaster method for FEC. All pre- treatment fecal egg numbers were multiplied by 25 as per this method. Two weeks after treatment, samples were collected and counted once again in the same manner to obtain the post-treatment results. The pre- treatment and post-treatment numbers for each horse were compared and the average fecal egg count reduction was calculated to be 90.01%. This number shows that there is suspected resistance to the treatment. The fecal egg count reduction needs to be between 95% - 100% in order for the parasites to be considered susceptible to the anthelmintics used. This research, when applied to a broader context, can help determine whether or not anthelmintic resistance is common in nematodes. It can highlight the importance of regulation when using these anthelmintics as overuse can cause resistance. Future studies in this area should continue to focus on the how of anthelmintic resistance because if it is known what is happening to render treatment ineffective, it can be slowed or stopped. (**105**)

Donovan, Angelena*, Kara Selesky*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Surveillance of tick-borne diseases at DeSales University's campus*.- Tick borne diseases, caused by microbial infectious agents, are a prominent issue across the state of Pennsylvania. Ticks acquire these pathogens through blood meals of small mammals and transmit them via blood meals of larger hosts such as deer and humans. Tick borne diseases are commonly transmitted in the spring and summer months when these ticks are most active. At DeSales University, pesticide use was decreased and "grow zones" were introduced to improve the environment, however, this has led to a noticeable increase of ticks on campus. In this study, nymph, larva, and adult stage ticks were collected from wooded and grassy areas at DeSales University. The ticks collected are *Ixodes scapularis*, commonly known as deer ticks, and *Dermacentor variabilis*, or American dog tick. Ticks were sized and the species identified before performing DNA extraction, PCR, and agarose gel electrophoresis to detect the presence of multiple different microbial infectious agents. These infectious agents include *Borrelia burgdorferi*, *Anaplasma phagocytophilum*, *Ehrlichiosis chaffeensis*, *Babesiosia microti*, and *Rickettsia rickettsii*. In this study, out of the 82 collected ticks, 3 tested positive for *B. burgdorferi* and 4 tested positive for *A. phagocytophilum*. By looking at these infectious agents across multiple species on DeSales University's campus, the likelihood of contracting a tick-borne illness in Pennsylvania can be better understood and can help determine what proactive measures can be taken to prevent these diseases. (**173**)

Dotta, Austin, Jonathan Katzenmoyer, Caroline Maciejewski, Kade Lippit, James Knowles, Afaf Nazif*, and Alex Huynh DeSales University, Center Valley, PA 18034. *Measuring avoidance of predator odor cues in wild birds*.- It was historically thought that birds were anosmic (Caro and Balthazart, 2010). However, recent work has shown that birds have both functional olfactory bulbs (Balthazart and Taziaux, 2009) and a diverse set of olfactory receptor genes (Steiger et al., 2008; Driver and Balakrishnan, 2021). The use of odor by birds has recently been established as an important mode of communication in a variety of contexts (Bonadonna and Mardon, 2010; Whittaker et al., 2010; Whittaker et al., 2013; Van Huynh and Rice, 2019; Krause et al., 2023). Olfaction has also been shown to play a role in recognition of territory (Caspers et al., 2013) and some species have even been shown to use odor cues for foraging (Potier et al., 2019; Hiltpold and Shriver, 2018; Nguyen et al., 2022). However, fewer studies have investigated the ability of birds to respond to predator odors as a potential threat cue and what findings have been made in this context are mixed (Roth et al., 2008, Dotta et al., 2024). We had previously found nonsignificant but interesting trends that avian species tend to avoid predator odors in a natural context (Dotta et al., 2024) (Figure 1). Here, we aim to quantify birds' responses toward predator odors in the context of foraging in an agricultural setting. (**171**)

Doyle, Aidan*, Liam Semmler, and Vaughn Shirey Immaculata University, Immaculata, PA 19345. *Invertebrate abundances change with the presence of slugs (Gastropoda: Pulmonata) in pitfall traps*.- Studying invertebrates is invaluable because they provide humans with essential ecosystem services such as pollination, pest control, and nutrient cycling. Additionally, since invertebrates are the most biodiverse animal group in the world, they make the most ideal study organisms to test ecological and conservation hypotheses. Pitfall traps have been a foundational method to study surface-active invertebrates historically and currently. However, we observed that pitfall traps that collected slugs (Gastropoda: Pulmonata) seemed to have collected less invertebrates. Therefore, we predict that pitfall traps that collected slugs will have (1) less insect abundance and (2) less non-insect invertebrate abundance on Hog Island, Bremen, Maine, managed by the National Audubon Society. We visited Hog Island in 2023 and 2024, and sampled eight field sites using 4-6 pitfall traps per site. Invertebrate specimens collected from each pitfall trap were then sorted to taxonomic order. We then used a mixed-effects model to determine if insect and non-insect invertebrate abundance decreased with the presence of slugs from our pitfall traps. In total, 6,798 invertebrates were collected which included 175 slugs from 54 pitfall traps. We found that insect abundance had no change with the presence of slugs. However, we found that non-insect invertebrates increased with the presence of slugs. More importantly, we found that certain taxonomic orders significantly increased or decreased in abundance. Even though our two original predictions were rejected, we found that beetles, true flies, pillbugs, and springtails increased with slug presence while ants/wasps and mites decreased with slug presence. Our research is impactful because the relationship between slugs and invertebrates caught in pitfall traps have not been previously explored. Given the presence of slugs does increase or decrease certain invertebrate orders, all future pitfall trap studies need to address this relationship. (**144**)

Driver, Ashley* University of Scranton, Scranton, PA 18510. *Elucidating the role of Hsd17b7 during mammalian neurogenesis*.- Mammalian cells obtain cholesterol from either dietary sources or from internal de novo biosynthesis. During embryonic development formation of the blood-brain barrier restricts cells of the developing brain from utilizing dietary cholesterol, thus increasing reliance on internal biosynthesis. Loss of individual enzyme function in this pathway in both humans and mice can manifest as a variety of deleterious brain phenotypes. While a common feature of enzyme loss is reduced cholesterol production, the unique nature of the brain phenotypes suggests novel roles for these proteins within the neural cell. Therefore, increasing research is needed to resolve the underlying mechanisms of both enzyme function and loss. My lab has focused on characterizing the enzyme Hydroxysteroid (17-beta) dehydrogenase 7(Hsd17b7) using mouse Neuro2a cells. We have recently established the subcellular localization of this enzyme in both undifferentiated and differentiated cells. Our data suggests that the localization of this protein is dynamic during neurogenesis. Moreover, using CRISPR-Cas9 genome editing we have generated unique cell lines for molecular and biochemical analysis. Development of these cells enables a high-resolution exploration on individual enzyme function, specifically in the context of the neural cell. Together, we are generating novel information to further our understanding of the cholesterol biosynthesis pathway and brain development. (**65**)

Dugger, Tobias*, and Thomas Kwiatkowski West Chester University, West Chester, PA 19383. *Copper complexes as catalysts for cleavage of molecular oxygen by the particulate methane monooxygenase enzyme, using N=O as an O2 Substitute*.- Methanotrophs, prokaryotes that use methane as their sole source of energy and carbon, contain enzymes known as methane monooxygenase, of which there are two forms, soluble (sMMO) and particulate (pMMO). pMMO is a copper containing transmembrane protein that has three major subunits, pmoA, pmoB, and pmoC, of which subunit pmoC holds the copper complex that acts as a methane binding site for catalysis of methane oxidation into methanol. Currently the structure of the copper complex is unconfirmed, though prior research has suggested it is either a one or two copper complex. Recreation of the binding site and confirmation of the degree to which two copper complexes reduce oxygen containing double bonds allows for upscaling and, ideally, use in sustainable removal of methane from the atmosphere. Additionally, nitroso groups have been shown to engage in similar reactions to oxygen - oxygen double bonds allowing for its substitution in the recreation of the binding site. This, in conjunction with known FTIR spectra for the appearance of nitrogen - oxygen double bonds, makes nitroso a suitable replacement for molecular oxygen in the recreation of the pMMO binding site. (**30**)

Edwards, Alison*, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining the impact of post-translational modifications on the bridging interactions of cancer associated protein Ddc2p with Replication Protein A and Mec1p using the budding yeast Saccharomyces cerevisiae*.- In 2024, there were over 611,000 deaths caused by cancer in the United States alone. Cancer is often characterized by its uncontrolled cell division and can arise from a variety of DNA mutations that affect the proteins involved in cell cycle regulation. One protein that helps regulate the cell cycle and maintain genomic integrity is Replication Protein A (RPA). RPA is a major eukaryotic single-stranded DNA-binding protein with major roles in DNA replication, recombination, and repair. RPA can undergo post-translational modifications, including phosphorylation, when DNA is damaged as a part of the cell’s DNA damage response. This post-translational modification may aid in cell cycle regulation. The model organism, *Saccharomyces cerevisiae*, was used in this study due to the similarities between the yeast and animal cell cycles, the high level of protein homology between yeast and human cells, as well as the ease with which the yeast cells can be genetically manipulated. We hypothesized 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. Sequencing data was also collected from the yeast in the study to confirm the presence of our desired plasmids. 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 these proteins involved in regulating the cell cycle in response to DNA damage, we may be able to provide insights for novel cancer treatments. (**122**)

Elchin, Benjamin*, and Dawn Elchin Methacton High School, Eagleville, PA 19403. *Fantasy football correlation study*.- This study explores the correlation between fantasy football player performance and defensive rankings, with the aim of identifying mathematical relationships that can inform lineup decisions. By analyzing NFL data from the 2017-2020 seasons, the study evaluates how defensive rankings impact fantasy football points, specifically in the Points Per Reception (PPR) scoring system. Utilizing Python programming within the Replit IDE, the research calculates the correlation coefficient between player performance and opposing defense rankings. Findings reveal that players with weak correlation values (below 0.3) perform consistently regardless of defense strength, suggesting they should not be benched based on defensive matchups. Conversely, players with strong correlations (0.7 or above) demonstrate a notable dependency on defense rankings, highlighting the importance of considering defensive strength in fantasy lineup decisions. The study acknowledges the limitations of excluding factors like injuries, coaching, and home-field advantage, and suggests future research could incorporate these variables to refine predictions. (**11**)

Ellis, Gianna*, Dylan Walter, and Laurie DiRosa Immaculata University, Immaculata, PA 19345. *Assessing the validity of the Garmin Vivosmart 4 in estimating VO2 Max in male athletes*.- Given the critical role of VO2 max in assessing cardiovascular fitness and its inverse correlation with mortality, accurate measurement is essential. This study evaluated the accuracy of the Garmin Vivosmart 4's VO2 max estimations against the Queens College Step Test in male collegiate athletes. Five participants, screened via the Physical Activity Readiness Questionnaire, completed both tests. The Garmin device recorded VO2 max during normal activity, while the step test estimated VO2 max based on post-exercise heart rate. A dependent t-test was conducted to compare the two measurements. The results showed no significant difference between the Garmin Vivosmart 4 and the Queens College Step Test. Surprisingly, the mean VO2 max for both methods was 50 ml/kg/min, with a t-statistic of 0 and a p-value of 1.0. This indicates that the observed variations were due to random chance, not a systematic difference between the measurements. Therefore, the hypothesis that the Garmin device would achieve ≥85% accuracy was supported, as the device produced estimates comparable to the step test. This study suggests that the Garmin Vivosmart 4 offers a valid alternative for VO2 max estimation in this population, providing a convenient and accessible tool for cardiovascular fitness monitoring. (**45**)

Epp, Matthew*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Using AI and proteomics data to uncover new Histone Locus Body members and interactions in Drosophila melanogaster (fruit flies)*.- In both humans and *Drosophila Melanogaster*, DNA and other genetic material is held in the nucleus of each cell. In each of these species, there is a large amount of DNA that must fit into extremely tiny amounts of space. To make this possible, DNA is wrapped extensively around histone proteins, which are crucial for regulating gene expression. Since histone proteins are extremely important for genetic regulation and modification, they themselves are impacted by a nuclear body called the Histone Locus Body (HLB). The function of the HLB is to regulate the expression of histone genes, and contains a myriad of different interconnected known and unknown proteins that aid in this process. The goal of our lab's research has been to identify new members of the HLB and investigate how they connect to the overall nuclear body. In order to investigate some of the HLB unknown members, our lab analyzed proteomic data which provided various notable proteins that are new potential HLB members, including srp54, ran-GAP, cul2, and rpn2. Following proteomic analysis, our lab utilized recently developed AI software including Alphafold and ChimeraX in order to simulate potential interactions with these prospective members and MXC, which is the largest known protein in the HLB and a key component in HLB functioning. Simulations were run to see if they could be candidates for the HLB composition. Here, AI simulations have also been useful for gaining an enhanced understanding of where both known and unknown proteins in the HLB dimerize or bind to other proteins. Given that little is known even for how known HLB members interact with one another, AI has shed light on how the pieces of the puzzle that is the HLB may be put together. (**19**)

Fanning, Connor*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Prescribed burns as an invasive species management strategy in Jacobsburg State Park, PA*.- After decades of systemic fire suppression, prescribed burns are gaining popularity as a restoration and management strategy. Previous studies conducted in the western United States and Australia have shown that prescribed burns can maintain biodiversity, prevent woody species encroachment, replenish soil nutrients, and potentially suppress invasive species. However, more research is needed to determine how timing and frequency of burns and the characteristics of target invasive plants interact to determine the efficacy of this management strategy. The objective of this study is to compare plant species composition, including frequency and percentage cover of invasive species, among ten experimental burn units receiving burns in different seasons (i.e., five burned during the growing season and five burned during the dormant season) and frequencies (i.e., burned once or twice since 2021) in Jacobsburg State Park (JSP) in Nazareth, PA. Using a stratified random sampling design in fall 2023 and 2024, plant species coverage was determined using 1m2 quadrats along transect lines in each burn unit (N ≥ 10 per year). The most abundant invasive species within the meadows are *Celastrus orbiculatus*, *Lonicera japonica*, *Microstegium vimineum*, and *Rosa multiflora*. Although burn season and frequency are not yet significantly altering mean coverage of invasive species, preliminary data suggest that burns are generally suppressing invasive species, as well as a localized, sporadic pathing behavior of specific species like *Lonicera japonica*. The data collected so far represent a baseline against which future changes in plant diversity, structure, and function can be compared. In collaboration with park staff, our intention is to collect at least ten years of monitoring data that can be used to inform adaptive management practices for grassland management. (**157**)

Feczko, Allison*, Madison Bailey*, Marisa Powell, and Daniel Strömbom Lafayette College, Easton, PA 18042. *SIS-type COVID-19 and Influenza spread with collective effects*.- Pandemics driven by Susceptible-Infected-Susceptible (SIS) infections, like COVID-19 and Influenza, strain health and economic systems. The COVID-19 pandemic highlighted the role of collective behavior in shaping epidemics. A recent SIS model incorporating collective effects explained features of ancestral COVID, including recurrent waves and cooperation-driven shifts, with cooperation thresholds significantly altering disease dynamics. However, the generality of these findings remains unclear. We extend this study to assess the impact of collective behavior on the Delta and Omicron variants of COVID-19 and Influenza. Our results demonstrate that cooperation influences the spread of these diseases differently, even with the same cooperation threshold. For example, Omicron may exhibit oscillatory behavior, Delta may stabilize at equilibrium, and ancestral COVID may reach a stable low-prevalence state. We also find that as transmission rates increase, cooperative behavior becomes more critical. These dynamics highlight the need for tailored strategies based on disease characteristics and transmission rates. By comparing the impact of collective behavior across variants and diseases, our findings emphasize the importance of customized public health interventions, with cooperation-driven strategies being potentially more effective for certain COVID-19 variants but less so for Influenza. (**66**)

Ferguson-Richards, Adore*, Zahra Imrani*, Antonio Rinaldi*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Tetrahydrocannabinol (THC) destabilizes trinucleotide repeat tracts in Saccharomyces cerevisiae*.- Trinucleotide repeats (TNR) are repetitive regions of DNA which are variable in length. TNR tracts are unstable and prone to sudden expansion events due to DNA polymerase slippage. The expansion of TNR tracts is associated with several human diseases, including Huntington's Disease (HD), myotonic dystrophy, and spinocerebellar ataxia (SCA). *Saccharomyces cerevisiae* is a eukaryotic model organism which is useful for the study of TNR tract stability. We employed a *S.cerevisiae* strain engineered with 25 CAG repeats between the promoter region and open reading frame of the URA3 gene. In the presence of 5-fluoroorotic acid (5-FOA), expression of the URA3 gene leads to the formation of a lethal compound. If the TNR tract expands, however, the distance between the promoter and open reading frame increases. URA3 is no longer expressed and yeast become viable on 5-FOA. Our laboratory has previously demonstrated that nicotine, a component of tobacco smoke, destabilizes TNRs. Tetrahydrocannabinol (THC) is a psychoactive component of cannabis smoke with many similarities to nicotine. Both substances are lipophilic molecules that interact with neural receptors after inhalation and absorption through the lungs, leading to systemic effects on the cardiovascular, endocrine, and nervous systems. Given the structural and functional similarities between nicotine and THC, we hypothesized that THC might likewise influence TNR stability. We show that THC also promotes expansion of TNR tracts in *S. cerevisiae*. (**118**)

Fitz, Faith A.*, and John F. Harms Messiah University, Mechanicsburg, PA 17055. *Determining the efficacy of anti-fibrotic treatment in advanced pancreatic cancer using whole-slide imaging*.- Pancreatic Ductal Adenocarcinoma (PDAC) remains a lethal malignancy as the third most common cause of cancer death in the United States and has a 9% five-year survival rate. PDAC is one of the most aggressive forms of cancer due in part to its dense desmoplastic tumor microenvironment (TME). This fibrotic TME collapses blood vessels, which impedes chemotherapy delivery and decreases immune access. Proglumide, an oral gastrin/CCK receptor antagonist, has been shown to reduce tumor fibrosis up to 70% and improve chemotherapy in mice. To date, studies have initiated treatment early in tumor growth which does not accurately reflect clinical treatment in progressed stages of PDAC. We hypothesize that proglumide treatment of advanced tumors will exhibit decreased fibrosis similar to immediate treatment. Mice received subcutaneous injection of Panc02 murine PDAC cells and were randomized to control, immediate treatment (3 days post-injection), and late treatment (6 weeks post-injection). Tumors were isolated at 10 weeks for histological analysis by Masson’s trichrome staining. Historically, significant tumor heterogeneity has complicated quantification of fibrosis utilizing random photomicrographs. In a pilot analysis, we demonstrated that use of whole-slide imaging reduced sampling bias and provided a more accurate assessment of fibrosis. Applying this approach, imaging analysis (Fiji/ImageJ) on a wider array of tumor samples is currently underway. (**132**)

Flask, Isabella*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Screening of Bacillus isolates suggests conserved mechanisms of heat and salt tolerance*.- *Bacillus* species are an important group of bacteria, known to induce food spoilage, cause disease in animals and promote plant growth. Various *Bacillus* species are recognized for their stress-tolerance capabilities; however, the connection between the mechanisms by which they perform these capacities is not thoroughly understood. In this study, we screened sixty-six *Bacillus* isolates (including 23 unknown species) for heat-tolerance on tryptic soy agar (TSA) at 48°C, and salt-tolerance on TSA with 10% sodium chloride at 37°C. We found that, while individual species varied, several species successfully displayed tolerance to both heat and salt stress. *Bacillus altitudinis*, *Bacillus atrophaeus*, *Bacillus pumilus*, and *Bacillus subtilis* consistently showed resistance to both stressors and phylogenetically clustered within the same group, suggesting that the stress tolerance may be derived from a common ancestor. Our results also suggest that heat and salt tolerance within the same *Bacillus* species may be from overlapping stress tolerance mechanisms. Understanding the stress tolerance of *Bacillus* species has important implications for their applications in agriculture and their control in food industry and healthcare. (**92**)

Flores, Maria F.*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Investigating the impact of the Y56D MDH1 mutant on the activity of malate dehydrogenase*.- The citric acid cycle is an essential metabolic pathway that converts fuels such as carbohydrates, lipids, and proteins into energy. Malate dehydrogenase (MDH) is one of the enzymes in the citric acid cycle that forms metabolons with other enzymes. Metabolons are non-covalently associated sequential enzymes in metabolic pathways that impart enhanced efficiency by effectively shuttling metabolites between enzyme active sites. Malate dehydrogenase is present in cytosolic (MDH1) and mitochondrial (MDH2) isoforms, whose activity and metabolic outcomes are dependent on both the needs of the cell and formation of various metabolons. Phosphorylation, a method of post-translational modification, is proposed to affect metabolon formation and alter MDH activity, which is the area of interest in this study. Site-directed mutagenesis was used to create cytosolic MDH mutants called phosphomimics, whereby a Ser (S), Thr (T), or Tyr (Y) residue is substituted with a Glu (E) or Asp (D) residue that would mimic the size and negative charge created through phosphorylation. Y56D is of interest as Y56 is an essential residue in the MDH and citrate synthase (CS) interface and the phosphorylation state may play a critical role in facilitating (or inhibiting) metabolon formation. This protein was overexpressed in E. coli, cells were lysed using sonication, and purified using FPLC and Ni-NTA affinity chromatography. Fractions containing protein were characterized by Bradford assay to quantify total protein and SDS-PAGE to evaluate protein purity. Enzyme assays will be performed to assess the effect of the Y56D mutation on enzymatic activity of the protein. The effects of temperature, pH, and the addition of allosteric regulators on enzyme activity will also be investigated. This has significant disease implications, as altered cellular pH is a hallmark of dysregulated metabolism in cancer cells. As the overexpression and purification of this mutant has been particularly challenging, we are also currently evaluating purification strategies to maximize both yield and purity of our target protein. (**3**)

Fogarty-Harnish, Oliver*, Jill K. Yeakel, Ted L. Pauley, Ed T. Svirbely, and Shawn P. Barry Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Ethanol depletion dynamics in open-system breath alcohol simulators*.- Breath alcohol simulators are devices that are used to simulate human breath and are commonly used to calibrate alcohol breath testing instruments. In the field it has been noted that as you continue to perform tests using the same solution, ethanol concentration depletes. The goal of this study was to analyze this ethanol depletion in open system breath alcohol simulators and find the correlation between volume of air through the simulators and the observed depletion. Simulators were filled with certified alcohol reference solutions and air was pumped through the simulator and output to the analyzer, repeatedly until significant concentration depletion was observed. The main instruments used in the study were the Guth Model 12V500 Alcohol Breath Simulator and the CMI Intoxilyzer 9000 breath-alcohol analyzer. Analysis of our results shows that the depletion of ethanol concentration in breath alcohol simulators was correlated to the total liters of air that passed through the system. It was observed that ethanol depletion rates when having different flow rates or times was very similar when the total liters of air through the system was similar. When using different starting ethanol concentrations, an increase in ethanol depletion was observed as the ethanol concentration in the solution increased. Combining the aforementioned findings, we determined that the total ethanol depletion in an open system breath alcohol simulator can be described as a percentage of the original concentration being lost when a specific volume of air is passed through the system. (**133**)

Ford, Daniel*, and Thomas Kwiatkowski West Chester University, West Chester, PA 19383. *Phthalates in e-cigarettes and toxicity to male reproductive tissue*.- Endocrine-disrupting phthalates have been associated with declines in fertility, yet the underlying biochemical mechanisms affecting male reproductive tissues remain poorly understood.

