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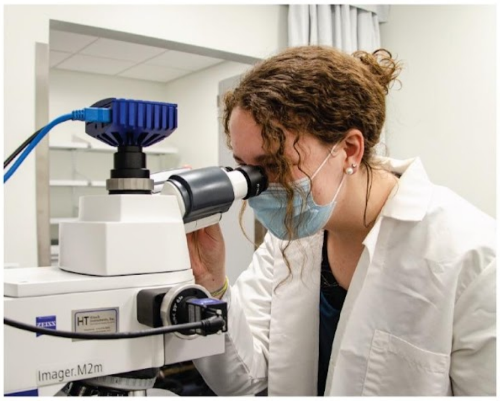

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Adams, Samantha*, and Garrett Barr King's College, Wilkes-Barre, PA 18711. *Effects of fish on salamander feeding*.- Predators can have lethal and non-lethal impacts on their prey. In the presence of fish, larval salamanders may reduce their foraging activity, and laboratory experiments show this results in decreased prey consumption. Our study compares the stomach contents of larval salamanders in fish and fishless streams. We collected 10 two-lined salamander larvae (Eurycea bislineata) from each of 3 fish and 3 fishless streams in Northeastern Pennsylvania. In the lab, we removed and identified prey items from stomachs and used length-mass relationships to estimate the biomass of prey in each salamander. Our results will help us better understand the non-lethal impacts of fish on salamander larvae. In addition, we will compare our results from this study to previous experiments that addressed similar research questions in a laboratory. (**24**)

Adedokun, Hope*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Characterization and impact of chemical hypoxia on oligodendrocyte myelination of Danio rerio (zebrafish)*.- During hypoxia, oligodendrocyte precursor (OLPs) are prevented from generating functional oligodendrocytes, causing disruption of myelination. This study aims to continue prior exploration of the effectiveness of a sodium sulfite hypoxia model, as well as its effectiveness in studying oligodendrocyte development in Danio rerio (zebrafish) embryos. In chemical hypoxia, zebrafish embryos (55 hours postfertilization) are placed in one of two solutions: the control or sodium sulfite (less than 0.5 mg/mL dissolved oxygen). After zebrafish embryos were exposed to chemical hypoxia and underwent a subsequent recovery period, a mortality rate of nearly 0% was observed. We also examined hypoxia’s effects on *OLIG1* and *SOX10* expression at 24 hours post-hypoxia. In addition, protocols for nuclear isolation were developed in order to study the translocation of *FOXO1A*, a regulator of responses to oxidative stress, recently linked to oligodendrocyte myelination in zebrafish. (**121**)

Ajirotutu, Adesewami*, Amber Marble, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *Exploring the link among visible signs of aging, age perception, stress, and telomere-associated qPCR Ct values*.- In humans, telomeres are repeats of TTAGGG sequences. They are found at the end of chromosomes, serving as protective caps that help to preserve genomic stability. Telomeres play a key role in cellular aging by protecting the ends of the chromosomes from degradation and inappropriate repair mechanisms. Over time, telomere length shortens with each cell division, contributing to visible and physiological signs of aging. However, telomere length does not decrease solely as a result of biological processes; research shows that TL can shorten as a result of environmental and lifestyle stressors. This research examined the relationships between visible aging signs, age perception, perceived stress, and quantitative polymerase chain reaction (qPCR) cycle threshold (Ct) values. DNA samples were collected through buccal swabs and analyzed using qPCR. Participants provided demographic information, completed the Perceived Stress Scale (PSS), and submitted photographic data; used to assess visible and perceived age. Perceived age assessment was conducted using Copilot AI to provide objective comparison of perceived and chronological age. A strong positive correlation was found between chronological age and perceived age ($r = 0.867$, $p < 0.001$), showing that the perceived ages were generally close to participants chronological ages. However, sample telomere Ct values did not show significant relationships with chronological age, perceived stress, physical activity, or visible aging measures. The telomere Ct values were also not significantly associated with whether participants appeared older or younger than their chronological age. In all, this research suggests that in a small sample, biological aging markers and visible aging does not always align. (**118**)

Al-Maleki, Shahraban*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Characterization of endophytic Sphingomonas from aerial plant tissues*.- Sphingomonas species are recognized as aerobic, Gram-negative, non-fermentative, rod-shaped bacteria commonly found in the environment, water, and clinical settings. However, Sphingomonas species have many different prevalences and functions depending on where they were isolated from. In this study, we isolated six Sphingomonas species from fruits, ivy leaves, and flower petals from diverse environments and examined their general characteristics. Using 16S rRNA sequencing, we found that the isolates corresponded to the Sphingomonas species, S. faeni, S. gacialis, S. endophytica, and S. aerolata. All or nearly all isolates tested were pigmented and psychrotolerant at 4°C, along with sugars promoting growth. The exception was the fruit S. sanguinis that appears to have thermotolerance (up to 45°C) since it was isolated from a tropical fruit. Finally, all isolates were able to promote growth with sugars such as lactose, maltose, mannitol, and sorbitol. Thus, this study documents common traits and adaptations in various Sphingomonas species, and the presence of these isolates in plant, floral, and fruit organs implies certain characteristics of inheritance of these isolates. (**8**)

Amram, Juliette*, Sara Gill*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Mucin and tight junction gene expression in OKF6 cells after E-cigarette aerosol treatments*.- The rising prevalence of electronic cigarette (ECIG) use, particularly among youth, has prompted growing concern regarding its impact on oral health. Although ECIGs are often marketed as a safer alternative to traditional cigarettes, emerging evidence suggests they may exert harmful effects on the pulmonary and cardiovascular systems. As the oral cavity serves as the primary site of exposure to ECIG aerosols, recent studies have begun to associate vaping with the development of periodontal disease. Understanding how ECIG use alters the oral microbiome is essential, given its broader implications for systemic health. This study examines the effects of flavored E-liquid aerosols on the expression of mucins and tight junction proteins in oral epithelial cells. OKF6 cells were grown as monolayers and exposed to media with 100 puffs of aerosol for 24 hours. Total RNA was extracted, reverse-transcribed into complementary DNA (cDNA), and amplified by quantitative polymerase chain reaction (qPCR). Specifically, gene expression levels of MUC1, MUC4, MUC5B, TJP1, occludin, claudin, and human beta-defensins 2 and 3 were analyzed. Upregulation was observed in the majority of these genes, mirroring gene expression patterns commonly associated with carcinogenesis. These findings support the hypothesis that flavored ECIG exposure induces significant pathophysiological changes in the OKF6/TERT-2 in vitro model, highlighting potential cancer risks associated with ECIG use. Such alterations may contribute to the development of more severe oral conditions. Given the well-established link between oral and systemic health, further investigation into the toxicological and pathological effects of flavored ECIGs on oral tissues is warranted. (**62**)

Apiolaza, Rachel*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Extraction, quantification, and antioxidant potential of tannic acid from various oven-dried fruit flesh and skin*.- The results of this study are part of an investigation to extract, identify, and quantify the antioxidant tannic acid present in the flesh and skin of select fruit samples. Soxhlet extractions using 95% ethanol as a solvent were performed on oven-dried flesh and skin of lemon (*C. limon*), lime (*C. x latifolia*), grapefruit (*C. x paradisi*), persimmons (*D. kaki*), and dragon fruit (*H. undatus*). Extracts were analyzed using ultraviolet (UV) spectroscopy at a maximum absorbance wavelength of 276 nm to identify and quantify tannic acid compounds present in each sample. Quantification was performed using a standard calibration curve to determine tannic acid equivalents across all samples. The antioxidant potential and properties of each extract were further evaluated using a Ferric Reducing Antioxidant Power (FRAP) assay and compared to known antioxidant standards. Antioxidant activity was determined through the reduction of ferric ions and the formation and detection of reactive oxygen species, which were measured using visible spectroscopy at 590 nm in a 96-well plate. Citrus fruits exhibited higher tannic acid concentrations compared to the non-citrus fruits analyzed. In several cases, fruit flesh contained greater tannic acid content than the corresponding skin samples. FRAP assay results followed similar trends, with citrus fruits displaying greater antioxidant capacity than the non-citrus fruits. Although overall patterns between tannic acid content and antioxidant activity were consistent, the relationship was not strictly proportional, suggesting the presence of additional phenolic compounds contributing to antioxidant activity within the fruit extracts. (**42**)

Atroshyna, Daryana*, Kendra Schlitzer, Amber O'Connor, and Florence Ling La Salle University, Philadelphia, PA 19141. *Effects of saturation index, ion competition, and salinity on As and Cr coprecipitation into barite BaSO4*.- Engineered systems, e.g., oil and gas operations and geothermal energy power plants, often produce saline wastewaters rich in Ba2+ and other hazardous metals. One proposed treatment method involves adding Na_2SO_4 to produce barite ($BaSO_4$) solid solutions that coprecipitate with the hazardous ions. Here, we examine coprecipitation of toxic As and Cr anions into barite. We conducted experiments with varying saturation indices (SI) of $BaSO_4$, $BaHAsO_4$, and $BaCrO_4$, ranging from 0.37 to 3.27, -2.22 to 0.18, and –2.94 to 2.74, respectively. Experiments were conducted with no NaCl and at 1.0 M NaCl. As, Ba, and Cr concentrations were measured using inductively coupled plasma-atomic absorption spectroscopy (ICP-AES). Experiments showed that higher $SIBaSO_4$ produced more solids that removed fewer trace ions. Low $SIBaSO_4$ resulted in greater total As and Cr removal, suggesting slower nucleation and growth may cause inclusion of more trace elements into the solid. When comparing As and Cr trace ion coprecipitation into solid solution, the less soluble solid $BaCrO_4$ incorporated more readily into $BaSO_4$ solid solution than the more soluble $BaHAsO_4$ phase. Removal of As increased with the product of the individual mineral saturation indices, $SIBaHAsO_4$ with $SIBaSO_4$, suggesting dependence on both saturation indices. Similarly, Cr removal increased with the product of $SIBaCrO_4$ and $SIBaSO_4$ when $SIBaCrO_4$ was low. At higher $SIBaCrO_4$, Cr removal decreased with the product of $SIBaCrO_4$ and $SIBaSO_4$. Furthermore, high salinity conditions favored coprecipitation of trace elements into $BaSO_4$. (**32**)

Bachman, Delilah*, Jessica Nolan, and Bridgette Hagerty York College of Pennsylvania, York, PA 17405. *Basking behavior of red-bellied turtles (Pseudemys rubriventris)*.- Basking is necessary for thermoregulation of freshwater turtles and may be influenced by environmental conditions and seasonal variation. Red-bellied turtles (Pseudemys rubriventris), a threatened species in Pennsylvania, were of particular interest. This study investigated the basking behavior of aquatic turtles in two lakes in Pennsylvania during the 2025 active season. To analyze basking behavior, basking observations were conducted from June to September using field observations and trail camera data, allowing for the quantification of the number of turtles basking, timing of basking events, and duration of basking periods. The basking surveys revealed that basking occurred at 65% of potential basking locations and were associated with specific habitat characteristics. Sites with surrounding water depths of approximately 0.8-1.5 m and lower canopy cover supported greater basking. Environmental conditions also influenced basking, where the greatest number of turtles were observed basking at air temperatures of approximately 22-24°C. Trail camera data indicated that basking activity was greatest in June and declined into the months of late summer, with no basking recorded in September. Daily patterns varied greatly between the months. In early summer, turtles basked more often earlier in the morning, with red-bellied turtles basking the longest between 06:00 and 10:00. Later in the summer, basking events occurred later between 10:00 and 14:00, and overall basking time decreased. These findings suggest that both seasonal temperature conditions and time of day strongly influence basking behavior. The data collected was included in an ArcGIS dashboard to aid in the analysis of these patterns, providing a greater understanding of habitat use and creating a foundation to develop management strategies for threatened freshwater basking turtle populations in Pennsylvania. (**53**)

Badstubner, Jonah*, Aunja Richards, Katie Dunleavy, Mei Lin Chen-Lim, and Florence Ling La Salle University, Philadelphia, PA 19141. *Comparison of environmental pollutants in the Nicetown and Frankford neighborhoods in Philadelphia, PA*.- The Frankford (19124) and Nicetown (19140) neighborhoods in Philadelphia have similar socioeconomic conditions, although Nicetown has a higher incidence rate of cancer. In this work, we compared exposure to environmental pollutants between both neighborhoods. We installed one air quality monitor in each neighborhood to compare PM1.0 and PM2.5. Tap water samples were collected from residents and local businesses and tested for Pb using inductively coupled mass spectrometry (ICP-MS). Soil samples in both the Frankford and Nicetown areas were also collected for metals analysis using X-ray fluorescence (XRF). Air quality data collected showed that Frankford's measurements of PM2.5 exceeded the EPA's 2024 PM2.5 standard of 9.0µg/m3 at 9.05 ± 8.57µg/m3 while Nicetown's average PM2.5 did not (8.15 ± 7.82 µg/m3). Frankford (202 ± 221ppm) also had higher Pb than Nicetown (111 ± 89ppm) in their soil. Welch's t-tests indicated that both soil and air quality averages were significantly different between the two neighborhoods. Water samples from both neighborhoods showed that neither neighborhood had tap water samples that exceeded the EPA limit of 15ng/L of Pb in their drinking water and there were no significant differences between the two neighborhoods. Our data suggests that Frankford may be more polluted than Nicetown which points towards other potential causes of cancer in Nicetown. (**115**)

Banis, Acadia*, Amber Marble, and Sherri Buerdsell Wilson College, Chambersburg, PA 17201. *Natural versus traditional: comparative effects of essential oil-based and veterinary-grade canine topical repellents on the behavior of Ixodes scapularis*.- The eastern black-legged tick *(Ixodes scapularis)* is a primary vector of Lyme disease and other tick-borne pathogens, posing ongoing challenges for canine ectoparasite management. While veterinary-grade topical repellents are widely recommended and used, the emergence of essential oil-based formulas represent an alternative approach to canine tick prevention. Currently, a direct comparative evaluation of their behavioral effects in decreasing tick activity on canines is limited. This study systematically evaluated the efficacy and behavioral impacts of veterinary-grade topical tick repellents and their essential oil-based alternatives against adult *I. scapularis*. A total of 57 adults (29 female and 28 male) were obtained from the Tick Rearing facility at Oklahoma State University. Three laboratory experiments were conducted. The first consisted of an immediate exposure behavioral assay, with tick movements recorded 30 seconds posttreatment. The second involved an extended exposure behavioral assay, with movements recorded four hours after application of the treatment. The third experiment utilized an artificial feeding chamber to evaluate repellent efficacy under controlled, host-mimicking conditions. Behavioral parameters, including movement patterns and avoidance responses, were quantified and statistically compared across treatment groups. Product cost was additionally analyzed to assess economic considerations alongside efficacy. Across all experimental conditions, veterinary-grade tick products consistently demonstrated greater repellency than essential oil-based treatments. Within the essential oil-based treatment group, turmeric and frankincense produced the highest levels of avoidance behavior, indicating greater repellency than the other essential oil-based products. Collectively, these findings provide a more informed, evidence-based framework for comparing natural versus traditional canine tick prevention strategies by integrating behavioral efficacy with economic considerations. (**19**)

Becotte, Rachel*, Kelsey Cole*, Joe Adserias-Garriga, and Sydney Carlson Mercyhurst University, Erie, PA 16546. *Exploring the use of zygomatic arch extension as a cranial sex indicator*.- An important part of the forensic anthropological analysis of human remains is the reconstruction of the biological profile, which includes estimating sex, population affinity, stature, and age at death. Sex estimation mainly relies on features observed in the os coxa and the cranium. Walker (2008) developed a widely used method for sex estimation of the cranium that is based on five nonmetric cranial traits: the glabella, mastoid process, supraorbital margin, nuchal crest, and mental eminence. Some traits like the glabella and nuchal crest, are reliable for producing accurate results, while the mental eminence is known to perform poorly compared to the other traits. This preliminary study evaluates the use of the zygomatic arch extension (ZAE) as an indicator for sex estimation. A sample of 50 skulls from the Dirkmaat and Symes skeletal collection at Mercyhurst University was scored following the established guidelines of Walker (2008), the presence or absence of the ZAE according to Adserias et al. (2017), and the ZAE scoring according to Langley et al.

(2018). This study highlights the importance of exploring reliable sex indicators that may have their value, especially in cases of fragmentary remains where other indicators might be damaged or missing. (**43**)

Blymire, Elizabeth*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Examining tumor fibrosis in lung metastases of pancreatic cancer*.- Pancreatic ductal adenocarcinoma (PDAC) has a poor prognosis, due in part to the highly fibrotic nature of the tumors, which hinders the delivery of therapeutics to the tumor cells and lowers the survival rate. In addition, patients are usually diagnosed after tumors have grown substantially and spread outside of the pancreas, often resulting in metastases in the liver and lungs. Studies have pointed to cholecystokinin-2 receptor (CCK2R) signaling as a significant contributor to increased tumor fibrosis. Proglumide is a CCK2R antagonist, which has been shown to decrease fibrosis in primary pancreatic tumors in mice; however, the efficacy of proglumide in decreasing fibrosis in metastases requires further investigation. To address this, PANC02 cell line metastases in murine lungs were sectioned and stained using a Masson's trichrome regimen. Whole slide imaging revealed intravascular growth of the metastases and margins difficult to distinguish from surrounding compressed lung tissue. To quantify fibrosis, the images were edited to isolate metastases from surrounding pulmonary tissue and fibrotic pixels were quantified by color thresholding in ImageJ. In preliminary quantification, the lung metastases exhibit substantially less fibrosis compared to the primary subcutaneous tumors, regardless of treatment. (**123**)

Bonnet, Ashley*, and Akeisha Belgrave Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Investigating the role of Myxococcus xanthus in iron bioremediation under varying environmental ferric iron conditions*.- Excess environmental iron can pose significant ecological and public health risks, particularly in areas impacted by acid mine drainage (AMD), where concentrations often exceed regulatory limits and contribute to metal toxicity and reduced biodiversity. Biological remediation offers a sustainable alternative to conventional chemical treatments, and the soil bacterium Myxococcus xanthus is a promising candidate due to its ability to tolerate, uptake, and store iron through specialized regulatory pathways and encapsulin-based storage systems. This study evaluated the metabolic responses, extracellular iron depletion, and intracellular iron accumulation of M. xanthus exposed to 0–200 µM Fe^{3+} over 96 hours using a WST-8 metabolic assay, a Ferrozine colorimetric assay, and flame atomic absorption spectroscopy (FAAS). Results indicate that M. xanthus exhibits optimal metabolic activity under moderate iron conditions (25–50 µM), rapidly depletes extracellular Fe^{3+} within the first 24 hours, and gradually accumulates intracellular iron with peak storage efficiency at 75–100 µM. At the highest iron concentrations, cells exhibited metabolic decline, plateaued or reduced intracellular iron retention, and slight re-release of iron into the environment, indicating stress-induced dysregulation. Together, these findings demonstrate that M. xanthus effectively removes and stores environmental iron but exhibits reduced stability under extreme metal stress, supporting its potential use as a bioremediation tool while highlighting important physiological limits relevant to real-world applications. (**73**)

Brophy, Emily*, Tabeth Mwema, Isabel Molineros, Zoie Jackson-Lawrence*, Sophie Melissen, and Carla Garzon Delaware Valley University, Doylestown, PA 18901. *A nucleic acid-based study of hemp-infecting viruses and their aphid carriers*.- Since hemp was legalized in 2018, its cultivation has skyrocketed. However, new diseases and pests are now threatening the stability of the industry. In indoor and greenhouse farms, aphids—tiny sap-sucking insects—have become a major concern. Aphids hurt hemp plants in several ways. They cause physical damage by feeding on the plants and leaving behind a sticky waste called "honeydew." More importantly, they act like needles, spreading harmful viruses from plant to plant. Even "visitor" aphids that don't live on the hemp can start a massive disease outbreak just by taking a quick "test bite" and passing on a virus. A big problem for farmers is that many aphid species look almost identical, making it hard to tell which ones are dangerous. In this study, we looked at the different viruses found in aphid groups collected from sick hemp plants in the campus of Delaware Valley University in eastern

Pennsylvania. To get accurate results, we used two methods: 1) Traditional Identification: Looking at the insects' physical features under a microscope; 2) DNA Barcoding: Checking their genetic "fingerprints" to confirm exactly which species they were. We then used specialized lab tests (called RT-PCR and sequencing) to identify the specific viruses the aphids were carrying. Our study highlights which aphid species are the main culprits and the wide variety of viruses they are spreading in the area close to our campus. (**64**)

Browning, Matt*, Sherri Buerdsell, and Amber Marble Wilson College, Chambersburg, PA 17201. *Environmental factors and their impact on bat box preference in Pennsylvania over the warm season*.- Habitat destruction, degradation, and fragmentation are some of the biggest threats to bats, leading to a decrease in population. Bat boxes were used to collect samples of guano to measure activity levels in five bat boxes in Pine Grove Furnace State Park. Two of the five boxes were inhabited by bats. Samples were collected over a period of 24 weeks with a total of 236 samples being collected. Temperature, humidity, box color, and the orientation of the boxes were recorded. A preference of box color was observed, the two boxes inhabited were painted black while the other three boxes were unpainted wood. Temperature and humidity had no impact on the activity levels of the bats. Placement and orientation of the boxes was observed to play a role in choosing what box to inhabit. This study revealed the preference of bat box choice based on orientation, color, and height. More research is needed into what other environmental factors cause preferences to determine where and how bat boxes should be constructed. (**116**)

Burda, Jeremy*, and Mahita Kadmiel Allegheny College, Meadville, PA 16335. *CTZ1: a novel small molecule to inhibit in vitro angiogenesis*.- Retinal angiogenesis is an important step in maintaining homeostasis in the eye by creating new blood vessels, generally when hypoxia takes place to deliver more oxygen to the tissue. In various stimuli however, we see an overexpression of angiogenic molecules, such as vascular endothelial growth factor (VEGF), which leads to abnormal and uncontrollable blood vessel growth. Abnormal growth can lead to serious conflicts like significant vision loss or blindness. Current anti-angiogenic therapeutics are expensive and require several intraocular injections that the patient must come back several times to get. The need for a more cost effective and easier way to treat abnormal angiogenesis is very important for patients whose vision is deteriorating due to unwanted neovascularization in the retina. This project aims to find an improved solution by using a novel small molecule, CTZ1, a bipartite molecule with anti-angiogenic and antioxidant properties. These properties are thought to be beneficial to retinal cells maintaining homeostasis when faced with diabetic retinopathy (DR) or age-related macular degeneration (AMD). Our preliminary results show that CTZ1 inhibits tube formation in Human Umbilical Vein Endothelial (HUVEC) cells compared to the control treatment, indicating that CTZ1 is exerting an antiangiogenic action. The aim of this proposal is to determine the lowest concentration of CTZ1 to inhibit tube formation and to evaluate the effect of CTZ1 on angiogenic gene expression in HUVECs. Compared to dexamethasone (Dex), which is known for its anti-angiogenic properties as well as undesirable side effects, particularly threatening vision when used at high doses or in chronic treatment. Results from this proposal would allow us to test if CTZ1 is a more effective candidate to disrupt angiogenesis. (**109**)

Chadwick, Mason*, and Jessica Nolan York College of Pennsylvania, York, PA 17405. *The impact of addressing common misconceptions about pit bull type breeds on individual perceptions*.- Widespread misconceptions about pit bull type dogs contribute to negative stereotypes, which often subjects these dogs to higher rates of euthanasia in animal shelters, societal stigma, and targeted legislation. 'Pit bull' is used colloquially as an umbrella term for multiple different breeds (or mixes) that share similar physical characteristics. The statistics of bites attributed to 'pit bulls' are highly inflated due to a combination of different purebred and mixed dogs being considered as one breed. Mislabeling multiple breeds as 'pit bulls' reinforces the belief that dangerous behaviors are disproportionately performed by pit bull type dogs, thus fueling negative individual perceptions and fear-based decisions in broader public policy. This research investigated the effectiveness of educational content that addressed common misconceptions about pit bull type breeds in changing the way individuals perceive different behaviors of dogs. A survey was distributed to 245 individuals to determine their baseline perception on different breed categories as well as both pit bull type and non-pit bull type dogs performing various behaviors. Participants were shown a four minute video before being given another set of dogs to determine if their perception of pit bull type dogs became more positive. The amount of experience participants had with dogs had an impact on how they perceived pit bull type breeds, as those who had experience within the pet industry described pit bull type breeds more positively than those who did not. It was also found that after being exposed to educational content, participants' perception of pit bull type dogs became more positive, with the magnitude of increase being the highest for individuals with little experience with dogs. Thus, efforts to educate the general public about inaccurate stereotypes surrounding pit bull type dogs can help address both conscious and subconscious biases, improving overall perception. (**36**)

Chang, Tristan*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Characterization of bacteria isolated from snow*.- Microbes are present in every conceivable environment, but little research exists on culturable bacteria that inhabit snow. In this study, we sampled snowfall and snow mounds from six snow events and isolated bacteria on tryptic soy agar. We identified some of the isolates using 16S rRNA sequencing. Interestingly, we found the same bacteria in multiple apparently independent snowfall events. We observed over 80% of the isolates were pigmented, most likely with carotenoids. As expected, most isolates were cold tolerant, able to grow at 4°C. We also found that some of the isolates displayed tolerance to UV-B radiation. The cold tolerance, pigmentation and UV tolerance all support the idea that the bacteria isolated in snow originated in the clouds, where these characteristics may have provided survival benefits. Further research on these isolates could reveal the stress tolerance mechanisms in play that enable the bacteria to survive in the unique environment of snow. (**7**)

Clark, Joshua*, Ashlyn Crawford, and Ann Yezerski King's College, Wilkes-Barre, PA 18711. *Effects of dietary quercetin on infection success of <u>Hymenolepis</u> <u>diminuta</u> in the flour beetle <u>Tribolium</u> <u>confusum</u>*.- Parasites strongly influence host biology, behavior, and ecological interactions, shaping evolutionary dynamics across taxa. The rat tapeworm, *Hymenolepis diminuta* develops its intermediate stage, a cysticercoid, within flour beetles such as *Tribolium confusum*, providing a tractable model for experimental studies of host–parasite relationships. Plant-derived secondary metabolites are an important source of biologically active compounds with potential antiparasitic properties. The flavonoid quercetin has demonstrated inhibitory effects on several parasites, including adult *H. diminuta* in its terminal rat host. This leads to the question of whether this compound could also be effective on the cysticercoid stage. This study tested whether dietary quercetin affects infection success or parasite burden of *H. diminuta* in *T. confusum*. Beetles from a single Recombinant Inbred line (to control for genetics) were fed *H. diminuta eggs* via a standardized protocol and then maintained in flour containing 0%, 1%, 10%, 20%, and 40% quercetin by weight. Percent infected and parasite loads in each treatment were determined via microdissection of the beetles. The presence of quercetin had no detectable effect on parasite establishment. Neither the percent infected nor parasite load differed among treatment groups, indicating that dietary exposure did not reduce infection. While previous studies have demonstrated inhibitory effects on adult worms in vertebrate hosts, those effects did not translate to cysticercoid development in the insect intermediate host. The findings suggest that the reported anti-helminthic activity of quercetin may depend on parasite life stage or host environment. Future work should investigate the mechanism of quercetin action in infected vertebrate hosts and determine why this activity does not occur during the cysticercoid stage in beetles. (**132**)

Crookston, Justin*, Dominic DePaul*, and M. Logan Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *Nuclear receptor interactions with JAZF1/SUZ12*.- JAZF1 in humans can undergo translocations that result in gene fusions that cause different cancers, including endometrial stromal sarcomas (ESS). The hallmark of ESS is the JAZF1/SUZ12 fusion protein. These fusions always occur between chromatin modifying proteins with JAZF1. Because of the conserved nature of chromatin modifying proteins between humans and Drosophila, and their unique genetic tools. We can form a disease model in Drosophila to address some basic functional questions about these diseases. Therefore, we plan to use a JAZF1/SUZ12 in vivo model to study the effects of this fusion in the cell. Previous studies demonstrate that JAZF1 acts through a nuclear receptor NR2C2, homologs of Drosophila Hr78 and Hr51. This research aims to determine whether JAZF1/SUZ12 maintains JAZF1's ability to interact with the highly conserved nuclear receptors Hr78 and Hr51. To investigate this, we performed a Yeast Two-Hybrid Assay (Y2H) to analyze protein-protein interactions. Y2H fuses Gal4 activating domains to Hr78 and Hr51 and DNA-binding domains fused to the JAZF1/SUZ12 fusion. If JAZF1/SUZ12 interacts with these nuclear receptors, the association between the Gal4 domains will activate the synthesis of essential amino acids in selective yeast cultures. Successful yeast growth will indicate a protein-protein interaction between JAZF1/SUZ12 and each Hr78 and Hr51. Positive interactions will demonstrate that JAZF1/SUZ12 maintains its nuclear receptor interaction function. Understanding if this function is maintained is critical to understanding the molecular mechanisms responsible for JAZF1/SUZ12's ability to induce endometrial stromal sarcomas. (**113**)

Dalal, Shaunak*, Christopher Tseng, Daniel Otchere, and Neerav Goyal Hershey High School, Hershey, PA 17033. *Multi-modal prediction of laryngeal cancer recurrence*.- Purpose: Laryngeal squamous cell carcinoma (LSCC) causes over 100,000 deaths annually worldwide. While adjuvant radiotherapy after surgical resection can reduce the risk of recurrence and improve disease-free survival (DFS), accurate stratification of recurrence risk for optimized treatment planning remains challenging. This study aimed to develop a multi-modal deep learning-based model to predict DFS outcomes and identify patients who may benefit from adjuvant radiotherapy. Methods: Primary tumor whole slide pathology images (WSI) and clinicopathological features were collected from 177 LSCC patients who underwent curative local surgery from the HANCOCK dataset. A multiple-instance learning algorithm extracted histopathological features from WSI to generate a risk score, which was combined with clinical variables in a Cox regression model to predict DFS. Propensity score matching with stratified Cox regression evaluated radiotherapy benefit across model-defined risk groups. Results: The multi-modal model achieved a C-index of 0.78 (95% CI: 0.64–0.90) and average AUC of 0.86 (95% CI: 0.72–0.97) over four years on the test set (n=36), significantly stratifying patients into high and low-risk groups (p=0.002). Low-risk patients showed no benefit (p=0.085), while high-risk patients demonstrated significant benefit from adjuvant radiotherapy in DFS (p=0.001; interaction p=0.001). Conclusions: This study demonstrates a multi-modal deep learning approach for predicting LSCC recurrence and identifying patients who would benefit from adjuvant radiotherapy, potentially enabling personalized, AI-driven treatment recommendations. (**136**)

Davies, Keira*, and Jeanne Berk Cedar Crest College, Allentown, PA 18104. *Comparison of the sensitivity of azo dyes as a replacement for beta-naphthol in the Modified Griess Test used in Forensic Science*.- A common technique used in the field of Forensic Science to examine gunshot residue (GSR) on fabric is the Modified Griess Test (MGT). The MGT is a reaction where the nitrites in the GSR are reacted with the reagents beta-naphthol and sulfanilic acid in the presence of acid to form a bright orange dye upon heating on photosensitive paper. This study compared replacing beta-naphthol (A) with either 2,7-dihydroxynaphthalene (B) or 3-aminophenol (C) to see if the chemical sensitivity of the reaction could be improved. Using UV-Vis, solutions of sodium nitrite (50 -250 ppm) were reacted with the three sets of reagents (A, B or C with sulfanilic acid) to compare absorbance versus concentration. The reaction with both the beta-naphthol (λmax = 484 nm) and 2,7-dihydroxynaphthalene (λmax = 474 nm) produced an orange solution, whereas the 3-aminophenol (λmax = 439 nm) resulted in a yellow solution. The Beer's Law plot of the three reactions showed that 3-aminophenol is the most sensitive for the detection of sodium nitrite. (**66**)

Devine, Natalie*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Using Yeast Two Hybrid analysis to study how phosphorylation affects the interactions of Replication Protein A with cancer proteins*.- Cancer is the second leading cause of death in the United States and can be caused by mutations in the genome that inactivate or modify genes required for proper regulation of cell cycle regulation or 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. One protein of interest involved in these processes is Replication Protein A (RPA), which is a highly conserved ssDNA binding protein that has previously been shown to interact with numerous 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-associated proteins. To assess 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 upregulated by phosphorylation, suggesting that RPA phosphorylation may play a significant role in regulating DNA repair and cell cycle pathways by modulating physical interactions. We have systematically isolated and sequenced candidate proteins that interact with RPA in a phosphorylation-dependent manner and will be sharing any that interact in novel ways. Some notable proteins that may provide insights into new treatments for cancers caused by abnormal protein-protein interactions found via sequencing include IXR1 (increases sensitivity to chemotherapy), TAH11 (replication licensing factor), FREMSR (oxidative stress response), and IRC22 (Rad52 recruiter). A better understanding of RPA's protein-protein interactions may lead to insights for novel cancer treatments. (**128**)

Dhar, Arna*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Annual documentation project of spring mushrooms using simple PCR-based identification*.- Foraging and consumption of mushrooms has gained popularity in recent years, especially post-pandemic. While many mushrooms are edible, some of them may contain toxins and other compounds that could require medical attention and, in some cases, could be lethal. Mushrooms are typically identified visually, and genetic tests could be used to confirm their identity. The genetic tests, however, are not standardized and not accessible for general use. In this study, we seek to standardize a method to identify 15 representative mushrooms rapidly through the amplification of the 18S rRNA gene and internal transcribed spacer (ITS) from diverse mushrooms. We will sequence the amplicons using Sanger sequencing to determine possible universal primer sets. We will then try to simplify the DNA extraction procedure to optimize a low-cost genotyping procedure. The simple genotyping method could be used for rapid and inexpensive identification of mushroom samples, and possibly be combined with visual identification to determine the safety of edibility of mushrooms. (**9**)

Donovan, Angelena*, Nai Ri Lin, Conner Zimmerman, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *kefF is a novel regulator of rpoS expression in E. coli*.- Sigma factors control the transcription of target genes in bacteria. rpoS is a sigma factor which activates the bacterial stress response. Because antibiotics induce stress in bacteria, the expression of rpoS is vital to the development of bacterial antibiotic resistance. The investigation of genes which influence rpoS expression is a first step in determining how to mitigate the bacterial stress response to antibiotic treatment. We synthesized an E. coli genomic library, which we transformed into cells containing a rpoS-lacZ fusion. Transformants with altered levels of rpoS expression were selected by atypical colony color on Xgal-containing medium. Inserts were sequenced and identified by BLAST analysis. We found four genes which affected rpoS expression. Literature searches revealed three are known interactors of rpoS, thus validating our assay. The fourth gene, kefF, has no known interactions with rpoS. We believe kefF is a previously uncharacterized regulator of rpoS. (**34**)

Dormer, Molly*, and Robert Kurt Lafayette College, Easton, PA 18042. *Using cell sorting to quantify macrophage activation and function in order to understand anti-tumor immunity*.- Macrophages are large phagocytic white blood cells that can polarize into M1 or M2 macrophages with M2 macrophages promoting immunosuppression and tumor development, while M1 macrophages support inflammation and anti-tumor immunity. Macrophage polarization from M1 to M2 represents a key event in tumor development, but little is known about the cellular conditions behind this shift *in vivo*. The purpose of this study was to understand and quantify the signaling cross-talk that is occurring between the immune cells in the tumor microenvironment. Bone marrow-derived macrophages were generated from stem cells, isolated from the hind limbs of mice, treated with macrophage colony stimulating factor. The macrophages were then activated using Toll-Like Receptor agonists; LPS for TLR4 signaling, flagellin for TLR5 signaling, and R848 for TLR7 signaling. The cells were treated with one, two, or three of these agonists under different concentrations to generate anti-tumor (M1) macrophages. Next, the cells were delivered with EMT6 tumor cells into BALB/c mice and tumor volumes were measured over the course of the study. Results showed that mice that received BMDM treated with a low dose of LPS had smaller tumors and higher survival rates than mice that received LPS, flagellin, and R848 treated BMDM. The number of F4/80+ macrophages infiltrating the tumor site was collected using magnetic cell sorting and ongoing studies are analyzing mRNA and protein levels to quantify the signaling cross-talk that is occurring at the tumor site *in vivo*. Thus far, these findings indicate that the type of macrophage activation influences tumor progression, highlighting the important role of macrophage polarization in shaping and supporting the tumor microenvironment. (**68**)

Economidou, Ariana*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Characterization of endophytic bacteria from the parasitic plant, <u>Monotropa</u> <u>uniflora</u> (Indian Pipe)*.- *Monotropa uniflora*, a parasitic plant that feeds on the roots of mycorrhizal fungi colonizing the roots of trees such as the American beech. These plants are ephemeral with short life cycles and typically survive summer months. We collected stems and flowers from these plants, surface-sterilized them and isolated endophytic bacteria using serial dilution plating. We identified eleven distinct bacterial isolates, mostly belonging to the class Gamma Proteobacteria, including several species of fluorescent *Pseudomonas*, *Rouxiella Rahnella* and *Ewingella* species. Interestingly, nearly all isolates were nitrate-reducing and glucose-fermenting and not surprisingly, the flower isolates had distinct metabolic preferences including sugar metabolism, compared to the stem isolates. Given that non-photosynthetic plants like *Monotropa* rely on parasitism for survival, they may possibly rely on microbial partners for vital metabolic services. This study provides a window into the unexplored world of microbial inhabitants of parasitic plants. (**49**)