Vaping exposes the user's lung epithelial tissues and pulmonary circulation to varying concentrations of phthalates from both the e-liquid and the vaping devices themselves. In this project, our aim is to assess the biochemical impact of phthalates derived from e-cigarettes on male reproductive tissues using rat and cell culture models. Our hypothesis is that phthalates, particularly dibutyl phthalate, negatively impact male reproductive tissues through inhibiting spermatogenesis and testosterone synthesis, along with elevated inflammation signaling cascades. To examine the mechanisms, we exposed several rats and primary derived testicular Sertoli cells to vaporized phthalates and measured protein expression changes through western blot analysis and cell viability assays. Our preliminary findings indicate that several phthalates exhibit cytotoxic effects on primary-derived rat testicular Sertoli cells. Additionally, exposure of male rats to vaporized DBP at the lowest concentration found on the market for 72 hours did not result in significant alterations in serum testosterone concentrations compared to control groups exposed to vehicle or air alone. Similarly, the protein expression of enzyme CYP11A1, a key enzyme involved in testosterone synthesis, did not display significant differences with and without dibutyl phthalate. Future investigations will extend exposure durations and concentrations of dibutyl phthalate to rats, as well as exploring the changing expression patterns of other testosterone synthesis pathways. (**130**)

Foriska, Isabella*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Sigma Factor B as a potential regulator of high salinity induced conditional bacterial filamentation*.- Filamentation is a type of anomalous cell growth in which bacteria undergoing either DNA damage or exposure to environmental stress continue to grow laterally through the preliminary stages of binary fission, however, no septal wall is formed and cell division is therefore blocked. The resulting structures are called filaments. Filamentation is unique to certain bacterial species and reversible. Filamentation has been suggested to have survival benefits for the bacteria and has even been suggested to assist certain bacteria in their pathogenicity. With all that is known about the effects of bacterial filamentation, much is still unknown about the mechanism(s) bacteria use to initiate filamentation. In this study, we aim to identify a possible mechanism of initiating bacterial filamentation through studying the genetic expression of the wild type and a catalog of knockout mutants of the model species *Bacillus subtilis*. Preliminary data from completed simple staining screenings have shown the gene sigB as a promising candidate for controlling stress-induced filamentation. Under high salinity conditions (TSB + 10% NaCl), these bacteria did not form filaments while the wild type, wt1A1, clearly demonstrated their filamentous capabilities. These results indicate that this transcriptional regulator, or some of its 255 regulon members, may be involved in the initiation of stress-induced filamentation in *B. subtilis*. Future experiments aim to test and quantify the expression of sigB under a time course study of filamentous conditions and perform a genetic complementation experiment to restore filamentation in the sigB mutant. (**15**)

Franchina, Abigail*, Courtney Williams, and John Harms Messiah University, Mechanicsburg, PA 17055. *Characterizing the effect of a gastrin/CCK antagonist on post-translational processing of collagen in pancreatic cancer*.- A major contributing factor to significant pancreatic cancer mortality is the obstacle to treatment presented by dense collagen-rich fibrosis permeating the tumor. This fibrosis, which increases pressure in the tumor, collapses blood vessels and prevents delivery of chemotherapy and immune cells. The gastrin antagonist, proglumide, has been shown to significantly decrease the amount of fibrosis within murine pancreatic tumors, but the mechanism is yet unknown. Parallel work in our laboratory has shown proglumide does not change the RNA expression of collagen. As such, we hypothesize proglumide changes the post-translational processing of collagen. Type 1 collagen is a heterotrimer formed by two α1 chains and one *α*2 chain. These pro-collagen strands are secreted from the cell before both termini are cleaved, and the strands are crosslinked to form mature fibrils. Four major collagen processing enzymes were investigated including intracellular PLOD2 and extracellular ADAMTS2, BMP1, and LOX. Human pancreatic cancer (PANC-1) and pancreatic stellate (RLT-PSC) cell lines were treated with proglumide for 72 hours before RNA isolation. While no significant differences in PLOD2, ADAMTS2, and LOX expression were observed in either cell lineage, preliminary studies suggest a difference in BMP1 expression between treated and untreated RLT-PSC cells. Confirmatory studies are ongoing. (**189**)

Franz, Allison*, Alexander Hurtado*, and Quyen Aoh Gannon University, Erie, PA 16541. *Evaluating the role of SCAMP3 on CXCR4 trafficking*.- The G-protein coupled receptor CXC-Chemokine Receptor Type 4 (CXCR4) is involved in regulation of cell migration, growth, and differentiation. CXCR4 overexpression has been linked to metastatic cancer growth. When CXCR4 is bound to its agonist CXCL12, CXCR4 is downregulated through endocytosis and ubiquitin-dependent trafficking through the endolysosomal pathway. The trafficking of CXCR4 to the lysosomes for degradation requires the Endosomal Sorting Complexes Required for Transport (ESCRTs) proteins, including the ubiquitin adaptor Hrs and Tsg10. The Secretory Carrier Membrane Protein 3 (SCAMP3) has been shown to oppose the ESCRT proteins Hrs and Tsg101 in regulating degradation of the Epidermal Growth Factor Receptor (EGFR), which follows a similar degradative pathway. In this project, we will investigate if SCAMP3 also regulates CXCR4 trafficking. To do this, we are using complementary approaches to assess CXCR4 trafficking and degradation in cells where SCAMP3 is knocked down. We have been able to knock down SCAMP3 using small interfering RNAs with >95% efficiency. We have optimized a pulse-chase immunofluorescence assay to observe fluorescently labeled CXCR4 in endosomal and lysosomal compartments following stimulation with its agonist CXCL12. Finally, we are using western blotting to observe degradation of stimulated CXCR4 in cells where SCAMP3 is knocked down. (**178**)

Garcia, Naiara Bernice*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Using CRISPR-Cas9 to delineate the antibiotic potential of uncharacterized genes in Paenarthrobacter nicotinovorans*.- The rise of antibiotic resistance, driven by the overuse, misuse, and lack of new antibiotic development, is a growing global health crisis. Soil offers potential solutions in the search for antimicrobials due to having a rich reservoir of antibiotic-producing microorganisms. This study investigates *Paenarthrobaccter nicotinovorans*, a soil bacteria that has been previously identified to inhibit the growth of *Eschericia coli*, *Bacillus subtilis*, and *Staphylococcus epidermidis* ESKAPE pathogen safe strains. In our lab, we identified biosynthetic gene clusters (BCG) encoding for a secondary metabolite similar to stenothricin (38%). Stenothricin is a known antimicrobial compound, however its function is poorly characterized. Previous work by others has suggested that certain genes within this BGC are also involved in arginine production. To distinguish the antibiotic properties of this pathway from its role in arginine synthesis, we pursued two uncharacterized genes, CTG21_59 and CTG21_74 within the stenothricin-like BGC. Specifically, we plan to silence these genes using CRISPR/Cas9 gene editing, and compete against ESKAPE pathogen safe strains using both wild-type and mutant isolates. This will allow us to assess differences in antibiotic production before and after gene sequencing. We have cloned gRNA into the pCasi-ART plasmid in preparation for CRISPR-Cas9 gene editing, with the intent of transforming *P. nicotinovorans* to induce gene silencing. We expect the mutant isolates of CTG21_59 and CTG21_74 to exhibit decreased zones of inhibition (ZOIs), thus indicating their role of antibiotic potential in the stenothricin-like pathway. These results would further characterize the function of the stenothricin-like BCG, separate roles in antibiotic production versus arginine synthesis, and contribute to the development of novel antibiotics. (**128**)

Gautam, Saradha*, Brayden Robicheau*, and Quyen Aoh Gannon University, Erie, PA 16541. *The role of secretory carrier membrane protein 3 (SCAMP3) in amyloid precursor protein (APP) and beta-amyloid production*.- Alzheimer's disease is a progressive neurodegenerative disorder characterized by cognitive decline and memory loss. Studies have shown that the accumulation of β-amyloid plaques plays a role in its pathogenesis. These plaques result from the cleavage of amyloid precursor protein (APP), a process closely linked to APP trafficking within the trans-Golgi network (TGN) and endosomal system. Previous studies have shown that Secretory Carrier Membrane Protein 3 (SCAMP3) interacts with key ESCRT (endosomal sorting complexes required for transport) proteins, such as Hrs and Tsg101, which regulate the trafficking of proteins like APP and the epidermal growth factor receptor (EGFR). We have found that SCAMP3 colocalizes with APP in both the TGN and early endosomes, suggesting that SCAMP3 may have a role in APP trafficking in concert with Hrs and Tsg101. This study aims to investigate whether SCAMP3: 1) affects the trafficking of APP within the TGN and endosomes and 2) influences the production of β-amyloid. To examine SCAMP3's effect on APP trafficking from early endosomes, we will use immunofluorescence with SCAMP3 knockdown. Separately, to assess SCAMP3's impact on beta-amyloid production, we will use an ELISA assay with SCAMP3 knockdown to quantify β-amyloid levels in N2a cells. Together, these complementary approaches will provide insight into the role of SCAMP3 in APP trafficking and β-amyloid production. (**20**)

Geditz, Diana*, Brianna Hong, Stephen Mason, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Comparing cave cricket (Orthoptera: Rhaphidophoridae) communities on Harbor Island, Maine*.- Island ecosystems make ideal study areas due to their unique flora and fauna. Therefore, collecting baseline data about the biodiversity on islands is critical, particularly with anthropogenic global change. Insects make ideal study organisms because of their foundational role in food webs and trophic levels. More specifically, cave crickets (Orthoptera: Rhaphidophoridae) provide essential ecosystem services such as decomposition and food sources for other animals. This research aims to (1) start determining the cave crickets to species on Harbor Island, Maine, co-managed by the National Audubon Society, and (2) determine if there is a difference between cave cricket abundance between a red spruce (*Picea rubens*) forest and an adjacent fern (*Dennstaedtia punctilobula*) field. During one week in July of 2022, 10 pitfall traps were set up at our spruce and fern sites to collect cave crickets. We used DNA barcoding to determine the cave crickets to species. Additionally, we used a Mann-Whitney Wilcoxon analysis to determine if there was a difference between cave cricket abundance between our two sites. Out of the 43 cave crickets collected, 42 were found in the spruce forest and 1 was found in the fern field. We determined two species: *Ceuthophilus guttulosus* and *Ceuthophilus brevipes*. We also found that cave cricket abundance was significantly higher ($p = 0.007$) at our spruce site compared to our fern site. By doing this research, these data will help better understand Maine's biodiversity on island ecosystems. These data will also be uploaded to the Global Biodiversity Information Facility to help other researchers studying island biogeography and cave cricket biodiversity. (**170**)

Giardini, Francesca*, Jessica Wolfgang, Vaughn Shirey, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Testing the plant vigor hypothesis on oak (Fagales: Fagaceae) leaves after wildfires in the Pinelands National Reserve, NJ*.- 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 herbivore attack. Our former research has shown that oak (*Quercus spp.*) leaves in the PNR are undergoing rapid growth after wildfires. Therefore, we predict that oak leaves from our wildfire site will have more insect herbivore and pathogen damage, (phytotroph damage) compared to our prescribed fire and unburned sites in the NJ Pinelands National Reserve

(PNR). In 2018, 1,724 oak leaves (Wildfire: 319; Prescribed fire: 696; Unburned: 709) were collected between May to September to count phytotroph damage on each leaf. We then used a Kruskal-Wallis analysis to compare the phytotrophic damage on the leaves from our wildfire, prescribed fire and unburned study sites. Our preliminary results show that there was significantly more ($p < 0.001$) insect damage in the wildfire site compared to the prescribed fire and unburned sites. However, the pathogen damage was significantly less ($p < 0.001$) at our wildfire site compared to the prescribed fire and unburned sites. Therefore, our hypothesis is supported with insect herbivore damage, but rejected with pathogen damage. Subsequently, insects and pathogens could have different recolonization strategies after a wildfire. For future research, we will analyze Ericaceous shrubs to test the PVH and test if plants growing more vigorously are actually less chemically defended. (**75**)

Gibbs, Evan* York College of Pennsylvania, York, PA 17405. *Elucidating the heterogeneity of wing morphology in D. melanogaster using Wasserstein geometry*.- Quantitatively understanding variation in the morphology of an organism is a difficult task regardless of species. In our research, we aim to tackle this problem with the wings of wild-type *D. melanogaster*. Through the novel application of Wasserstein Geometry, we interpret the boundaries and veins of a given wing as the support of a probability measure on $\mathbb{R}2$ and calculate the 2-Wasserstein distance (W2) between wings. This embeds the space of all wings as a submanifold of the Wasserstein manifold, allowing us to effectively leverage its structure to learn about the modes of variation of *D. melanogaster* wings. We discuss the process by which we are able to represent the movement between wings via Riemannian logarithms of this submanifold, thereby providing a more intuitive representation of the morphological differences compared to previous works. In doing so, we construct visualizations of the optimal transport of mass between wings, demonstrating how the vein and boundary structures of wings transform between flies stemming from distinct strains, environmental conditions, and sexes. Further, as we can locally represent the manifold linearly, we make use of a unique linear technique, multiscale Singular Value Decomposition (mSVD), to gauge the intrinsic dimensionality and degrees of freedom of our space at a given wing. An exploratory implementation of mSVD on the medoids of wing-strain subsets has revealed a local, low dimensional structure of our space. Through both techniques, we aim to effectively characterize the ways in which *D. melanogaster* wings can vary and present a new methodology for realizing morphological variation. (**142**)

Glenn, Madeline*, Kade Lippitt*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Homo sapiens DNA in the Tannersville Cranberry Bog*.- Bogs are ecologically important wetland biomes which develop from the gradual accumulation of Sphagnum moss and other partially-decayed detritus (jointly referred to as peat). These create an acidic and oligotrophic (low-nutrient) environment which impedes the decomposition of organic materials. The abundance, diversity, and composition of organismal communities within bogs remains relatively unknown. We metagenomically analyzed soil samples from the Tannersville Cranberry Bog, a ~13,000 year old bog located eight km northwest of Stroudsburg, PA. We sampled soil in triplicate at a depth of 15cm from seven sites within the bog: the center of the bog, the bog's shore, and at six meter intervals from the shore. We extracted genomic DNA using the Qiagen Powersoil Pro kit. We ligated adapters and barcodes to create a DNA library, which we then sequenced using the Oxford Nanopore MinION sequencer. Fastq files were analyzed with the EPI2ME platform and taxonomic assignment was made by the wf-metagenomics workflow. Remarkably, the initial metagenomic analysis of the bog revealed high numbers of Homo sapiens reads in all sampling sites. To rule out the possibility of contamination introduced by sampling, we repeated the sampling and extraction/sequencing after donning PPE including surgical facemasks, nitrile gloves, and full body Tyvek suits. Even after these measures, we again found high numbers of Homo sapiens reads in all bog samples. We postulate that the Tannersville Bog is contaminated with human DNA of unknown origin. (**81**)

Gramlich, Arthur*, and William Wagner Immaculata University, Immaculata, PA 19345. *How professional sports teams assess injury risk*.- Professional sports teams continually seek technological advancements to optimize player performance and minimize injury risks. This research explores the integration of machine learning models into injury risk assessment. These models have shown a varying success rate of anywhere from 74.2%-97.7% but have proven to be much more accurate when assessing musculoskeletal injuries. This study focused on a case study analysis of real-world applications of these machine learning models. The first practical application to be analyzed was the NFL's "Digital Athlete". This program uses Amazon Web Services (AWS) to run a multitude of simulations on when players are the most at risk. In the 2024 season, all 32 teams were given access to the full software with league wide benchmarks and trends about player performance and injury recurrence. The second case study was an analysis of FC Barcelona's process mining application. Process mining is a retrospective analysis of workflow. In this situation, it was an analysis of post-Preparticipation medical evaluation for recurring injuries. It was found that there was a high recursion rate for thigh muscle injuries. Issues like data variability and accuracy still remain but it is clear how useful these models can be. This research intentionally focused on machine learning for assessing injury risk but there are alternatives that are widely recognized. GPS and wearable technology, biomechanical analysis, and functional movement screening are similar processes at the forefront of sport injury assessment and reduction. (**53**)

Grimes, Sydney*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Naphthalene induces UV fluorescence in Pseudomonas species isolated from Polycyclic Aromatic Hydrocarbon-polluted soil*.- Some *Pseudomonas* species are known to produce porphyrin or amino acid-derived compounds that are fluorescent under ultraviolet light (UV-C). Stresses such as chemical starvation, pH changes, and temperature can induce the production of these compounds, many of which are iron-scavenging fluorescent siderophores. In this study, we discovered several *Pseudomonas* species from polycyclic aromatic hydrocarbon (PAH)- contaminated soils outside of the now defunct Erie Coke plant in Erie, PA using 16S rRNA sequencing. To test for their ability to tolerate toxic PAH, we grew the bacteria in the presence of naphthalene, a PAH, and found that some of the isolates not only tolerated naphthalene but also thrived on naphthalene media, suggesting an ability to utilize naphthalene as a carbon source. Furthermore, naphthalene triggered UV fluorescence in certain *Pseudomonas* species leading us to speculate that the fluorescence could be an indication of iron sequestration, presumably to support the degradation of naphthalene. Indeed, iron supplementation of naphthalene media suppressed UV fluorescence, supporting the idea that an iron-requirement triggers UV fluorescence. Using sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), we found proteins that were inducible by naphthalene and identified putative proteins in a 55 kD band using tandem mass spectrometry. To understand gene expression changes in response to naphthalene, we will test the expression of naphthalene-degradation genes in these isolates using quantitative RT-PCR. We will also test the bioremediation potential of the bacteria by testing if the plants grown in the presence of these naphthalene-metabolizing bacteria can better tolerate naphthalene. The study of naphthalene-induced fluorescence could provide insights into the mechanisms of pollutant degradation with future prospects in bioremediation. (**16**)

Haddad, Joy*, Taylor DeHaven, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Unlocking antibiotics: The role of soil microbes*.- Antibiotic resistance is a major global health concern, largely driven by the misuse or overuse of antibiotics. Many of these antibiotic resistant infections are caused by the ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*). Our study aims to identify novel antibiotics produced by soil bacteria. Since many soil bacteria naturally produce antibiotics, we collected samples from our campus in Center Valley. Bacterial colonies were isolated from these soil samples and incubated at 25°C to select for non-pathogenic strains. Once isolated, we first tested the bacterial isolates for antibiotic production using bacteria that are closely related to the ESKAPE pathogens (*Staphylococcus epidermidis*, *Enoterococcus raffinosus*, *Bacillus subtilis*, *Mycobacterium smegmatis*, *Escherichia coli*, *Erwinoia carotovora*, *Acinoetobacter baylyi*, *Enoterobacter aerogenoes*, *Psuedomonoas putida*). One of eight isolated bacteria produced zones of clearing and was further characterized. The isolate did not cause any change in the color of the media around the bacterial colonies on the blood agar plate, indicating that it does not lyse red blood cell and is gamma-hemolytic as one of its characteristics. A catalase test confirmed that the bacteria produces the catalase enzyme, which breaks down hydrogen peroxide into water and oxygen gas, as indicated in the formation of bubbles. Further tests will be conducted to determine additional characteristics of this bacterial isolate. Additionally, ongoing work will assess whether these antibiotics are novel. (**172**)

Haldaman, Alanna*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Gene expression analysis of Phytophthora infestans AA17 gene PITG_04947 in Solanum tuberosum during disease development*.- The oomycete *Phytophthora infestans* is the causal agent of potato late blight, a disease that leads to approximately 6 billion USD in crop losses worldwide. Shortly after contact with the plant, *P. infestans* secretes proteins known as effectors, which modulate the host resistance response, thus facilitating penetration and colonization. Because of their predicted enzymatic activities, some effectors have been classified within a large group of enzymes referred to as carbohydrate-active enzymes (CAZymes). A significant number of CAZymes also play an important role in *P. infestans* pathogenesis by targeting and hydrolyzing cell wall polysaccharides in the host plant. *Phytophthora infestans* gene PITG_04947 belongs to the recently discovered auxiliary activity 17 (AA17) family of CAZymes. This family is composed of copper-bound lytic polysaccharide monooxygenases, a class of CAZymes that degrade pectin. Previous studies have shown that some AA17 genes are upregulated during infection of potato by *P. infestans*. Despite its importance, very little is known regarding the role of PITG_04947 in *P. infestans* pathogenicity. This study aimed to further characterize PITG_04947 gene by cloning and sequencing it and quantifying its expression at 12, 24, 36, and 48 hours after infection of *Solanum tuberosum* leaves with *P. infestans*. Using qPCR analyses, we found that PITG_04947 is upregulated during infection, displaying its highest transcriptional activity at 12 hours post inoculation. The elucidation of PITG_04947 transcriptional profile during pathogenesis establishes the basis for future research on the AA17 family of CAZymes. (**56**)

Hansell, Madison*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *How does temperature affect DNA yield in blood samples?*- DNA has proved valuable in all manner of legal matters from proving the innocence of the accused to identifying the true culprit. For samples left at a crime scene, there are many factors that may lead to DNA degradation, including high temperature, low humidity, UV exposure, and the material on which the DNA is left. We were interested in the effects of temperature cycling on DNA stability. We expected that the more temperature cycles a DNA sample was subject to, the more the DNA would degrade, and the less likely it would be to provide useful PCR products. To test this hypothesis, we subjected 100 µL bovine blood in plastic petri dishes to temperature cycles of 24 h at 37 °C and 24 h at -20 °C. We found that the amount of DNA recovered by Qiagen DNeasy Blood & Tissue Kit decreased by ~67% through three temperature cycles but did not decrease further out to six temperature cycles. DNA fragment size was not dramatically affected by the temperature cycling. Surprisingly, there did not seem to be any correlation between our ability to amplify the MC1R (melanocortin 1 receptor) gene and the number of temperature cycles. These results suggest that there may be a limit to how much DNA will degrade due to temperature cycling and that DNA fragment size and concentration is not sufficient to predict the success of PCR amplification. (**60**)

Heidel-Roberts, Ethan*, Dominic DePaul*, and M. Logan Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Seeing gene regulation: Histone modifying complex and nuclear receptor roles in Drosophila melanogaster eye development*.- Gene regulation is often a delicate balance between proteins that control transcription and can reshape how tissues are formed. The protein Jazf-1 has been suggested to regulate genes in the eye and has been shown to modify a Lobe-2 (L2) allele, an allele which causes a smaller eye. As a member of the NuA4 histone modifying complex that also interacts with the nuclear hormone receptor Hr78, we wanted to examine Jazf-1 in the eye. Using the GAL4-UAS system we investigated Jazf-1, members of the NuA4 complex, and Hr78's role in regulating eye development. One of these lines drove GFP expression in tissues where Jazf-1 is endogenously expressed and showed robust expression in the adult eye. We also used several lines that reduced or overexpressed Jazf-1, other members of the NuA4 complex, and Hr78. When found the development of the eye was more sensitive to these manipulations on a L2 mutant background. When NuA4 complex members were reduced with L2, eye reduction was severe, often resulting in a complete loss of the eye. The opposite was observed in Hr78, where downregulating Hr78 resulted in a restored eye, and increasing Hr78 reduced eye size. An Hr78 allele that should not interact with Jazf-1 is placed on a L2 background, the eye is also reduced. Taken together, we find that Hr78 is working as an enhancer to the L2 phenotype, and that Jazf-1 and other members of the NuA4 complex are repressing the phenotype. (**18**)

Hoitt, Julianna*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Modeling coral reef and crown of thorns starfish Acanthaster solaris interactions to conserve reef health*.- Coral reef ecosystems face increasing threats from population surges of crown of thorns starfish (*Acanthaster solaris*, COTS). At high densities, COTS can consume up to 90% of coral cover, resulting in widespread coral loss. Current management strategies often focus on eliminating COTS only after outbreaks occur, which may be too late to prevent ecosystem collapse. Here we introduce a mathematical model of coral and starfish interactions to identify optimal population thresholds for intervention. Our model incorporates coral growth dynamics, COTS predation patterns, and intervention strategies to determine ecologically sustainable population levels. Our findings indicate that total COTS elimination is not necessary nor viable, as a small, controlled population supports coral diversity. Specifically, reef hectares with less than 6 COTS should remain untouched, as COTS at this density are contributing to ecosystem stability. Instead, we find that intervention methods should prioritize reefs with densities between 6 and 15 COTS per hectare, as the success rate of coral recovery is highest. Beyond 15 COTS per hectare, intervention becomes less effective due to rapid coral loss. Additionally, we show that reefs experiencing higher COTS consumption rates suffer from greater coral loss, underscoring the need for site-specific intervention strategies. By quantifying these interactions, we provide a framework for proactive reef management, offering a decision-making tool for policymakers and conservationists to prevent irreversible reef degradation. (**149**)

Hong, Brianna*, Diana Geditz, Kelly Orlando, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Comparing ant (Hymenoptera: Formicidae) communities on Harbor Island, Maine*.- Insects are the most biodiverse group of organisms in the world and provide ecosystem services such as pollination, pest control, and clean water. Ants (Hymenoptera: Formicidae) are mostly known for their role in ecosystem engineering and having symbiotic relationships with other organisms. The goals of this research are to (1) start determining the ant species richness on Harbor Island, Maine, co-managed by the National Audubon Society, and (2) determine if there is a difference between ant abundance between a red spruce (*Picea rubens*) forest and an adjacent fern (*Dennstaedtia punctilobula*) field. During one week in July of 2022, 10 pitfall traps were set up at the spruce and fern sites to collect ant specimens. We used DNA barcoding to determine the ants to species. Additionally, we used a Mann-Whitney Wilcoxon analysis to determine if there was a difference between ant abundance between the two sites. We collected 27 specimens, 20 in spruce and 7 in the fern sites, and currently identified two species: the Hercules carpenter ant (*Camponotus herculeanus*, Linnaeus, 1758) and the silky ant (*Formica fusca*, Linnaeus, 1758). We found there is no significant difference (p = 0.20) in abundance between the spruce and fern sites. We will continue to barcode other collected ant specimens from Harbor Island. These data will help better understand island biodiversity in Maine. Most importantly, these data will be uploaded into the Global Biodiversity Information Facility to help other researchers test their own local and global hypotheses. (**169**)

Inch, Olivia*, and Nik Tsotakos Penn State University-Harrisburg, Middletown, PA 17057. *Genetic and environmental factors that affect the natural history of chronic kidney disease*.- Chronic Kidney Disease (CKD) is a progressive condition characterized by the gradual loss of kidney function over time. It affects the kidneys' ability to filter waste and excess fluids from the blood, leading to serious complications such as cardiovascular disease, anemia, and metabolic imbalances. CKD is a major public health challenge, affecting 10% of the population. For the purpose of this study, all diagnosed CKD stages were included, regardless of cause. Exclusion criteria included organ transplantation and pregnancy. This research study involved an in-depth coding-based analysis using the All of Us database. In totality, 28,851 individuals were included in the study and calculations. Of this amount, 5,843 were diagnosed with CKD. White, African American or Black individuals had the highest occurrence of CKD. In the African American and Black grouping, 28.7% of the population were diagnosed with CKD. The white population had a 20.3% CKD diagnosis. These findings were found to be significant based on a Chi-Squared test (P<2.26e-16). The investigated SNPs did not show statistical significance, as expected for a multifactorial condition, like CKD. The work is ongoing, exploring possible confounding variables in the population. CKD is a multifactorial disease influenced by both genetic and environmental factors. This study confirms significant disparities in CKD prevalence across racial and sex-based demographics, with African American/Black individuals and males exhibiting higher diagnosis rates. Despite analyzing genetic variants, no statistically significant associations were found for the investigated SNPs. Future research should focus on identifying environmental and lifestyle contributions. (**61**)