Edwards, Talia*, Sophia Firneno, Kaixin Li*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Oscillation of the X chromosome in metaphase I in male spiny flower mantids is associated with changes in attachment to the spindle*.- Errors in chromosome movements during cell division can lead to congenital conditions like Down Syndrome or Turner Syndrome. Some species have odd chromosome movements in their natural state that can open a window on how congenital conditions develop. One of these species is the spiny flower mantis, *Pseudocreobotra wahlbergi*, which acted as a model system for our study. We fixed and stained testis samples and observed that there was an unpaired (univalent) X chromosome in all meiosis I cells. When we looked in living cells, we observed that the X chromosome in male *P. wahlbergi* meiosis I does not align with the autosomes on the metaphase plate. Instead, the X chromosome exhibits random movements between the spindle poles that can be more rapid than the movements of autosomes. Using confocal microscopy of primary spermatocytes with either stained microtubules or stained kinetochores, we observed that some X chromosomes have a visible connection to spindle microtubules, while others don’t appear to connect to microtubules in metaphase I. Sometimes the X chromosome appeared to associate with microtubules from only one spindle pole, while in other cases, the X chromosome was aligned on the metaphase I plate and appeared to have microtubule connections to both poles. All of the autosomes had robust attachments to microtubules at both kinetochores in metaphase I. In metaphase II, all chromosomes appeared to have robust microtubule attachments at both kinetochores. Our results suggest that X chromosome movements are associated with detachment and reattachment to spindle microtubules. (**117**)

Flyte, Haley*, Colleen Fejes, Adore Ferguson-Richards, Gabrielle Seagreaves, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Identifying genetic regulators of rpoS in Escherichia coli*.- Sigma factors are proteins in bacteria that bind to RNA polymerase, helping it recognize specific promoter regions, therefore regulating gene expression. rpoS, a sigma factor in Escherichia coli, is a key regulator of genes involved in the bacterial stress response. It allows bacteria to adapt to environmental stressors, including exposure to antibiotics. Antibiotics induce a stress response which can lead to the development of antibiotic resistance in bacteria over time. To explore the regulation of rpoS, a genomic library of E. coli was grown in the presence of the antibiotic kanamycin. Mutants that up or down regulated rpoS were chosen and examined using qPCR. Analysis revealed the gene, bamB, is a down-regulator of rpoS with a fold change of 0.0016. Another gene, der, is an up-regulator of rpoS with a fold change of 3.173. These genes may serve as potential targets for modulating rpoS expression, which can lead to the development of novel antibiotics. (**35**)

Galanti, Gianina*, McKenna Horst*, Madison Poladian*, Alexander Korin*, Erica Hollister, and Carrie Wise Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Documentation and biological profiling of a legacy skeletal collection*.- Undocumented skeletal collections maintained within academic institutions present both educational value and potential ethical and forensic considerations when provenance and documentation are incomplete. This study documents and analyzes a skeletal teaching collection housed at Harrisburg Area Community College (HACC) to evaluate the biological profile and condition of the remains and assess their potential for forensic anthropological analysis. A total of 21 specimens were systematically documented and assigned unique identification numbers. The collection consisted primarily of cranial elements along with articulated skeletons and prepared anatomical display specimens. Standard forensic anthropological methods were applied to specimens that retained sufficient anatomical features for analysis. Sex estimation was conducted using morphological assessment of cranial and pelvic traits. Age estimation relied on adult skeletal indicators where observable. Ancestry estimation was conducted using morphoscopic trait analysis, craniometric analysis with FORDISC, and mandibular assessment using the (hu)MANid database. Sex estimation was possible for thirteen specimens, resulting in classifications of five males and seven females, with one specimen classified as indeterminate due to conflicting trait expression. Ancestry estimations produced variable classifications across analytical methods, reflecting differences in reference populations and the limitations associated with incomplete skeletal elements. Stature estimation was conducted for two articulated skeletons using long bone regression equations, producing estimated statures of approximately 148 cm (±4 cm) and 162 cm (±4 cm). Examination of the collection also identified evidence of anatomical preparation and modification consistent with historical teaching practices. These findings highlight both the research potential and interpretive limitations of legacy skeletal teaching collections and emphasize the importance of systematic documentation and evaluation for responsible curation and future forensic analysis. (**87**)

Garcia, Naiara*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Elucidating the function of uncharacterized genes in an antibiotic biosynthesis pathway in P. nicotinovorans via CRISPR interference*.- The consistent overuse and misuse of antibiotics have contributed to the global rise of antibiotic resistance. Therefore, there is a critical need to develop new therapeutic strategies to combat bacterial infections. Soil offers a highly competitive, pressurized environment where millions of microbes compete for limited resources – a promising source for novel antibiotics. In our lab, we are specifically investigating a soil-isolated bacterium Paenarthrobacter nicotinovorans, which we found to inhibit the growth of several ESKAPE pathogen-safe strains. Using bioinformatics analyses, we identified a biosynthetic gene cluster (BGC) encoding a secondary metabolite similar to stenothricin, a known antimicrobial compound. Uncharacterized to date, we sought to discern the function of this potentially novel compound by knocking down the expression of genes within the pathway. Previous work in our lab established that BGC genes also involved in arginine production (argB, argC, argG, and argJ) were important for antibiotic production; however, we could not separate that function from the essential process of arginine production. Therefore, we are pursuing two uncharacterized genes in the pathway, CTG21_59 and CTG21_74 that have proposed functions of promoting antibiotic activities. Using a CRISPR interference system, we have designed and cloned plasmids containing gRNAs to disrupt each gene and successfully electroporated the constructs into P. nicotinovorans. After generating successful mutants, I am conducting competition assays against ESKAPE pathogen-safe relatives and measuring rates of growth to determine how these genes are influencing secondary metabolite production and its morphology. By further characterizing the function of the stenothricin-like BGC, we can contribute to the development of novel antibiotics. (**39**)

Geditz, Diana*, Brianna Hong, Stephen Mason, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Comparison spricket (Orthoptera: Rhaphidophoridae) species richness and abundance on Harbor Island, ME*.- Ecosystems of islands are valuable study locations 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) determine if there is a difference between cave cricket abundance between two habitats, and (2) start to determine the cave crickets to species on Harbor Island, Maine. During one week in July of 2022, ten pitfall traps were set up between a spruce forest and fern field sites to collect sprickets. DNA barcoding was used to identify the collected sprickets to species. We used a Mann-Whitney Wilcoxon analysis to determine if there was a difference between spricket abundance between our two sites. Out of the 87 sprickets collected, 86 were found in the spruce forest and one was found in the fern field. We found that cave cricket abundance was significantly higher ($p = 0.007$) at our spruce site compared to our fern site. We also determined two species: Ceuthophilus guttulosus Walker, 1869 and Ceuthophilus brevipes Scudder, 1862. By doing this research, baseline data was gathered for Harbor Island, which gives greater insight on island diversity and ecosystems throughout the coasts of Maine. The data will also be uploaded to the Global Biodiversity Information Facility to help other researchers studying island biogeography and cave cricket biodiversity. (**97**)

Ghazi, Jamal*, M. Dana Harriger, and Natasha Clarke Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The relationship between macronutrient adherence and salivary cortisol response during academic stress*.- Academic examinations are reported to be a source of acute stress for college students associated with increased activation of the hypothalamic-pituitary-adrenal (HPA) axis, resulting in cortisol release. Dietary intake and macronutrient balance may influence physiological stress responses however, studies have not examined this relationship using real-time macronutrient tracking software applications. This study investigated whether adherence to recommended macronutrient ranges (% carbohydrate/fat/protein) affects exam-related cortisol responses in undergraduate students. Five participants tracked their daily food intake using Nutritionix and provided three morning salivary samples each (baseline, exam day, and post-exam). Salivary cortisol concentrations were quantified using a competitive ELISA and analyzed using a four-parameter logistic (4PL) standard curve. Participants with higher macronutrient adherence tended to show more stable cortisol responses and improved post-exam recovery compared to those with lower adherence. Based on these trends, the findings were consistent with the hypothesis that balanced macronutrient intake may be associated with improved regulation of cortisol during academic stress. Although limited by the sample size, these findings suggest that proper macronutrient intake may influence stress responses in students during academic examination periods. (**2**)

Goldring, Morgan*, Lily Decker*, Jenny Hayden, and Jeanne Berk Cedar Crest College, Allentown, PA 18104. *Synthesis and antibacterial studies of novel Mannich bases from lawsone, vanillin and 1° aromatic amines and copper complexes*.- Antibacterial medicines are fundamental to modern healthcare. Recently, there has been a concerning increase in the rate of antibacterial resistance in commonly used drugs, which poses a significant threat to the future of medical treatment. The Mannich base reaction is a three-component reaction involving an amine, an aldehyde and an enolizable ketone allowing the formation of complex nitrogen-containing molecules, known as Mannich bases. These Mannich bases often exhibit stronger antibacterial effects than their parent compounds, and their three components can be easily substituted, allowing for great versatility in drug design. Another well-studied strategy in medicinal chemistry is to bind the Mannich base with copper (II) to enhance toxicity and reactivity. To that end, a series of Mannich bases were successfully synthesized from the biologically active compound lawsone using various aldehydes and primary amines. Selected Mannich bases were subsequently complexed with copper(II) to form corresponding metal complexes. The antibacterial activity of all synthesized compounds was evaluated against a range of Gram-positive (*B. cereus* and *S. saprophyticus*) and Gram-negative (*E. coli*) bacteria using the Kirby–Bauer disk diffusion method. The results indicate that Mannich bases and their copper complexes derived from lawsone—particularly those incorporating heterocyclic aromatic amines and morpholine carbaldehyde—exhibit substantial antibacterial activity against both Gram-positive and Gram-negative bacterial strains. (**57**)

Gonzalez, Marlyne*, Jacobus De Roode, Nadya Muchoney, Ehsan Sanaei, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Evaluating the effects of antibiotic treatment on microbial load in second instar monarch caterpillars*.- The gut microbiome plays an essential role in animal health by supporting digestion, shaping immune responses, and defending against pathogens. In monarch butterflies (Danaus plexippus), microbial communities may influence disease resistance and the ability to process toxic cardenolides found in milkweed plants (Asclepias spp.), their primary host. While monarchs have evolved tolerance to these compounds, it is still unclear how gut microbes may assist or interfere with toxin breakdown and immune function. Monarch larvae can potentially acquire microbes through their diet, the environment, or maternal transfer; however, the specific pathways and their relative importance remain poorly understood. This study explored whether antibiotic treatment could reduce the bacterial load in second instar monarch caterpillars while developing an experimental framework involving antibiotic application, whole-body DNA extraction, and microbial quantification using qPCR. To test this, four gravid female monarchs were allowed to lay eggs on two Asclepias curassavica plants. Eggs were split into control and antibiotic-treated groups. A combination of tetracycline, streptomycin, and ampicillin was applied to the leaves fed to the treatment group. All caterpillars were raised in sterile Petri dishes for approximately three days and fed only their assigned leaves. DNA was extracted from whole caterpillars using the CTAB method, and bacterial load was quantified with 16S rRNA qPCR. DNA quality and quantity were confirmed by Nandrop, and successful qPCR amplification validated the efficiency of the methodology. Unexpectedly, antibiotic treatment did not consistently lower microbial levels. Treated caterpillars showed variable bacterial counts, while the control group had relatively lower and more stable values. These findings suggest either minimal microbial communities due to sterile rearing conditions or that antibiotic concentrations were too low to be effective. These results point to the need for refining experimental designs when studying monarch microbiomes, especially in terms of antibiotics delivery and rearing conditions. (**41**)

Graff, Isabella*, and Cathy Greco St Joseph High School, Natrona Heights, PA 15065. *Bioyarn and fishing: a new approach to sustainable fishing*.- Worldwide, fishing is one of the biggest industries, with roughly 600 million people relying on fishing for their livelihood. But with fishing comes the concern of ghost fishing. Ghost fishing is the phenomenon where abandoned, lost, or discarded fishing gear (ALDFG) continually catches fish and harms ecosystems. Ghost gear is one of the ocean's biggest polluters and has led to many researchers attempting to find a solution. This has led to the question: Can bioyarn be used to create an alternative form of fishing nets? Bioyarn is derived from sodium alginate powder (brown algae) and, when combined with calcium chloride, forms into a rope. Using this rope, a strength test was performed by hanging increasing weights from the bioyarn. Additionally, pieces of yarn were submerged in saltwater and freshwater and placed under UV light to test for biodegradability. The yarn was then crafted into a standard fishing net and used to catch fish. Nylon netting was also tested as a control. The bioyarn either worked on par or surpassed that of the nylon control net in all tests except the strength test, where the control net performed significantly better. Additional calculations showed that the bioyarn net would degrade 150 times faster than the control net, taking only 90 days. After the project was concluded, a new method of making the bioyarn was discovered, which has shown higher signs of flexibility; however, this new yarn has shown signs of shrinkage. This new method is continuing to be tested, and in the future, further tests will be run to develop stronger nets and explore more possibilities. These nets can potentially be used to ensure a more sustainable approach to fishing. (**79**)

Graham, Jillian*, and Anna Fedor Misericordia University, Dallas, PA 18612. *Characterization and analysis of polyphenol extracts from almonds using UV-Vis spectroscopy*.- Almonds are recognized as a nutrient dense superfood rich in polyphenols including *proanthocyanidins*, *tannins*, and *flavonoids*. These polyphenolic compounds contribute to the antioxidant capabilities of almonds. This study examined the antioxidant content of almond extracts using the *Folin-Ciocalteu* (FC) method to calculate the total phenolic content. A new extraction technique was developed in order to optimize the amount of extracted polyphenols. Raw almonds (5.0 g) were processed using a coffee grinder and added to a 70% ethanol/water solution. The samples were dissolved using ultrasonic-assisted extraction (UAE) for durations of 10 and 20 minutes. A series of gallic acid standards were prepared and analyzed using UV-Vis spectroscopy at 765 nm to create a calibration curve for determining total phenolic content. The total phenolic content was calculated for both time intervals and compared. This experimental protocol and results from this study will be implemented into an upper-level instrumental analysis course for biochemistry and chemistry majors. (**30**)

Guest, Catherine*, Gaige Selvey, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The cultivation of Ocimum basilicum (sweet basil) in hydroponic vs. aquaponic environments*.- Over the past 10 years, the United States has gradually increased reliance on the imports of herbs to meet consumer demand. In 2024, the imports of Ocimum basilicum into the U.S. totaled $121 million. Given the economic importance of sweet basil specifically and herbs in general, this study aims to identify the best alternative growth environment (hydroponic or aquaponic) that minimizes growing time, cost and space to potentially shift the ability to meet the basil demand to domestic alternative growth conditions. This study compared, on a small-scale, hydroponic and aquaponic growth environment impact on O. basilicum compared to a control. Quantitative measurements included stem height, stem diameter, and wet plant weight twice a week for 4 weeks in addition to qualitative assessment of leaf color. The cumulative findings suggest that growth of O. basilicum in a hydroponic system outperforms aquaponic and control systems with respect to the measured parameters, both quantitative and qualitative. (**76**)

Haddad, Joy*, Cora Zilinski, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Exploring quercetin as a natural inhibitor of coronavirus 3CLpro*.- 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, antimicrobial, anti-inflammatory, and antiviral activities. Several studies have demonstrated the antiviral potential of quercetin due to its ability to inhibit several stages of viral infection and interact with proteases essential for viral replication. In case of SARS-CoV-2, quercetin has been shown to inhibit its viral entry, absorption, and penetration. This could be partially explained by having inhibitory activity against the coronavirus 3C-like proteases (3CLpro) from SARS-CoV 2 and some inhibitory activity against the papain-like protease (PLP). Using chimeric reporter mouse hepatitis virus (MHV), that expresses the 3CLpro of HCoV-HKU1 or HCoV-OC-43 in place of the MHV protease, we tested for virus inhibition by quercetin. All three have a firefly luciferase reporter as a nsp2-fusion, and the difference lies in their nsp5 (3CLpro). We tested for viral 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 quercetin at the time of infection, it decreases viral syncytia formation. Results from the co-treatment antiviral assay, quantified using a firefly Luciferase assay, showed that the percentage of remaining virus decreases at higher concentrations of quercetin. Overall, our data suggests that quercetin may have broad anti-coronaviral activity. (**23**)

Haddad, Joy*, Joshua Rizzardi, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Curcumin as a potential therapeutic inhibitor of coronavirus 3CLpro*.- 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. Curcumin has gained significant attention due to its properties that were discovered through in vitro, in vivo studies and clinical trials. Curcumin is a naturally occurring plant-based compound derived from turmeric, that has been shown to have anti-inflammatory, antioxidant, antibiotic, anticancer, antibacterial, antifungal and antiviral activities. Multiple studies through clinical trials addressed the pharmacokinetics, safety and efficacy of this drug against various huma diseases. There is a study that showcased curcumin inhibiting the replication of SARS-CoV-2 through photodynamic therapy. However, it is unclear whether curcumin targets 3CLpro other human coronaviruses including HCoV-HKU1 that cause the common cold. Using chimeric reporter mouse hepatitis viruses (MHV), that expresses the 3CLpro of either HCoV-HKU1 or HCoV-OC43 in place of the MHV protease. Three different strains of MHV were used. All three have a firefly luciferase reporter as an nsp2-fusion, and the difference lies in their nsp5 (3CLpro). We tested for viral inhibition by curcumin. All the experiments were tested on Delayed brain tumor cells (DBT-9), which is a murine astrocytoma cell line. First, a broad range of concentrations were tested for cell viability. High concentrations of curcumin were found to be highly toxic; therefore, lower non-toxic concentrations were used to test for antiviral activity. Co-treatment, pre-treatment, and post-treatment assays were performed to determine the inhibitory effects of curcumin using the firefly luciferase assay. When cells are treated with curcumin and infected at the different time-frames, viral syncytia formation was reduced. Overall, our data suggests that curcumin may have broad anti-coronaviral activity. (**11**)

Hansen, Brice*, and Tyler Goerge Mercyhurst University, Erie, PA 16546. *Effect of a polyculture system on arthropod abundance and diversity in a fruit tree microhabitat*.- Arthropods are the foundation of the world's food web and various ecosystem functions. Agriculture poses a significant threat to global arthropod diversity and abundance through the use of insecticides, habitat destruction, and climate change. Therefore, feeding the Earth's growing population while nurturing and amplifying arthropod biodiversity is an important issue to address. Implementing polycultures, originally used in traditional indigenous farming systems, amplifies the diversity of crops, arthropod habitats, and arthropod food sources. I analyzed the biodiversity of arthropods in the microhabitat of ten fruit trees on a small organic farm in Franklin County, PA, where I implemented a polyculture system under half of the trees and left the other half bare (monoculture). I found a significant interaction between the treatment type and the type of fruit tree on the Mean Inverse Simpson Diversity of arthropods. The tree where this interaction most significantly impacted diversity was the Prunus americana (American Plum) tree, where I found a higher arthropod diversity in the microhabitat of the polyculture tree than in the monoculture tree. I also found a greater abundance and diversity of strictly beneficial pollinator species in the polyculture habitats, likely due to the increased food and habitat that the flowers provided. Ongoing research is necessary, but these results demonstrate that a polyculture system in an orchard setting has the potential to enhance arthropod biodiversity and contribute to a positive relationship between agriculture and arthropods. (**77**)