Ivory, Leigh*, and Michael Foulk Mercyhurst University, Erie, PA 16546. *Development of a larval salivary gland culturing system for the black fungus gnat, <u>Bradysia</u> <u>coprophila</u>*.- The black fungus gnat , *Bradysia coprophila*, is a non-canonical fly model organism that exhibits several unique biological phenomena that merit further investigation. We have focused on the developmentally regulated, site-specific DNA amplification that occurs in the larval salivary glandpolytene chromosomes. This phenomenon has been extensively characterized in vivo. In the research presented here, we attempted to develop a salivary glands culturing system to further characterized DNA amplification in explanted salivary glands. The glands from early eyespot larvae were microdissected for culture in Cannon's media. Two different batches of Cannon's media were tested; a bottle that was already opened (old) and a bottle that was unopened (new). Both bottles were over a decade old. In both cases, the media was supplemented with glutamine, Penn/Strep, and Amphotericin to control microbial contamination. The requirement for Fetal Bovine Serum (FBS) was also tested. All culture conditions preserved the morphology of the cultured glands for up to 7 days, with the new

Cannon's media -FBS preserving gland morphology the best. Giant polytene chromosome squashes demonstrated that the morphology of the polytene chromosomes were also well maintained under all culture conditions. We attempted to induce DNA amplification and puffing by adding 20-hydroxyecdysone to the cultures. Unfortunately, no DNA puffing was observed in the squashes. Moreover, genomic DNA was prepared and used for quantitative real-time PCR. Across a range of ecdysone concentrations, no DNA amplification was observed for the well characterized II/9A locus. In the future, this culturing system can be used to develop a system for RNA interference (RNAi) and other experimental techniques for studying DNA amplification. (**119**)

Jenkins, Owen*, David Rothblat, and Jaimy Joy La Salle University, Philadelphia, PA 19141. *Exploring quiescence-specific protein markers in human fibroblasts*.- Cellular senescence is a phenomenon whereby a cell undergoes permanent cell cycle arrest, which can occur due to DNA damage, oxidative stress, and/or telomere shortening. Quiescence is a reversible cell cycle arrest, which can result from nutrient deprivation, contact inhibition, or loss of adhesion. When environmental factors are changed to more favorable conditions, cells can be brought out of quiescence and begin proliferating. Unlike quiescent cells, however, senescent cells cannot re-enter the cell cycle. Cell cycle regulatory proteins, such as p16 upregulated in senescent cells, and Ki67, upregulated in proliferating cells, have important functional roles and can serve as markers of cell cycle states. Identification of proteins that can be used as markers of a cell's proliferative state may lead to a better understanding of these cellular phenomena. Many studies have identified proteins that are uniquely upregulated in senescence, whereas proteins uniquely expressed in quiescence are relatively underexplored. A previous study identified AT-Rich Interactive Domain-Containing Protein 5a (ARID5a), as a quiescence associated gene in an osteosarcoma cell line. ARID5a is involved in positively regulating the inflammatory response by stabilizing selective inflammation-related mRNAs. We seek to investigate whether this protein is also uniquely upregulated in quiescent primary human fibroblasts. We will apply qPCR, immunofluorescence, and immunohistochemistry to assess the levels of cell cycle proteins in proliferating, quiescent, and senescent human fibroblasts. Our results may provide insights into the unique molecular signatures of the different cell cycle states of primary human cells. (**191**)

Kafley, Prashila*, Aiden Reynolds*, Meghan Ziegler*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Optimizing organic waste treatment processes to facilitate the food, water, and energy nexus in prototype biological life support systems*.- This research investigates the optimization of coagulation and flocculation processes for treating Nile tilapia (*Oreochromis niloticus*) effluent from a recirculating aquaculture system (RAS) to enhance downstream waste valorization. It supports the National Aeronautics and Space Administration's (NASA) mission to develop bioregenerative life support systems (BLSS) for food production during long-duration space exploration. Aquaponic systems utilize the nutrients produced by RAS as a naturally derived fertilizer in hydroponic systems. They are a promising foundation for a BLSS because they facilitate the production of protein and vegetables within a closed-loop nutrient economy. The effectiveness of using ferric chloride ($FeCl_3$) and aluminum sulfate ($Al_2(SO_4)_3$) in coagulating suspended solids from RAS effluent into a nutrient-dense and highly organic thickened sludge was assessed. This is intended to serve as a novel pretreatment step to optimize sludge characteristics for anaerobic digestion (AD), facilitating nutrient recovery for plant fertilization and biogas production, while removing solids and organic matter from the clarified water prior to reverse osmosis to achieve drinking standards in alignment with NASA life support objectives. Treatment success was determined by supernatant clarity and the concentration of solids, organic material, nutrients in the sludge. Forthcoming results are dependent upon ongoing analysis of data. Full results, discussion, and conclusions will be determined and incorporated prior to the conference. By integrating experimental findings into bioregenerative system design, this study addresses the unique demands of space habitation while providing a framework for improved nutrient management and resource optimization within the terrestrial controlled environment agriculture industry. (**38**)

Kang, Genelia*, and Ajaipal Kang Gannon University, Erie, PA 16541. *Giant basal cell cancer: characteristics of a rare, deadlier skin cancer*.- Basal cell carcinoma (BCC) is the most common skin cancer worldwide. BCC rarely spreads to other tissues. However, a rare and poorly understood subset known as Giant Basal Cell Carcinoma (GBCC), defined as tumor size between 5 cm to 20 cm, has a higher likelihood of metastasis and mortality. Clinically, GBCC behaves differently than just “advanced” BCC. That is, if BCCs are allowed to grow unchecked, they do not all proceed to GBCC. To better understand characteristics of patients presenting with GBCC, we conducted a systematic review of all the relevant articles in the English literature from 1972 to 2024. We studied age (in years), tumor size (in cm2), general location of the tumor, and time to presentation (in years). Statistical analyses of the pooled data revealed that females were diagnosed at an older age than males (p=0.029). Patients with lesions on the extremities were older than to patients with head/neck and trunk lesions (p = 0.019 and p = 0.012); patients with extremities lesions had a larger area (marginally significant, p=0.056) compared to head and neck, while those with trunk lesions had a significantly larger area than head/neck (p=.002). Trunk location also had a longer time to presentation compared to head and neck (p=.030). This comprehensive review offers valuable insights into GBCC demographics and clinical patterns to help clinicians identify risk factors that inform targeted screening and lead to earlier diagnosis. Further studies are needed understand the cellular differences that lead to GBCC, as untreated BCCs do automatically proceed to GBCC. (**67**)

Kapushinski, Isabelle*, Lilia Wiest, Elizabeth Levin, Madison Sangrey, Brianna Livezey, Isaiah Bomboy, Ashley Marchessault, and Delana Spencer Susquehanna University, Selinsgrove, PA 17870. *Herbicide and surfactant effects on eggsac eclosion and spiderling survival in the wolf spider Tigrosa helluo*.- Different herbicides are often applied to crops in combination and with surfactant additives yet the toxicity of combining these agrochemicals has rarely been assessed among beneficial non-target species such as spiders. Surfactants increase absorption of herbicides through plant leaves but may also increase toxicity to spiders by enhancing penetration through eggsacs or the spider’s exoskeleton. We measured the separate and combined effects of the herbicides glufosinate ammonium and mesotrione with the organosilicone surfactant Sil-Fact®. We measured the interactive effects of these agrochemicals on eggsac eclosion and spiderling survival in the agrobiont wolf spider *Tigrosa helluo*. We applied water (control) or field doses of agrochemicals in all combinations to spider eggsacs (eight treatments) and measured eclosion for all eight treatments over a 50-day period. We conducted a dye test to measure absorption of herbicides and surfactants into the eggsacs across the eight treatments. We also measured spiderling mortality when maintained on freshly sprayed soil or 3-day aged residue of agrochemicals alone or in all combinations (32 treatments) with comparison between previous agrochemical eggsac exposure compared to water controls. We found no difference in eclosion frequency across agrochemical treatments. Agrochemicals significantly increased herbicide eggsac penetrance when combined with surfactant. Exposure to fresh or aged glufosinate increased mortality among spiderlings while only aged mesotrione residue significantly increased mortality. Sil-fact® alone did not significantly increase mortality but acted synergistically or antagonistically with some herbicide treatments. Spiderlings exposed to glufosinate and Sil-fact® in the eggsac showed lower mortality to secondary exposure than spiderlings that were not pre-treated with agrochemicals prior to eclosion. Results indicate that agrochemical combinations impacted survival and that glufosinate and mesotrione are both powerful araneocides. The timing, frequency, and combination of agrochemicals can dramatically impact spider reproduction and survival within integrated pest management systems and likely influence their effectiveness as biocontrols. (**168**)

Katona, Charles*, and Rebecca Urban Lebanon Valley College, Annville, PA 17003. *Using benthic macroinvertebrates to indirectly determine water quality*.- Pollution levels are a critical concern for watershed health, particularly in systems that provide sustainable drinking water to their surrounding communities. Freshwater benthic macroinvertebrates serve as bioindicators of stream water quality due to their varying pollution tolerances. The Quittapahilla Creek Watershed Association conducts annual assessments at six stream sites as part of a long-term monitoring protocol to evaluate the success of restoration efforts. Historically being considered unrecoverable, the watershed has shown notable improvements in water quality in recent years. This study examines macroinvertebrate composition from fall 2019 to fall 2023, utilizing the Shannon-Weiner Index (SWI), EPT Index, and Family Biotic Index (FBI) to quantify water quality trends across sites. We plan to use these metrics to assess improvements in the stream's health and the effectiveness of restoration initiatives conducted by the Watershed Association. (**160**)

Kemper, Heather*, and Elise Heiss King's College, Wilkes-Barre, PA 18711. *Development of a two-part electrochemistry experiment for analytical chemistry lab*.- The purpose of this research is to develop a new, two-part electrochemistry experiment for the King's College Analytical Chemistry Laboratory course to provide students with a better understanding of electrochemistry through hands-on experience. The first part of the experiment involves constructing a galvanic cell, which can then be used to determine the concentration of Fe2+ in an unknown solution. The second part of the experiment involves a redox titration as an alternate method to determine the concentration of Fe2+ in the same unknown solution. The focus of the research thus far has been on building the galvanic cell such that when concentrations of Fe2+ are varied in one half-cell, a calibration curve from the resulting cell voltages can be constructed. The galvanic cell was created using a constant concentration of acidified CuSO4 solution in one half cell, varying concentrations of an acidified solution of FeSO4 in the other half cell, a filter paper salt bridge to connect the half cells, and a multimeter to measure the cell voltage for each concentration. As the concentration of Fe2+ decreased within a range of 1.0M to 0.1M using 1.0M H2SO4 as the solvent, the cell voltage increased linearly as expected. (**32**)

Kersten, Elise*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Characterization of a chemical hypoxia model in developing zebrafish*.- Oligodendrocytes (OLs) are specialized cells of the central nervous system that produce myelin. Myelin is composed of tightly wrapped layers of plasma membrane around the axon of a neuron, providing insulation for rapid transduction of electrical signals. The process of myelination during development is coordinated by induction of signaling cascades, expression of transcription factors, various inhibitors, and myelin-specific proteins. This process is derailed when oligodendrocyte progenitors are damaged due to reduced blood flow to the brain in utero as seen in perinatal hypoxia-ischemia, leading to permanent myelin deficits in humans. Investigating mechanisms of OL damage, recovery and remyelination is the focus of this research. Limited remyelination occurs in humans, but regeneration is especially robust in zebrafish (*Danio rerio*). We have characterized a new method to induce hypoxia in developing zebrafish using a chemical oxygen scavenger, sodium sulfite. Zebrafish larvae (55 hours post fertilization) were divided in three groups: 1x E3 media, .2 mg/mL sodium sulfate in 1x E3 media, and .2 mg/mL sodium sulfite in 1x E3 media to analyze effects on developmental myelin production. Oxygen levels in the sodium sulfite decreased to an average .25 mg/mL but remained at approximately 10.5 mg/mL in the sodium sulfate control for the duration of the 1-hour hypoxia treatment. Fluoromyelin staining and analysis of myelin gene expression were used to examine the impact of hypoxia on myelin levels compared to the sodium sulfate control treatment. Ultimately, the chemical hypoxia model successfully created a hypoxic environment for the fish treated with sodium sulfite with which the myelin levels were analyzed. (**138**)

Kianersi, Hedyeh, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Chromosome segregation dynamics in meiosis I, meiosis II, and mitosis in the cells of milkweed bugs (Oncopeltus fasciatus)*.- Our aim in this study is to characterize mitosis, meiosis I, and meiosis II in the milkweed bug *Oncopeltus fasciatus*. Milkweed bugs have holocentric chromosomes in mitosis, but in meiosis, the chromosomes appear to designate a position on the chromosome to act as a monocentric kinetochore. While milkweed bugs have been studied for more than 100 years, this work is the first study of chromosome movements in living cells of the species. Meiosis I and II spermatocytes were isolated from adult males, while mitotically-dividing spermatogonia were isolated from juvenile males. For each cell we measured pole to pole distances and rates of chromosome movement through anaphase. The preliminary data show that rate of chromosome movement and spindle pole separation vary at different time points, and that chromosomes in mitotic anaphase move significantly faster than chromosomes in either meiotic division. (**186**)

Kiederling, Jessica*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *How do different DNA double strand break repair pathways contribute to resistance to chemotherapy?*- Double strand breaks (DSBs) are one of the most dangerous types of DNA damage, because they can completely block replication and transcription. Additionally, the broken ends can also lead to chromosomal fusions. Thus, the cell has four pathways for repairing such breaks. Multiple cancer therapies work by inducing DNA breaks in rapidly dividing cancer cells. Unfortunately, the effectiveness of these therapies can be reduced by the endogenous double strand break repair pathways present in the cancer cells. This study examines how different DSB repair mechanisms contribute to chemotherapy resistance by investigating how loss of specific repair pathways in the yeast *Saccharomyces cerevisiae* affects cell survival following treatment with carboplatin. We treated strains deficient in homologous recombination (HR) or nonhomologous end joining (NHEJ) with carboplatin for five hours, plated the cultures, and counted colonies. Carboplatin killed ~80% of WT cells, ~65% of cells lacking NHEJ, and ~50% of cells lacking HR. Interestingly, loss of DSB repair pathways seemed to lead to carboplatin resistance. This could be due to the compensatory effects of other DSB repair pathways or reduced cell cycle arrest and apoptosis. These findings provide insight into the interplay between repair pathways and suggest potential targets for enhancing chemotherapy efficacy in resistant cancers. (**126**)

Kitzhoffer, Ashlee*, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *Isolation and genetic characterization of antibiotic-producing bacteria from water samples*.- Antibiotic resistance is a growing global health crisis, underscoring the urgent need for new antibiotics derived from natural sources. Natural sources like the sedentary water, which my sample is sourced from, are ideal as they commonly have diverse microbes and have been previously shown to be environments where antibiotic producers can be identified. As part of the Tiny Earth mission, this study aims to identify, isolate, and genetically characterize waterborne bacteria with antibiotic-producing capabilities. Water samples were collected and plated on R2A media to encourage the growth of diverse bacterial colonies. Potential antibiotic producers were screened against *Escherichia coli* and *Staphylococcus saprophyticus*, and promising isolates underwent antibiotic extraction to facilitate further understanding of the antibiotic. This research contributes to the ongoing search for novel antimicrobial compounds to combat antibiotic-resistant pathogens. (**107**)

Klews, Cristoph*, Samantha Orosz*, and Emily Stowe Bucknell University, Lewisburg, PA 17837. *Minimal heterocyst formation distance and akinete density in a filamentous cyanobacteria isolate*.- Cyanobacteria are photosynthetic microorganisms that are of interest for their potential as a biofuel source but also in their role in diagnosing the environmental conditions of a given waterway. *Anabaena sp*. strain WFMT 1a is a filamentous cyanobacterium initially collected from a cut slope drain along Big Mountain Road near Whitefish, Montana. Many filamentous cyanobacteria, such as WFMT 1a, form specialized cells within a filament called heterocysts. The primary function of the heterocyst is to fix atmospheric nitrogen for the benefit of the whole filament. As other bioavailable nitrogen sources become scarce within an aquatic environment, heterocysts are formed at higher frequencies along a filament up to a minimal distance between heterocysts as determined by intracellular signaling and gene regulation. Thus identifying the density of heterocyst per filament can allow us to extrapolate the nitrogen status if a waterway. Filamentous cyanobacteria can also differentiate into a resilient, dormant, spore-like cell-type referred to as an akinete under environmentally unfavorable circumstances. To better characterize WFMT 1a, we grew cultures from this isolate in nitrogen replete or nitrogen free BG-11 media for five and seven days. We then compared the ratio of heterocysts to vegetative cells to akinetes and counted the minimal number of vegetative cells between heterocysts or the end of the filament (marked by smaller, young vegetative cells) to determine average filament length. This work allows us to begin to understand cellular differentiation in this organism which we can then couple to molecular analysis of gene expression. (**106**)

Kline, Vaughn*, Benjamin McNertney*, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Determining the partition coefficients of pigments*.- Butterfly Pea Flowers (BPF) contain a large amount of blue ternatins, which are polyacylated derivatives of delphinidin 3,3′,5′ -triglucoside and serve as a natural blue pigment within the plant. Currently, there are few stable natural blue pigments for use in food and other materials. To better understand the chemistry of the blue pigment, a partitioning coefficient was determined. Partition coefficients are a measure of the hydrophobicity associated with a molecule. This research aimed to investigate the partitioning of butterfly pea flower (BPF) pigments in comparison to another well known pigment crystal violet. The method involved measuring the absorbance spectra of different aqueous dilutions of BPF extract before and after partitioning with toluene. Dilutions of 1:20, 1:15, 1:10, 1:5, 1:4, and 1:2 were measured using UV-Vis spectroscopy to create a standard curve, and three solutions were left to partition over 24 hours. The results revealed that BPF blue pigment does not distribute well across an organic/aqueous interface and prefers to stay in the aqueous phase. The findings suggest that BPF extract is insoluble in organic solvents and a hydrophilic pigment. (**28**)

Kowalski, Sarah*, and Cosima Wiese Misericordia University, Dallas, PA 18612. *The inhibitory effects of duckweed on germination and growth of common weed species*.- Weeds are plants that are not desired in given environments. Weeds can affect the habitat as well as the growth of other plants for competition of space, sunlight, water, and important nutrients. To control these weeds, farmers have used herbicides to control or eliminate their growth. Herbicide resistance has increased over time and the weeds are able to survive these chemicals since they are being overused. Along with resistance, herbicides can be very harmful, with the potential of the toxic chemicals posing environmental risks. Allelopathy can be used as an alternative strategy for herbicides to reduce the use of toxic chemicals and still apply a natural approach. Duckweed has allelopathic properties and can be investigated to determine if they control the growth of weeds. The goal of this research project is to understand the inhibitory effects of two duckweed species, *Lemna minor* and *Spirodela polyrhiza*, on the growth of common weed species when grown with different concentrations of an aqueous methanol extract. The species of duckweed were grown and dried to collect plant tissue which was ground up and placed in methanol. Cress (*Lepidium sativum*) and red clover (*Trifolium pratense*) seeds were grown in petri dishes with varying concentrations of the duckweed extract, and germination rate and shoot growth were measured. Preliminary results reveal a difference in germination and shoot growth between control and duckweed extract for both cress and red clover. There is an inhibition of shoot growth observed as the concentrations of the *L. minor* and *S. polyrhizia* extract increase. (**39**)

Kritikson, Athena*, and Alismari Read Immaculata University, Immaculata, PA 19345. *Testing different surfactants to reduce dynamic surface tension in PSA*.- The Dow Chemical Company is a producer of pressure sensitive adhesives (PSAs). A key research focus is to make products more effective for customers. The goal of this research project is to test different surfactants in a commercial adhesive to see which surfactant is the most suitable for lowering dynamic surface tension (DST) without changing the PSA performance. A pressure sensitive adhesive (PSA) works when two surfaces are bound together upon application of pressure. When formulating PSAs, surfactants are added to decrease dynamic surface tension (DST), which enables customers to sandwich adhesives between two liners of different surface energies. This ensures the final adhesive film is smooth with no defects. To make the PSA in this project, an acrylic polymer backbone was formulated by adding surfactants of different chemistries. Then, these formulations were diluted to 36% solids for testing DST. Finally, PSA laminates were also prepared using undiluted samples. These laminates were used for PSA testing such as peel strength, loop tack, and shear resistance. The results showed that formulations including the newly added surfactants are better at reducing DST compared to surfactants regularly used in acrylic adhesives. Data for shear resistance shows that formulations with the new surfactants exhibit lower cohesion than the backbone alone as expected when adding surfactants to PSAs. They also provide similar or additional adhesion performance compared to the control. In conclusion, based on these results, the new surfactants show promising performance. (**27**)

Kuehner, Laura*, and Isis Rivera-Walsh Messiah University, Mechanicsburg, PA 17055. *Establishing a model system to study inflammatory signaling in human macrophages*.- Inflammation is a natural immune response in the body, but its long-term implications are often associated with disease. In the intestine specifically, Irritable Bowel Disease (IBD) results from the overexpression of inflammatory genes within gut tissue. Previous research has demonstrated that the microtubule-associated serine/threonine-protein kinase gene 3 (*MAST3*) is upregulated in patients with inflammatory bowel disease. MAST3 is a kinase found to be pro-inflammatory and to exacerbate symptoms in IBDs. Our goal is to elucidate the mechanism by which *MAST3* gene expression induces inflammatory signaling, specifically its role in activation of Nuclear Factor-kappa B (NF-kB) transcription factors. We hypothesize that the downregulation of *MAST3* expression will correlate with reduced NF-kB activity, thereby identifying *MAST3* as a therapeutic target for treatment of IBD. To investigate this, we utilized a human monocytic cell line (THP-1) with a well characterized NF-kB signaling pathway. We induced inflammatory signaling within these cells via treatment with bacterial lipopolysaccharide (LPS). A protocol and experimental design for LPS stimulation of differentiated THP-1 cells were determined, and an initial run-through of the entire procedure was completed. Preliminary data showed that the induced differentiation of THP-1 cells was present with the phorbol ester PMA at a concentration of 25 ng/ml. We investigated the effect of LPS stimulation of differentiated THP-1 cells on levels of the NF-kB inhibitor I-kappa B alpha (IκBα) as well as on levels of the MAST3 protein. Current data show that cytoplasmic protein extraction enabled loading and transfer of equal protein amounts before immunoblotting. Similar efforts are being conducted to look at *MAST3* mRNA levels after LPS stimulation of THP-1 cells. (**125**)

Kuhn, Nicholas*, and Diane Bridge Elizabethtown College, Elizabethtown, PA 17022. *Using genetically modified Hydra vulgaris to investigate the role of the inhibitory protein Axin in Wnt signaling*.- Wnt/β-catenin cell signaling plays important roles in embryonic development, homeostasis of normal adult tissues, and many types of cancer. Wnt/b-catenin signaling pathways are evolutionarily conserved, making the well-studied invertebrate *Hydra* an ideal, simple model to use in investigating Wnt signaling. Wnt causes its own production, creating a positive feedback loop. This project aims to determine whether Wnt production is limited within tissue by up-regulation of Axin expression by Wnt itself. Axin is an intracellular scaffolding protein which inhibits effects of Wnt. This study uses *Hydra vulgaris* that have been genetically modified to produce green fluorescent protein (GFP) when Axin is transcribed, so that time and location of Axin production can be detected using fluorescence microscopy. To test the hypothesis that Wnt causes Axin production in *Hydra vulgaris*, animals were bisected and allowed to regenerate a head. Regenerating head tissue produces Wnt mRNA. GFP upregulation was detected in regenerating head tissue by 33-37 hours after bisection, a result consistent with the hypothesis. To test the idea that transient production of Wnt is sufficient to cause Axin production, animals were bisected and allowed to regenerate a basal disk. Regenerating basal disk tissue only produces Wnt mRNA transiently within the first 6 hours post-bisection. GFP was not detectable in regenerating basal disk tissue, indicating that transient Wnt production did not cause Axin production. Experiments in progress include treatment with alsteraullone, which mimics Wnt, as well as exposing *Hydra* body column cells to cells that secrete Wnt to determine whether this induces Axin production. (**35**)

Larick, Connor*, Alyson Cooper, Marina Evert, and Amy Parente Mercyhurst University, Erie, PA 16546. *Investigating the role of phosphorylation in malate dehydrogenase activity and metabolon formation*.- The citric acid cycle is important for breakdown of carbohydrates, proteins, and lipids into CO2, NADH, and FADH2 which are turned into usable energy for the cell. Malate dehydrogenase (MDH) is a key enzyme in the citric acid cycle. There are two isoforms of MDH, mitochondrial MDH (mMDH) and cytosolic MDH (cMDH). These isoforms are responsible for the interconversion of malate and NAD+ to oxaloacetate (OAA) and NADH. Post-translational modifications, such as phosphorylation, can impact the activity and metabolon formation of MDH, which is the focus of this research. Phosphorylation is the result of kinase enzymes targeting hydroxyl residues on amino acids to add a phosphate group. This study utilizes a fusion protein of MDH and green fluorescent protein (GFP), which also contains an C-terminal Histidine tag (a.k.a. MGH). MGH is a model system to master methods of protein overexpression, purification and characterization, as the GFP domain allows for easy tracking of the protein. In addition, the MDH catalytic domain retains enzymatic activity, allowing for easy mastery of enzyme assay techniques. Transformation of MGH plasmid to BL21(DE3) *E. coli* allows for overexpression at 22°C by addition of IPTG. Lysis of cells followed by FPLC purification using a Ni-NTA affinity column generated significant quantities of high-purity protein as determined by Bradford assay and SDS-PAGE. Enzyme assays are performed under varying pH and temperature conditions as well as in the presence of various allosteric modulators including glutamate, glutamine, and citrate. A future goal for this project is to generate phosphomimic mutants of MDH which may have altered enzyme activity and/or ability to form metabolons with neighboring proteins. This is accomplished by substituting key serine (S), threonine (T), or tyrosine (Y) residues with aspartic acid (D) or glutamic acid (E), mimicking the negative charge and size of a phosphate group. (**120**)