Harrel, Michael*, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Comparison of poly(styrene-b-acrylonitrile) diblock copolymer syntheses: optimizing atom economy and product properties*.- Diblock copolymers have numerous potential applications, from the medical field as drug delivery vehicles to the technological world in electronics. One example is poly(styrene-b-acrylonitrile) (PS-b-PAN), which has been explored for use in supercapacitors, with some blocks of the polymer being sacrificed to produce electrode materials. Our work explores different synthetic strategies to create PS-b-PAN, while considering atom economy and mass efficiency. Three living polymerization strategies to create a starting hydroxyl-terminated polystyrene macroinitiator (PS-OH) were explored; the first used a premade nitroxide-based hydroxyl-functionalized initiator to start each chain, the second used the same premade initiator with a protected OH group, and the third used the straightforward benzoyl peroxide and 2,2,6,6-tetramethylpiperidinoxy (TEMPO) system. All PS polymerizations utilized the living technique of nitroxide-mediated polymerization (NMP) for the PS block, with future research using atom transfer free radical polymerization (ATRP) to grow the second PAN block. It was found that the atom economy was similar, but the mass efficiencies were less favorable when using the premade nitroxide-based initiators. These results and properties of the resulting PS-OH that is formed will be discussed. (**45**)

Heckman, Isabella*, Owen Walker, Michael Shin, and Scott Kieffer Messiah University, Mechanicsburg, PA 17055. *Impact of caffeine on anaerobic capacity and the influence of genes linked to caffeine signaling and processing*.- This study aims to assess caffeine's influence on anaerobic performance metrics and whether genes involved in caffeine signaling and processing (*CYP1A2*, *ADORA1*, *ADORA2*, *DRD1*, *DRD2*, *HTR2A*, and *AHR*) play a role in determining intraindividual differences. Fifteen participants from the Messiah University athletic population underwent two 30-second Wingate Anaerobic cycle trials using a randomized, counterbalanced design with placebo (maltodextrin) and caffeine (5mg/kg-1•BW) conditions. Paired t-tests showed that the placebo condition had significantly greater anaerobic power (10.66 ± 1.12 W/kg) than the caffeine trials (10.05 ± 1.12 W/kg), p = 0.03. There were no significant differences between placebo and caffeine for anaerobic capacity (7.57 ± 0.94 W/kg vs 7.62 ± 0.96 W/kg, p = 0.61) or AUC (219.37 ± 32.37 J/kg vs 219.73 ± 31.61 J/kg, p = 0.87). To determine genetic influence, subjects were genotypically categorized at 7 genes using SNP genotypic assays. Independent t-tests found no significant difference (p > 0.05) between placebo and caffeine in anaerobic power, anaerobic capacity, or AUC for each of the SNPs analyzed. The results suggest that a relatively higher caffeine dose may have a detrimental effect on anaerobic power. No SNP-related differences were identified, potentially due to limited statistical power from small sample sizes within each genotype group. Further research is planned with larger sample sizes per SNP to better understand the potential effects of caffeine supplementation on anaerobic performance. (**131**)

Heisler, Evan*, and Siobhan Fathel Susquehanna University, Selinsgrove, PA 17870. *Experiments evaluating the effects of beaver dam analogs (BDAs) on streambed complexity*.- This study evaluates how model Beaver Dam Analogs (BDAs) influence streambed development and sediment transport in stream channel flumes, motivated by field observations of bedform transformations that appeared as a result of BDA implementation in a stream at Susquehanna University's CEER Field Station. We used recirculating flumes with adjustable slope segments and a uniform pea gravel as substrate to investigate bedform dynamics. The model BDAs, while permeable, restrict the water's flow like their real-world counterparts and force it to move around the structures. Experiments were conducted at a discharge of 6.9 m3/s with runs lasting 1, 4, and 16 hours. Near the end of each experiment, we measure the centerline water depth. We record bedform changes by taking photos using a camera setup consisting of two GoPros (one parallel and one 30° oblique to the bed), then importing images into Agisoft Metashape to create digital elevation models (DEMs) of channel topography before and after experimental runs. We quantify sediment movement, bed elevation changes, and spatial variations in channel roughness from the DEMs. We observed that BDAs increase streambed complexity, effectively shaping a flat sloped bed into one that shows the beginning stages of riffle development downstream. The magnitude of bed elevation change and morphological complexity was greater in runs with multiple BDAs compared to single-structure configurations. For example, we often saw intense scour down to the flume liner; in runs with more than one BDA, there was a quantifiable difference in the water depth of upstream pools. (**133**)

Hong, Brianna*, Diana Geditz, Stephen Mason, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Comparing ant (Hymenoptera: Formicidae) abundance and species richness on Harbor Island, Maine*.- Insects are the most biodiverse group of organisms in the world and provide essential ecosystem services such as pollination, pest control, and clean water. One well-studied insect group are ants (Hymenoptera: Formicidae), which are specifically known for their role in ecosystem engineering and having symbiotic relationships with other organisms. The goal of this research is to (1) determine ant abundance and species richness at two sites on Harbor Island, Maine, and (2) compare ant abundance and species richness between those two sites. During one week in July of 2022, 5 pitfall traps were set up at red spruce and hay-scented fern field sites (n=10) to collect ant specimens. A total of 29 specimens, 20 in the spruce and 9 in the fern sites, were collected. We then used a Mann-Whitney Wilcoxon analysis to determine if there was a difference in ant abundance between the two field sites. We found that there is no significant difference ($p = 0.20$) in abundance between our sites. We then used DNA barcoding to determine the ants to species. We have currently identified 5 species: the Hercules carpenter ant (Camponotus herculeanus), the silky ant (Formica fusca), the slave-making mound ant (Formica aserva), the light bronze mound ant (Formica subaenescens) and the woodland fuzzy ant (Lasius americanus). We will continue to barcode other collected ant specimens from Harbor Island to determine if there is a difference in ant species richness. These data will help the National Audubon Society, who co-manages the island, make more informed conservation decisions in future projects to better understand island biodiversity in Maine. Most importantly, these data will be uploaded into the Global Biodiversity Information Facility (GBIF) to provide information that other researchers can use to test their own local and global hypotheses. (**98**)

Hope, Sarah*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Comparing LLM-generated practice exam questions for a molecular biology course*.- Artificial intelligence tools are becoming increasingly prevalent in generating course materials for both students and instructors. Despite AI's rapid expansion in higher education, limited research has compared how effectively different large language models (LLMs) generate practice exam questions or how well these questions align with course content. This project aims to identify which LLM is most effective at producing exam-aligned practice questions for an undergraduate molecular biology course. Three widely used models: ChatGPT, Microsoft Copilot, and Google Gemini, will receive identical lecture slides and a standardized prompt to generate college-level practice exam questions. These questions will be compiled into a randomized practice exam administered to students prior to the first course exam. Students will complete each question and rate it on clarity and alignment with lecture material. Additional measures will include students' confidence, familiarity with AI, GPA, and grades in prerequisite courses. Student performance on the practice exam will be analyzed and compared with scores on the subsequent course exam. The course instructor will also conduct a blinded review of each question to assess accuracy, alignment with learning objectives, and suitability for exam use. We will examine whether student performance varies by LLM and whether certain models produce questions that more closely reflect instructor expectations and testable material. We anticipate meaningful variation between models, suggesting that some LLMs may be more effective than others at generating high-quality practice materials. Understanding these differences can help educators and students make informed decisions about integrating AI tools to support learning. (**33**)

Huynh, Alex Van, Kade Lippitt, Caroline Maciejewski, Madeline Frederick, Afaf Nazif*, and James Knowles DeSales University, Center Valley, PA 18034. *Analyzing observations of various taxonomic groups through iNaturalist*.- As biodiversity loss intensifies, large digital datasets function as providing a source of crucial information in addressing critical ecological and conservation issues. Researchers may now leverage these datasets to gain key insights faster and across much broader scales. A source of crucial importance of biodiversity data comes through platforms dependent on citizen science observations. One of the most popular citizen science platforms, iNaturalist, is used increasingly in biodiversity research, including monitoring species distributions. Despite its usefulness, iNaturalist remains an unstructured citizen science platform and presents sampling artifacts and other sources of errors such as taxonomic biases in observations logged by the public. We demonstrate how the volume of iNaturalist observations are highly skewed towards specific taxonomic groups. As a result, this data may be more applicable to some taxonomic groups than to others. Through these important suggestions and cautions, we aim to assist scientists worldwide in effectively utilizing this dataset for future ecological and conservation research. (**47**)

Javia, Dhara*, and David Glick King's College, Wilkes-Barre, PA 18711. *Microbial community composition as a determinant of electrical output variability in microbial fuel cells*.- This pilot study investigated whether differences in microbial community composition contribute to variation in electrical output in microbial fuel cells (MFCs). Twelve MFCs were constructed using a standardized MudWatt protocol developed over multiple prior experiments, representing six conditions in duplicate: regular setup, no cellulose, no acetate, no iron, inoculation with mud from a previously productive MFC, and supplementation with orange peel material. Electrical output was monitored for 49 days, and the highest performing MFC from each condition was selected for 16S rRNA microbiome sequencing. Peak power output varied across conditions, with the regular and orange peel MFCs producing the highest outputs, the inoculant and no acetate MFCs showing intermediate performance, and the no cellulose and no iron MFCs generating the lowest outputs. Microbial community analysis showed that five dominant classes, *Gammaproteobacteria, Alphaproteobacteria, Bacilli, Anaerolineae, and Bacteroidia,* accounted for most of the community structure across all conditions. Differences in electrical performance were associated with shifts in the relative abundance of these classes. Understanding the factors that contribute to stable MFC output is valuable because stable and high performance is essential for advancing MFCs toward practical applications in renewable energy and waste management. These findings suggest that the balance of a small number of metabolically important microbial groups influences MFC output, and they provide preliminary support for the idea that guiding community composition may improve the productivity and reliability of MFC performance. (**59**)

Jennings, Keira*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Cloning and sequencing of <u>Phytophthora</u> <u>infestans</u> polysaccharide lyase genes PITG_02368, PITG_02331, and PITG_02332*.- Phytophthora infestans, the causal agent of “late blight” in potatoes, is a damaging pathogen that impacts the lives of many through its destruction of potato crops, and is estimated to lead to annual losses of more than $6.8 billion worldwide. One essential focus of current research on P. infestans is its production of cell wall degrading enzymes (CWDE) that facilitate the pathogen’s penetration of the plant cell wall, followed by the successful infection of its host plant. Many CWDE produced by P. infestans belong to the CAZyme superfamilies carbohydrate esterases, glycoside hydrolases, glycosyl transferases, and polysaccharide lyases, all of which perform specific functions that facilitate the breakdown of various parts of the plant cell wall. This study aimed to gain a better understanding of three P. infestans genes that encode polysaccharide lyase family 4 proteins, PITG_02368, PITG_02331, and PITG_02332, by cloning and sequencing these three genes, and analyzing their expression in mycelial tissue using Kelch as a reference gene. Gel electrophoresis done following the amplification of the genes by PCR, which was accomplished using primers designed with NCBI Primer BLAST, revealed the approximate length of PITG_02368, PITG_02331, and PITG_02332 to be 1800 bp, 800 bp, and 1900 bp respectively, which was confirmed by Sanger sequencing. Following the use of the Expasy Translate Tool to determine the open reading frames of the genes, the proteins encoded by PITG_02368, PITG_02331, and PITG_02332 were found to have amino acid lengths of 437, 110, and 376 amino acids respectively. Finally, the NCBI Conserved Domain Search revealed that all three genes have carbohydrate-binding module domains. Expression analysis using quantitative PCR is underway to determine whether these genes are transcriptionally active in mycelial tissue. (**93**)

Jensen, Caitlyn*, and Jane Cavender Elizabethtown College, Elizabethtown, PA 17022. *CD44 isoform selection in virally transformed cells*.- Cancers such as HPV, HTLV1 and Merkel Cell Carcinoma are directly correlated with viral infection. Post-infection, viral oncoproteins disable host tumor suppressors and activate oncogenes to promote uncontrolled cell growth. Recently the generation of oncoproteins via alternative splicing has been implicated as a driver of tumorigenesis. One potential driver of transformation is the transmembrane glycoprotein, CD44. The RNA encoding CD44 can be alternatively spliced to contain no variable regions (CD44s) or include any combination of ten variable regions. Studies have found upregulated CD44v3, v6, v9, v6-10, and v8-10 isoforms in pancreatic, prostate, colorectal, and bladder cancer. Correlating isoform expression to specific tumors is useful; however, matched controls are not always available. To investigate the role of splice variants of CD44 in viral transformation, this study used immortalized human diploid fibroblasts (HDFs) transfected with the early coding region of SV40 to produce transformed cells (HDFT). CD44 alternative splicing was determined using RTPCR with variable-region-specific primers and protein was detected with v6-specific antibody. Data show that CD44s accumulation was inversely correlated to T-antigen expression levels; and the isoform containing v6-10 appears up-regulated as shown by RTPCR and Immunoblot in HDFT cells. Sequencing confirmed that the most abundant isoforms containing variable 6 are CD44v6 and CD44v6-10. To assess v6-isoform contribution to aggressive growth, CRISPR was used to knockout/down SAM68, the factor responsible for CD44 splicing. Preliminary results indicate that the v6-isoform is decreased in SAM68-KO cells; however, growth rates, metabolic activity and anchorage independence are indistinguishable from the SAM68-expressing HDFT2 cells. This indicates that the CD44v6-containing isoform is not directly responsible for those growth characteristics. Overall, results suggest CD44 isoform selection is altered in virally transformed cells but not responsible for the transformation or measured aggressive phenotypes. (**139**)

Keja, Aiden*, and Jeffrey Thompson York College of Pennsylvania, York, PA 17405. *CRISPR/Cas9-mediated functional knockout of the human interleukin 13 receptor alpha 1 gene*.- The objective of this study was to create a stable Human Embryonic Kidney sensor (HEK293) cell line with a functional knockout of the human interleukin-13 receptor alpha 1 (IL-13ra1), with the long-term goal of implementing a similar knockout in a glioblastoma cell line. The functional knockout of the IL-13ra1 gene was accomplished with the introduction of an active Cas9 enzyme and an associated anti-IL-13ra1 sgRNA. A culture of HEK293 sensor cells was transfected with an expression vector containing GFP for expression visualization, Cas9, the anti-IL-13ra1 sgRNA, and a G418 selection marker. Subclone colonies were repeatedly selected and transferred to new flasks to obtain a monoclonal expansion of a high-GFP-expressing population. A functional SEAP assay performed with a final population of monoclonal cells showed a statistically significant (ANOVA comparison; $p < 0.0001$) decrease in SEAP expression in response to IL-13 treatment compared to wild-type HEK293 sensor cells. This indicated that a functional disruption of the IL-13ra1 subunit was achieved after transfection. Total RNA of the knockout cells was extracted and converted to cDNA. PCR amplification of the IL-13ra1 gene sequence was conducted with the cDNA as a template. Sanger sequencing of the PCR amplicon was obtained, and the sequence was put through the NCBI BLASTn tool. Sequence comparison to the wild-type human IL-13ra1 gene showed that an approximately 20-base pair deletion had occurred upstream of the expected Cas9-induced DSB, and the downstream sequence had an erratic pattern of mismatched bases. This indicated that the functional disruption observed was likely due to the creation of a deletion within the IL-13ra1 gene sequence. Future experimentation will include conducting a rescue experiment to reintroduce a CRISPR-resistant, synonymous IL-13ra1 variant to a subpopulation of the knockout cell line, restoring functionality. (**127**)

Kelly, Raine*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Do microplastics affect growth patterns of placental cells?*.- Plastic pollution has become a significant environmental and human health concern, with current research showing evidence suggesting microplastics (MPs) and nanoplastics (NPs) could have negative effects on our reproductive systems. The placenta, an integral gestational organ that facilitates maternal-fetal exchange, has been utilized in various research studies to understand the cellular and overall biological effects of MPs/NPs. This project aimed to investigate the effects of polyethylene nanoplastics on trophoblast cell viability using a HTR8-Svneo trophoblast (placenta) cell line. A RT4-D6P2T schwannoma cancerous cell line was first treated with increasing doses of polyethylene nanoplastics (0.001–100 μg/mL) to standardize assay conditions prior to treating the HTR8-Svneo trophoblast cell line with identical doses. Both the RT4-D6P2T and HTR8-SVneo cells were cultured under standard conditions and treated with polyethylene NPs for 24 hours. To ensure the NPs would enter the cell, a Tween 20 (0.01%) surfactant solution was employed. To rule out the Tween20's possible role in altering the trophoblast cell growth pattern, a separate optimization experiment using various concentrations of Tween20 (0.0001%, 0.001%, 0.01%) was completed. The results of this experiment showed that Tween20 at all concentrations increases viability compared to the control, excluding the treatment using the smallest dosage of nanoplastics (0.001 ug/ml). Cell viability was quantified using the CellTiter-Glo assay, with luminescence measured using relative luminescence units (RLU). Results exhibited a dose-dependent increase in HTR8-Svneo trophoblast cell viability from NP doses 0.001 to 10 μg/mL, while treatment dose 100 μg/mL demonstrated a significant reduced viability compared to the control. In contrast, RT4 schwannoma cells exhibited an increase in viability for all NP treatment doses. These results indicate that MPs/NPs have the ability to elicit abnormal cellular responses depending on the cell type and concentration of plastic particles used. This work highlights the importance of observing MP/NP effects on reproductive models. (**90**)

Kersten, Elise*, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Investigating effects of chemical hypoxia on myelination in Danio rerio*.- Myelin, composed of tightly wrapped layers of plasma membrane around the axon of a neuron, provides insulation for rapid transduction of electrical signals. Myelination can be derailed when oligodendrocyte (OL) 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 and recovery and resulting impacts to myelination is the focus of this research. We have characterized a new method to induce hypoxia in developing zebrafish using the chemical oxygen scavenger sodium sulfite. Zebrafish larvae 55 hours post-fertilization were treated with 0.2 mg/mL sodium sulfate (control) and 0.2 mg/mL sodium sulfite (hypoxia) to analyze effects on developmental myelin production. The sulfite solution decreased oxygen levels to 0.25 mg/L compared to 10.5 mg/L in the sulfate control. qPCR confirmed a 1.5–fold decrease in *mpz* gene expression post-hypoxia compared to the normoxic controls, indicating that hypoxia decreases myelin concentrations. This trend was corroborated by fluoromyelin staining for concentrated myelin in the spinal cord. Additionally, whole mount in situ hybridization (WISH) analysis was performed to examine the localized gene expression of *daam2*, a key regulator of the WNT signaling pathway, in hypoxic and control zebrafish OLs compared to the localized expression of myelin-specific *mbpb* and OL-specific *olig2*. (**111**)

Kimmel, Katherine*, Deborah Austin, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *Concentration of iron in the equine hoof wall and its relationship to veterinarian-diagnosed laminitis*.- Laminitis is a painful and disabling condition in horses caused by inflammation of the laminae that connects the hoof wall to the coffin bone and frequently results in severe lameness and impaired quality of life. Imbalance in trace minerals such as iron and copper may increase the risk of laminitis since these elements are crucial for the structure of the hoof wall and the integrity of the connective tissue. This study examined the iron content in the hoof wall and possible correlations with body weight and brand of food. During routine farrier visits, samples of the hoof wall were taken, and a survey was completed. The hoof wall material was digested using hydrogen peroxide and nitric acid. Atomic absorption spectroscopy was used to measure the concentration of iron. One-way ANOVA and Pearson correlations were done. The content of iron in the hoof wall varied statistically between laminitic and non-laminitic horses ($p = 0.002$), with the average iron levels being greater in non-laminitic horses. The iron content in the hoof wall varied significantly with brand of food ($p < 0.05$). The body weight of the horse and the iron content of the hoof wall were also shown to be somewhat positively correlated ($r = 0.630$, $p = 0.038$). This indicates that iron content is at a lower level when laminitis is present. Further studies should include an analysis of copper in the hoof wall to better understand the role of mineral composition and the incidence of laminitis. (**20**)

Kitzhoffer, Ashlee*, and Jenny Hayden Cedar Crest College, Allentown, PA 18104. *Exploring stagnant water as a source of antibiotic-producing bacteria: isolation and genetic characterization*.- Antibiotic resistance is one of the most pressing global health challenges of the twenty-first century, contributing to increased morbidity, mortality, and healthcare costs worldwide. This growing crisis highlights the urgent need to discover new antibiotics, particularly from natural environments that remain underexplored. While soil has traditionally been the focus of antibiotic discovery, aquatic habitats such as stagnant water may also contain diverse microorganisms with antimicrobial potential. As part of the Tiny Earth initiative, this study aimed to isolate and genetically characterize antibiotic-producing bacteria from stagnant water samples collected on the Cedar Crest College campus. Water samples were plated on R2A media to encourage the growth of diverse bacterial colonies. Individual isolates were then screened for antimicrobial activity against safe relatives of clinically relevant human pathogens, including *Pseudomonas putida, Alcaligenes faecalis, Bacillus cereus, Staphylococcus saprophyticus, Escherichia coli, Streptococcus pyogenes,* and *Staphylococcus aureus*. Isolates demonstrating zones of inhibition were selected for further study through morphological and biochemical characterization, antibiotic extraction, and 16S rRNA gene sequencing. By expanding antibiotic discovery efforts beyond traditional soil-based searches, this research contributes to the identification of potentially novel antimicrobial producers while also improving our understanding of microbial diversity in aquatic environments. Overall, this work supports the broader mission of Tiny Earth by exploring alternative ecological niches in the ongoing search for new antibiotics with future therapeutic relevance. (**58**)

Klews, C. Cristoph*, and Emily Stowe Bucknell University, Lewisburg, PA 17837. *Relationship between benthic microbial communities in the Susquehanna River and the environmental river conditions across multiple sites*.- Microbial communities are essential in the process of nutrient cycling in river ecosystems. They function to fix abiotic molecules involved in various metabolic processes into bioavailable nutrients. The Susquehanna River in Central Pennsylvania forms at the convergence between the North Branch and the West Branch of the Susquehanna River. These branches are geochemically distinct and show limited mixing after the convergence, creating water condition continuity across the main branch. This research explored the degree of correlation between the geochemistry of distinct river sites along the Susquehanna River and the community composition in the form of both taxonomic identities and metagenomic metabolic profiles. This correlation may allow future research into methods for untargeted water quality assessment based on community adaptations. Five fluvial islands were selected from the river, one from the west branch, one from the north branch, and three from the mainstem. These sites had in situ water probe readings taken, nine soil samples in a 3x3 grid for DNA Extraction, and four water samples were taken from the offshore shallows for the purpose of chemical analysis. This data was analyzed using multivariate statistical tests to determine community clustering patterns and the statistical significance of these clusters. The community clustering patterns were then compared to the clustering pattern of the environmental data to determine which had the strongest correlation. Preliminary results indicate that while each site is distinct from each other, there is a branch associated pattern to river condition and the community data is distinct from each other. (**81**)

Krainer, Melissa*, Alexis Dell, and Yimin Zhu Penn State University-Altoona, Altoona, PA 16601. *Exploring the complexation of sinapyl alcohol and cyclodextrins*.- We look at a plant cell model and observe the structure of the major polymer lignin in the cell wall. Two different types of lignin coupling linkage (-O-4 and -) are shown, each composed of two oxidized sinapyl alcohol radicals: -O-4 (composed of a and O-4 radical), and - (composed of two radicals). The auxiliary agents -cyclodextrin and -cyclodextrin are discussed with their unique hydrophobic cavities that are able to trap/encapsulate other molecules. To investigate whether hydrophobic sinapyl alcohol will become trapped within these cavities in an aqueous solution to form a “complexation,” solutions with sinapyl alcohol and increasing concentrations of cyclodextrin are prepared and analyzed with Nuclear Magnetic Resonance (NMR) spectroscopy. Titration curve graphs comparing the NMR signal to the concentration of cyclodextrin present in the solutions are shown in addition to the qualitative observation of spectra peak shifts as concentration changes. A quantitative analysis is performed to determine the equilibrium constant of the reaction of sinapyl alcohol and -cyclodextrin to produce complexations. The analyses confirmed complexations are formed with a high equilibrium constant value of 10.2. (**17**)

Lally, Madison*, and Robert Kurt Lafayette College, Easton, PA 18042. *An agent-based model of chemokines and white blood cells responding to tumor growth*.- Chemokines and white blood cells are critical to fighting cancer, but they can also contribute to cancer progression. However, the interactions between the immune system and cancer cells are difficult to visualize and study. For this reason, we developed an agent-based model that incorporated tumor cells, chemokines, macrophages, and T-cells to represent the tumor environment. The agent-based model was used to predict how changes in T-cell numbers and chemokine diffusion rates would affect tumor size. The model platform was NetLogo, and the code was generated with ChatGPT and then adjusted to take into account chemokine diffusion rates, and the number of tumor cells and white blood cells. Variables considered by the model included the diffusion coefficients for CXCL2 and CXCL12 (.25 to .40) and the number of T-cells (10 to 20). The modeling data showed that tumor growth slowed as T-cell numbers and the CXCL2 diffusion rate increased. On the contrary, tumor growth increased as CXCL12 diffusion increased, with over 7,000 tumor cells compared to over 3,000 tumor cells with CXCL2. These findings suggest that T-cells and chemokine diffusion rates play essential roles in regulating tumor growth. Additionally, the findings suggest that an increase in CXCL12 will increase tumor growth and an increase in CXCL2 will decrease tumor growth. We are currently generating bone marrow-derived macrophages and treating them with varying concentrations of CXCL12 to determine the impact on macrophage function. Preliminary data indicate that CXCL12 increases the protumor activity of macrophages, suggesting that it may contribute to tumor growth through macrophage signaling. Together, these findings will help improve the understanding of how immune cells and chemokines interact within the tumor microenvironment and influence tumor growth. (**101**)

Lenkiewicz, Nicole*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Expression analysis of Phytophthora infestans AA17 gene PITG_09799 in mycelium using quantitative PCR*.- The oomycete *Phytophthora infestans* is the pathogen responsible for potato late blight, a disease that causes approximately 6 billion USD in agricultural losses worldwide. The pathogen relies on carbohydrate-active enzymes (CAZymes), which are able to break down the cell wall components of plants, such as hemicellulose, cellulose, and pectin, thus allowing the pathogen to have access to nutrients from the plant and invade its tissue. Among these enzymes, PITG_09799 is predicted to belong to the auxiliary activity 17 (AA17) CAZyme family. Members of this family are lytic polysaccharide monooxygenases that oxidatively break down resistant polysaccharides. However, the expression of PITG_09799 in *Phytophthora infestans* has not been well characterized. This study aimed to further characterize PITG_09799 by cloning and sequencing the gene, and evaluating its expression in *Phytophthora infestans* mycelium using quantitative PCR (qPCR). After cloning and sequencing the gene, *P. infestans* was cultured in pea broth, and RNA was extracted from the harvested mycelial tissue. The RNA was converted into complementary DNA (cDNA), which was used as a template for quantitative PCR (qPCR) analysis using PITG_09799-specific primers and Kelch as a reference gene. The *Phytophthora infestans* gene PITG_09799, approximately 2000 bp in length, encodes a 692–amino acid glucan 1,3-β-glucosidase containing a glycosyl hydrolase family 1 catalytic domain and an X8 carbohydrate-binding domain. Preliminary results indicate the gene is actively expressed in mycelium. Analyzing the expression of PITG_09799 in mycelial tissue will contribute to a better understanding of gene activity in this pathogen and help support future studies investigating its potential role in pathogen development. Future work will focus on detecting expression of this gene *in planta* during host infection. (**95**)

Lewis, Kylie*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Exploring the mouse fecal microbiome using ONT sequencing of 16S and ITS amplicons*.- The gut microbiome is a critical player in host immune system function, metabolism, and overarching organism health. Characterizing the microbiome of an organism, especially a model organism like the mouse, is beneficial for understanding the interactions between the microbial community and the host as well as validating the techniques used to isolate DNA and compare sequence data. This study, done as part of the genome analysis course, aims to identify the microbial communities present in mouse fecal material using amplicon sequencing. The Fecal sample was collected from a C57 lab mouse at Lycoming College and genomic DNA was extracted using the Zymo Fecal/Soil DNA extraction kit. Bacterial communities were identified using the 16sRNA amplicon, and fungal communities were characterized using the internal transcribed spacer or ITS sequence. Both sequences were amplified using the polymerase chain reaction or PCR. Amplicons were then sequenced using Oxford Nanopore Technologies on a Flongle flow cell in a MinION sequencing device. The resulting data was analyzed to determine the identity of the organisms within the microbial community found in the sample. Analysis of the sequencing data showed many bacterial species commonly associated with the murine microbiome including Ligilactobacillus murinus and Muribaculum gordoncarteri, as well as several fungi associated with plant decomposition. Many of the organisms found have been previously identified as associated with the murine gut microbiome. This study showed that ONT can be utilized to rapidly characterize both the bacterial and fungal murine gut microbiome. (**126**)

Liebmann, Caroline*, and Isaac VonRue King's College, Wilkes-Barre, PA 18711. *Biodegradation of shape memory polymer foams*.- Shape memory polymers (SMPs) are smart materials that can undergo shape changes when an external stimulus, like heat, light, or moisture is applied. When the stimulus is applied, the SMP changes from its permanent shape to a temporary shape that is maintained until the stimulus is reapplied. SMPs have a variety of biomedical applications including being used as minimally invasive implants, sutures, and tissue scaffolds. The purpose of the research project was to synthesize biodegradable SMP foams from two different crosslinkers, hexamethylenediamine (HMDI) and disulfide diester dihydroxyl

(DSDEDH), and compare their respective degradation rates. SMP foams were first synthesized using a 1:1 ratio of polyvinyl alcohol to cornstarch and crosslinked with HMDI. Solid NaCl was added during the SMP synthesis to create pore spaces in the foam. The DSDEDH crosslinker was synthesized via an esterification reaction of dithioglycolic acid and diethylene glycol. Future directions include synthesizing SMP foams with the DSDEDH crosslinker and comparing the degradation rates of HMDI-crosslinked SMP foams to DSDEDH-crosslinked SMP foams. (**37**)

Lighting, Mikayla*, and Whitney Leach DeSales University, Center Valley, PA 18034. *Temperature effects on sex ratios in the tidal cnidarian Nematostella vectensis*.- *Nematostella vectensis* has previously been shown to exhibit circadian behavior, reproduce both sexually and asexually, and regenerate body parts following severe injury. Despite its widespread use as a model organism, the mechanisms underlying sex determination, and even the sex ratio within a clutch of eggs, remain unknown. The objective of this study is to investigate whether developmental temperature influences sex ratios in *N. vectensis*. Offspring from three clutches of eggs were collected, fertilized, and reared under three temperature conditions (17°C, 21°C (room temperature control), and 26°C). Replicate cultures were maintained either in an incubator or at room temperature. At one month post-fertilization, developmental differences among temperature treatments were observed, with individuals raised at 21°C and 26°C developing substantially faster than those maintained at 17°C. Upon reaching sexual maturity and spawning for the first time, male and female individuals will be identified, allowing this study to determine the resulting sex ratios across temperature treatments and assess whether developmental temperature influences sex determination in *N. vectensis*. (**29**)

Li, Jayden*, and Andrea Nerozzi Wyoming Seminary Upper School, Kingston, PA 18704. *Enzymatic resilience: analyzing the effect of dehydration on β-Glucosidase activity across fungal species*.- This study evaluates the viability of dehydration as a preservation method for β-glucosidase, an enzyme used in food processing and energy development. Because fresh fungal samples degrade rapidly, this research sought to determine if desiccation could effectively slow metabolic activity for delayed analysis without compromising enzymatic function. Cap tissue from Agaricus bisporus variants (Button, Portabella, Crimini) and non-Agaricus species (Lentinula edodes, Pleurotus sp.) was analyzed in both fresh and dehydrated (24-hour) states. Extracts obtained by grinding and filtration were incubated with a p-nitrophenyl glucopyranoside substrate under room temperature, and reactions were stopped at timed intervals using an alkaline solution. Enzyme activity was quantified via spectrophotometry (410 nm), utilizing a pigment-corrected blank to account for the intrinsic coloration of mushroom. Results indicated a taxonomic divide in enzymatic stability: while the Agaricus group maintained stable or slightly enhanced activity post-desiccation, the non-Agaricus species (Lentinula edodes, Pleurotus sp.) lost approximately 46% and 27% of their activity, respectively. These findings demonstrate that dehydration is a viable protocol for preserving enzymes in specific fungal groups like Agaricus, though unsuitable for species such as Lentinula edodes and Pleurotus sp. This study provides a practical procedure for optimizing sample processing in mycological and biochemical research. (**112**)

Lippitt, Kade, Caroline Maciejewski, James Knowles, Afaf Nazif, Madeline Frederick*, and Alex Van Huynh DeSales University, Center Valley, PA 18034. *Usage of iNaturalist for observation of morphologically similar species and disease-causing pathogens*.- As Earth's biodiversity is faced with ever-escalating threats, large digital datasets have become a vital source of information in addressing critical ecological and conservation issues. With important biodiversity data acquired in the form of citizen science initiatives, iNaturalist has become one of the most popular citizen science platforms used increasingly in biodiversity research. Already, iNaturalist has been utilized in a wide variety of ways, including monitoring species distributions, phenological changes, biological invasions, at-risk species, and even investigating a wide variety of interspecific interactions. Still, iNaturalist is ultimately an unstructured, citizen science platform, resulting in several sampling artifacts and other sources of error that must be taken into consideration by researchers. These commonly include spatial, temporal, and taxonomic biases in observations logged by the public. Here we discuss the ability for iNaturalist to be used when species identity is questionable, especially in the context of morphologically similar species through spatial and temporal lenses and for pathogens identifiable through disease symptoms in their hosts. By outlining these important uses and limitations we hope to inspire scientists around the globe to leverage this dataset for future ecological and conservation research. (**51**)

Lippitt, Kade*, Caroline Maciejewski, James Knowles, Afaf Nazif, Madeline Frederick, Natalie Skuza, Nia Tempest, and Alex Huynh DeSales University, Center Valley, PA 18034. *Analysis of iNaturalist observations of visually distinct species*.- Faced with ever-accelerating threats to Earth's biodiversity, large digital datasets have become a vital source of information in addressing critical ecological and conservation issues. These data now allow researchers to attain key insights more rapidly and at larger scales. An important source of biodiversity data comes in the form of citizen science initiatives. iNaturalist is one of the most popular naturalist citizen science platforms and is being increasingly used in biodiversity research, including monitoring species distributions, biological invasions, at-risk species, phenological changes, and even investigating a wide variety of interspecific interactions. Still, iNaturalist is ultimately an unstructured, citizen science platform, resulting in a number of sampling artifacts and other sources of error that must be taken into consideration by researchers. Species with visually distinct morphology and coloration (i.e charismatic species) have a skewed distribution of observations compared to similar species that are less charismatic. With this in mind, future large-scale iNaturalist research may need to correct for this disparity when comparing species of varying charismatic levels. (**61**)

Lippitt, Kade*, Caroline Maciejewski, James Knowles, Afaf Nazif, Madeline Frederick, Nia Tempest, Natalie Skuza, and Alex Huynh DeSales University, Center Valley, PA 18034. *Analysis of acoustic activity database 'BirdWeather' reveals temporal shifts of diurnal species vocalizations in response to wildfire smoke*.- The increase in size, regularity, and duration of wildfires globally has occurred in tandem with anthropogenic climate change. While previous studies have examined the habitat destruction of wildfires and have even shown the detrimental health effects of long-term exposure to smoke particulate in the air. Research focusing on wide-ranging ecological impacts of the smoke plumes themselves has been largely neglected. In 2023 the Northeastern United States experienced severe record-breaking smoke pollution originating from the Canadian wildfires. To investigate how these smoke plumes may have affected avian behaviour at a large scale during this period, we utilized the publicly available database BirdWeather. BirdWeather sources its data from a network of autonomous audio recording devices which utilize artificial intelligence to identify bioacoustic signals to the species level. By spatiotemporal mapping over 550,000 vocalizations across nine states, these bioacoustic signals revealed a significant shift in timing of the early morning 'dawn chorus' of diurnal species which correlated with the increase in air pollutants within that geographic area. (**84**)