Lass, Melissa*, Amanda Pratt*, Robert Kurt, Chun Wai Liew, and Molly Dormer Lafayette College, Easton, PA 18042. *Optimizing anti-tumor RNA longevity in murine bone marrow-derived macrophages and validating the role of NFkB in the anti-tumor response*.- Here, we explored methods to generate a long-lasting and strong anti-tumor immune response using murine bone marrow-derived macrophages (BMDM). For this purpose, BMDM were treated with single (flagellin), dual (flagellin and LPS), and triple (flagellin, LPS, and R848) toll-like receptor (TLR) agonists and the strength and length of the immune response was studied. Actinomycin-D, which shuts down RNA production, was used to determine how long the RNA lasted using qPCR at 0, 1, and 8 hour time points. Utilizing more than one agonist generally resulted in RNA staying around longer. We found that RNA encoding il-1b, il-6, il12, il18, ccl5, cxcl9, and cxcl10 lasted longer after dual and/or triple treatments than single agonist treatments. IL-1b and IL-6 represent inflammatory cytokines important for starting an immune response. CXCL5, CXCL9 and CXCL10 are important for recruiting CD8+ T cells and NK cells, while IL-12 and IL-18 are essential for activating them. These results are being used to improve our computational model which considers the TLR4, TLR5 and TLR7 interconnected signaling cascades. To validate the model and verify the importance of NFkB in producing an anti-tumor immune response, we used GeneXplain to locate NFkB binding sites in the gene promoters relative to other transcription factors (STAT, IRF, GATA, HIF1, NFAT). The results showed that the most common transcriptional factor binding site was for NFkB followed by NFAT and IRF, suggesting that these transcriptional factors are important for expressing our panel of genes. Future studies can use this information to investigate regulation of anti-tumor immune responses. For instance, why cxcl11 had significantly more gene expression than the other cytokines despite the lack of relevant transcription factor binding sites on the cxcl11 promoter. (**115**)

LeBaron, Mikaela*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Effects of temperature, pH, and allosteric regulators on the enzymatic activity of S8D mutant of malate dehydrogenase compared to wild-type*.- Metabolism is essential for energy production in organisms, with the citric acid cycle (TCA) playing a key role in carbohydrate oxidation. Malate dehydrogenase (MDH), present in cytosolic (MDH1) and mitochondrial (MDH2) isoforms, is crucial in this process. MDH plays a role in cancer, as cancer cells rely on glycolysis even with oxygen present. Studies show that MDH1 supports glycolysis in proliferating cells, and its deletion slows cancer cell proliferation, suggesting MDH1 as a potential therapeutic target in cancer treatment. Knowing how different mutations affect the enzymatic activity of MDH could target the citric acid cycle in cancer cells to slow tumor growth. Mutants are created by a process of site-directed mutagenesis, which substitutes a different amino acid with one that was already there. The mutation S8D has an aspartic acid (D) substituted for the serine (S) that was at position 8. After overexpression of mutant S8D protein, purification using FPLC, with characterization by Bradford assay and SDS-PAGE, enzyme assays were used to see the effect of this mutation on enzymatic activity. The S8D mutation introduces a negative charge while maintaining approximate residue size, mimicking what would occur during in vivo phosphorylation of this residue by a native kinase. This mutation has the potential to alter protein structure, which could lead to a change in the enzyme's response to allosteric regulators. Overexpression of the S8D mutant has been particularly challenging. We are testing various overexpression methods to optimize the preparation of this mutant. Once suitable concentrations of protein are obtained for study, we will investigate how temperature, pH, and the presence of various allosteric regulators affect the activity of S8D compared to wild-type. (**2**)

Lippitt, Kade*, Caroline Maciejewski, Jonathan Katzenmoyer, Emily Ringholm, and Alex Huynh DeSales University, Center Valley, PA 18034. *Using Google Trends to improve monitoring of the invasive spotted lanternfly in the United States*.- Invasive species pose significant threats to ecosystems and human industry and are being rapidly exacerbated by increased globalization and climate change. Effective monitoring of invasive species is crucial for control and eradication efforts, but traditional methods can be costly and resource-intensive. This study explores the use of Google Trends, a tool that quantifies internet searches made on the Google search engine, to monitor the spread of the spotted lanternfly

(*Lycorma delicatula*), a recent invasive insect in the United States. We analyzed Google search data from 2014 to 2022 and compared it to official occurrence data pooled from a variety of government and citizen science-based sources. Our results show a significant relationship between the number of Google searches and the presence of the spotted lanternfly. Yearly patterns in Google search data align with observed population sizes and seasonal patterns with the emergence of mature adult spotted lanternflies. Our results indicate that Google Trends may be particularly useful in complementing traditional monitoring methods. This approach could enhance future monitoring of the spotted lanternfly and possibly other invasive species to better inform conservation efforts. (**143**)

Longwell, Daniel* Methacton High School, Eagleville, PA 19403. *The power of sound: the effect of pitch on power usage*.- In this project, research is performed on the power output of an electronic speaker system for different sound frequencies. An alternating current signal generator was used in a circuit to vary the frequency supplied to a 4-ohm computer speaker. The power output of the speaker was measured at frequencies between 100 and 523 Hz. A conclusion is drawn about the degree to which frequency impacts the power used by the speaker. As the frequency increases there is an increase in the amount of power required to produce that sound. (**13**)

Lugo, Adrian*, Amber Marble, and Deborah Austin Wilson College, Chambersburg, PA 17201. *The effects of serotonin transporter gene variations on major depressive disorder treatment and anxiety*.- The serotonin transporter gene (SLC6A4) has been found to play a role in the development of mental disorders such as major depressive disorder. Previous research suggests that variations in the serotonin transporter-linked polymorphic region (5-HTTLPR) may influence susceptibility to these disorders, but evidence remains inconclusive, especially regarding response to medications. This study investigated the relationship between genotypes in the 5-HTTLPR region of the serotonin transporter gene and the prevalence of depression and anxiety disorders, as well as the effectiveness of medications. It was hypothesized that individuals with the homozygous long allele (L/L) genotype would show a better response to selective serotonin reuptake inhibitors (SSRIs) and lower levels of anxiety and depression. Volunteers completed a survey and provided DNA samples, which were analyzed to determine their 5-HTTLPR genotypes. The results revealed a majority of individuals had the heterozygous (S/L) genotype, with the homozygous long (L/L) genotype observed in 9.1% of individuals. Interestingly, those with the L/L genotype reported both higher levels of depression and a significant presence of anxiety, challenging previous findings that suggested the L/L genotype provided protective effects. Multivariate analysis of variance showed no significant differences in depression and anxiety scores across genotype groups. These findings underscore the complexity of the relationship between genetic factors and mental health outcomes and highlight the need for further research. Future studies should involve larger, diverse populations, include additional genetic variants, and investigate the mechanisms by which serotonin transporter gene variations affect mood regulation and treatment efficacy. (**134**)

Maamari, Jessica*, Lauren Heiland, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *Antimicrobial potential of bacterial isolates from Ficus carica leaves*.- Antibiotic resistance has been an ongoing threat to world health for many years. The search for new antimicrobial agents, particularly from natural sources like plants, is becoming popular among researchers because of their value in traditional medicine. This study aimed to investigate the antimicrobial potential of bacterial isolates from *Ficus carica* (Brown Turkey fig) leaves by screening for silent antibiotic producers under two different laboratory conditions. A total of 36 bacterial isolates were obtained, with 11% exhibiting antimicrobial activity against *Staphylococcus saprophyticus*. All active isolates were obtained from starch agar, suggesting that different types of media may trigger the production of secondary metabolites. Isolate LHJM3 was chosen for further characterization using a series of bacterial identification assays, yielding mixed results. A negative result on MacConkey agar, indicating possible Gram-positive identification, while the Gram stain showed pink staining typical of Gram-negative bacteria. Secondary metabolite extraction from isolate LHJM3 on starch agar produced a 1.1 cm zone of inhibition against *S. saprophyticus*, confirming its moderate antimicrobial potential. These findings support the hypothesis that antibiotic biosynthesis can be triggered by varying conditions. Further research is needed to clarify the bacterial characteristics and suggested antimicrobial activity of bacterial isolates from *Ficus carica* (Brown Turkey fig). Natural products have been shown to have many clinical applications. It is essential to investigate natural products in order to increase the probability of finding novel antibiotics and combating the issue of antibiotic resistance. (**102**)

Maciejewski, Caroline*, Kade Lippitt, Jonathan Katzenmoyer, Emily Ringholm, and Alex Huynh DeSales University, Center Valley, PA 18034. *Using Google Trends to improve monitoring of the invasive spotted lanternfly in the United States*.- Google Trends allows users to collect data on keyword searches made in the Google search engine and has been used as a predictive tool in forecasting sociological and biological phenomena, including the spread of infectious diseases. However, no studies have used this tool for predicting the spread of invasive species. The spotted lanternfly (*Lycorma delicatula*) was first introduced to the United States in September 2014. The origin of this invasion stemmed from a single introduction event from South Korea to Berks County, Pennsylvania (Du et al. 2020). This species has caused profound ecological and economic damage since its arrival in the United States. This pest damages native trees and disrupts local industry, particularly in vineyards, which are nationally valued at $6 billion annually. This pest notoriously feeds on grape vines, causing damage and decreasing yield (Leach & Leach, 2020). Additionally, spotted lanternflies produce honeydew as a waste product, which can promote the growth of sooty mold or attract other insect species, causing further damage to host plants (Urban & Leach, 2021). As such, the population spread of the spotted lanternfly has been closely tracked in the wild (De Bona et al. 2023). In general, monitoring efforts of invasive species can be time-consuming and costly. We sought to determine if Google Trends can be used as a cheap and effective method for tracking the spread of the spotted lanternfly based on where/when it is Googled. (**161**)

Maldonado, Vincent*, and Emily Basile Delaware Valley University, Doylestown, PA 18901. *Meiofauna community composition and vertical zonation in intertidal mudflats, Chincoteague Bay, Virginia*.- The meiobenthos are an abundant and diverse biota found in ocean and littoral sediments that is often overlooked due to its niche following when compared to other branches of ecology, its novelty as an area of study, and the overall esoteric nature in meiofaunal organisms and research on them. But meiofauna are vital to larger ecosystems and take up a unique role as accessible bioindicators of their environment. Meiofauna was systematically collected from sites in Chincoteague Bay, Virginia, and analyzed using R for abundance and diversity between sites, as well as for meiofaunal distribution between the most oxygenated and least oxygenated horizons. Analysis of samples identified 20 different taxa in varying quantities across sites, with Nematoda being the most abundant animal across all sites. Animal count proportions between sediment layers suggest meiofauna greatly prefer the uppermost oxygenated layers of sediment over the deeper anoxic layers, with over 70% of all animals counted being found in the oxygenated layers, and all taxa identified being partially if not entirely found within the oxygenated layers. Animal density per cm^3 of sediment was found to vary between sites, but also between sediment layers. Average animal density in samples across all sites was found to be about four times denser in the oxygenated layers than in the anoxic layers. Shannon-Weaver Indices of diversity also found low diversity and evenness across all sites but found comparably more diversity and evenness in the oxygenated layers over anoxic layers. The reasons for the specific patterns of distribution found here could be related to microhabitat distribution between sites, the natural temporal variations in meiofauna composition throughout the year, but also could be due to higher heavy metal content and lower pH than average, human disturbances of the area, or possibly due to other factors not measured in this study. (**148**)

Maley, Mackenzie*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Thyme (Thymus vulgaris) to thrive: exploring the most effective controlled environment agriculture (CEA) system for sustainable growth*.- Thyme (*Thymus vulgaris*) is a versatile herb used for teas, cooking, essential oils, holistic medicines, and many other purposes. In 2023, 2.94 billion dollars' worth of thyme was imported to the United States from China. Domestic agriculture is limited by a growing population of 335-340 million people by 2025 and decreasing arable land by 33 percent in the past 40 years. Controlled environment agriculture (CEA) can address these limitations through location-independent and season-independent growth of diverse crops, including herbs. Hydroponics, soilless plant production using synthetic fertilizers, and aquaponics, where dissolved nutrients from fish culture are used as a natural fertilizer, are two prominent CEA methods. This research explored the most effective methods for cultivating thyme, integrating considerations for economic viability, rate of production, and carbon emissions. It was hypothesized that thyme would grow more efficiently in an aquaponics system compared to hydroponics and hybrid systems, as measured by wet and dry weight. Three independent nutrient film technique systems were used for thyme cultivation. One system was a hydroponic control, operated under the standard procedure for growing thyme. The second system was an aquaponics system. The third system was a hybrid system, with a base of an aquaponics system and supplemented with nutrients to meet the same electrical conductivity as the control hydroponic system. Trial 1 yielded statistically lower wet (0.26g) and dry (0.045g) weights, respectively, in aquaponics compared to hybrid (1.18g and 0.207g) and hydroponics (1.55g and 0.220g). Trials are ongoing and additional statistical analysis will be completed. This study will advance knowledge of thyme growing requirements or new ways of understanding by informing readers of what exactly aquaponics and hydroponics are and how they differ. (**159**)

Marchiori, Jared*, and Quyen Aoh Gannon University, Erie, PA 16541. *Secretory carrier membrane protein 3's (SCAMP3) role in amyloid precursor protein trafficking*.- According to the Journal of the Alzheimer's Association (2024), approximately seven million individuals in America are living with Alzheimer's Disease (AD), and this is projected to grow to 13.8 million Americans by 2060. AD is a neurodegenerative disease resulting in nerve damage that ultimately leads to cognitive decline as the disease progresses. A pathogenic characteristic of AD is associated with an abnormal accumulation of B-amyloid plaques in the extracellular matrix of the brain. B-amyloid is produced from the amyloid precursor protein (APP) when cleaved by beta secretase (BACE) and its production is associated with its trafficking within the TGN-endolysosomal system. We have determined that the Secretory Carrier Membrane Protein (SCAMP) 3 colocalizes with APP and BACE in the trans-Golgi Network (TGN). SCAMP3 has also been shown to interact with the endosomal sorting complexes required for transport (ESCRT) proteins Hrs and Tsg101, both of which have been implicated in APP trafficking and B-amyloid production. In this study we will use immunofluorescence to test the effect of a SCAMP3 knockdown on APP trafficking within the TGN-endosomal system. (**63**)

Maslin, Valoria*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Chromosome number and segregation behavior in the green lacewing Chrysoperla rufilabris*.- All previously studied species of the insect order Neuroptera display a phenomenon called distance segregation during male meiosis I, in which the X and Y chromosomes move apart from one another in anaphase I without being previously connected in metaphase I. This study investigates chromosome number, spatial arrangement, and patterns of segregation of a previously unstudied Neuropteran insect: the green lacewing, *Chrysoperla rufilabris*. To collect comprehensive chromosomal information, testes of male *C. rufilabris* were collected, fixed, and then prepared following a chromosome squash method. The data from squash experiments revealed a chromosome number of 2n=22 with XX-XY sex determination and evidence of distance segregation of X and Y chromosomes in meiosis I spermatocytes. Further analysis of chromosome movements in living cells and spindle structure using immunofluorescence will reveal more of the mechanistic details of distance segregation in green lacewings. (**185**)

McHenry, Emily*, and Robert Mishur Widener University, Chester, PA 19013. *Evaluating the cytotoxicity of novel phosphaplatins in breast cancer cells*.- Cisplatin has been a cornerstone in chemotherapy for various cancers, significantly improving cure rates, notably for testicular cancer. However, its use is often limited by severe side effects such as nausea, vomiting, hair loss, hearing loss, and kidney toxicity, along with the development of resistance in certain tumors. Consequently, there is a pressing need for alternative platinum-based drugs that are less toxic and can overcome resistance. Phosphaplatins represent an emerging class of platinum drugs with promising antitumor activity and potentially novel mechanisms of action. This study aims to evaluate the cytotoxicity of two newly developed phosphaplatins, dicyclobutylaminepyrophosphatoplatinum(II) and dicyclopentylaminepyrophosphatoplatinum(II) against a metastatic breast cancer-derived cell line, MDA-MB-231. Cytotoxicity was assessed using an MTT assay by exposing the cells to varying concentrations of either cisplatin or a phosphaplatin and measuring cell viability compared to untreated controls. Preliminary results indicated that our compounds induced a dose-dependent decrease in cell viability at high concentrations. As we continue to develop new phosphaplatins and evaluate their effectiveness, the findings will contribute to the understanding of the potential of phosphaplatins as effective chemotherapeutic agents for breast cancer, as well as other cancers. Further studies are necessary to elucidate the detailed mechanisms of action and optimize the therapeutic potential of this class of compounds. Ultimately, this research aims to contribute to the development of novel, less toxic platinum-based therapies that can significantly improve outcomes for patients with breast cancer and other malignancies. (**108**)

McKeague, Sean*, and Issac VonRue King's College, Wilkes-Barre, PA 18711. *Controlling the glass transition temperature of shape memory polymers for biomedical applications*.- The purpose of the research project was to determine what controls the glass transition temperatures of biodegradable shape memory polymers (SMPs). Biodegradable SMPs were synthesized using varying mass ratios of polyvinyl alcohol and cornstarch crosslinked with hexamethylenediamine. The samples were tested using a differential scanning calorimeter to determine the glass transition temperature. The preliminary results showed that there was a correlation between high PVA content and decreased glass transition temperatures. The results also indicated the presence of water in the samples can significantly decrease the glass transition temperature. (**29**)

McNertney, Benjamin*, Yiben Wang, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The quantification and analysis of microplastics in Central Pennsylvania springs*.- The ever-growing use of plastic worldwide has led to plastic pollution in unwanted locations such as lakes, rivers, streams, oceans, and more. These waste plastics in the environment break down into smaller materials over time called microplastics, which are characterized as plastic particles less than 5 mm in size. The quantity of microplastics have been found in numerous bodies of water worldwide but have not been studied extensively in natural springs, with no known studies occurring in the United States. In this study, FTIR spectroscopy and fluorescence microscopy were used to identify microplastics at three Central Pennsylvania natural springs which differ with respect to surrounding development: the Artesian Spring (urban), The Bubble (suburban), and the Laurel Forge Pond Spring (rural). A stainless-steel mesh filter stack combined with a 1.1 mm glass fiber filter was used to filter water from each location for microplastics. The particulates collected were analyzed and the findings suggested that microplastics were present in all three central Pennsylvania natural springs. (**83**)

Miller, Rebecca*, Albert Sarvis, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *A GIS analysis of the impacts of climate change on distribution and biodiversity of elasmobranch species*.- Shark and ray populations have declined by 71% since 1970 due to human activities, including climate change, habitat destruction, and overfishing, which pose significant threats to marine biodiversity. As key regulators of ocean ecosystems, elasmobranch species play crucial roles in maintaining ecological balance. However, rising ocean temperatures and acidification are altering their distribution, behavior, and physiology. This study analyzes a decade-long dataset (2015-2024) from the Coastal Marine Education and Research Academy (CMERA) to assess the correlation between rising water (or air) temperatures and the distribution of elasmobranch species in the Gulf of Mexico. Rising ocean temperatures can force species to migrate to cooler waters, disrupting predator-prey relationships and habitat stability. ArcGIS Pro will be used to visually represent and analyze changing temperatures and elasmobranch population shifts in distribution. By employing statistical analyses and correlation analyses, this research looks to determine the extent to which temperature fluctuations and other environmental factors influence species presence and movement patterns. Preliminary results suggest distribution changes including a Northward shift in the shark species and a Southward shift in the ray species, indicating that warmer waters are driving migration patterns. This shift raises concerns about long-term ecosystem disruptions and competition for resources. Findings from this study will contribute to addressing knowledge gaps in elasmobranch distribution and support conservation efforts through improved monitoring and policy recommendations. Understanding these temperature-related and other environmental cue shifts is essential for developing adaptive conservation strategies and protecting marine biodiversity in the face of climate change. (**156**)

Milligan, Scott*, Sara Ashcraft, and Matt Wilson Susquehanna University, Selinsgrove, PA 17870. *Fishing out invasives: how are native tessellated darters reacting to the presence or absence of invasive banded darters?*- Invasive species have caused multiple large scale ecological issues, including the extinction of many species. These invasive organisms directly affect native species by ways of outcompeting them or forcing them outside of their ecological niche. Understanding these relationships can be key in attempting to slow the spread of invasive species. In the Susquehanna River Basin, native tessellated darters, *Etheostoma olmstedi*, and invasive banded darters, *Etheostome zonale*, have similar substrate preferences and they both tend to prefer larger substrate. It is believed that banded darters entered the Susquehanna River Basin in the late 1960s from the Ohio River Basin via a bait bucket transfer and since then have become the most abundant darter species in this basin (Gray and Stauffer, 2001). Banded darters are more aggressive than their tessellated counterparts, so are likely affecting their behavior. To investigate this, I used a mock stream channel system at Susquehanna University's Freshwater Research Institute. This system has three independent 10 ft. x 2 ft x 2 ft. channels that are each split into three sections. Each section contained two fish in three pair combinations: tessellated and tessellated, banded and banded, and tessellated and banded, and had four substrate sizes available, from gravel to large cobble, with preference of substrate size observed over a two hour trial. Preference is determined by the amount of time spent in each substrate. Number of interactions between the two fish were also observed. I hypothesize that both tessellated and banded darters both prefer the larger substrate sizes when the species are independent, however when placed together the aggressive behavior of the banded darters will force the tessellated darters away from the substrate that they prefer and to the smaller substrate sizes. (**154**)

Molineros, Isabel*, Danielle Bowman, Emily Brophy, Matthew Izuka, Ameer Awawda*, and Carla Garzon Delaware Valley University, Doylestown, PA 18901. *A study of fungal pathogens of hemp in Bucks County PA*.- Since hemp legalization in 2018, Pennsylvania has had continued production of hemp varieties for grain, fiber, and flower cannabinoid production. Plant health is fundamental for obtaining high quality products, including grain for food, animal feed and oil production, fiber for textiles and construction, and flower for cannabinoid and terpene production. Fungal diseases compromise the quality of these materials by degrading their nutritional and nutritional value, as well as by the integrity and strength of fibers. To identify the most common fungal pathogens of hemp present in Bucks County, annual collections were conducted at the Delaware Valley University campus and nearby farms for three years. Leaves displaying symptoms, such as necrotic spots or yellowing, were collected and brought to the laboratory for examination. Small leaf pieces (approx.1 cm2) cut from the margins of the lesions were surface sterilized and placed on water agar. Hyphal tips were transferred to potato dextrose agar after one to three days and incubated for 5 to 10 days to induce spore production. Pure cultures were examined for tentative morphological identification and then transferred to PDB. After 3 to 5 days of incubation at room temperature, mycelia were collected by filtration and processed for DNA purification using the CTAB protocol. Sequences of the ITS region and the RPB2 gene were obtained and used for molecular identification by comparing them against the NCBI Nucleotide Database using BLAST. Among the most frequently fungal species identified were the known hemp pathogens *Alternaria spp.*, *Nigrospora sp.*, and *Epicoccum sp.* Sequencing additional genetic barcodes is in progress for accurate identification of these pathogens. Additionally, *Epicoccum* isolates were inoculated on diverse herbs to identify potential alternative hosts of this fungus. (**167**)

Morgan, Nyicia*, and Yiben Wang Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Exploring the effect of a combined cannabidiol and chlorhexidine treatment against the Streptococcus mutans*.- According to the World Health Organization (WHO), dental caries impacts 60-90% of children and most adults (Pitts et al., 2017). Conventional oral hygiene products - like toothpaste and mouthwash - typically contain antimicrobial agents such as triclosan and chlorhexidine (CHG) to prevent and treat caries, though their effectiveness can be affected by factors including diet and medication. Recently, cannabidiol (CBD), a compound used both recreationally and for pain management, has been shown to lower both the metabolic activity and biomass of the oral *S. mutans* biofilms when used in conjunction with triclosan (Avraham et al., 2023). In this study, we evaluate the combined effect of CHG and CBD on *S. mutans* biofilms using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assay to measure metabolic activity and crystal violet staining to assess biofilm biomass. Our findings indicate that at lower concentrations (1.25 μg/mL), the CHG/CBD blend decreases metabolic activity by 42.8% ($p<0.001$) and biofilm biomass by 44% ($p<0.001$), while higher concentrations (5.00 μg/mL) achieve reductions of 66.6% in metabolic activity and 99.5% in biofilm biomass. This synergistic treatment strategy shows considerable promise for improving oral care products by offering a natural, effective alternative to traditional antiseptics for preventing biofilm formation and bacterial growth. (**77**)

Morrow, Torianne*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Phosphomimic mutations of malate dehydrogenase: investigating the impact of post-translational modifications on enzyme activity and metabolon formation*.- Metabolism is the process of converting food into energy (ATP). An important pathway in this process is the citric acid cycle. Complexes of sequential enzymes called metabolons can increase the efficiency of a pathway. These enzymes benefit from non-covalent association that can shuttle metabolites between active sites. Malate dehydrogenase (MDH) is a citric acid cycle enzyme that is known to form metabolons with a variety of other enzymes. Adding to this diversity is the fact that MDH is found as both cytosolic and mitochondrial isoforms. The enzymatic activity of MDH can be altered with post-translational modifications like phosphorylation, which is the focus of this work. Mutant enzymes called phosphomimics are prepared by replacing a serine (S), threonine (T), or tyrosine (Y) residue in the wild-type (WT) cytosolic MDH with a glutamic acid (E) or aspartic acid (D) residue to mimic the size and negative charge that would have been created by phosphorylation at a single site. This strategy is essential, since it is not possible to accomplish this site-specific phosphorylation through other methods, such as through the use of kinase enzymes. The mutant examined in this study is S45D. Mutant proteins are overexpressed in *E. coli*, the cells lysed by sonication, and protein purified using fast-protein liquid chromatography (FPLC) that uses an affinity column to easily separate our proteins which contain a C-terminal histidine tag. The purified fractions are then quantified by Bradford assay and SDS-PAGE was used to determine purity. In this study we will be testing the effects of temperature, pH, and the inclusion of allosteric regulators on the activity of the mutant enzyme as compared to both WT and other mutants that are studied in the lab. This could have implications for cancer biology since dysregulated metabolism can alter cellular pH which could impact the ability of MDH to properly function. (**1**)

Moyer, Michaella*, and Tammy Tintjer King's College, Wilkes-Barre, PA 18711. *Comparison of isolation techniques for Epichloë endophyte*.- *Festuca arundinacea* seeds were used to isolate *Epichloë* samples in order to artificially inoculate grass seedlings. An initial attempt using an established protocol only resulted in one isolation of the fungal endophyte. It was suspected that the sterilization process was too harsh which possibly killed the fungal endophyte. This led to a literature search for additional seed sterilization procedures. Another procedure conducted on *Phragmites australis* seeds was found and parts of that procedure were used and compared to the previous technique. In a second attempt *Festuca arundinacea* seeds were sterilized with the two different techniques. The first technique used a Clorox® solution as well as the second technique, but in addition to the Clorox® a 90% ethanol rinse was added. The seeds were plated and incubated at 25°C for six weeks and during this period the number of contaminates as well as fungal growth was documented. The first technique had a 5.5% contamination rate while the second technique had an 11.1% contamination rate. The first technique produced no endophyte isolates while the second technique produced three possible isolates. This isolate confirmation is unclear at this stage due to the slow growth period of the endophyte. When comparing techniques, the second method had twice the contamination rate of the first method but produced a higher rate of possible endophyte growth. (**165**)

Muhl, Courtney*, Maral Ganzorig*, and Cecilia Bove York College of Pennsylvania, York, PA 17405. *Identification of a putative pathophysiological mechanism for dysregulated gastrointestinal transit in fluoroquinolones-associated disability*.- Fluoroquinolone (FQ) antibiotics have been shown to have potentially lifelong adverse effects in various ways, yet continue to be prescribed despite the proposed existence of Fluoroquinolone-associated Disability. In addition to their antimicrobial capabilities, FQs act on off-targets in the human body, including the Central Nervous System. Here, FQs have been shown to inhibit GABAA receptors while enhancing glutamate activity by acting as NMDA receptor agonists. These are critical neurotransmitters of the vagus nerve, the main nerve of the parasympathetic nervous system, which innervates the gastrointestinal tract (GI), playing a role in digestion and mood. The hormone cholecystokinin (CCK) controls gastric emptying by acting on vasovagal reflexes, and elevated levels of CCK were associated with dyspepsia and panic disorders. Previous data from our laboratory demonstrated that 14 daily doses of ciprofloxacin (CPX), a commonly prescribed FQ, permanently accelerated gastrointestinal transit together with an increase in anxiety-like behavior in rats. The goal of this study is to evaluate whether the CPX-mediated dysregulation of GI and mood are caused by altered CCK plasma levels in rats. To test our hypotheses, ~30 days old Sprague Dawley rats received oral administration of 20 mg/kg CPX daily for 14 days. Before the treatment, baseline levels of CCK were established by sampling venous blood from the lateral tail vein; this procedure was repeated once a week for 4 consecutive weeks to match the timeline of anxiety-like behavior and GI transit. Plasma concentrations of CCK will be quantified using an ELISA kit. Given the physiological role of CCK, we expect to find elevated levels of CCK following the treatment. Understanding the involvement of this hormone in the gastrointestinal symptoms that accompany FQAD may allow us to characterize a pathophysiological mechanism of this disorder and potentially propose a non-invasive, pharmacological intervention to ameliorate these symptoms in patients. (**127**)

Murray, Mackenzie*, and Luis Cabo-Perez Mercyhurst University, Erie, PA 16546. *Analyzing the sources of variation that influence biological sex and population affinity estimations when using postcranial skeletal measurements in Fordisc 3.1*.- Being able to accurately estimate components of a biological profile, which include sex, age, stature, and ancestry, is vital for the positive identification of unidentified skeletal remains. Multiple methods for estimating these elements exist, ranging from non-metric methods for sex estimation with the pelvic and cranium to metric methods for stature utilizing the entire skeleton. This project looks at the use of metric methods on postcranial skeletal remains for the purpose of sex and ancestry estimation. One of the most complete analytical programs with comparative datasets is *Fordisc* 3.1, which allows users to estimate conditional probabilities of group classification for sex and populational labels through stepwise Discriminant Function Analysis (DFA). However, the database limits its application to a small subset of standard analyses, which results in a black box model in which it is possible to infer approximate individual variable weights and precise output accuracy rates, but not which specific components are more influential in the final classification. This study aims to identify the sources of variation that are most influential for the estimation of biological sex and population affinity. A dataset consisting of 15 postcranial skeletal measurements from over 200 individuals under “Black” and “White” population labels were utilized. Principle Component Analysis was performed to identify the main sources of variation in terms of size and different components of size-free shape. The same dataset was then introduced and analyzed in *Fordisc* 3.1, to estimate the correlations between the *Fordisc*-generated discriminant functions and the principal components, in order to infer the main morphological basis of the DFA classifications. Our results suggest that *Fordisc* 3.1 postcranial analyses can be useful for sex classification based primarily on body size, and maybe for populational comparisons of sexual size dimorphism, but less so for estimates of sample affinity or populational distances. (**86**)

Naugle, Grace*, and Cosima Wiese Misericordia University, Dallas, PA 18612. *Effects of commonly found microplastics on terrestrial plant growth and reproduction*.- Plastic pollution is extremely abundant in both terrestrial and aquatic environments. Common plastic sources include grocery bags, water bottles, packaging, and clothing. In addition, plastics are an important component in the agricultural industry, and are commonly used in irrigation systems, row covers, greenhouses, and mulch. As plastics degrade over time, they break down into smaller pieces called microplastics. However, there is little known about how these plastics may affect crops, especially as they break down over time and pollute the soil. In aquatic environments, microplastics can reduce plant and algae growth and reproduction. In terrestrial environments, microplastics can alter soil structures and composition of soil microorganism communities, and in some cases, can be absorbed by terrestrial plants.

However, the general effects of microplastics on terrestrial plant growth and reproduction are not well understood. This experiment seeks to investigate the effects of commonly found microplastics, including some biodegradable plastics, on terrestrial plant growth and reproduction. Kidney beans were grown in a greenhouse with PE, PLA, PVC, and PCL microplastics added to the soil in concentrations of 0.1% and 0.01% w/w. Height measurements of each plant are currently being taken for a total of eight weeks. Plants will then be harvested, and aboveground biomass, number of pods and seeds, and weight of pods and seeds will be measured and compared. Total chlorophyll content as well as chlorophyll a and b content will also be calculated by measuring the absorbance of leaf extracts at 663 and 647nm. Preliminary results show that 0.1% concentrations of PLA, a biodegradable plastic, significantly reduce the weight of pods, number of seeds, and weight of seeds produced. (**164**)

Naugle, Grace*, Maya Luse*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *The effects of BPF on tail resorption in Rana catesbeiana larvae*.- Bisphenol F (BPF) is an analogue to bisphenol A (BPA), a compound found in plastics that is known to be an endocrine disruptor. After a partial BPA ban, BPF was introduced as a replacement, but has shown similar endocrine disrupting properties. In the American Bullfrog (*Rana catesbeiana*), thyroxine is required for metamorphosis and endocrine disruptors can interfere with this process. To determine BPF's effects on development of *Rana catesbeiana* larvae, 5 mm of the tail was removed (except in one control group), and treated for 21 days with BPF (1x10-8M), thyroxine (1x10-9M), and a combination of BPF (1x10-8M) and thyroxine (1x10-9M). Given current literature indicating BPF may have endocrine disrupting effects like BPA, it was predicted that tadpoles treated with BPF would see a decrease in tail resorption. The purpose of this experiment is to investigate BPF's potential as an endocrine disruptor, particularly as an inhibitor of thyroxine. Results show the percent changes for all tail lengths were reduced from the initial length: uncut (-2.719837% ± 0.7777801) and cut (-1.559428% ± 1.0038211) controls, thyroxine (1x10-9M) group (-2.759918% ± 2.0757950), combination BPF (1x10-8M) and thyroxine (1x10-9M) group (-2.614874 ± 0.3817254), and BPF (1x10-8M) group (-2.665747% ± 2.2275206). The percent changes for weight (grams) show that weight decreased from the initial weight for uncut (-12.042945% ± 3.978612) and cut (-4.447881% ± 5.556454) control groups, thyroxine (1x10-9M) group (-16.876518% ± 6.640281), and combination of BPF(1x10-8M) and thyroxine (1x10-9M) group (-2.740807% ± 3.402720), while the body weight for BPF (1x10-8M) group (9.104056% ± 4.453320) increased. This indicates BPF is associated with a decrease in tail resorption, and an increase in weight, whereas the control and thyroxine treated groups saw a greater decrease in tail length and a decrease in weight. Given this, it is likely that BPF has similar endocrine disrupting effects to BPA. (**41**)

Nerozzi, Andrea* Wyoming Seminary Upper School, Kingston, PA 18704. *Science Research Group: An example high school science research program*.- The Science Research Group (SRG) at Wyoming Seminary is an extracurricular activity in which high school (HS) students conduct STEM research projects for enrichment or competition. SRG serves as an example of an apprenticeship program, which relies almost exclusively on internal support rather than placement of students into professional labs. Since 1996, c.200 students have voluntarily participated in SRG with many engaging the maximum amount of time possible based upon their grade level at entry. The group demographics provide insight into what types of students are interested in research, and the outcomes of participation. The majority of students participated in the Region 2 and State level Pennsylvania Junior Academy of Science (PJAS), which has played a central role in the SRG student experience, providing incentive for enhanced effort. This seminar will focus on how the group is organized, how students select projects and in what areas, what mentorship looks like at this level, and how students progress through the program. Reflections of current students and alumni on how participation in STEM research helped them in high school, college and their careers will also be presented, providing evidence that doing research on the HS level, and participating in PJAS, aids in retaining students in the STEM pipeline.Suggestions for how to improve this experience, and potential roles of higher education, will be presented. (**62**)

Njogu, Alphaxand*, Callum Shutack, Veronica Jakubikova, Helene Hartman, and Dylan Shropshire Lehigh University, Bethlehem, PA 18015. *Mapping a bacterium's cryptic journey across animal hosts*.- The most widespread animal-associated bacterium on Earth is *Wolbachia*, found in the cells of over half of insect species. *Wolbachia* is being used in at least 14 countries to slow the spread of mosquito-borne diseases like dengue and Zika. Therefore, understanding *Wolbachia*'s transmission dynamics has become increasingly important. While *Wolbachia* is primarily transmitted from mothers to offspring, growing evidence suggests it can also move between host species. However, the mechanisms and conditions that enable *Wolbachia* to switch hosts remain poorly understood. For a *Wolbachia* cell to switch hosts, it must first separate from its original host's cells, through processes that are poorly understood. Here, we test the hypothesis that food acts as a conduit for *Wolbachia*'s transmission into the environment, using *Wolbachia*-bearing fruit flies as a model. We allowed fruit flies to feed for defined intervals, collected the exposed food, extracted DNA, and performed digital droplet PCR (ddPCR) to count *Wolbachia*. Our experiments revealed that *Wolbachia* separates from its host, transmission rates vary across life stages, and *Wolbachia* is present in fly feces. We conclude that *Wolbachia* is consistently released into the environment through larval feces during feeding, suggesting a potential fecal-oral transmission route for *Wolbachia* host switching. These findings shed light on *Wolbachia*'s broad distribution and inform risks associated with efforts to use *Wolbachia* to block the spread of mosquito-borne diseases. (**7**)

Ortega, Meghan*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Forskolin-mediated cAMP activation in Schwann cells shows upregulated PKAc expression and downregulation of PP2A expression*.- Schwann cells play a crucial role in the peripheral nervous system including regulation of axonal growth. Proliferation of Schwann cells is facilitated by cyclic-AMP (cAMP), the universal cellular second messenger. In vitro, when the cAMP pathway is stimulated by the plant extract forskolin (FSK), expression of protein phosphatases such as PP2A are decreased, while catalytic subunits of kinases such as protein kinase A (PKAc) are increased. Since phosphatases regulate cAMP levels, decreased PP2A expression should show increased Schwann cell proliferation and higher levels of PKAc expression. Although the relationship between protein phosphatases and kinases is well documented, minimal research is available about the role of PP2A in the peripheral nervous system. It is hypothesized that the expression of the protein phosphatase PP2A in forskolin-treated Schwann cells will decrease while PKAc expression will increase. Schwann cell lysates treated with and without forskolin extract were tested for expression of PKAc, PP2A, and actin (control) proteins through Western blotting, and analyzed via densitometry. Detected expression levels of actin were used to normalize all Western blots. Cells treated with forskolin showed a decrease in the expression of PP2A (13.92%) and an increase in expression of PKAc (42.659%) in comparison to control (11.11% and 16.6%) respectively. These results suggest that activation of cAMP results in a decrease in phosphatases and an increase in kinase activity. A better understanding of the relationship between protein phosphatases and kinases like PKAc and PP2A may help to identify potential signaling partners within the cAMP pathway to stimulate Schwann cell proliferation and lead to breakthrough therapies for the treatment of peripheral nerve injury. (**91**)

Oye-mba, Angele*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Eaf's effect on NuA4 histone acetylation*.- NuA4 is the only essential lysine acetyltransferase (KAT) complex in yeast. It plays critical roles in transcription and DNA repair through acetylation of histones H4 and H2A as well as almost 100 other targets. Its human homolog Tip60 has been implicated as a tumor suppressor or oncogene in different cancers as well as neurodegenerative diseases like Alzheimer's. While the functions of some of the complex's thirteen subunits have been determined, we investigated the role of the Eaf6 subunit in histone H4 acetylation. If Eaf6 contributes to the ability of NuA4 to acetylate histones, cells lacking Eaf6 should have less histone acetylation than cells with Eaf6. Thus, histone H4 tetra-acetylation (H4-Ac) was measured by western blotting in strains with and without EAF6. We found that eaf6Δ cells had a reduction in H4-Ac of ~25%, which was comparable to cells lacking Yng2, a protein known to stimulate the activity of the catalytic subunit of NuA4. This suggests that Eaf6 stimulates NuA4's acetylation of H4, possibly through binding to nucleosomes, RNA polymerase II, or directly stimulating the acetyltransferase activity of subunit Esa1. Understanding the function of Eaf6 as a part of NuA4 will help elucidate how the complex contributes to important cellular processes like cell cycle control and how the human homolog Tip60 may contribute to diseases like cancer. (**111**)

Panitz, Alexandra*, Jazmyn Davis*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Identification of human bodily fluids commonly found at crime scenes through analysis of DNA methylation status*.- In the forensics field, there are numerous presumptive tests for the identification of bodily fluid trace evidence commonly found at a crime scene (e.g., ninhydrin for fingerprints, luminol for blood, acid phosphatase test for semen). These tests typically identify specific proteins that are relevant to the functions of those fluids. Unfortunately, low level of expression of some of these proteins in multiple fluids confounds protein-level analysis. The aim of this project is to shift to epigenetic analysis for forensic confirmatory testing. The epigenome helps to regulate gene expression through the methylation of CpG islands in the promoter regions of the genes that encode differently expressed proteins. The DNA methylation status of these promoter regions can be assessed through bisulfite conversion (converting unmethylated cytosine to uracil, which is subsequently converted to thymine during PCR amplification) followed by qPCR with high-resolution melt curve analysis. This study focused on the PFN3 (Profilin 3) and USP49 (Ubiquitin-Specific Protease 49) genes, both of which play important roles in the function and development of male sperm cells, and therefore would be expressed in seminal fluid, and have a methylation pattern that is different in semen versus blood, urine, and vaginal fluid. Similarly, the DACT1 (Disheveled Binding Antagonist of Beta Catenin 1), MDFI (MyoD Family Inhibitor), PRMT2 (Protein Arginine Methyltransferase 2), MMP7 (Matrix Metallopeptidase 7), and MMP11 (Matrix Metallopeptidase 11) genes are differentially expressed in seminal fluid, saliva, venous blood, menstrual blood, and vaginal fluid respectively; thus, high resolution melt curves for qPCR amplicons of promoter regions for these genes reveal differential melt curves depending on the fluid analyzed. This preliminary work demonstrates the potential for distinguishing semen, saliva, menstrual blood, and vaginal fluid crime scene stains based on melt curve data. (**52**)

Paterson, Rhiannon A.*, and Ronald Brown Mercyhurst University, Erie, PA 16546. *Analyzing hydrogen abstraction, vinylacetylene addition (HAVA) reaction pathway for polycyclic aromatic hydrocarbon (PAH) synthesis in dark molecular clouds (DMCs)*.- Polycyclic aromatic hydrocarbons (PAHs) are believed to line millimeter-sized dust grains in the interstellar medium (ISM) and account for ~20% of the interstellar carbon budget. As such, they heavily influence the chemistry and physics of the ISM, and possible pathways of formation are continually sought after. The formation of catacondensed PAHs in dark molecular clouds (DMCs) has been theorized as possible via utilization of the hydrogen abstraction, vinylacetylene addition (HAVA) reaction mechanism. The barrierless conditions of this reaction mechanism support the possibility of PAH formation in the 10-50 K conditions of DMCs, as does the detection of vinylacetylene molecules in DMCs such as Taurus Molecular Cloud-1 (TMC-1). Using ab initio calculations, we seek to investigate the favorability of the HAVA mechanism as a bottom-up pathway to PAH formation in DMCs. The energetics of pathways for ring formation in PAHs via the HAVA mechanism have been studied at the B3LYP/6-311G(d,p) level of theory. The steps in these pathways and their relative energetics will be presented. (**82**)

Perneta, Nicholas*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Brew-tal for bacteria: Investigating coffee as a natural antimicrobial agent*.- The emergence of antibiotic-resistant bacteria poses a significant risk to public health, reinforcing the need to explore other antimicrobial strategies. Coffee, one of the most consumed drinks worldwide, has bioactive molecules including caffeine, polyphenols, and acids that could be used against bacterial growth. While previous studies have established the antimicrobial activity of coffee, its effect on pathogenic and beneficial bacteria remains largely understudied. This study aims to establish the potential of coffee in inhibiting pathogenic bacteria growth while demonstrating the impact of coffee on probiotics and other beneficial microbes. Coffee was made through eight common methods of brewing - espresso, moka pot, instant, cold brew, Keurig, pour-over, drip pot, and French press - in an attempt to analyze if coffee's antimicrobial activity varies with different extraction techniques. Bacterial growth and viability were assessed to establish coffee's potential as a natural antimicrobial compound and its selectivity between a variety of microbial populations. By gaining an understanding of coffee's interaction with pathogens and probiotics, this research aims to contribute to a greater exploration of natural antimicrobial compounds within food and beverage science. If coffee is found to be selectively inhibitory, it may have applications in food safety, microbiome health, and even diet-based antimicrobial approaches. Preliminary data suggests that the espresso, moka pot, and pour-over brew methods have an antimicrobial effect against *Staphylococcus aureus*. As antibiotic resistance continues to grow, research into natural products such as coffee can help pioneer different approaches to regulating bacterial growth. (**88**)

Perneta, Nicholas, Victoria Kenney*, Colin Cloud, Emaleigh Kramer, Joshua Rizzardi, Cassandra Zellner, Sarah James, and Nandana Varier DeSales University, Center Valley, PA 18034. *From ocean to ointment: Evaluating the anti-inflammatory effects of Lampire Lobster Hemocyanin*.- Heart disease stands as the foremost cause of death in the United States. Atherosclerosis, marked by the accumulation of lipids within blood vessels alongside the release of inflammatory cytokines and leukocyte adhesion, plays a significant role in the development of coronary heart disease. Another pertinent medical issue linked to heightened inflammation is the rejection of implantable medical devices like pacemakers, vascular stents, and cosmetic implants. In the search for a natural compound capable of reducing excessive inflammation, human pulmonary aortic endothelial cells (HPAECs) and THP-1 cells served as model cell lines. Lampire Lobster Hemocyanin (LLH), a natural compound found within the base of the tail in lobsters, is suggested to have anti-inflammatory properties. Preliminary viability assays suggest that LLH shows no toxicity between 1:10 and 1:160 µg/mL concentrations.THP-1 adhesion assays on polyurethane films were conducted with LLH to determine the impact of LLH on biocompatibility. There was a noticeable decrease in adhesion by THP-1 cells after 1:80 µg/mL LLH treatment, indicating that LLH may have an impact on the biomaterial rejection of a common polymer used in medical devices. To further evaluate LLH's anti-inflammatory effects, TNF-α assays and wound healing assays will be conducted. Overall, LLH was found to have anti-inflammatory effects in the cell models evaluated herein, suggesting that it may be suitable as an anti-inflammatory supplement. (**181**)

Perneta, Nicholas*, Victoria Kenney, Colin Cloud, Emaleigh Kramer, Joshua Rizzardi*, Cassandra Zellner, Sarah James, and Nandana Varier DeSales University, Center Valley, PA 18034. *Galangin gains: Evaluating galangin as a natural ally against inflammation*.- Heart disease is one the most common causes of death in the United States. Atherosclerosis is a widely observed cause of heart disease, including coronary heart disease and ischemic stroke. Atherosclerosis involves the narrowing of the blood vessels caused by lipid accumulation, accompanied by the release of inflammatory cytokines and leukocyte binding. This plaque formation can lead to thrombosis, venous rupture, and cell death. Bovine Aortic Endothelial Cells (BAOECs) were used as models of vascular endothelium to determine the anti-inflammatory effect of galangin on vascular endothelium. Galangin is found in honey and *Alpinia officinarum* (a plant in the ginger family). In previous studies, galangin has shown potential as an anti-inflammatory treatment. To evaluate the anti-inflammatory effects of galangin, BAOECs and THP-1 cells served as model cell lines. Preliminary viability assays show that galangin is not cytotoxic to either cell line. TNF-alpha inflammation assays and wound healing experiments plan to be conducted to test the hypothesis that galangin would ameliorate inflammation in BAOEC cells. (**180**)

Persons, Kelsey*, and Matthew Persons Susquehanna University, Selinsgrove, PA 17870. *Reading between the draglines: The effect of male and female fishing spider Dolomedes triton silk on whirligig beetle Dineutus assimilis behavior and predation*.- The six-spotted fishing spider, *Dolomedes triton*, is semi-aquatic and deposits hydrophobic silk across the water surface while anchoring it on emergent objects. This silk, used to attract mates by females, could also act as a trip-line to increase the detection of nearby prey or act as an aquatic tangle web. Alternatively, silk deposited on the neuston may be used as an enemy-avoidance kairomone and alert aquatic prey to the presence of predators. The whirligig beetle, *Dineutus assimilis*, swims across the water surface and may encounter fishing spider silk. We measured the activity level and space use of pairs of whirligigs in the presence or absence of male or female *Dolomedes* silk. We also compared the quantity of silk deposited by adult male versus female spiders. In a second 2x2 factorial experiment, we measured survival of pairs of beetles in the presence of live adult male or female *Dolomedes* with or without their associated silk. Female *Dolomedes* deposited significantly more silk on the water surface than males and females showed significantly higher predation than males. The presence of female silk significantly decreased the time to prey capture by female spiders compared to when silk cues were absent. The beetles also showed significantly higher avoidance of areas with spider silk present and showed greater avoidance of female rather than male silk. Our results suggest a trip-line function to *Dolomedes* silk that enhances the detection range of moving prey on the water surface, but this effect is most pronounced with female spiders. Beetle behavior also suggests an enemy avoidance kairomone function, but their behavioral shifts were ineffective to avoid predation within our testing environment. Fishing spider silk may mediate a number of trophic interactions within the neustonic arthropod community, but additional studies are needed. (**153**)

Pierce, Liv*, and Clinton Jones Mercyhurst University, Erie, PA 16546. *Total phenolic content in herbal teas*.- Tea is the second most popular beverage in the world, next to water. Herbal tea has recently grown in popularity due to an increase in health and wellness and mindful consumption. The growing interest in herbal teas is attributed to their high levels of antioxidants, vitamins, and minerals. The antioxidants in herbal teas largely come in the form of polyphenols and are often associated with potential health benefits. It has been found that the preparation condition of tea brewing, such as infusion time and temperature, can directly affect the levels of polyphenols. Spectrometry, using the Folin-Ciocalteu reagent, is the standard method of determining total phenolic content in teas. Using this experimental method, we are hoping to estimate the total phenolic content for herbal teas when they are prepared according to the distributors packaging. The temperature, the amount of water, and the weight of the tea will all be measured following the recommended amounts on the packaging, and the traditional brewing method of infusion will be used. It is expected that herbal teas with known health benefits will contain more polyphenols. Estimating the total phenolic content for herbal teas may reflect the antioxidant levels consumer receive when preparing tea at home, which would allow health-conscious consumers to make informed choices when buying tea. (**33**)