Lippitt, Kade*, Desmond Purchla*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Metagenomic analysis of a peat bog reveals persistent Homo sapiens* <u>*reads*</u>.- Bogs are ecologically important wetland biomes that develop from the gradual accumulation of Sphagnum moss and other partially decayed detritus, collectively referred to as peat. Despite their importance, the abundance, diversity, and composition of microbial communities within bog ecosystems remain relatively understudied. We performed metagenomic analysis of soil samples collected from the Tannersville Cranberry Bog, a ~13,000-year-old bog located approximately 8 km northwest of Stroudsburg, Pennsylvania. Soil was sampled in triplicate at a depth of 15 cm from seven distinct sites within the bog. Genomic DNA was extracted, adapters and barcodes were ligated to construct sequencing libraries, and samples were sequenced using the Oxford Nanopore MinION sequencer. FASTQ files were analyzed using the EPI2ME platform, and taxonomic assignments were performed with the wf-metagenomics workflow. Unexpectedly, initial metagenomic analysis revealed a high abundance of Homo sapiens reads across all sampling sites. To address the possibility of contamination during sampling, we repeated collection and sequencing using enhanced personal protective equipment. Despite these precautions, H. sapiens reads were again detected at high levels in all samples. To further evaluate potential laboratory contamination, we analyzed the data using the R package decontam, assessing the relationship between read abundance and DNA concentration. This analysis suggested that the H. sapiens reads are unlikely to originate from laboratory contamination. Collectively, these findings raise the possibility that the Tannersville Cranberry Bog contains human DNA, the origin of which warrants further investigation. (**88**)

Love, Wesley*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Gamma proteobacteria are the dominant culturable endophytes in the Indian Pipe, Monotropa uniflora*.- *Monotropa uniflora*, commonly called the ghost plant or Indian pipe, is a parasitic, non-photosynthesizing flowering plant known to feed off the nutrients from underground mycelia of fungi colonizing tree roots. While they are known to be parasitic, there is no knowledge of microbes that colonize *Monotropa*. In order to explore the inner lives of these mysterious plants, we collected their stems and flowers, surface-sterilized them and isolated endophytic bacteria using serial dilution plating. We identified eleven distinct bacterial isolates, mostly belonging to the class Gamma Proteobacteria including several species of fluorescent *Pseudomonas, Rouxiella Rahnella* and *Ewingella* species. Multiple *Pseudomonas* isolates displayed exceptional cold tolerance, being able to grow at temperatures as low as -2°C. Interestingly, nearly all isolates were nitrate-reducing and glucose-fermenting and not surprisingly, the flower isolates had distinct metabolic preferences including sugar metabolism, compared to the stem isolates. Given that non-photosynthetic plants like *Monotropa* rely on parasitism for survival, they may possibly rely on microbial partners for vital metabolic services. This study provides a window into the unexplored world of microbial inhabitants of parasitic plants. (**18**)

Ma, Beth*, Mitchell Devore, David Almeida, and Mahita Kadmiel Allegheny College, Meadville, PA 16335. *Effect of glucocorticoid receptor, dexamethasone, and CTZ1 interactions on human Müller glia inflammatory response and regenerative potential*.- Affecting over 100 million individuals worldwide, diabetic retinopathy (DR) is the leading cause of blindness in working-age adults in the United States. As a major contributor to the global disease burden, DR is projected to affect an additional 60 million individuals over the next two decades. Current treatments target glucocorticoid receptors (GR), which modulate immune responses and gene expression. While synthetic glucocorticoids (GC) like dexamethasone effectively suppress inflammation by inhibiting cytokine production, their direct effects on neurogenesis are still underexplored. Chronic GC use is associated with significant side effects such as immunosuppression and increased risk of cataracts, making the development of novel therapeutics critical. This study investigates CTZ1 (Citrus Therapeutics), a novel vascular-disruptive and antioxidative agent, as an alternative therapeutic to modulate cellular function in ocular inflammation. As primary retinal support neurons, Müller glia (MG) maintain homeostasis and possess the capacity to reprogram into progenitor cells in non-mammalian species—a process governed by transcription factors including anti-proliferative PROX1 and the pro-neurogenic ASCL1. While current studies are primarily focused on direct initiation of MG regeneration towards treating retinal degeneration, this study aims to map GR immunomodulation across physiological and hyperglycemic states, and associated effects on known regulators of MG neurogenesis. Immortalized MIO-M1 cells were cultured under normal (NG) and high (HG) glucose to simulate the diabetic environment, with siRNA transfection applied to knock down GR. RT-qPCR quantification was performed to confirm knockdown (NR3C1), inflammatory (IL1RN), and differentiative (PROX1, ASCL1) states. Immunocytochemistry (ICC) was employed to observe morphological changes and assess reactive gliosis (GFAP) and proliferation (Ki-67). Results suggest that IL1RN expression is GR-independent in NG and GR-dependent in HG conditions when treated with dexamethasone, while

GFAP expression in NG is GR-dependent and GR-independent in HG. Future investigation of the MAPK and VEGF pathways may elucidate GR-specific mechanistic contributions towards neuronal retinal survival. (**70**)

Maciejewski, Caroline*, Kade Lippitt, James Knowles, Afaf Nazif, Madeline Frederick, and Alex Huynh DeSales University, Center Valley, PA 18034. *The use of iNaturalist in ecological and conservation research: methodological guidance and considerations*.- Faced with ever-accelerating threats to Earth's biodiversity, large digital datasets have become a vital source of information in addressing critical ecological and conservation issues. These data now allow researchers to attain key insights more rapidly and at larger scales. An important source of biodiversity data comes in the form of citizen science initiatives. iNaturalist is one of the most popular naturalist citizen science platforms and is being increasingly used in biodiversity research, including monitoring species distributions, biological invasions, at-risk species, phenological changes, and even investigating a wide variety of interspecific interactions. Still, iNaturalist is ultimately an unstructured, citizen science platform, resulting in a number of sampling artifacts and other sources of error that must be taken into consideration by researchers. These commonly include spatial, temporal, and taxonomic biases in observations logged by the public. Here we outline and highlight these important sources of error in iNaturalist data using case studies that span various ecosystems and taxa in the United States, where the usage of the platform remains highest. Together, we provide comprehensive guidance, suggestions, and notes for caution in using iNaturalist data to better help scientists around the globe leverage this dataset for future ecological and conservation research. (**82**)

Mallette, Jessie*, Aiden Keja*, and Brian Gray York College of Pennsylvania, York, PA 17405. *CRISPR/Cas9-mediated knockout of potential biosynthetic gene cluster responsible for the antimicrobial properties of Pantoea eucrina*.- The emergence of antimicrobial resistance among pathogenic bacteria is creating global health concerns that necessitate the discovery of novel antibiotics. An effective method for discovering novel antibiotics involves isolating antimicrobial compounds that environmental bacteria naturally produce. A bacterium isolated from a soil sample from York, Pennsylvania (39°56'48" N 76°43'40" W), isolate JAD10_F22WB, produced a zone of inhibition less than 1 mm when plated on an LB plate against Pseudomonas aeruginosa. Genomic sequencing combined and BLASTn showed a high percent identity of JAD10_F22WB to Pantoea eucrina. Using the antiSMASH suite, we identified a putative biosynthetic gene cluster (BGC) sharing 6% similarity to a previously studied BGC associated with production of the antibiotic Yatakemycin. Two genes from the cluster, ctg3.47 and ctg3.48, were putatively identified as biosynthetic enzymes: a methyltransferase and a YcaO family protein, respectively, by NCBI BLASTp. These enzymes have been noted to be crucial in the formation of other ribosomally synthesized and post-translationally modified peptide products (RiPPs) with antibiotic properties. We used Geneious to design two unique single-guide RNA (sgRNA) targeting the genes of interest. These sgRNA oligonucleotides were ligated into the pCasCure-Kan expression vector using HiFi assembly for later transformation into isolate JAD10_F22WB. Future studies will include the transformation of the synthesized vectors into isolate JAD10_F22WB, LB agar competition plates against Pseudomonas aeruginosa to observe phenotypic changes in antimicrobial production, and gene-specific PCR and sequences of the target genes to identify a gene-level functional knockout of the targets. (**50**)

Mamari, Angela*, Angela McMahon*, and Giancarlo Cuadra Cuadra Muhlenberg College, Allentown, PA 18104. *SDS-PAGE characterization of glycoproteins released from OKF6 cells following exposure to e-cigarette aerosols*.- Studies from our laboratory have shown that exposure to E-cigarette aerosols can alter oral epithelial cell responses, however, little is known about their effect on glycoprotein secretion, which is important for maintaining oral barrier function. So, the aim of this study was to evaluate glycoprotein release from OKF6 cells (cell model for oral epithelial cells) following 24-hour exposure to aerosolized flavored E-liquids. Supernatants were collected, concentrated, and analyzed using SDS-PAGE, with glycoproteins detected by Alcian Blue staining and quantified using ImageJ. Across treatments, glycoprotein band intensities showed variability, with some conditions (tobacco, menthol, air, flavorless, blueberry, cinnamon, and strawberry aerosols) exhibiting higher average glycoprotein to control ratios. However, substantial variability between experimental replicates resulted in large standard deviations, limiting the significance of these differences. Overall, these results suggest that no consistent effect of aerosol exposure on glycoprotein release was observed. (**135**)

Marcellino, David*, Ibrahim Salahi*, and Robert Mishur Widener University, Chester, PA 19013. *Investigation of the effects of branched-chain keto acids on Drosophila lifespan*.- Alpha-ketoglutarate is a naturally occurring metabolite that has been shown to influence longevity across multiple organisms including *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Mus musculus* by affecting metabolic pathways involved in energy metabolism, oxygen response, and resistance to cellular stress. Interestingly, several branched-chain keto acids (BCKAs), which are structurally analogous to AKG, have also been demonstrated to increase lifespan in *C. elegans*. These metabolic intermediates are derived from branched-chain amino acids and include 3-methyl-2-oxobutyrate (3M2OB), 3-methyl-2-oxovalerate (3M2OV), and 4-methyl-2-oxovalerate (4M2OV). However, it is unknown if these compounds can extend lifespan in *D. melanogaster*. To investigate this, the diets of adult flies were supplemented with various BCKAs by incorporating them directly into their food at a concentration of 10 mM, and survival assays were performed. A statistically insignificant increase in lifespan was observed in male flies treated with 3M2OV, while supplementation of other BCKAs resulted in lifespans similar to those of control animals. Female flies had reduced lifespans on dietary supplementation with all three BCKAs at this dosage. To investigate whether the shortened lifespans were due to hormesis, we repeated this experiment using 1 mM concentrations of BCKAs. At the lower dosage, no significant increase in overall lifespan was observed in any of the animals. However, male flies supplemented with 1 mM 3M2OV showed a slower decline in survival during early and mid-life stages, suggesting a possible improvement in health span. Future studies will examine the effect of administering BCKAs to *D. melanogaster* during larval development. (**107**)

Marley, Kaitlyn S.*, Hannah M. Werle, and John P. Morgan Misericordia University, Dallas, PA 18612. *Green modification of a coupling reaction between N-acetylated amino acids and p-nitrophenol*.- We report an improved green synthesis of *N*-acetylphenalanine p-nitropheylthioester as originally reported in Hondal, R. J.; Nilsson, B. L.; Raines, R. T. *J. Am. Chem. Soc.* 2001, *123*, 5140-5141. This literature synthesis uses *N,N*-dimethylformamide (DMF) as solvent in the final thioester coupling step due to the limited solubility of *N*-acetylphenylalanine in less polar solvents. We report that water solvent is an acceptable alternative to DMF, improving both the greenness and the reaction workup of the desired thioester product. (**140**)

Martinez, Nicole*, and Robert Kurt Lafayette College, Easton, PA 18042. *Early immune cell recruitment may determine tumor fate: modeling and in vivo studies*.- The development of a tumor depends on complex mechanisms between cancer cells and the host's immune response. An agent-based model of the early immune response to cancer was created to explore how initial immune conditions impacted tumor outcome. The model included different types of functionally identical immune cells (including macrophages and cytotoxic T cells) in an environment initially containing a single cancer cell. In the model if an immune cell was near a cancer cell, then the immune response was triggered, and an attack on the tumor was initiated. The primary objective of this model was to predict the outcome of the immune response (tumor elimination or progression) across three different treatment trials. Baseline simulations showed the immune system successfully eliminated the tumor ~30% of the time. Based on these results, three experiments were conducted within the model: (1) increasing the initial number of immune cells, (2) increasing signaling between activated immune cells, and (3) removing the limits on the number of immune cells that could be present simultaneously. The three trials had similar results; the immune system success rate rose to 50% (a

66% increase), and the rate of tumor growth was slowed. Examination of successful runs revealed that the outcome was decided within 50-100 ticks of initiation of the simulation (the total run time was 250 ticks), suggesting that an effective early immune response was more efficient than an aggressive later immune response. An ongoing *in vivo* study is being conducted to evaluate this hypothesis. For this purpose, four groups of mice will be injected with breast cancer cells with increasing concentrations of the chemokine CXCL1 (starting at 0 ng) to stimulate early immune cell recruitment. (**104**)

Martin, Natalie*, and Whitney Leach DeSales University, Center Valley, PA 18034. *Sex-based differences in circadian rhythms in Nematostella vectensis*.- *Nematostella vectensis*, commonly known as the starlet sea anemone, is a burrowing cnidarian found in salt marshes, lagoons, and mudflats along the Atlantic and Pacific coasts of the United States and in southern England. This species is tolerant of a wide range of salinities and temperatures and has become increasingly popular as a model research organism. Despite this, little information is known about the circadian clock of *Nematostella*. Unlike many organisms, *Nematostella* lack eyes or any type of known specialized light sensing organs, suggesting they detect light and regulate circadian rhythms differently than other animals. Much of this research will focus on the potential differences in circadian rhythmic activities between male and female *Nematostella*. The animals will be exposed to alternating 12 hour light and 12 hour dark cycles (LD) for a total of 36 hours using a light ring composed of LED and IR lighting to stimulate daytime and nighttime conditions. Images captured during the experiment will be compiled into timelapses and analyzed using Fiji to observe behavioral activity patterns. This research aims to determine whether sex-based differences exist in the circadian behavior of *Nematostella vectensis*. (**28**)

Mazza, Gia*, Leah Rudolph, Jazzlyn Dominguez, Sarah Parent, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Effects of information and collective behavior on SIS disease spread*.- Infectious disease dynamics are strongly influenced by human behavior. A recent modeling study introduced an SIS epidemic model with collective behavioral effects, where individuals adopt protective behavior in response to disease prevalence. That model showed that feedback between disease prevalence and cooperation can produce different epidemic regimes depending on how readily populations respond to infection risk. However, responses to epidemics are also strongly shaped by the information environment, including the consistency and quality of public messaging. Here we extend the previous model by explicitly incorporating information dynamics. The new model includes a variable representing the level of coherent information encouraging cooperative behavior. Disease prevalence influences the production of coherent information, information coherence affects whether cooperation grows or declines, and cooperation in turn reduces disease transmission. We analyze the resulting system to determine its equilibria and explore how information dynamics influence epidemic outcomes. These models provide a framework for studying how information environments interact with collective behavioral responses during epidemics. Understanding how information coherence affects cooperation and disease spread may help clarify how communication environments shape epidemic dynamics. (**1**)

McDermott, Owen*, and Anna Fedor Misericordia University, Dallas, PA 18612. *Analysis of lead concentration in soil samples using atomic absorption spectroscopy*.- Lead-contaminated soils are routinely analyzed using highly concentrated acids, which present safety and environmental drawbacks. This project investigates a safer alternative using a dilute nitric acid extraction combined with atomic absorption spectroscopy (AAS) to determine the concentration of lead in soil. Soil samples collected from Dallas, PA (1.0 g) were digested with 0.43 M nitric acid and extracted under shaker-bath conditions for varying durations (2-96 hr) to evaluate the effect of extraction time on calculated lead concentration. Samples were centrifuged, filtered, and analyzed by AAS using prepared lead standards for calibration. Method optimization, including extraction time and standards used for the calibration plot, improved the reproducibility of results. These results suggest that prolonged extraction with dilute nitric acid is a viable, lower-risk approach for forensic and environmental lead analysis in soil. (**100**)

Mendola, Jyanna*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Pro-inflammatory and anti-inflammatory cytokine secretion in lipopolysaccharide-treated RT4-D6P2T Schwann cell line*.- Schwann cells play a key role in inflammation and repair following damage of the myelin sheath. The process of repair starts by stimulating macrophages to make pro-inflammatory cytokines, Tumor Necrosis Factor-Alpha (TNF-a), and anti-inflammatory cytokines, Interleukin 10 (IL-10), which promotes healing and injury. Although it is clear that Schwann cells play a role in nerve repair, the exact mechanisms are unknown. To further explore the effects of forskolin in LPS-stimulated Schwann cells, the role of IL-10 secretion was examined. The RT4-D6P2T Schwann cell line were treated with 0.1,1, or 10 μg/mL of LPS, or 1, 2, or 3 μM forskolin (F), or combinations of LPS and F treatments for 3 and 24 hours in growth media (N2). Cell culture supernatants were collected and assayed for IL-10 secretion using ELISA. Secretion of IL-10 was augmented by forskolin in LPS-treated cells compared to LPS or forskolin treatment only. For instance, IL-10 secretion was increased at 1 μg/mL of LPS with all treatments of forskolin at 24 hours (404 +231.3%, 586 + 226.2%, 474 + 299.1%). Surprisingly, cells treated with 0.1 μg/mL of LPS for 3 hours secreted more IL-10 when stimulated with forskolin at concentrations of 1 μM (155.85+16.85%) and 3 μM (140.1+37.23%) compared with 24 hours (126.8+24%, 135+35.8%). It appears that LPS and forskolin may act in unison to upregulate IL-10 secretion. Moreover, these findings suggest that, during nerve injury, the ability of the cAMP pathway to counteract inflammation by secreting IL-10 in LPS-stimulated Schwann cells is dependent on concentration and time. Ongoing studies are investigating the effects of forskolin on LPS-stimulated Schwann cells, with particular emphasis on the role of TNF- α at corresponding time points. A better understanding of the balance between pro- and anti-inflammatory cytokines during nerve injury may potentially unlock the mechanisms that mediate these pathways. (**99**)

Miller, Emmit*, and Derek Straub Susquehanna University, Selinsgrove, PA 17870. *Evaluating fog liquid water content through capacitive sensing to assess fog harvesting potential*.- Fog water harvesting has emerged as a potential supplementary water source for communities facing increasing water scarcity, yet its reliability depends heavily on the amount of liquid water present in fog events. Current fog-collection systems mainly rely on passive mesh structures and do not directly measure fog liquid water content (LWC), making it difficult to predict water yield or assess long-term productivity. This project investigates whether capacitive sensing can be used as a practical method to quantify the LWC of fog, with the broader goal of determining whether fog harvesting can serve as a sustainable water resource in water-limited regions. The experimental design consists of a parallel plate capacitor with polypropylene filter material as the dielectric. As air is drawn through the capacitive sensor, fog droplets accumulate on the filter material, increasing its capacitance. By monitoring the change in capacitance over time, LWC can be derived. Background research on fog formation, droplet behavior, and moisture-responsive sensing technologies provides the foundation for exploring this approach. Over the course of the project, relative humidity tests revealed slight increases in measured capacitance, suggesting that ambient moisture influences the sensor more than expected. Additional tests using incremental droplet deposition, simulating fog collecting on a surface, produced consistent and measurable increases in capacitance, demonstrating that the system is highly responsive to changes in surface water content. By analyzing these trends, this study aims to determine whether capacitance data can be reliably correlated to fog LWC and, ultimately, to the volume of water that could be harvested during fog events. If successful, this approach could offer a low-cost, low-energy tool for evaluating fog density and predicting water yield, supporting efforts to develop sustainable fog-harvesting technologies for regions experiencing chronic water shortages. (**108**)