Popoola, Esther*, and Jacquelyn Maddox Harrisburg University of Science and Technology, Harrisburg, PA 17101. *A CRISPR-Cas approach to combat ampicillin resistance in Enterobacter cloacae*.- The rise of antibiotic resistance among bacteria poses a significant threat to public health, with infections caused by antimicrobial-resistant bacteria leading to elevated mortality rates globally. ESKAPE pathogens, including the *Enterobacter species*, are particularly concerning due to their ability to cause severe infections and develop resistance to multiple antibiotics. One of the principal forms of resistance is the development of enzymes that inactivate β-lactam antibiotics such as ampicillin. *Enterobacter cloacae*, a member of the *Enterobacter* genus has developed the ability to express β-lactamase enzymes allowing it to degrade β-lactam antibiotics, rendering treatments ineffective. Researchers have focused on understanding the genetic mechanisms behind antibiotic resistance and developing innovative strategies to combat it. One promising approach involves utilizing CRISPR technology. This project explores the use of CRISPR-Cas to resolve ampicillin resistance in *E. cloacae*. A wild-type (WT) strain of *E. cloacae* was modified to create an ampicillin-resistant (AMP-R) strain. This AMP-R strain was then modified using CRISPR to presumably disrupt the β-lactamase gene (AMP-C). The growth kinetics of each cell line was determined under normal conditions as well as with ampicillin. Preliminary results show that the CRISPR edited AMP-C line has an increased sensitivity to ampicillin when compared to the AMP-R line. AMP-C also grows at a higher rate than both WT and AMP-R under normal conditions. Results are currently being analyzed to determine significance. This study serves as a proof-of-concept for using CRISPR to combat antibiotic resistance. The findings from this research could offer insights into the genetic regulation of antibiotic resistance in hospital-associated pathogens. By continuing to refine approaches to antibiotic resistance, this study contributes to the broader effort to mitigate the public health crisis posed by multidrug-resistant bacteria. (**76**)

Rasa, Christina*, Angela Asirvatham, and Cosima Wiese Misericordia University, Dallas, PA 18612. *Cell-free expression of a genetically encoded fluorescent ATP sensor*.- Adenosine triphosphate (ATP) provides the energy necessary for all chemical reactions at the cellular level. When cells lack adequate amounts of ATP, they are unable to complete functions related to metabolism, growth, and protein expression, leading to cell death. Loss of cellular function due to lack of ATP causes oxidative stress, accelerates the aging of cells, and leads to development of degenerative diseases. For these reasons, several ATP biosensors have been developed. One such sensor is a protein called HHM-iATPSnFR1.0 which has subunits containing superfolder green fluorescent protein. When ATP binds to this protein, it causes a conformational change and an increased intensity of fluorescence. Thus, the increase in fluorescence is directly correlated to the amount of ATP in the sample. Typically, this protein would be expressed via *E. coli* cells and then isolated in a tedious and time-consuming process. The goal of this study is to validate the use of a cell-free expression system called BioBits™ to simplify production and application of the HHM-iATPSnFR1.0 protein. It is hypothesized that upon binding to ATP, HHM-iATPSnFR1.0 expressed by BioBits™ will undergo a conformational change, resulting in an increase of fluorescence intensity which will be directly related to the amount of ATP in the sample. To test this hypothesis, the fluorescence of samples containing BioBits™ pellets, HHM-iATPSnFR1.0 plasmid, and water was measured using a fluorimeter. Then the fluorescence of the samples was measured again after different amounts of ATP solution were added. As a negative control, the same measurements were carried out on samples containing just the BioBits™ pellet and water. Preliminary results show that the fluorescence intensity of samples with the plasmid increased by 169% upon addition of ATP, and fluorescence of samples without the plasmid did not increase. This indicates that HHM-iATPSnFR1.0 was successfully expressed by BioBits™, supporting the hypothesis. (**110**)

Richards, Abigail*, and Joy Karnas Cedar Crest College, Allentown, PA 18104. *Characterization of BetI expression on antibiotic drug sensitivity*.- *Leclercia adecarboxylata*, a bacillus of the Enterobacteriaceae family that is highly similar to *Escherichia coli*, is found in environmental and clinical aquatic settings. This species is slowly gaining recognition as an emerging opportunistic pathogen in immunocompromised patients. While it is susceptible to common antibiotics, there have been reports of resistant strains isolated from clinical and wastewater settings. We demonstrated repeated exposure to triclosan (TCS) can lead to the appearance of TCS-resistant *L. adecarboxylata* strains. Whole genome sequencing of a resistant isolate indicated a mutation in the betaine inhibitor (betI) gene, the first gene in the betIBA operon, which is activated under osmotic stress and negatively autoregulated by BetI. To better understand this novel betI mutation and its relationship to *L. adecarboxylata* antibiotic resistance, wildtype and mutant forms of this gene were subcloned into an expression plasmid. The constructs were overexpressed in *E. coli* cells which were subsequently exposed to TCS and other antibiotics via Kirby-Bauer disk diffusion assay. This project aims to help provide insight into spontaneous antibiotic resistance mechanisms as well as aid in the development of new methods to combat this ongoing issue. (**131**)

Richards, Cale*, and Derek Straub Susquehanna University, Selinsgrove, PA 17870. *Monitoring carbon dioxide concentration patterns with inexpensive NDIR sensors through a mobile platform*.- Carbon dioxide (CO2) in the atmosphere has negative impacts on human health and the environment, and comes primarily from the extraction and burning of fossil fuels such as coal, oil, and natural gas. Monitoring carbon dioxide concentrations has become more critical due to the rising levels outdoors and the prolonged time spent indoors, where CO2 can accumulate. In addition, CO2 monitoring is becoming more prevalent due to the development of inexpensive CO2 sensors and supporting electronics that have been used by the HVAC industry and citizen scientists. This study aims to assess the ability of the SCD30, an inexpensive nondispersive infrared carbon dioxide sensor created by Sensirion, and monitor the concentrations of CO2 in indoor locations on Susquehanna University campus, and in the atmosphere in the area around Selinsgrove, Pennsylvania by attaching this sensor to a mobile platform. Attached to the SCD30 is a microcontroller from Adafruit Industries that was used to control the SCD30 and log data, including CO2 concentration, temperature, relative humidity, and GPS coordinates every 10 seconds. When collecting data with the SCD30, the measured concentrations were slightly lower but still within the uncertainty range specified by the manufacturer. A pattern of elevated CO2 concentrations was observed in high-traffic areas, particularly during stops, with similar higher levels ranging from 430-560 ppm detected along specific sections of Route 147, on the other side of the Susquehanna River. (**40**)

Rogers, Madison*, and Clint Jones Mercyhurst University, Erie, PA 16546. *The effect of crosslinkers on nanogel colloidal crystals*.- This study investigates the effect of crosslinker type and concentration on the optical properties of self-assembled colloidal crystals from thermoresponsive poly(N-isopropylacrylamide) (pNIPAm) nanogels. Nanogels were synthesized with varying concentrations (2, 5, 10, 15, 20%) of *N*,*N*-methylenebisacrylamide (BIS) and ethylene glycol dimethacrylate (EGDMA) crosslinkers. Colloidal crystals were formed through temperature-controlled centrifugation and annealing. UV-Vis spectroscopy was used to characterize the diffraction of the crystals. Preliminary results suggest that higher crosslinker concentrations correspond to smaller spacing between particles, while lower crosslinker concentrations maintain a larger particle spacing. These findings show control over Bragg diffraction properties through manipulation of crosslinking type and concentrations, which has implications for the development of colloidal crystal-based optical materials and pigments. (**21**)

Roman Jordan, Alfredo*, and Mitchell Powers Gettysburg College, Gettysburg, PA 17325. *Short tails and shorter interactions: insights into molecular structure and the behavior of columnar liquid crystal mesophases*.- This work focuses on a set of fluorinated triphenylene based discotic liquid crystals (DLCs) that posses an unusual structural motif: where DLCs typically consist of a rigid molecular core surrounded by long flexible (highly entropic) tails, this set of materials have increasingly short tails or even lack tails entirely. Despite this, these molecules self-assemble into long columns while still allowing molecules to move, twist and spin. Conventional DLCs rely on their tails to form a buffer between columns that prevent short range inter-columnar interactions between the molecular cores. As the tails become shorter, these interactions take on a new significance. Of particular interest is the changing role of fluorine, which is a popular substituent often added to molecular cores in order to manipulate long range electrostatic interactions between molecules from distant columns. As the range between columns decreases, the interactions become more complicated, and fluorination begins to play a more prominent role in the formation of networks of short range intermolecular bonds. The nature of these interactions, and resulting phase behavior, have been studied through x-ray scattering and molecular dynamics simulations in order to identify key features that shed light on the structural factors that can be used to create new short-tailed DLCs with similar properties. In this contribution we present details of the structures and phase properties of these materials and current efforts to better understand the formation of weak hydrogen bond networks in the materials as a means of balancing crystal-like order while preserving the liquid-like dynamic freedom of the molecules. (**47**)

Rossiter, Taylor*, Matt Vogan, 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 to discover novel antibiotics or new ways to increase antibiotic efficiency to try and solve this crisis. Previously, we isolated a bacterial sample from soil and showed that it demonstrated antagonistic activity against the ESKAPE pathogen-safe relatives *B. subtilis*, *P. aeruginosa*, and *S. epidermidis*. The isolate (3TR12_21) was identified as *Paenarthrobacter nicotinovorans*, and the secondary metabolite identification/analysis software, antiSMASH, revealed a stenothricin-like biosynthetic gene cluster (BGC; 38% identical) that previous literature suggests could be an antibiotic. This study aimed to determine how disrupting this BGC using a modified CRISPR/Cas9 system would affect *P. nicotinovorans* antibiotic production. We downregulated several genes in the stenothricin-like biosynthetic pathway, StenK, StenM, StenL, and StenF, and compared their antibiotic-producing activity to that of the wild-type isolate. Preliminary results have shown that there were changes in antibiotic production against various ESKAPE pathogen-safe relatives, and changes in the overall growth rate were observed when comparing the mutant strains with the wild-type strain. (**79**)

Ruccolo, Maria*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Co-segregating X1 and X2 chromosomes in yellow sac spiders are not connected in metaphase I*.- Spiders show unusual sex chromosome movements during male meiosis I that can be informative for learning general principles of chromosome behavior in cell division. Here we are studying the movements of the X1 and X2 chromosomes of the yellow sac spider *Cheiracanthium mildei*. We used live-cell imaging and histological staining to determine that

C. mildei exhibits a X1X20 (male) and X1X1X2X2 (female) sex-determining system. Our data show that, in male meiosis I, the X1 and X2 chromosomes move together to the same spindle pole. Micromanipulation reveals that X1 and X2 are not physically connected in metaphase I or anaphase I. We show using immunofluorescence staining of microtubules that the X1 and X2 chromosomes associate with a single spindle pole during prophase I, prior to nuclear envelope breakdown. We propose that this early attachment guarantees the coordinated movements of the X1 and X2 chromosomes throughout meiosis I. (**188**)

Safi, Sabeen*, Danna Berro*, Juliette Amram*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Porphyromonas gingivalis growth is disrupted by oral commensal metabolites and e-liquids*.- Electronic cigarettes (ECIG) are popular as a perceived safer alternative to traditional cigarettes, but their impact on oral health is concerning. E-liquid components like cinnamon and menthol flavorings can disrupt the oral microbiome. Oral commensal *Streptococci* maintain oral health by inhibiting pathogens like *Porphyromonas gingivalis*. We investigated how cinnamon and menthol flavorings affect commensal metabolites' interactions with *P. gingivalis* growth. *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus mitis*, and *Streptococcus oralis* were cultured in TSBY until late exponential phase. Supernatants were collected, filter-sterilized, and stored at -20°C. *P. gingivalis* was cultured anaerobically in TSBY with 1% cinnamon or menthol E-liquids and 10% commensal supernatants. Growth kinetics were monitored by absorbance at 595 nanometer wavelength. *P. gingivalis* growth is affected by 10% commensal spent media, where *S. mitis* supernatant has the highest effect, followed by the spent media of *S. gordonii* and *S. oralis*. No effect is observed with the spent media of *S. intermedius*. *P. gingivalis* growth is severely affected by 1% cinnamon and, to a lesser extent, 1% menthol. All supernatants interfered with the E-liquids' suppressing effects, where *P. gingivalis* growth is slightly higher when grown with both E-liquid and supernatants as compared to growth with E-liquids alone. This research is critical for understanding the health implications of ECIG. (**103**)

Saintillien, Berrangere*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Mutating yeast for faster fermentation*.- Commercial beer-making takes approximately two weeks for ales and four to eight weeks for lagers with one week of fermentation for ales and two to six weeks for lagers. Being able to make beer faster by reducing fermentation time would provide a great benefit to the beer industry as well as recreational brewers who are interested in trying out different recipes. The goal of this project was to screen a library of yeast for faster fermenters and then see how the finished beer was affected by the faster fermentation. Brewing yeast strain US-50 was mutagenized with ethyl methanesulfonate (EMS) and individual clones were screened in small-scale fermentation reactions. Almost 25% of clones appeared to ferment faster than the parental strain. The fastest fermenters were used to brew one-gallon batches of beer. Fermentation time decreased by 20 and 30% with the two mutant clones compared to the parental US-50 strain. Interestingly, the flavor profiles of the three beers were different with beer from clone 2 described by tasters as fruitier, sweeter, and lighter than beer from US-50. Beer from clone 24 was sharper, spicier, more bitter, and fuller than beer from US-50. Our results suggest that yeast can be mutated to reduce fermentation time, but that more work is needed to maintain a beer's flavor profile. (**124**)

Seagreaves, Gabrielle*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Effects of pesticide pyrethrins on the soil microbiome*.- The soil microbiome plays an important role in plant growth, soil nutrition, and plant fertility. Pesticides are an inexpensive method of inhibiting insect pests in agricultural environments. Application of pesticides can lead to degradation of soil richness and alter the composition of soil microbial communities. The recovery of a microbiome after damage contributes to the overall health of plant ecosystems, but the extent of this resilience is unknown. We hypothesized that the application of a standard treatment of pesticides to soil samples would alter its microbiome. We selected the pesticide PyGanic, containing the organic compound pyrethrins as its active ingredient. Soil was taken from a local untreated nature preserve and separated into six samples. Two controls received only water, two samples were treated with the recommended dosage according to package instructions, and two samples were treated with quadruple the recommended dosage. Samples were taken before and during application of PyGanic. We extracted genomic DNA using the Qiagen Powersoil Pro kit, then prepared a DNA library by ligating adapters and barcode sequences. We sequenced the library using the Oxford Nanopore MinION portable sequencer before analyzing the results with the EPI2ME platform using the wf-metagenomics workflow. We report here on the impact of pyrethins on the soil microbiome. (**58**)

Selesky, Kara*, Angelena Donovan*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Resveratrol demonstrates antiviral activity toward the Mouse Hepatitis virus 3C-like protease*.- Traditional Chinese herbal medicines have been known to treat various respiratory infections, such as coronaviruses. *Polygonum cuspidatum*, also known as the Japanese knotweed, is a plant native to eastern Asia that contains resveratrol and is commonly used in herbal preparation of Chinese traditional medicines. Resveratrol is a polyphenol, which is an organic chemical that can also be extracted from peanuts, berries, and grapes and exhibits antioxidant, anti-inflammatory, and antiviral properties. Three novel coronaviruses have emerged in the last 25 years, including the SARS-CoV 2 which caused a global pandemic in 2019. In the future, it is possible that new coronaviruses will emerge and require broadly acting antivirals. Resveratrol has been shown to have potent inhibitory activity against both the coronavirus 3C-like proteases (3CLpro) and papain-like protease (PLP) from SARS-CoV 2 and MERS-CoV. However, it is unclear whether resveratrol targets 3CLpro in other coronaviruses, including mouse hepatitis virus (MHV). Both MHV and SARS-CoV 2 belong to the Betacoronavirus genus, which allows MHV to work as a model for SARS-CoV 2 based on their similarities. Resveratrol has no significant cytotoxicity in mouse DBT-9, delayed brain tumor-9, astrocytes. During co-treatment, resveratrol had inhibitory activity towards MHV as measured by a firefly luciferase assay. However, when cells were pre-treated or post-treated within 6 hours, decreased efficacy of resveratrol is shown. This work provides insights into the inhibitory effects of resveratrol as an antiviral for MHV. (**80**)

Selner, Melanie*, and Gerardo Giordano King's College, Wilkes-Barre, PA 18711. *Using Quantum Computers to Study the Effects of Thermal Noise in Computation*.- *Quantum computers* execute computations using *quantum bits (qubits)* based on their quantum mechanical properties. While quantum computers have the potential to outperform classical systems in specific tasks, *qubits* are highly sensitive to thermal interactions with their environment. During computations, qubits are initialized to a state, manipulated through quantum logic gates, and then measured to observe the final result. *Thermal noise* disrupts all these processes, leading to poor computational accuracy. The purpose of this project is to observe the effects of thermal noise on quantum computing using IBM's quantum computing services. To do so, jobs are sent to different systems that can then be retrieved and analyzed when completed. *Quantum circuits* and *algorithms* were executed on both an ideal (no noise) *simulator* and on real IBM quantum *hardware* that did have noise. Comparing the outputs showed the impact of noise on expected outputs and results. Using these observations, various error mitigation techniques were tested to reduce computational error. This research aimed to provide insight on ways to improve *quantum error correction* methods so quantum computing can ultimately become more practical than classical systems. (**48**)

Semmler, Liam*, Aidan Doyle, Vaughn Shirey, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Predicting beetle (Insecta: Coleoptera) communities* *through biotic and abiotic variables 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. Beetles (Insecta: Coleoptera) are the most species rich insect group and provide essential ecosystem services such as pollination, pest control, and nutrient cycling. For this research, we predict that (1) our study site without any trees will have the most unique beetle community, and (2) leaf litter will be the most impactful environmental variable that influences beetle communities on Hog Island, Bremen, Maine, managed by the National Audubon Society. 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). At each site, we set up 4-5 pitfall traps to target and collect surface active beetles. Each pitfall trap location was then surveyed for biotic and abiotic variables (e.g., vegetation height classes, ground cover percentage, canopy density). We then determined all the collected beetles to morpho-species. A non-metric multidimensional analysis (NMDS) was conducted to determine how distinct the beetle community compositions were for each study site. Additionally, an adonis2 was conducted to determine which environmental variables had the highest impact on predicting the beetle communities. Out of 182 beetle specimens collected, our milkweed field had the most unique beetle community with our other four sites having some overlapping similarities. Additionally, we found two significant predictors for beetle communities: foliage percentage ($p = 0.01$) and downed wood layers ($p = 0.004$). Our two original predictions were supported. This research is impactful because being able to predict beetle communities based on environmental variables present allows for making more informed conservation management decisions in the interest of protecting biodiversity. (**145**)

Sennett, Rachael*, Madeline Solomon, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *The effects of bisphenol-F on RT4 schwannoma cell proliferation, viability, and TNF-α*.- Bisphenol A (BPA) is a harmful chemical found in plastics. The FDA has banned its use in certain products due to its toxicity, but similar, modified versions of this compound are being used as substitutes, such as Bisphenol F (BPF). Recent studies have shown that low concentrations of BPF induced proliferation in human breast cancer MCF-7 cells and inflammation in macrophages. Reports in the literature reveal that the addition of BPA and BPF to rat neural stem cells interfered with characteristic morphology and its differentiation into astrocytes, oligodendrocytes, and neurons along with an increase in proliferation. Based on these results, it was hypothesized that the addition of BPF in incremental doses to RT4 Schwannoma cancer cells will increase viability, cell proliferation, and TNF alpha production in comparison to cells without BPF. To evaluate this hypothesis, RT4 Schwannoma cancer cells were incubated with control media (N2), ethanol, and BPF at various concentrations ranging from 1x10-7M to 1x10-2M for various time points. Using the EdU proliferation assay, an increase in cell proliferation was observed with a BPF treatment at 1x10-7 M. Quantification of cell viability with the ATP Glo titer assay revealed that it was enhanced in doses ranging from 1x10-7 M to 1x10-4 M in 4.5, 24, and 48-hour cultures. Compared to other doses, cells treated with 1x10-7 M BPF for 24 hours had the highest percent change in proliferation (43.6% +/-0.107214), viability (99.7+/-31.14%) and secretion of TNF-α (4132.667 pg/ml) as measured by the ELISA. These results suggest that minute concentrations of BPF are adequate to promote RT4 Schwannoma cell proliferation and pro-inflammatory cytokine production. (**55**)

Shaver, Bridget*, Diego Zelaya, Robert A. Kurt, and Chun Wai Liew Lafayette College, Easton, PA 18042. *An experimental and computational approach to studying anti-tumor activation of mouse macrophages*.- Macrophages are immune cells that can play a role in cancer growth, spread, or treatment. We focused on cancer treatment by optimizing the best way to activate the anti-tumor activity of bone marrow-derived macrophages (BMDM) using a computational model and lab-based experiments. For this purpose, Toll-like receptor (TLR) agonists were used to trigger macrophages to activate and defend the body against cancer. The macrophages were stimulated with the TLR agonists Flagellin, LPS, and R848 to measure signaling and gene expression under different activation conditions. Stimulated macrophages were then lysed and the RNA was isolated, cDNA was synthesized and then used for quantitative PCR (qPCR). Primers specific for il-1, il-6, tnf, il-12, il-18, ccl5, cxcl9, cxcl10, cxcl11, and ccr7 genes were used to measure the BMDM response to single (flagellin), double (LPS and flagellin), and triple (LPS, flagellin, and R848) signaling. The data showed that gene expression was generally higher under triple stimulation than dual or single stimulation, results that validated the model. A similar experiment was conducted to determine how TLR agonist concentration affected the strength of gene expression. For this purpose, high and low concentrations of the TLR agonists were added to the BMDM. The model showed that single, dual, and triple high treatments led to higher RNA responses than the single, dual, and triple low treatments. The lab-based results were generally consistent with the model for single and dual doses; however, the results for the triple treatment contained more variability between genes. The complex interplay between dose and stimulation of multiple signaling cascades underscores the importance of investigating interconnected signaling cascades in total rather than in isolation. These data suggest that for the most effective anti-tumor activation, the dose and number of agonists should be carefully considered concerning the gene(s) of interest. (**114**)

Simbar, Gwen*, Patricia Strazdus, and Andrea Nerozzi Wyoming Seminary Upper School, Kingston, PA 18704. *The effect of starch source on the characteristics of bioplastics*.- This study investigates the properties of biofilm produced from three different starches (potato, corn, and cassava) as an eco-friendly alternative to petroleum-based plastic packaging, which is resistant to degradation and difficult to recycle. Starch is composed of both branched (amylopectin) and unbranched (amylose) polymers. The ratio of these two forms may affect biofilm properties by altering granule size, with potato starch and cornstarch, which have a higher amylose content, exhibiting larger granule structure than cassava starch. Each biofilm was prepared by a procedure that includes gelatinization, heating, and plasticization. The thickness, biodegradability and tensile strength of the resulting films were compared. Thickness was measured directly with a Vernier Caliper, and strength was determined by the mass required to break a sample. Degradation was examined by exposing biofilm samples to 1.0 M NaOH and measuring the release of yellow dye using a spectrophotometer (380 nm). The results demonstrate that corn starch is able to produce the most effective biofilm because it exhibited the fastest degradation rate, and moderate thickness and tensile strength. However, qualitatively, potato starch produced a more flexible product. The greatest limitation of this protocol is the uneven distribution of material during plasticization. Future research opportunities include improving the plasticization protocol, utilizing alternative degradation methods, developing methods to assess flexibility and investigating thermal properties. This study provides valuable insight into developing sustainable packaging solutions. (**34**)

Sizemore, Anne, Elise Heiss, Shannon Corcoran, Jillian Snook*, and Jillian McCue King's College, Wilkes-Barre, PA 18711. *Evaluating student learning outcomes across three teaching modalities using the same set of flipped classroom materials*.- Upon the onset of the COVID-19 pandemic, the transition to online learning caused a great deal of uncertainty for students and instructors as to how course material would be adequately delivered and assessed. In preparation for the 2020-2021 academic year, three professors at King's College in Wilkes-Barre, Pennsylvania, USA, each contributed one-third of the course content to a shared set of flipped classroom materials for General Chemistry I & II. The course materials were designed to be versatile and applicable to each modality offered: online, hybrid, and traditional face-to-face. This arrangement provided for a natural experiment to measure the effects of course modality on student learning outcomes independent of the professor during the same term. Student performance was evaluated quantitatively by comparing exam grades, and student perceptions were evaluated qualitatively using student survey data. We evaluated the data collected in the fall 2020 and spring 2021 to determine: (1) if exam scores differed by modality in General Chemistry I when students were assigned a random course section; (2) if exam scores differed by modality in General Chemistry II when students had a choice in course section; (3) how the students rated their experience in a flipped-classroom format; (4) whether or not they preferred, hybrid or online-only over a traditional course format. There was no statistically significant difference in exam grades between modalities in both General Chemistry I and II, although students generally preferred hybrid and traditional courses over those delivered fully online. (**23**)

Slusser, Andrea* Methacton High School, Eagleville, PA 19403. *Determining the correlation of nodal patterns from resonating two dimensional standing waves on Chladni plates and the amplification qualities of a cello using Chladni's law*.- This experiment utilized modern adaptations of Ernst Chladni’s visualization of nodal patterns to demonstrate the formation of standing waves on the body plates of a cello. An amplifier and a frequency generator projected vibrations of contrasting frequencies to resonate across a thin, circular plate that was made of metal and coated in sand. The standing waves formed from interference oscillate across the plate with heightened amplitudes at natural resonant frequencies, which were then localized to compare to Chladni’s law for waves driven transversely through a centrally fixed circular plate: F ~ (m+2n)^2. By comparing the collected data to his law, a polynomial, mathematical relationship and R^2 correlation of 0.994 can be established between nodal patterns and frequency. Such values were then statistically analyzed on a graph with values applied to Chladni’s law, F ~ (m+2n)^2, to determine the linear relationship and R^2 correlation, 0.994, between nodal patterns created with modern devices and his original visualization. The data found was finally examined to demonstrate the amplification qualities of standing waves acting upon the body plates of a cello. (**12**)

Snyder, Jillian*, Chris Needham, and Thomas Kwiatkowski West Chester University, West Chester, PA 19383. *Effects of alcohol and nicotine e-cigarette co-exposure on biochemical changes in developing mice*.- Fetal Alcohol Spectrum Disorders arise from prenatal ethanol exposure, often compounded by concurrent nicotine use, both of which can significantly impact fetal metabolism. Despite the high prevalence of co-exposure, little research has examined how these substances interact to alter lipid metabolism and hepatic drug-metabolizing enzymes. This study investigates the effects of combined prenatal ethanol and nicotine exposure on triglyceride levels and liver enzyme expression in neonatal mice, compared to exposure to each drug alone. Pregnant dams were exposed to vaporized ethanol and nicotine during a developmental window equivalent to the human third trimester, modeling real-world maternal substance use. Offspring serum triglyceride concentrations were quantified using a colorimetric assay to assess metabolic disruptions, while western blot analysis determined changes in alcohol dehydrogenase expression in liver tissue. This study will clarify whether ethanol and nicotine have additive, synergistic, or independent effects on metabolic and enzymatic pathways, providing insight into potential long-term consequences of prenatal substance exposure. (**5**)

Solomon, Madeline*, Rachael Sennett, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *The effects of bisphenol S on the viability and proliferation of glial cells in the peripheral nervous system*.- Schwann cells are glial cells in the peripheral nervous system that support nerve function and myelination. Endocrine-disrupting chemicals, such as bisphenol A (BPA) and its derivative, bisphenol S (BPS), can adversely affect Schwann cell proliferation. While BPA has been banned in many industries, BPS is commonly used in the production of plastic water bottles, containers, and various everyday products. Previous research indicates that BPS promotes the proliferation of breast cancer cells by accelerating the cell cycle. Additionally, BPA exposure on macrophage cells suppressed the pro-inflammatory cytokine TNF-α mRNA levels. Based on these studies, it was hypothesized that BPS treatment would enhance Schwann cell viability and proliferation in a dose-dependent manner and decrease TNF-α production. To test this hypothesis, Schwann cells were incubated for 4.5 hours, 24 hours, and 48 hours with control media, ethanol, and incremental concentrations of BPS ranging from 1x10-7 M to 1x10-3 M. The ATP Glo titer assay revealed that 1x10-3 M BPS had a significant effect ($p<0.05$) on ATP production across all time points. Significant effects were also observed at 4.5 hours (1x10-7 M to 1x10-4 M, $p=0.0009238$), 24 hours (1x10-6 M to 1x10-3 M, $p=0.001082$), and 48 hours (1x10-7 M to 1x10-3 M, $p=0.00015$). The EdU proliferation assay showed the percentage of proliferating cells as 75.95%±5.95 at 1x10-7 M, 79.5%±4.5 at 1x10-6 M, 79.25%±1.75 at 1x10-5 M, and 87.35%±1.35 at 1x10-4 M, compared to the control at 69.3%±1.3, indicating an increase in proliferation for all treatments. Preliminary findings suggest a reduction in TNF-α production for all BPS treatments compared to the control. The results suggest that BPS stimulates cell proliferation, affects viability, and potentially inhibits inflammation in Schwann cells. An overproduction of Schwann cells due to BPS exposure in the environment can lead to cancer, autoimmunity, and limit their ability to support endogenous repair. (**179**)

Sontheimer, Danielle*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Regulation of malate dehydrogenase by phosphorylation: Exploring the role of T85 in enzyme function*.- The citric acid cycle is an important metabolic pathway in fuel metabolism. Metabolic pathways often utilize 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. Enzymes can be post-translationally modified which can affect both enzyme activity and metabolon formation. 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. In this study, T85D was of interest because of the importance of a phosphorylated T85 as a key residue in the MDH interface with citrate synthase (CS), as well as the role it may play in the mobile loop domain. The MDH-CS interface is of interest because citrate acts as an allosteric inhibitor towards malate dehydrogenase. Putative roles for T85, which occupies a key position within the mobile loop surrounding the enzyme active site, include regulating substrate specificity and positioning of the substrate for efficient catalysis. In the short term, this study will address whether phosphorylation of T85 is important for enzyme activity and has any dependence on changes in pH or temperature. A long term goal of this project is to assess whether this post-translational modification will affect interactions with key citric acid cycle enzymes, like citrate synthase. (**4**)

Soukup, Maria*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *What factors influence foraging group formation in house sparrows Passer domesticus*.- House sparrows (*Passer domesticus*) and other social birds often form dynamic subgroups while foraging. While the composition of these groups varies across foraging events, it is not entirely random, and the factors influencing individual foraging partner choices remain unclear. Here, we use field data, statistical analyses, and modeling to investigate the roles of genetic relatedness and kin recognition in shaping these foraging associations. Linear regression models were constructed to assess the relationships between number of clutch siblings and probability of foraging with clutch siblings, non-siblings, and alone, based on data collected from an RFID tagged house sparrow population foraging at two feeder stations. Results showed a positive correlation between number of clutch siblings and probability of foraging with siblings, as well as a negative correlation between number of clutch siblings and probability of foraging with non-siblings. Such preferential foraging tendencies indicate a previously unobserved clutch sibling effect and contribute to a larger dynamic subgroup formation framework. (**6**)

Sowers, Cassidy*, Amber Marble, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *Influence of anthelmintic medications on the aerobic bacterial populations of the equid gastrointestinal tract microbiome*.- Parasitic infections are a prevalent issue throughout equid populations. Anthelmintic medications are readily used to treat parasitic infections. These medications are selective toxins meant only to target parasites by interfering with the vital processes or structural dexterity required for the parasite to survive and reproduce. Research has not yet determined if anthelmintic medications influence the gastrointestinal tract (GIT) microbiome because a complete understanding of the microbiome has not yet been determined. There is a determined symbiotic relationship between the microbiome and the equid; the microbes have a safe place to propagate, and when the microbes break down highly fibrous materials (via fermentation), the equid is provided with the nutrient byproducts. The microbiome offers a majority of the equid's daily nutrient requirements. The influence of these medications on the aerobic bacterial populations within the GIT was tested by serially diluting fecal samples onto agar plates treated with Ivermectin, Panacur, or Pyrantel. Colony-forming units per milliliter (CFU/mL) were calculated, and a one-way analysis of variance indicated no significant difference between treatment groups. This implies that anthelmintics do not influence the concentration of bacterial growth in the equid GIT microbiome. Subsequent gram staining was used to determine whether anthelmintics influence the composition of bacterial populations in the equid GIT microbiome. Eight out of nine isolates tested were gram positive. Future research examining the entirety of the microbiome will be required to understand anthelmintics' impact on the equid GIT microbiome fully. (**8**)

Spencer, Gabrielle*, M. Dana Harriger, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Analysis of the digestibility of protein in canine pet food*.- The growing numbers of dog owners have increased the demand for commercial dog food production. An important parameter in product selection is the digestibility and nutrient availability of the dog food, specifically the protein content. Currently, the pet food industry produces several types of dog food; including kibble, bone and raw food (BARF), and freeze-dried, which all differ in processing, convenience, and potential health benefits. Kibble, the most common, offers convenience but is produced by high-temperature extrusion, having a potentially negative impact on the nutritional availability. BARF diets are typically fresh or frozen and consist of uncooked meat and bones to mimic a dog's ancestral diet. Freeze-dried dog food is lyophilized, removing water from frozen food producing a dry product using no heat and little processing. Protein content and bioavailability is key when assessing the final product for pet food as protein is crucial for growth, development and physiological functions. Gastric digestion was simulated to determine the protein digestibility of each dog food type. Freeze-dried dog food had the highest quantity of digestible proteins and the largest difference in protein concentration before and after simulated gastric digestion. Results of this study may help inform dog owners on food selection when considering digestibility and nutrient availability for their pets. (**9**)

Steele, Hailey*, Kathryn Sarachan, Amber Marble, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *The cytotoxicity of synthetic dye Red 40 and its metabolites* *cresidine-4-sulfonate and 1-amino-2-naphthol-sulfonic acid on the Caco-2 human colon cell line*.- The most consumed artificial dye in the United States is Red 40. This chemical, classified as an “azo dye”, is used in processed foods to enhance color and to entice the attention and desire of young consumers. As the consumption of ultra-processed foods has increased markedly over the past few decades, there has been an increase observed in the number of early onset colorectal cancer cases (EOCRC) along the same timeline. One contributing factor to the increase in colorectal cancer is the consumption of a high-fat diet, including these ultra-processed foods, which are likely to contain artificial dyes. This high-fat, low nutrient “Western diet”, has been shown to cause inflammation of the colon. A state of chronic inflammation is understood to pose a threat to healthy tissue and provide optimal conditions for carcinogenesis over time. This research aimed to assess the effect of Red 40 on the viability of human colon cells using an MTT assay. Since Red 40 is metabolized into cresidine-4-sulfonate and 1-amino-2-naphthol-6-sulfonic acid in the colon, the effects of the metabolites themselves were also tested. This study showed that Red 40 and cresidine-4-sulfonate, at varying concentrations, had statistically significant impacts on the viability of the human colon cells. The results of this study provide insight into potential preventative measures against the increasing cases of early onset colorectal cancer. In addition, the results are educational for the general public when selecting foods to purchase and consume. (**136**)

Stube, Judah*, Jordan Wilson*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Characterizing the role of QbsC and QbsD in antibiotic production in Alcaligenes faecalis strain DS8_19 from York County*.- The rise of antibiotic resistance necessitates innovative strategies for antibiotic discovery. Antibiotic-resistant bacteria pose a major threat to public health as traditional drug discovery efforts approach a standstill. Many antibiotics originate from soil-dwelling microbes that produce secondary metabolites with antimicrobial properties. DS8_19, an Alcaligenes faecalis strain isolated from the soil in York County, exhibits antibacterial activity against Bacillus subtilis. Due to this inherent capability, it is a promising candidate for the antibiotic crisis. Genome sequencing and antiSMASH analysis identified a biosynthetic gene cluster with homology to quinolobactin, an antimicrobial siderophore. While previous research links quinolobactin gene clusters to antibiotic activity, the specific contributions of the sulfur-transporting genes QbsC and QbsD within this cluster remain untested. The main objective of this study is to evaluate QbsC and QbsD to assess if they are responsible for antibiotic production in isolate DS8_19. The CRISPR/Cas9 gene editing system will be utilized to create a targeted knockout for QbsC/D. Disrupting these genes will reveal their role in antibiotic production. A loss of antimicrobial activity in the mutant strain compared to the wild type would suggest that QbsC/D contributes to antibiotic production. CRISPR plasmids were successfully constructed by HiFi Assembly and transformed into *E. coli*. The insertion of gRNAs was successful, as confirmed by colony PCR and sequencing. Future work should focus on transforming DS8_19 with the CRISPR construct to assess changes in antibiotic production, linking biosynthesis to the genes. This research contributes to efforts to link biosynthetic gene clusters to antibiotic production by performing a targeted gene disruption. Investigating the role of QbsC and QbsD will provide feedback on whether this gene cluster is responsible for antimicrobial activity in DS8_19. Ultimately, this work accentuates the promise of genomic mining in identifying new antibiotic candidates and expanding our understanding of bacterial secondary metabolism. (**96**)

Stults, Isabelle*, Roseann Sachs, and Janet Barroga-Matanguihan Messiah University, Mechanicsburg, PA 17055. *Agronomic evaluation and oil analysis of flax varieties (<u>Linum usitatissimum</u> <u>L.</u>) in South-Central Pennsylvania*.- Flaxseed (*Linum usitatissimum L.*) is a rich source of dietary fiber, alpha-linolenic acid, vitamin E and lignans. As a functional food, flax can be incorporated in people’s diet to prevent chronic diseases such as diabetes, colon cancer and cardiovascular diseases. In this study, six varieties were evaluated for their agronomic performance to identify those best suited to the environmental conditions of South-Central Pennsylvania. The varieties ‘Omega’, ‘Bright’, ‘Glas’, ‘Rowland’, ‘Hammond’, and ‘York’ were laid out in 3 m x 1.5 m plots in a randomized complete block design 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, 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 2024), weeds were removed manually and pesticides were not applied. The oil composition of each variety was determined by cold pressing oil from seeds and derivatizing as FAMEs, followed by analysis using GC-MS. Agronomic data show that ‘Omega’ flowered first at 42 days while ‘Rowland’ flowered last at 48 days (p=0.05). ‘Glas’, ‘Omega’, and ‘Bright’ had higher average plant height than the rest of the varieties (p = 0.05). ‘Bright’ had more seed capsules per plant than the other varieties (p=0.05). Oil analysis of the flax seed control samples and the 2023 harvested samples showed that ‘Rowland’ had the highest relative percentage of alpha-linolenic acid at 79% and 72%, respectively. ‘Bright’ and ‘Omega’ can be grown in areas with prolonged periods of high temperature, while ‘Rowland’ grows better in areas with cooler summers. Results show that flax can be grown successfully under environmental conditions in South-Central Pennsylvania, laying the foundation for incorporation of this crop in sustainable farming systems. (**147**)

Suter, Gavin*, Nicole Flanders, Gracie Harlow, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Evidence for enemy release in the invasive New Zealand mud snail*.- New Zealand Mud Snails (NZMS), *Potamopyrgus antipodarum*, are an invasive species that are widespread throughout the world and cause large-scale ecological damage. One of the most prominent hypotheses to explain why an invasive species is more successful in its invaded territory when compared to their natural habitat is the enemy release hypothesis. The enemy release hypothesis states that invasive species are able to outcompete native species due to the absence of natural enemies in the invaded environment. The purpose of this study was to examine populations of *Potamopyrgus antipodarum* from multiple locations in the mid-Atlantic region for infection and compare the rates of infection to the infection rates of native snails found in the same locations. We hypothesized that NZMS would be less parasitized when compared to native species collected from the same site. We sampled 461 NZMS and 289 native snails from 3 sites in the Musconetcong River, NJ. The most common symbiont was the annelid, *Cheatogaster limnaei*. A total of 10 NZMS and 47 native snails were infected with endoparasitic *Chaetogaster limnaei*, yielding a 2.2% and 16.3% infection rate respectively; 67 NZMS and 99 native snails presented with ectosymbiotic *Chaetogaster limnaei*, yielding a 14.5% and 34.3% association rate respectively. Statistical analysis demonstrated significant differences in endoparasitic and ectosymbiotic prevalence in NZMS compared to all natives, and when compared to individual natives. These results support the enemy release hypothesis. (**152**)

Tabakha, Maya*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *E-liquids disrupt macrophage phagocytosis against <u>Escherichia</u> <u>coli</u>*.- The use of e-cigarettes by adolescents has sparked concerns pertaining to its safety, especially its impact on oral health. Recent studies show that e-liquids result in aberrant morphology in macrophages and a change in gene expression involved in the immune response. Macrophages play a role in defense by phagocytosing bacteria. The aim is to explore this function under e-liquid treatment by performing phagocytosis assays using THP-1-derived M1 macrophages infected with *Escherichia coli*. CFU counts and qPCR reveal macrophages polarized with cinnamon e-liquids contain the least amount of bacteria compared to the control. The amount of bacteria found by CFU counts were less than those obtained through qPCR likely due to qPCR accounting for both intracellular and extracellular bacteria. This implies that the immune response is diminished under e-liquid treatment providing implications for bacterial defense specifically in periodontal disease. One major finding by our group is that oral pathogen, *Porphormonas gingivalis*, is able to escape macrophage phagocytosis and invade oral cells. Therefore, we plan to investigate its escape from macrophages and invasion into oral epithelial cells under e-liquid treatment. This research addresses the long-term health risks of e-cigarettes and provides a potential link between vaping and periodontal disease. (**184**)

Teisen, Rachel*, and David Foster Messiah University, Mechanicsburg, PA 17055. *Population of fishers (<u>Pekania</u> <u>pennanti</u>) in York County, Pennsylvania*.- *Pekania Pennanti* (fishers), were extirpated from the state of Pennsylvania in the early 1900's. The species was reintroduced approximately 90 years later in northern Pennsylvania. Surveys in 2007 and 2017 showed populations were established in all regions of the state except for the southcentral and southeastern. Images of fishers were captured on a camera trap in October and November of 2023 at Camp Tuckahoe in York County, which is the southcentral region of Pennsylvania. To confirm this presence, camera traps were set up in locations relative to the original cameras a year later. The motion-activated camera traps captured image bursts followed by video recordings and remained undisturbed for weeks. Multiple cameras captured images of fishers, indicating an established presence in the region. To determine that the captured images were of not a single animal, fixed points on the images (logs) were measured and compared to fisher body and tail length. This was used to create a scale on image software to measure the lengths of the animals. It was determined that two animals were captured due to their difference in size. One animal measured 145 cm, which, based on known size ranges, is indicative of a male. The other animal measured 90 cm, suggesting it is a female according to established size parameters. This provides strong evidence of the presence of both a male and female fisher in this region of Northern York County and suggests that fishers have been established in this area for at least 1.5 years. (**10**)

Thomas, Kloe*, Jordan Smith*, and Antonio Rockwell Susquehanna University, Selinsgrove, PA 17870. *The function of METTL3 during spermatogenesis in <u>Drosophila melanogaster</u>*.- The N6-methyladenosine modification (m6A) is the most abundant internal RNA modification. The m6A modification helps regulate gene expression in many developmental processes including spermatogenesis. METTL3 is an essential component of the writer complex required for the m6A modification. Our investigation aims to determine the role of METTL3 during spermatogenesis in Drosophila melanogaster. To study the function of METTL3, we used the Gal4/UAS system to ubiquitously knockdown METTL3. Specifically, we used an actin driver for the ubiquitous knockdown. In our knockdowns, we found a swollen tip morphology that often corresponds with a mislocalized hub. The swollen tip appears to also be closely related to abnormal muscle development suggesting a possible issue with gonad development. Additionally, we observed abnormal spermatid bundles and issues with waste bag localization. Overall, our preliminary results support previous studies and show a connection between the absence of the METTL3 gene and an abnormal spermatogenesis process in Drosophila. These findings may potentially contribute to a broader understanding of RNA modifications in biological systems and could have implications for future reproductive research. (**36**)

Thomas, Mercedes*, Ling Huang, and Jiangyue Zhang Immaculata University, Immaculata, PA 19345. *Comparison study of cannabis products using a benchtop NMR and a research grade NMR*.- The importance of analytical methods in forensic science remains relevant in seized drug analysis and its applications in law enforcement procedures. The testing of seized-drug samples is in high demand and requires sensitive and accurate instruments. Despite NMR spectroscopy being a highly regarded technique for identifying compounds through the spectra it produces, it is not a method commonly used in forensic laboratories. This forensic NMR project was undertaken in collaboration with Dr. Ling Huang of Hofstra University to contribute to the research being conducted comparing the capabilities of a benchtop 60 MHz NMR to that of a 400 MHz NMR. This is in part to make NMR spectroscopy a more widely used technique with more accessible options for smaller laboratories. There were 48 samples of cannabis-derived products containing THC, HHC, and CBD, which were tested using the Magritek benchtop 60 MHz NMR. Side by side comparison of the bench top NMR and high field NMR was performed. The results of our analysis provide quality spectra with identifiable features which has the potential to be used in the forensic field to identify cannabis derived products. (**31**)

Tomov, Sophie*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *The effects of cinnamon e-liquids on THP-1 macrophage differentiation and gene expression*.- While E-cigarette usage is continuing to increase in popularity, the notion that they are harmful to their 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 and CD80 are both 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 reversed transcribed to cDNA. The expression of MHC class II and CD80 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 expressed at lower levels 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 and CD80. E-cigarette usage is becoming increasingly more popular, a trend which depends on the notion that E-cigarettes are not harmful for the user. To challenge this misconception, it is imperative to understand the effects of E-liquids on the immune system and macrophage immunobiology in particular. (**109**)

Trainor, Maddy*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Evolving more alcohol-tolerant yeast for brewing*.- Ethanol tolerance is a key limiting factor in high-alcohol beer production, as most brewing yeast strains (*Saccharomyces cerevisiae*) cease fermentation around 12-14% ABV due to ethanol toxicity. This study aimed to enhance the ethanol resistance of the US-50 brewing yeast strain using ethyl methanesulfonate (EMS) mutagenesis to induce random point mutations. Mutant strains were screened on selective media containing increasing ethanol concentrations (12-18%), and those exhibiting sustained growth were used to brew beer. Mutagenesis resulted in five strains with alcohol tolerance up to 50% more than US-50. Mutant strains showed reduced fermentation rate compared to the parental US-50 strain. This suggests that while ethanol resistance increased, metabolic efficiency was compromised. Beer made with the parental and alcohol-tolerant strains were both found to contain isoamyl acetate and ethyl caproate by mass spectroscopy, while beer fron the alcohol-tolerant strain resulted in a slightly higher alcohol concentration. Future research will focus on identifying the genetic mutations responsible for ethanol tolerance, optimizing fermentation conditions, and evaluating the impact on flavor profiles to enhance both ethanol yield and beer quality. (**116**)

Tran, Thuy-Tien*, and Jiangyue Zhang Immaculata University, Immaculata, PA 19345. *Analysis of vitamin C antioxidant activity*.- This is a continuous quantitative study of Vitamin C (Ascorbic Acid) antioxidant activity using High-Performance Liquid Chromatography

(HPLC). In this redox reaction, Vitamin C reacts with Iron where the presence of this antioxidant stops the oxidation of Iron (II) to Iron (III) and is converted to dehydroascorbic acid. The initial concentration of the Vitamin C in “old” (expired) and “new” (fresh) commercially available Vitamin C supplements were also investigated. The expired Vitamin C supplement brands used were Osco (1995), Rite Aid (2018), 21st Century (2020), and Nature Made (2022) while the fresh Vitamin C supplement brands used were Force Factor, Bronson Basics, Nature’s Bounty, and Nature Made. All Vitamin C supplements were treated in the same procedure and extracted by distilled water. A calibration curve was created by obtaining the peak area through HPLC for various concentrations of stock ACS grade Ascorbic acid. The concentrations of Vitamin C in this study were determined using this calibration curve. Antioxidant activity was timed and quantified through the difference between the amount of Vitamin C before and after the addition of hydrogen peroxide to the reaction. Through the HPLC data, a decrease in Vitamin C concentration was observed which indicates that Vitamin C was consumed in this antioxidant activity. Through the use of ANOVA, no significant difference was observed ($p = 0.47$) for the antioxidant activity between expired and fresh categories, as well as between brands. A significant difference was observed ($p < 0.001$) for the initial amounts of Vitamin C for expired versus fresh categories for several brands, as well as for different brands within expired and fresh categories. (**22**)

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, and cadmium constitute abiotic stress and can be toxic to plants even in low concentrations in micromolar ranges. With the rise in industrialization, a need for hardy, genetically modified plants resistant to heavy metal ion toxicity has grown. In this study, we investigated the role of iron-regulated transporter 1, AtIRT1, in the response to nickel ion toxicity in *Arabidopsis thaliana* (*A. 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 plants accumulate more nickel in iron-deficient conditions. Nishida et al. (2011) showed qualitatively that irt1-1 (SALK_024525) and irt1-2 (SALK_054554) mutants were hypersensitive to nickel and showed chlorosis when grown in tissue culture in the presence of 50μM iron and 25μM nickel chloride ($NiCl_2$) compared to wild-type Col-0 plants. This study aims to extend the 2011 study quantitatively by investigating the effect of nickel on the average root length of wild-type and irt1 mutants in the presence of iron with a dosage response curve of nickel. Two T-DNA insertion irt1 mutants, irt1-1 (SALK_024525) and irt1-3 (CS869354), were studied. Both irt1-1 and irt1-3 mutants were shown to have no difference in root length compared to wild-type in the presence of $NiCl_2$. A third irt1 mutant, irt1-4 (SALK_097869), will also be studied to determine the effect of nickel toxicity on root length. (**146**)

Updegrove, Madelyn*, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *Finding antibiotic producers using the crowded-plate technique*.- Antibiotic resistance is estimated to cause up to 10 million deaths per year by 2050 and cost the world $100 trillion. One way to combat antibiotic resistance is to discover or develop new antibiotics. Tiny Earth is a non-profit organization that uses students to discover antibiotics from soil samples. A single gram of soil can contain up to 10 billion microorganisms, so soil is abundantly filled with bacteria. A crowded-plate method was used to obtain antibiotic producers by serially diluting & plating the soil samples on R2A media, then leaving them to grow for one to two months. After leaving the colonies to grow on the agar, the colonies were picked and patched, then screened against known bacterial species. Eight isolates were taken from six different soil samples, and one has been identified so far to be producing antibiotic properties against various bacterial species (MU1). MU1 was sequenced and its crude metabolites were extracted using ethyl acetate and methanol. Antibiotic resistance is a growing problem that needs to be addressed as soon as possible. (**99**)