Miller, Gennavieve*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Molecular identification of PETase genes and assessment of PET plastic degradation in marine bacteria*.- Polyethylene terephthalate (PET) is one of the most commonly used polymers in food and beverage packaging. Due to improper plastic waste management, plastic has become a pressing issue for both the environmental and human health. Microorganisms may respond to this stress by adapting an enzyme necessary to degrade the waste. Polyethylene terephthalate hydrolase enzymes (PETase) are used in the degradation of plastics and offer a sustainable solution for recycling PET. However, their prevalence and efficiency are not yet well understood. The objective of this study is to determine how prevalent PET-degrading enzymes are in the marine environment. In this study, we utilized marine bacteria isolated from various beaches along the United States East Coast to investigate the degradation of PET in tryptic soy broth agar (TSA) plates. To promote plastic degradation, we will use minimal media agar supplemented with PET to screen for plastic degradation activity. As a complementary approach, we will also screen the bacteria using primers designed to amplify PETase enzymes that are commonly employed for PET degradation. Through this study, we hope to find if there is enrichment of PETase enzymes in certain bacterial taxa. Understanding the genetic and functional aspects of marine microorganisms in response to plastic pollution may inform future bioremediation strategies and contribute to sustainable approaches to plastic waste. (**46**)

Molineros, Isabel*, Tabeth Mwema, Sophie Melissen*, Emily Brophy, Zoie Jackson-Lawrence, and Carla Garzon Delaware Valley University, Doylestown, PA 18901. *Characterizing thrips and their associated viruses in hemp grown at Delaware Valley University*.- As hemp farming grows across the U.S., tiny insects called thrips are becoming a major—and expensive—headache for growers. Whether grown outdoors or in climate-controlled indoor facilities, these pests change based on the environment and the age of the plant. Thrips hurt hemp in two main ways. First, they cause physical damage by feeding on the plants, which leads to scarred leaves, distorted flowers, and dead spots. Second, they are "super-spreaders" of plant viruses. These viruses can infect the entire plant, ruining its quality and making it impossible to sell. This is especially dangerous during the flowering stage, as the viruses can mess with the plant's growth and its ability to produce important compounds like CBD or THC. To stop these outbreaks, farmers need to know exactly which thrips they are dealing with. In this study, we looked at thrips found on indoor hemp plants that showed clear signs of sickness. To get the full picture, we used: 1) Microscope identification: Looking at their physical shapes; 2) DNA Barcoding: Checking their genetic code to confirm their identity; 3) Virus Testing (RT-PCR): Analyzing the insects to see which specific viruses they were carrying. Interestingly, the thrips in this study were found on plants that were also suffering also from aphid infestation, suggesting a "double whammy" of pests for the hemp. (**65**)

Moyer, Michaella*, and Tammy Tintjer King's College, Wilkes-Barre, PA 18711. *Evaluating alkaloid toxicity of Epichloë infected tall fescue seeds using brine shrimp assays*.- Fungal endophytes, in the genus *Epichloë*, form mutualistic relationships with cool season grasses such as tall fescue (*Festuca arundinacea*). The fungi live within the extracellular spaces of the host and infect the entire plant, including the seeds. *Epichloë* provides benefits to the host such as resistance to biotic/abiotic stressors through metabolic byproducts called alkaloids, but these compounds cause toxicity in mammals if consumed. Through artificial inoculation of wheat, we can use the alkaloids produced as a natural protection to stressors, making it more suitable, but it also puts humans at risk. By isolating the endophyte from infected tall fescue seeds, we hoped to artificially infect other grasses like wheat, but had minimal success which led to no artificial inoculations. To substitute, tall fescue seeds were used in place of the wheat seeds for the toxicity testing. Livestock friendly strains of *Epichloë* produce lower levels of alkaloids which decrease the toxicity risk. By using a livestock friendly strain, we could still use the insecticide benefits while preventing toxicity to mammals. This study tested various *Epichloë* strains by grinding the seeds of infected tall fescue into flour and adding them to water to create extracts. These extracts were then tested on a series of brine shrimp (*Artemia*) assays to observe differences in toxicity. At a 0.2 concentration there was a 40% mortality rate for ground seeds while the whole seeds had a 27% mortality rate. (**16**)

Mulholland, Brian*, Sherri Buerdsell, and Amber Marble Wilson College, Chambersburg, PA 17201. *The effect of glyphosate and atrazine on phenotypic variation in Brassica rapa*.- Herbicide exposure has been shown to cause phenotypic changes in plants. This study examined the effects of atrazine and glyphosate on *Brassica rapa* over a one-week period to determine the presence of epigenetic changes. Plant height, leaf area, chlorosis, necrosis, mortality, and dry biomass were observed. The data was organized in an Excel spreadsheet, and statistical analysis tests were performed. There was no significant difference in plant height, leaf area, or dry biomass. Necrosis occurred much less frequently than chlorosis, and no mortality was observed. There were seven glyphosate-treated plants that showed signs of chlorosis, and three atrazine-treated plants that showed signs of chlorosis. A Pearson correlation test was done comparing percentage necrosis and percentage chlorosis; there was no significant correlation. A Kruskal Wallis One-Way ANOVA for chlorosis percentage indicated a difference (p-value= 0.003). A Dunn's Post Hoc test showed that glyphosate-treated plants differed significantly from both atrazine-treated and control plants. A Kruskal Wallis One-Way ANOVA for necrosis percentage did not differ significantly. The results indicate chlorosis, but not necrosis, served as a reliable indicator of herbicide stress within the one-week observation period. While this study confirmed observable phenotypic changes, whether these reflect underlying epigenetic modifications remains unknown. Future studies incorporating epigenetic analysis could determine if these herbicide-induced stress responses are heritable. (**15**)

Nacua, Sophia*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Stage-dependent expression of circCUL2 in retinal development and neuroblastoma differentiation*.- Circular RNAs (circRNAs) are nucleic acids characterized by a covalently-linked closed loop, resulting in highly stable structures that have been investigated for potential roles in cell cycle regulation, neural differentiation, and gene expression. Circular RNA CUL2 (circCUL2) has previously been found to be downregulated in human retinoblastoma and colorectal cancer, with forced expression inhibiting tumor growth through microRNA modulation. However, it is unknown whether circCUL2 is expressed in other organisms and whether its expression patterns are associated with specific stages of nervous system development. This study thus tracks circCUL2 expression across select stages of nervous system development, using chicken (Gallus gallus) retinal cells and the human SH-SY5Y neuroblastoma cell line as model systems. Divergent CUL2 primers were designed to selectively amplify circCUL2 from samples of various stages via end-point and quantitative polymerase chain reactions (PCR). circCUL2 was found to be expressed in both Stage 29 (~6 days post-fertilization) and Stage 36 (~10 days post-fertilization) of chicken retinal development with multiple forms not previously found in human cells. Moreover, circCUL2 expression remains constant throughout stages of retinoic acid-induced differentiation in SH-SY5Y cells while its linear RNA counterpart CUL2 increases in expression. Future work centers around upregulating and downregulating circCUL2 in SH-SY5Y cells to observe whether this alters neuroblastoma phenotype. (**103**)

Nahon, Jess*, Chahinez Hennous*, Ayah Suleiman*, Hadeer Hamada*, and Whitney Leach DeSales University, Center Valley, PA 18034. *Mucus production in the tidal anemone, Nematostella vectensis*.- Antimicrobial mucus production in cnidarians is often associated with environmental stress, yet the specific conditions that induce this response remain unclear. In this study, we tested whether simulated low tide and changes in salinity influence mucus production in the intertidal sea anemone Nematostella vectensis. To mimic low tide conditions, we designed a "death hang" experiment in which anemones were placed in angled 6-well culture dishes with minimal water, creating partial aerial exposure and physiological stress. This treatment was applied across three salinity conditions representing the species' natural range and potential environmental variation: low (below 11 parts per thousand, ppt), normal (13–15 ppt), and high salinity (above

30 ppt). Preliminary observations showed no detectable mucus production at normal salinity under either control or death hang conditions. Limited mucus production was observed in the low-salinity death hang treatment. Based on these results and previous literature on intertidal stress responses, we hypothesize that tidal exposure, rather than salinity alone, may be the primary driver of mucus production in this species. Future experiments will separate tidal exposure from salinity treatments to better determine the relative contribution of these stressors. (**26**)

Nahon, Jessica*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Antimicrobials in coffee brew-methods*.- As antibiotic resistance grows over time, research into natural products such as coffee may help aid in a different approach to regulating antimicrobial growth and microbiome health. Studies have shown that coffee holds bioactive molecules that can combat bacterial growth. However, the pathologic effects and benefits from the coffee are not studied to the same degree. This project aims to establish the effects coffee has on inhibiting bacterial growth using eight different common brew methods of coffee. A popular brand of coffee, Starbucks, in a popular flavor brew profile, dark roast was chosen to test the antimicrobial effects. To test whether brew method altered the antimicrobial properties, the same coffee beans were used throughout. The beans were ground on site to the specificity of the brew method. To test if coffee has natural antimicrobial properties, a disk diffusion assay was performed. The coffee was tested on several bacteria. Overall, inhibitory effects were seen, however there were differences in the degree of inhibition with the individual microbes and the brew methods. The Majority of different brew techniques inhibited *Streptococcus pyogenes*. Specifically, espresso and drip inhibited *Staphylococcus aureus* and *Escherichia coli*. *Pseudomonas aeruginosa* was inhibited by espresso, pour over, moka pot, drip, and Keurig. Ongoing work will determine if coffee has effects on additional bacteria and whether the inhibition is dependent on caffeine. If coffee is determined as inhibitory, the data can be applied to areas such as microbiome health, food safety, and even sustainable diet-based antimicrobial approaches. (**31**)

Nerozzi, Andrea* Wyoming Seminary Upper School, Kingston, PA 18704. *Defining the continuity between high school and collegiate research*.- A veteran high school instructor shares her experiences leading a high school science research program. The structure of the program, as well as student outcomes, are described, with reference to the role of the Pennsylvania Junior Academy of Science. High school research starts at the level of the student and spans “discover-as-if-new” to novel projects, with students taking the lead in project development, execution and analysis, learning skills that go well beyond those encountered in a typical classroom setting. The author will discuss how this model fills an important role in developing future science professionals by fostering independence in scientific thought and action, and building transferable skills. The author advocates for more overt coordination between the high school and collegiate levels to provide more robust, accessible, opportunities for these young scientists. (**4**)

Ngo Bapa Ba Boumtje, Marianne*, Zuleikha Kurji, Kathryn L. Sarachan, and Deborah S. Austin Wilson College, Chambersburg, PA 17201. *Testing the photo-response of thin film elastomers of different thicknesses*.- Light-responsive liquid crystal elastomers (LCEs) can be used as actuators in biomedical devices and robotics. Thickness is an important engineering parameter that may affect the speed, force, and repeatability of the light-induced bend. Here we report the synthesis of azobenzene-containing thin film LCEs by sandwiching a still-crosslinking LCE reaction mixture between two glass slides with a release agent applied to make removal easier, using different layers of scotch tape as spacers to determine film thicknesses. After demolding, the sample was stretched and exposed to UV light at 405 nm to align the LC polydomain to the monodomain. This alignment concludes the second cross-linking. Using this method, thin films with thicknesses ranging from 50 -200 µm were successfully synthesized and aligned. Their light responses were measured using 405 nm light and the effect of increasing thin film thickness on LCE bending was analyzed. Establishing how different thicknesses of thin films react to light will help establish which different thicknesses will be more advantageous in an array of different fields, from biomedical to energetics technologies. (**54**)

Norris, Olivia*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Differentiating beer yeast strains with quantitative Polymerase Chain Reaction using High Resolution Melt Analysis*.- The first commercial brewery in the United States was established in 1632 in Jamestown, Virginia. Today, 135 billion dollars' worth of beer is sold annually in the United States. During the beer brewing process, yeast is added to ferment the liquid and produce alcohol, carbon dioxide, and other chemical compounds that contribute to distinctive flavorings of a beer. The two main species of beer fermentation yeasts are ale yeast (*Saccharomyces cerevisiae*) and lager yeast (*Saccharomyces pastorianus*). These two yeasts ferment at different temperatures and result in beers with significantly different characteristics, and within each species, different strains result in beers with different characteristics. Since the quality of beer is greatly impacted by the specific yeast used in the brewing process, it is important to monitor the purity of yeasts during the beer brewing process to ensure that the beer has the correct flavor profile. If yeast contamination occurs, either from environmental yeasts or cross-contamination from other beers, the resulting flavor profile is incorrect, and entire batches need to be discarded. A potential solution is to develop easier and more effective tools to quickly and accurately identify yeast contamination because existing methods are imprecise and time-consuming. We developed a technique to genetically identify beer yeast using quantitative Polymerase Chain Reactions (qPCR) and High-resolution Melt Analysis (HRM) of specific DNA loci with repeated sequences known as short tandem repeats (STRs). Using this technique, we were able to discern the different species of Ale yeast and Lager yeast from each other and were able to distinguish yeast strains from within each species. This new technique can effectively classify different yeast strains within only a few hours instead of the days required by earlier techniques, resulting in significant savings in time and money for breweries. (**130**)

Oliphant, Ava*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Amplification, cloning, sequencing, and expression analysis of Phytophthora infestans glycoside hydrolase genes PITG_19782.1 and PITG_11632.1*.- *Phytophthora infestans* is an oomycete responsible for infecting potato and tomato plants, causing diseases like potato late blight that ruin an estimated 6.7 billion USD worth of crops in the United States annually. Carbohydrate-active enzymes (CAZymes) are enzymes that contribute to *P. infestans'* destructive power by breaking down plant cell walls and aiding in infection. Among these enzymes are glycoside hydrolases, which degrade structural polysaccharides such as cellulose and pectin by cleaving glycosidic bonds. Glycoside hydrolase family 105 contains several genes that have not been thoroughly characterized, including genes PITG_19782.1 and PITG_11632.1. This study aimed to further investigate the sequence and expression of these genes within *P. infestans.* This was done by first cloning the gene through ligation and transformation in *E. coli,* followed by the purification and restriction digest of the plasmid to confirm successful cloning. Both PITG_19782.1 and PITG_11632.1 were sequenced using Sanger sequencing with universal (M13) and custom-designed primers. Both genes transcribe a protein containing a hydrolase domain similar to the YesR protein found in *Bacillus subtilis*, which catalyzes the hydrolysis of rhamnogalacturonan disaccharide in plant cell walls. Gene expression in mycelial tissue was measured using qPCR. This investigation provides a foundation for further research on glycoside hydrolases such as PITG_19782.1 and PITG_11632.1. (**94**)

ORourke, Anna*, and Micheal Foulk Mercyhurst University, Erie, PA 16546. *CLOCK Genotype, chronotype and seasonal light changes; implications for autumnal sleep and mood*.- College students frequently report poor sleep quality, a factor known to be correlated with poorer performance and mental health outcomes. A key challenge lies in the interplay of chronotype and epigenetic factors. One of the most studied single nucleotide polymorphisms (SNP), 3111T/C in the CLOCK gene, has been studied in relation to one's chronotype preferences. While the correlation has yielded inconsistent results, this study aims to clarify the correlation between the CLOCK gene 3111T/C alleles and the measured chronotype. Secondly, the study seeks to understand how the seasonal light changes may influence the fluid characteristics of one's chronotype with correlation to subjectively improved sleep quality among evening chronotypes. Thirdly, the study will test if poor sleep quality associates with higher negative affect scores. To test these hypotheses, the participants' genotype, chronotype, sleep quality, and mood data was collected. Following data processing, linear regressions were run to determine the relationships among the variables of the CLOCK gene, chronotype, sleep quality, and mood. The CLOCK 3111T/C gene correlation with chronotype was non-associative and non-significant along with the genotype's ties to sleep quality and mood. The MEQ measurement of chronotype in relation to sleep quality was found to be non-associative and non-significant as well. However, a weak non-significant correlation was found between poorer sleep quality and higher negative affect scores. By studying the interrelationships between one's genetics, sleep, and mood, this research adds to our understanding of the complex, dynamic environment-dependent expression of the human circadian system. (**3**)

O'Shea, Haley*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Molecular and phenotypic responses of tomato to Phytophthora infestans: the role of jasmonic acid and defense marker genes*.- Phytophthora infestans, the causal agent of tomato late blight, is a major constraint on global tomato production and a significant source of economic loss worldwide. Jasmonic Acid (JA) is a central regulator of plant defense signaling, especially against necrotrophic pathogens, yet the mechanisms by which it modulates specific JA-responsive genes during P. infestans infection remain poorly understood. In tomato (Solanum lycopersicum), wound-induced proteinase inhibitor 1 (SlWIPI1; locus LOC101248138) is a putative JA-responsive defense gene, but its transcriptional dynamics during pathogen infection have not been fully characterized. This study investigated the molecular and phenotypic responses of S. lycopersicum to exogenous JA treatment and P. infestans infection. Plants were assigned to five treatments: untreated control, ethanol control, JA-treated, pathogen-inoculated, and combined JA plus pathogen treatment. Disease progression was assessed using detached leaf assays, and SlWIPI1 expression was quantified by qPCR at defined time points following inoculation. Statistical analyses evaluated the effects of treatment and time on lesion development and gene expression. Our findings clarify how JA influences SlWIPI1 activation and disease outcomes during late blight infection, contributing to a better understanding of hormone-mediated defense regulation and informing the potential development of JA-based strategies for sustainable crop protection. (**14**)

Ospina-Wiese, Melina*, and Andrea Nerozzi Wyoming Seminary Upper School, Kingston, PA 18704. *Effect of nutrients on the proportion of heterocysts to undifferentiated cells in Anabaena filaments*.- Excessive growth of cyanobacteria poses a significant threat to many lakes in northeastern Pennsylvania and can harm organisms in and around the lake. Harmful algal blooms (HABs) happen when environmental conditions promote the growth of algae or cyanobacteria. Understanding the mechanisms that facilitate excessive cyanobacterial growth is a critical step in developing solutions to protect our local bodies of water. Heterocysts are specialized cells formed by certain cyanobacteria that contain nitrogenase, an enzyme that fixes atmospheric nitrogen (N2). They allow these cyanobacteria to survive in environments where nitrogen is limiting. This study explores the relationship between nutrient levels and the formation of heterocysts in Anabaena sp., a filamentous cyanobacterium (Carolina Biological Supply). The Anabaena was grown on plates composed of 1.5% agar and varying concentrations of Alga-Gro® Freshwater medium (Carolina Biological Supply), from 0x to the suggested concentration (20 mL 10x Alga-Gro® /L) of this commercial media. For cultures in each condition, the ratio of heterocysts to undifferentiated cells was counted using a bright field light microscope at 40x after c. 3 weeks of growth. A total of 225 cells were counted from multiple colonies on each plate, and means and standard error calculated. The results indicate that differentiation in