Usher, Helene*, Owen Jenkins*, Zahraa Muhammad*, and Jaimy Joy La Salle University, Philadelphia, PA 19141. *The cytoprotective effects of sulforaphane in IMR-90 cells*.- Sulforaphane is a natural compound heavily concentrated in cruciferous vegetables known for its potent antioxidant, anti-inflammatory, and anticancer properties. Mechanistically, sulforaphane blocks cancer-causing mutations, promotes the DNA repair pathway, and activates the redox-sensitive nuclear erythroid 2-related factor 2 (NRF2) pathway, which leads to upregulation of the cell's antioxidant response. Senescence is a permanent state of cell cycle arrest activated in response to various stressors, such as DNA damage and reactive oxygen species (ROS) accumulation. Though cells enter such senescence as a protective mechanism, an accumulation of senescent cells over time has been shown to lead to age-related decline and disease, including cancer. There are few studies addressing the relationship between sulforaphane and senescence. We seek to investigate the role(s) of sulforaphane on DNA damage and the onset of cellular senescence in a primary human fibroblast cell line, IMR-90. Towards this, we assess whether sulforaphane protects cells against DNA damage using single cell gel electrophoresis following treatment with etoposide, a chemotherapeutic agent. Given that etoposide treatment normally induces senescence in IMR-90 cells, we also assess the levels of cellular senescence in the presence of sulforaphane using a beta-galactosidase assay. As sulforaphane has antioxidant properties, we also investigate how the compound influences H_2O_2-induced ROS levels and oxidative stress-induced senescence. The results of this study may provide insights into the therapeutic effects of sulforaphane in the reduction of DNA damage, ROS accumulation, and cellular senescence triggered by these stressors. (**44**)

Vana, Aurora*, Rhiannon Toy*, and Joe Adserias-Garriga Mercyhurst University, Erie, PA 16546. *The use and prevalence of post-cranial antemortem trauma, pathology, and variation in human identification*.- One of the most important aspects of a forensic investigation is the identification of the remains. Forensic anthropologists can assist with identification through skeletal analysis. In this sense, skeletal pathology, antemortem trauma and anatomical variation offer critical information that may assist in the identification of the deceased. This preliminary study aims to evaluate the skeletal traits that could potentially be used for personal identification. This project included twenty-one individuals from the Donated Skeletal Collection of the Applied Forensic Sciences Department at Mercyhurst University. Antemortem trauma, pathological signs, and skeletal variation were analyzed and catalogued for each donor, noting the frequency and type of each. Pathology was the most common overall with seventeen out of the twenty-one donors. Fusion of the pelvis, fusion of vertebrae, and bony overgrowth were the most frequent pathological signs. Antemortem trauma was the second most common with ten donors having evidence of surgery or healed fractures, which are highly individualistic. Anatomical variation was the least frequent category with only three donors. Each of the three categories was then broken down into detailed traits or diagnosis. The pathological entities found in the sample were fusion and bony overgrowth of different skeletal areas. Antemortem trauma signs found included hip replacement, knee replacement, and healed fractures. Anatomical variations found consisted in scapular foramen and supernumerary vertebrae. Taking into account all the results obtained, supernumerary vertebrae, lower limb fusion, and hip replacement were the least frequent in the sample, although all healed fractures and surgery procedures and the presence of surgical devices are the most individualizing traits. (**85**)

Van Vlaenderen, Lore*, Jocelyn Lu, Josh Mirsky, and Dylan Shropshire Lehigh University, Bethlehem, PA 18015. *A bacterial weapon: a novel domain that enhances insect sterility*.- *Wolbachia* is a maternally transmitted bacterium that lives in the cells of over half of all insect species. Cytoplasmic incompatibility (CI), a *Wolbachia*-induced trait, increases the bacterium's rate of spread by killing *Wolbachia*-free embryos fertilized by *Wolbachia*-bearing males. However, CI strength varies, with strong CI (high egg mortality) being crucial for *Wolbachia*'s prevalence. The molecular basis of CI-strength variation is unknown. Knowing why CI strength varies is important because CI is used to spread pathogen-blocking *Wolbachia* strains through mosquito populations to protect humans from deadly diseases. CI is caused by the *Wolbachia* protein CI factor B (CifB). cifB transcript levels often align with CI strength. However, wBai *Wolbachia* of *Drosophila baimaii* are an exception, killing nearly all embryos during CI, yet expressing cifB at levels resembling *Wolbachia* strains that do not cause CI. Most CifB proteins, typified by those of the wMel *Wolbachia* used in mosquito interventions, possess three distinct functional regions. wBai's CifB maintains these familiar regions and has a novel domain with structural similarity to the AvrPphB protein in a plant pathogen. Known as a bacterial countermeasure against host defenses, AvrPphB might be the key that unlocks wBai's enhanced CI. To investigate this, we created transgenic *D. melanogaster* flies with cifB genes from both wBai and the reference strain wMel, demonstrating that cifB transgenes with the AvrPphB-like domain cause stronger CI than those without it. These findings directly link the AvrPphB-like domain to increased CI strength, represent the first successful genetic manipulation of CI enhancement, provide insights into novel CI mechanisms, and reveal a surprising parallel between insect-endosymbiont interactions and plant-pathogen warfare. Because strong CI is essential for *Wolbachia*'s prevalence in both natural and applied settings, understanding the mechanisms underlying CI strength variation is crucial. (**141**)

Velastegui, Michelle*, Chloe Benjamin*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *From bacteria to bugs: Bridging gene expression across domains*.- This research is the starting point for multiple parallel projects that utilize *Escherichia coli* for both the expression of protein products and dsRNA. The former allows for the exploration of protein structure and function in the prokaryotic cell with site-directed mutagenesis drawing a connection between specific amino acid residues and functionality. The bacterial enoyl-[acyl-carrier-protein] reductase (fabI gene product) that is essential for fatty acid biosynthesis and the impact of alterations to its triclosan binding site were investigated through these overexpression studies. In addition, overexpression of two isoforms of the insecticyanin blue biliprotein from *M. sexta* were also explored in *E. coli*. In contrast, the dsRNA produced by the *E. coli* cells will be used to evaluate the functional consequences of gene silencing via RNA interference (RNAi) when the cells are incorporated into the diet for the model organism, *Manduca sexta* (tobacco hornworm). Once proof of concept studies using the blue biliprotein have demonstrated the feasibility of RNAi in *Manduca*, studies will transition to investigation of lipidation and fatty acid biosynthesis. By analyzing the effects of reduced gene expression on organismal physiology, development, and behavior, this study aims to expand our understanding of gene function in both prokaryotic and eukaryotic systems and explore the potential of RNAi-based gene regulation in diverse biological contexts. (**129**)

Ventura, Caitlyn*, Christina Ventura*, and Austen Barnett DeSales University, Center Valley, PA 18034. *Exploring the genetic input of germline development in the arachnid Archegozetes longisetosus*.- The development of primordial germ cells (PGCs) in animals occurs through either the inheritance of maternal germline molecules (the inheritance model) or by signaling from other cells (the induction model). Studies of model arthropods (the clade including insects, crustaceans, and arachnids) have suggested that the inheritance model is ancestral to the clade. However, the observation of both mechanisms amongst different arthropod taxa suggests that this mode is evolutionarily labile. Studies into the formation of germ cells in the basal arthropod taxon Chelicerata, which includes arachnids and horseshoe crabs, has only been molecularly characterized in a single spider species, and a derived mite species. To expand upon the current state of our knowledge on chelicerate and arachnid

PGC formation, we followed the development of PGCs in the model mite *Archegozetes longisetosus*. We find that, like spiders, PGCs form from endomersodermal cells arising from the embryonic cumulus. Furthermore, these PGCs express the molecular parker piwi, but surprisingly, the germline marker vasa is not highly expressed in their PGCs. We conclude that the gene piwi is an ancestral factor in arachnid PGC formation, and that PGCs form through inductive mechanisms. (**37**)

Watson, Emilie*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Identifying Mushroom Species using Polymerase Chain Reaction*.- Mushroom species are typically identified using physical characteristics but sometimes these characteristics can be inconsistent due to environmental factors. Quick and accurate identification of mushroom could be beneficial for all different kinds of laboratory research. PCR is a laboratory technique that is can be used to detect and amplify sequences of DNA or RNA. PCR can be used to identify species of plants and fungi but the process is often long and tedious. To address this, in the study, we selected nine different species of mushroom cultures and we are going to modify and optimize a process for using PCR to identify mushroom species quickly and accurately. We selected *Agaricus bisporus*, *Coprinus atramentarius*, *Cortinarius sp.*, *Amanita pantheria*, *Russula brevipes*, *Boletinellus merulioides*, *Calvatia gigantea*, *Pleurotous ostreotus*, and *Lentinula edodes*. In order to prepare the mushroom cultures for DNA extraction we used a developed protocol that combines microwaving, cooling, and centrifuging. The DNA obtained will be used for PCR testing. We will use the results to see if we can accurately identify the mushrooms by knowing their species and then comparing the DNA sequencing we get from the PCR testing. (**177**)

Wiegand, Sydney*, Hannah Bojczuk, Brice Hansen, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Characterization of Endobacteria Isolated from Wild Mushrooms from Allegheny National Forest*.- Wild mushrooms, as well as bacteria are necessary in the environment for nutrient cycling and benefits to the overall health of the ecosystem. However, the interactions between mushrooms and bacteria and how they impact the environment are not well understood. There is especially limited knowledge on endobacteria living in mushrooms. To identify and characterize endobacteria from mushrooms, numerous tests were performed on bacterial strains isolated from ten different types of wild mushrooms. 16S ribosomal RNA sequencing revealed that the species *Ewingella americana* was found in 70% of the mushrooms, suggesting that similar bacteria are found in a diverse range of mushrooms. A citrate slant test displayed positive results for the citrase enzyme in most of the bacterial isolates, suggesting that they might be able to use citrate as an energy source. Several of the isolates were cold tolerant, exhibiting growth at freezing temperatures (0°C). This suggests that wild mushrooms typically harbor cold tolerant bacteria, which may be able to survive colder seasons. A phosphatase activity test on Pikovskayas agar revealed that many of the bacteria were able to solubilize phosphate, which could potentially aid growth in mushrooms. Further understanding of endobacteria in mushrooms is crucial because of their role in nutrient cycling and the consumption of mushrooms as a food crop. (**174**)

Wingard, Jacob*, and Meda Higa York College of Pennsylvania, York, PA 17405. *In search of novel silent antibiotics produced by Serratia marcescens*.- Since the discovery of antibiotics, scientists have been warning the world about the potential of antibiotic-resistant strains that would become invincible and render current treatments useless. Unfortunately, commonly resistant bacteria (known as ESKAPE pathogens) have already appeared. In past research, our goal was to identify and isolate bacteria that produce novel antibiotics that can be used to fight these ESKAPE pathogens. To do this, we have isolated soil bacteria that produce antibiotics against a panel of ESKAPE pathogen safe relatives. The isolate 1RB21_21 was identified as *Serratia marcescens* through whole genome sequencing, and the genetic informatics tool, antiSMASH was used to identify the secondary metabolite biosynthetic gene cluster, prodigiosin. The bacteria *S. marcescens* and the antibiotic prodigiosin are both highly studied; however, recent discoveries of “silent” or hidden antibiotics are being discovered in other well-known bacteria strains that produce known antibiotics. To do this, researchers disrupt production of the established antibiotic, and test the mutant strain against ESKAPE pathogens, looking for antibiotic production. We are attempting to test this idea by using a CRISPR/Cas9 construct to mutate the prodigiosin production pathway. We have successfully constructed a Cas9 and gRNA plasmid construct to mutate the gene pigC in the prodigiosin pathway; we are working to transform the plasmid into S. marcescens using electroporation. Upon completion, we hope to see zones of inhibition against ESKAPE pathogens safe strains change, telling us whether prodigiosin is the main antibiotic of S. marcescens. Further, this research could lead to the discovery of a silent and potentially novel antibiotic produced by S. marcescens. These perhaps obscured antibiotics can breathe life into “exhausted” bacterial strains that might still harbor antibiotics to combat antibiotic resistance. (**78**)

Wolfgang, Jessica*, Francesca Giardini, Vaughn Shirey, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Plant vigor is occurring on oak leaves after a wildfire in the New Jersey Pinelands National Reserve*.- Fires are becoming more frequent and severe due to anthropogenic climate change. Former studies have supported that fires have the ability to increase plant growth rate compared to adjacent unburned sites, which has been termed Plant Vigor (PV).In the NJ Pinelands National Reserve (PNR), wildfire frequency is at some of the highest in the country. To combat these wildfires, prescribed fires are often implemented, thus, it makes an ideal opportunity to test if plant vigor is occurring in the PNR. We predicted that oak (*Quercus spp.*) leaves would grow faster at our wildfire and two prescribed fire sites compared to our two unburned sites. At each site, 20 oak leaves were collected between May and September of 2018. To determine how vigorously the leaves were growing throughout the season, we calculated the leaf area by tracing each leaf on 0.5x0.5 cm^2 grid paper. We then used a linear regression to determine the growth rate for the oak leaves at different sites throughout the growing season. Using 1,724 leaves (unburned: 709 prescribed: 696, wildfire: 319), our preliminary results indicate that oaks grew fastest to slowest at our unburned, prescribed, and wildfire site, respectively, throughout the season. However, the average oak leaf area at the wildfire site was highest at the beginning of the season (May to June) compared to our other sites. Therefore, our prediction was supported, that oaks are going through plant vigor, but immediately in the beginning of the growing season and not throughout the season. It is possible that oaks have high resilience after wildfires because they immediately grew fastest sooner after the wildfire occurred. Additionally, oaks might be investing into their woody structures (e.g., trunk and branches) throughout the season which could explain why they were not going through plant vigor throughout the growing season. (**74**)

Wolf, Judith*, Amber Marble, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *The effects of lipid synthesis inhibitor ND-630 on fungal species Aspergillus fumigatus, Candida albicans, and Cryptococcus neoformans in comparison to fluconazole*.- The fungal species *A. fumigatus*, *C. albicans*, and *C. neoformans* are all WHO priority level fungal pathogens that are common in everyday environments. Excessive exposure or immunodeficiency can cause disbalance between host immune system and fungal virulence factors, leading to overgrowth and ultimately infection of all three species. Current prescribed antifungals, such as fluconazole, used to treat fungal infections are becoming less effective due to rising antifungal resistance. This study explores fatty acid synthesis inhibition as a potential antifungal route through fatty acid synthesis inhibitor ND-630. ND-630 is an allosteric inhibitor of acetyl-CoA carboxylase I. All three fungal species were tested against ND-630 and fluconazole, as well as synergistically at increasing concentrations. Cell viability was determined with an MTT assay. Individual results were analyzed utilizing a linear regression analysis and synergistic results were analyzed using a Bliss Independence test. Results of the individual test indicated that ND-360 had a lower minimum inhibitory concentration when exposed *C. albicans* than fluconazole, and fluconazole had a lower minimum inhibitory concentration when exposed to *C. neoformans* than ND-630. The linear regression analysis indicated a negative linear relationship between increasing ND-630 concentration and *C. neoformans* viability and increasing fluconazole concentration and *C. albicans* viability. Based on the minimal inhibitory concentrations, ND-630 was had more potent toxicity against *C. albicans* than *C. neoformans*. The Bliss Independence test determined that ND-630 and fluconazole did not have synergy when used in a one-to-one concentration ratio. Although the effects of ND-630 on fungal infections has yet to be determined in vitro or in vivo, this study was able to determine the validity of limiting fatty acid synthesis on cell viability for the given species. (**121**)

Wright, Grace*, and Rose Mulligan Immaculata University, Immaculata, PA 19345. *Differentiating raman spectra of plastics using principal component analysis*.- Recycling plastics can be challenging because there are various compositions the plastic can be made out of which require it to be recycled differently. The indicators placed on plastics during the time of manufacturing can be damaged in marine environments requiring further testing for identification. Raman Spectroscopy has been used to distinguish the different types of plastics, and the statistical analysis, Principal Component Analysis (PCA), has been used to organize large sets of spectral data. PCA clusters data based on similarities, helping the identification of plastics. By applying PCA on the spectrum data of recycled plastics, it was hypothesized that we would be able to see distinct clusters form, respective to a plastic type. This would allow an unknown sample to be analyzed and classified into a plastic cluster. However, the results showed insignificant evidence to support distinct spectral differences between plastic types. There is a single cluster that covers the score plot, which has data from 5 different types of plastics. The lack of separation does not support my hypothesis. This shows that there are spectral variations due to other components in the plastic formulations, such as dye. Further steps must be taken to take clearer spectrum data and account for additives. (**26**)

Wright, Kylie*, Deborah Austin, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *Assessing the correlation between California Mastitis Test results and somatic cell counts in caprine milk*.- As caprine dairy farming continues to grow, reliable diagnostic tools for mastitis are necessary for herd health and milk quality. The California Mastitis Test (CMT) is widely used for detecting mastitis in bovines. Its reliability in caprines is debated due to species-specific differences in lactation physiology. Unlike bovine somatic cell count (SCC), caprine SCC milk can be influenced by factors such as stage of lactation and stress. The CMT lyses somatic cells with a detergent, releasing DNA and forming a gel-like substance proportional to the SCC. The CMT scoring system assigns results of positive, negative, or trace, each corresponding to an estimated SCC value based on bovine data. While many countries do not rely on SCC for caprine mastitis detection, the U.S. Food and Drug Administration mandates a SCC limit of 1.5×10^6 per mL. This study examined the relationship between CMT results and SCC in caprine milk to evaluate the test's reliability and limitations. A total of 140 milk samples were collected and analyzed using both the CMT test and a SCC. Results indicated that positive CMT scores consistently corresponded with high SCC values and negative results generally aligned with low SCC. Trace CMT scores yielded variable SCC results. These findings suggest that while CMT is a useful screening tool, its accuracy is more reliable at the high and low ends of the spectrum but remains uncertain for trace infections. The findings of this study could help refine mastitis management strategies in dairy caprine herds, ultimately supporting milk quality and animal health. Additional diagnostic methods, such as bacterial cultures, should be evaluated to enhance mastitis detection accuracy in caprines. (**43**)

Zerebilov, Rozalia*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Comparison of ethanol and acetaldehyde exposure on developing zebrafish*.- Fetal Alcohol Syndrome (FAS) is a disorder caused by fetal exposure to ethanol in the womb. FAS causes an array of physical, behavioral, and mental disabilities. Some of which are attributed to myelin deficits in the central nervous system (CNS). Oligodendrocytes (OLs) are the myelinating cell of the CNS, that maintain the rapid signal transmission in myelinated axons. Ethanol has four metabolites, one being acetaldehyde. The contribution of acetaldehyde to ethanol toxicity is debated amongst the scientific community. We hypothesized that acetaldehyde is the driver of ethanol effects in myelination and will have similar but exaggerated effects to ethanol. The effects of two concentrations (0.2% and 0.5%) of acetaldehyde and ethanol were assessed in 36hpf and 56hpf zebrafish, which encompass two important stages in oligodendrocytes progenitor migration and myelination during development. Acridine Orange (AO) staining was completed to compare death in 36hpf embryo following 1- and 2-hour treatment of 0.2% and 0.5% acetaldehyde and ethanol. Gene expression of myelin and oligodendrocyte-specific proteins MAG, MPZ, Olig1 and nkx2.2a was analyzed. FluoroMyelin staining was used to compare overall myelination between treatment groups. It was concluded that the same concentrations of ethanol and acetaldehyde have significant differing effects on survival in our FAS zebrafish model. (**137**)

Ziegler, Benjamin*, Cora Zilinski, 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 a 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 expresses 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. (**89**)

Zilinski, Cora*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Quercetin shows no antiviral activity toward the Human Coronavirus 3C-like Proteases of HCoV-HKU1*.- 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. Quercetin is a naturally occurring flavonoid that can be found in many fruits and vegetables as well as some medicinal botanicals such as, *Ginkgo biloba*, and *Hypericum perforatum* (St. John’s wort). Quercetin has antioxidant and antimicrobial effects and has been shown to have antiviral activity. Specifically, polydatin has been shown to have potent inhibitory activity against the coronavirus 3C-like proteases (3CLpro) from SARS-CoV 2 and some inhibitory activity against the papain-like protease (PLP). However, it is unclear whether quercetin targets 3CLpro other human coronaviruses including HCoV-HKU1 that cause the common cold. Using chimeric reporter mouse hepatitis virus (MHV), that expresses the 3CLpro of HCoV-HKU1 in place of the MHV protease, we tested for virus inhibition by quercetin. First, a broad range of concentrations were tested for cell viability. The concentrations that did not kill cells were used for testing antiviral activity. When cells are treated with polydatin at the time of infection it decreases viral syncytia formation. Ongoing studies will further test the effects of this compound on the 3CLpro of HCoV-HKU1. (**90**)

Zinn, Hannah*, and Tej Man Tamang York College of Pennsylvania, York, PA 17405. *Exploring the role of glutaredoxin, GrxS16, in improving root development under salt stress*.- Over 6% of the world's total land area and 20% of irrigated land experience salinity stress. Salinity stress causes hormonal and nutritional imbalances, ion toxicity, and oxidative and osmotic stress. Salinity stress also leads to the overaccumulation of reactive oxygen species (ROS) that can significantly impair the biochemical activities of plants. Such impacts can be mitigated by strengthening the antioxidant defense system that detoxifies ROS. Glutaredoxins (GRXs) are small glutathione-dependent oxidoreductases that play a role in ROS scavenging. This study investigates the role of glutaredoxins in response to salinity stress using genetically edited tomatoes developed with the CRISPR/Cas9 approach. Wild-type (WT), Slgrxs14, Slgrxs16, and Slgrxs14:s16 mutant lines were treated with varying concentrations of NaCl (0 mM, 50mM, 100mM, and 200mM) and their phenotypes were documented. The results suggested that plants exhibited stunted growth and abnormal root development at increasing salt concentrations. Significantly longer root lengths and lateral root numbers were also observed in GrxS16 mutant plants, indicating that GrxS16 may play a role in lateral root development under salinity stress. Future studies will be conducted to explore the roles of GrxS16 in root development using a gene overexpression approach. (**163**)

Zivny, Kassandra*, and Jane Cavender Elizabethtown College, Elizabethtown, PA 17022. *Correlation of SV40 T-antigen Viral Oncoprotein Accumulation with Aggressive Growth Characteristics of Transformed Human Diploid Fibroblasts*.- It is estimated that 20% of human tumors have viral etiology yet the scientific community lacks data correlating the accumulated levels of viral oncoproteins to aggressive growth. This threshold effect is difficult to assess, due to the genetically diverse origins of tumors. Our study took advantage of two clonal cell lines isolated from telomerase-immortalized human diploid fibroblasts (HDFtert) stably transfected with the early region of simian virus 40. Upon screening clones, by immunoblot, it was found that HDFT1 accumulated less T-oncoprotein than HDFT2. These lines were used to investigate whether the increased level of oncoprotein expression translated to more aggressive transformed properties of increased metabolic activity and growth rate, anchorage independence, high-density growth, and growth in low serum. Metabolic activity was measured with MMT and CCK8 assays, and the soft agar assay was used to assess anchorage-independent growth. For growth rate, reliance on serum, and high density, cells were seeded in triplicate into 12-well dishes, harvested, and counted at 48, 72, and 120 hours. Our data showed that, unlike the immortalized HDFs, both transformed lines were anchorage-independent, proliferated in 0.1% serum, and exhibited increased growth rates. Interestingly, once confluent, cells expressing more T-antigen (HDFT2) maintained increased growth rates (p=), most notably in low serum (p=), and achieved higher cell densities (p-value 0.04). Thus, it appears that high oncoviral expression is advantageous under stressful environmental states but is unremarkable under favorable conditions. Experiments are underway to determine if oncoviral expression decreases under stress; thus, higher initial levels would persist longer allowing for the maintenance of aggressive growth characteristics. (**183**)

Zultevicz, Victoria*, and Brian Williams King's College, Wilkes-Barre, PA 18711. *Synthesis of bridged bicycles - compounds with medicinal applications*.- Bridged bicycles exist as important substructures of larger molecules, many of which exhibit biological activity. Carnosol, taxol, absinthin, eucalyptol, huperzine-A and epibatidine are examples of interesting compounds containing bridged bicycles. Previous research has shown the potential to form bridged bicycles by reactions of enamines with bis-electrophiles although the utility of this method has not been fully developed. The objective of this research was to explore the versatility of this cyclization reaction by varying the enamines and bis-electrophiles used in the cyclization process. In the research presented, 1,3-bis electrophiles were conjugated acid chlorides synthesized from the reaction of carboxylic acids with thionyl chloride followed by purification by distillation. Enamines were synthesized using a Dean-Stark trap to promote the reaction of cyclic ketones with morpholine. By incorporating cyclic 1,3-bis electrophiles and cyclic enamines in the cyclization reaction, four novel [n.3.1]-bridged bicyclic compounds with aromatic and non-aromatic five and six-membered fused rings were synthesized. Products were purified by filtration, extraction, and chromatography and analyzed by GC/MS, NMR, and X-ray crystallography. (**25**)