Anabaena is affected by nutrient level; the frequency of heterocysts increased as the nutrient concentration in the medium decreased, from 12±0.6 heterocysts per 225 cells in the medium lacking nutrients to no heterocysts in the full strength medium. In the medium without nutrients heterocysts represented 5.6% of cells in the filaments. The data indicate that heterocyst formation occurs when Anabaena receives ≤50% of the growth medium. To further this study, we would test the effects of specific nutrients, such as nitrate and phosphate, on cell differentiation in Anabaena. (**114**)

Palubinsky, Cody*, and Linda Auker Misericordia University, Dallas, PA 18612. *The combined effects of microplastics and parasite infection on NEPA crayfish*.- Microplastics have seen a large increase in public interest due to recent studies showing their impact on the ecosystem. Some major concerns for crayfish is their limited area as well as the impact microplastics have on them due to the nature of how they breathe. Any pollutants in their environment are taken in and processed in the hepatopancreas, a structure that acts as both a liver and pancreas for crayfish, with hormones such as glutathione providing an insight as to the stress from their surroundings. This study looked to determine microplastic contamination in local water, sediment, and crayfish organ structures. To determine microplastic levels in water, a simple filtration was utilized. For microplastic levels in sediment, a density filtration method was used involving a dense NaI solution to push microplastic particles upwards. For testing purposes, crayfish were bisected and tissue was split between microplastic and glutathione testing. Parasite infestation was determined using hepatopancreas tissue. Microplastic levels within crayfish were found by dissolving tissue in a 10% KOH solution in a 60℃ oven for 24 hours. Glutathione levels were found by preparing an assay and comparing levels of glutathione within the tissue to standards that were prepared, which was done by comparing light absorbance reading. Results indicated both microplastics contained within most water and sediment samples, as well as a lower level of glutathione than would be expected for crayfish, indicating an interaction that is potentially causing stress to the animals. P-values were analyzed to be >0.70 for each standardized parameter, showing confounding variables involved in lower glutathione levels. Parasites were found in approximately 8% of samples, much lower than literature values. These findings suggest that while microplastics may affect wildlife, there are more stressors that must be determined to preserve the safety and health of local crayfish. (**55**)

Parente, Amy, Vincent Armstrong*, Brynna King, Hailey Leisering, and Joseph Saxton Mercyhurst University, Erie, PA 16546. *Establishing an expression and purification framework for functional analysis of malate dehydrogenase*.- Malate dehydrogenase (MDH) is a highly conserved NAD$^+$-dependent enzyme that catalyzes the reversible interconversion of malate and oxaloacetate, a reaction essential to the citric acid cycle, gluconeogenesis, and cellular redox balance. Because MDH regulates NADH production and metabolic flux, dysregulation of its activity has been linked to metabolic disease, cancer metabolism, and altered mitochondrial function. The present work seeks to examine the functional properties of MDH and its regulatory mutants to better understand how enzymatic activity and protein–protein interactions contribute to metabolic control. The central hypothesis is that structural modifications, particularly mutations that mimic phosphorylation, alter active-site geometry and conformational dynamics, thereby modulating catalytic activity and metabolon formation. To establish experimental conditions for MDH characterization, a malate dehydrogenase–green fluorescent protein fusion construct (MGH) containing a His-tag was overexpressed in *E. coli*. Proteins were purified using Ni-NTA affinity chromatography through fast protein liquid chromatography (FPLC). Purity and molecular weight were verified by SDS-PAGE, while protein concentration was quantified using Bradford assays. Enzymatic activity was measured by monitoring NADH formation at 340 nm during the oxidation of malate to oxaloacetate. Preliminary results demonstrate successful expression and purification of the MGH fusion protein, with purified fractions showing high protein concentration and clear SDS-PAGE bands corresponding to the expected molecular weight. These findings establish a methodological framework for future biochemical studies. Future work will extend these methods to wild-type and phosphomimic MDH1 mutants to determine how specific residues influence catalytic efficiency, stability, and protein–protein interactions with metabolic partners such as citrate synthase. Understanding these regulatory mechanisms may reveal new insights into metabolic control and identify potential therapeutic targets in metabolic disease and cancer. (**110**)

Peckinpaugh, Jade*, Amanda Dorsey, Vanessa Funk, Langston Gash, Daniel Angelini, Jennifer Horsmon, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Toxicity and behavioral evaluation of VX on zebrafish (Danio rerio).*- Zebrafish (Danio rerio) are widely used as an experimental model for toxicity studies. The advantage of the zebrafish model is that it provides an ethically acceptable, cost-effective alternative to mammalian studies. In contrast to direct exposure to the toxicant in mammalian screenings, the aquatic environment of the fish is treated, and either single or multiple fish are subsequently monitored for a variety of endpoints ranging from aberrations of movement to death. Zebrafish are ideal models for high-throughput screenings due to their small size and rapid fecundity/development, making them ideal for large-scale drug discovery and toxicity testing. Their high genetic homology to humans (approximately 70%) allows for relevant, accurate insights into regular human toxicological responses. Studying the whole organism allows for real-time visualization of developmental and physiological changes in response to toxicants. For this experiment, zebrafish were screened for toxicity and behavioral changes caused by exposure to VX. (**91**)

Peluszak, Avery*, Helisa Nunez*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Investigating yggW as a novel regulator of rpoS-mediated stress responses in E. coli*.- Antibiotic-resistant bacteria pose a major global health threat, driven largely by the overuse of antibiotics in humans and animals. Antibiotic exposure induces metabolic stress responses in bacteria, including the activation of the sigma factor rpoS. In E. coli, rpoS regulates numerous stress response pathways that allow the cell to survive environmental and antibiotic stress. While the downstream genes controlled by rpoS are well characterized, the mechanisms regulating rpoS remain poorly understood. This study investigates the role of yggW, a gene with previously unknown function in the stress response pathway, as a potential regulator of rpoS activity and bacterial stress adaptation. Using genetic cloning and targeted modification of yggW expression in E. coli, we aim to determine whether changes in yggW influence the rpoS-dependent stress response. Understanding the relationship between yggW and rpoS may provide new insight into bacterial stress regulation and mechanisms that contribute to antibiotic resistance. (**38**)

Pete, Margaret*, and Christopher Dolanc Mercyhurst University, Erie, PA 16546. *Analysis of microclimate variations in a low-tech greenhouse*.- Low-tech greenhouses have the unique challenge of accounting for the climactic conditions of where it is located, while also satisfying the growing conditions of the selected plants. Greenhouses, like other enclosed environments, possess microclimatic heterogeneity, despite appearing more controlled than outdoor spaces. The Mercyhurst University greenhouse is located on a roof, with the building itself intermittently blocking light from the west. Seasonal changes in day length and sun angle create further variation in light intensity. This presents a complex dynamic from which to accommodate the wide range of plants in the greenhouse, all with different humidity and temperature requirements. To gain a better understanding of the microclimatic variation in the greenhouse, it was divided into ten sections (Loc 1-10) and light measurements were taken on random days from July 2025 to April 2026. From February to April of 2026, relative humidity and temperature data were collected from Loc 1-10. When comparing light levels across the months, Loc 1 (on the table in the west corner) had the highest average light intensity, reaching its peak at 951 umol m-2s-1. Loc 9 (under the table) had the lowest average light intensity, and its lowest point was 4 umol m-2s-1. When comparing the relative humidity and temperature of Loc 1 and Loc 9, it was found that the relative humidity of Loc 9 was consistently higher than that of Loc 1, but the temperature is constantly lower. This is consistent with the light regimes they typically experience, with Loc 1 exposed a majority of the day, whereas Loc 9 is beneath the shade of the table. With the use of temperature, humidity and light measurements, each section in the greenhouse can be characterized based on microclimate data throughout the year to better fulfill the plant's requirements. (**75**)

Pierce, Olivia*, 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. (**21**)

Portilla, Rosa*, Kathryn Sarachan, and Amber Marble Wilson College, Chambersburg, PA 17201. *The effect of ApoE3 glycosylation levels on its binding affinity for the CLEAR DNA motif*.- Alzheimer's disease is a neurodegenerative disorder characterized by beta-amyloid (Aβ) plaques and neurofibrillary tangles. The major genetic predisposition to Late-Onset Alzheimer's disease is apolipoprotein E4 allele (APOE4). In the brain, ApoE primarily functions to mediate lipid and cholesterol transport to neurons to support membrane homeostasis, synaptic integrity, and injury repair. ApoE4 demonstrates increased binding affinity for the Coordinated Lysosomal Expression and Regulation (CLEAR) DNA motif. When ApoE4 binds to CLEAR, it inhibits the expression of genes that aid in clearance of aggregates such as Aβ plaques. Decreased levels of glycosylation of ApoE4, relative to other isoforms, contributes to its pathophysiological mechanisms by affecting its binding affinity for various molecules. ApoE isoforms E2, E3, and E4 have decreasing levels of glycosylation, respectively. Conversely, E2, E3, and E4 have increasing binding strength to CLEAR DNA, respectively. This research set out to determine if there is a connection between ApoE glycosylation levels and its binding affinity for CLEAR. Evidence of ApoE3 binding to CLEAR DNA was confirmed with Electrophoretic Mobility Shift Assay. Varied concentrations of non-glycosylated and glycosylated ApoE3 were applied across a constant CLEAR DNA concentration for sedimentation velocity analytical ultracentrifugation to investigate the protein-DNA interaction; sedimentation behavior offered insight into molecular weights and shapes of the sedimenting species and suggested a possible stoichiometric binding model. Non-glycosylated and glycosylated ApoE3 displayed similar trends in the formation of higher order oligomers, with continuous distribution plots indicating concentration-dependent dimer and tetramer formation. (**137**)

Rasa, Christina*, Cosima Wiese, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Cell-free expression of a fluorescent ATP sensor*.- Adenosine triphosphate (ATP) provides the energy necessary for chemical reactions in all cells. Several biosensors have been developed to measure the dynamics of cellular ATP. One such sensor is a protein called HHM-iATPSnFR1.0. When this protein binds to ATP, a conformational change leads to increased intensity of a fluorescent subunit. Therefore, the sensor can be used to quantify the ATP concentration of a sample by measuring its fluorescence intensity. Since this ATP sensor is genetically encoded, the protein needs to be transcribed and translated from DNA. Currently, the protein must be purified from E. Coli cells transformed to express it. The goal of this project is to simplify production of HHM-iATPSnFR1.0 by using a cell-free expression system called BioBits™. Preliminary results indicate that the BioBits™ system is capable of expressing HHM-iATPSnFR1.0. Samples of BioBits™ pellets combined with the HHM-iATPSnFR1.0 plasmid and water were incubated at 37 °C for 30 minutes to allow for protein expression to occur. Upon the addition of ATP solution at 1 mM, a 1.15±0.06-fold increase in fluorescence intensity was measured in the samples. This increase was found to be significantly different from the change in fluorescence intensity after addition of ATP to control samples which were incubated without the plasmid. The proteins produced by BioBits™ should be identical to those expressed by E. Coli, so 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 directly related to the sample's ATP concentration. To test this hypothesis, the fluorescence intensity of HHM-iATPSnFR1.0 expressed by BioBits™ will be measured before and after treatment with increasing concentrations of ATP. The fold change for each concentration will be calculated, and a standard curve defining the relationship between ATP concentration and fluorescence intensity change will be constructed. (**89**)

Ridani, Idriss*, and M. Logan Johnson University of Pittsburgh at Greensburg, Greensburg, PA 15601. *The effects of JAZF1 manipulation on Drosophila melanogaster brain and oenocyte development*.- The misexpression of genes often disrupts tissues and can cause a wide range of phenotypes such as neurodegenerative and metabolic diseases. JAZF1 is a gene that has been implicated in neurodevelopment and in a predisposition to Type 2 Diabetes, a disease that disrupts vital processes, including glucose and lipid homeostasis. Overall, it helps regulate transcription as part of the histone modifying complex, NuA4/TIP60. With JAZF1 being involved in numerous bodily functions, we conducted a study looking at how JAZF1 manipulation affects morphology of two areas of the Drosophila melanogaster organism, the mushroom body of the brain, and the oenocytes, a bodily tissue analogous to human liver cells. Using the Gal4-UAS system, we specifically downregulated JAZF1 expression in the mushroom body, and manipulated expression in the oenocytes while simultaneously marking cells with Green Fluorescent Protein (GFP). After obtaining the resulting larvae, we dissected them to examine morphological changes. Within the brain we found that the morphology of the mushroom body developed abnormally compared to the control larvae. As we examine the oenocyte tissue, we expect to find a change in appearance and overall size. With these studies, we aspire to establish a relationship between JAZF1 expression and morphology of vital tissues. Additionally, we anticipate that examining both the mushroom body and the oenocytes through an RNA-seq analysis comparison of JAZF1 manipulation would provide insight into which JAZF1-associated genes get affected within those tissues. This relationship between JAZF1 and both the Drosophila brain and oenocytes may allow for better modeling of neurodegenerative disorders, such as Parkinson's Disease, and metabolic disorders, such as Type 2 Diabetes. (**124**)

Rinaldi, Antonio*, Zahra Imrani*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Effects of nicotine exposure on PEP1 expression in Saccharomyces cerevisiae*.- Alzheimer's disease (AD) is a progressive and irreversible neurodegenerative disorder. The gene SORL1 (sortilin-related receptor 1) has been implicated in AD risk due to its role in regulating the trafficking of amyloid precursor protein (APP), which can be processed to form amyloid-β peptide. Disruption of this trafficking pathway may contribute to amyloid-β accumulation and disease pathogenesis. Previous studies have shown that oxidative stress can disrupt protein trafficking in eukaryotic cells. Nicotine, a major component of cigarette smoke, is associated with oxidative stress, and cigarette smoking is a known risk factor for AD; however, the effect of nicotine-induced oxidative stress on SORL1 expression remains unclear. The unicellular eukaryote Saccharomyces cerevisiae serves as a tractable model organism for studying conserved trafficking pathways. PEP1, the yeast homolog of SORL1, is similarly involved in protein sorting and vacuolar trafficking. We hypothesized that nicotine exposure would alter PEP1 gene expression in S. cerevisiae. Wild-type yeast cells were incubated with 1 mg/mL nicotine for 8 hours, followed by RNA extraction and cDNA synthesis. PEP1 expression was quantified using quantitative PCR (qPCR), with ALG1 serving as an endogenous housekeeping control. Under these conditions, no significant difference in PEP1 expression was observed between nicotine-treated and untreated cells. These results suggest that nicotine exposure does not significantly alter PEP1 transcription in S. cerevisiae, indicating that any effects of nicotine-induced oxidative stress on this trafficking pathway may occur post-transcriptionally or require additional cellular factors. (**69**)

Roat, Grace*, David Andrew, and Mary O'Donnell Lycoming College, Williamsport, PA 17701. *Utilizing environmental DNA to survey elusive vernal pool salamanders*.- Indicator salamander species populations provide insight into the health of the local environment. The ability to unambiguously identify salamander species that are morphologically similar, such as Ambystoma maculatum and Ambystoma jeffersonianum, is crucial for monitoring potentially at-risk populations, as well as for investigating habitat vitality. Environmental DNA (eDNA) and its detection via quantitative polymerase chain reaction (qPCR) allow for noninvasive investigation of species presence and abundance. Utilizing previously published eDNA collection and qPCR detection protocols, we evaluated the A. maculatum population at Glacier Pools Preserve in Lycoming County, Pennsylvania. We collected water samples from two vernal pools to assess eDNA presence and benchmarked eDNA isolation against DNA obtained by swabbing live captive specimens and from preserved tissue. We confirmed that the published primers and probe for A. maculatum successfully produce signals with positive controls. Samples from a vernal pool provided a positive signal, but due to the limit of detection (LOD) and limit of quantification (LOQ) of qPCR testing with low DNA concentrations, we did not have enough data to quantify the A. maculatum abundance at Glacier Pools Preserve. We aim to apply the methods we have validated to the species A. jeffersonianum, a Pennsylvania species of special concern that has been reported to be present in Glacier Pools Preserve.. The data support the use of eDNA detection via qPCR for the confirmation of species presence and encourage future studies to quantify species presence, enhance conservation efforts, and simplify environmental monitoring. (**74**)

Rosas Ornelas, Adrian*, and Michael Foulk Mercyhurst University, Erie, PA 16546. *RNAi delivery method for Bradysia coprophila*.- Gene regulation through RNA interference (RNAi) is a conserved mechanism that utilizes small double-stranded RNAs to silence gene expression. RNAi is widely used for studying gene functions and has potential to be used to knockdown gene expression of specific gene in non-canonical model organisms such as the black fungus gnat, *Bradysia coprophila*. The purpose of this study is to develop RNAi delivery methods for *Bradysia coprophila* that silence genes essential for growth and development using *Saccharomyces cerevisiae* (baker's yeast) as a delivery vector for short hairpin RNAs (shRNAs). Prior to this study, plasmid vectors containing shRNA oligos targeting the *Bradysia* ecdysone receptor (EcR) were constructed. In this study, these plasmid constructs were transformed into yeast cells. Several different methods of delivering the shRNA containing yeast to *Bradysia* larvae in controlled feeding experiments were tested. These experiments are continuing and ongoing. Once the optimal delivery mechanism has been identified, Western blot and quantitative PCR will be used to confirm the knockdown of expression of *Bradysia* EcR. From this model, similar yeast-based RNAi delivery methods can be developed for analogous insects and present a basis for future yeast-based RNAi delivery methods relevant in pest management research. (**122**)

Rudenberg, Joanna*, and James Dearworth Lafayette College, Easton, PA 18042. *Attachment of radio transmitters to the carapace of freshwater turtles*.- The purpose of this investigation was to identify a method for long-term attachment of radio transmitters onto turtles to track their movements in the wild. Various ways of attaching were evaluated based on literature reviews. Methods read about included drilling into the shell to apply fasteners or using silicone, fiberglass, and epoxy adhesives. We first ruled out drilling and using fiberglass because of their potential harm and long curing time, and ultimately selected silicone- and epoxy-based methods. Effectiveness was compared by attaching pieces of wood, which were the same size and shape as transmitters, to a carapace available from a skeletal specimen of a red-eared slider turtle, Trachemys scripta elegans. A combination of JB Weld MarineWeld Epoxy Putty and JB Weld WaterWeld Epoxy Putty was found to work the best, curing with the least amount of time. We next used this combination in applying an ATS reptile glue-on Series R1800 radio transmitter to the carapace of a turtle, which was housed in a 200-gallon tank at the animal facility of Lafayette College. A board with Velcro straps was engineered to restrain the animal safely during fastening. The transmitter was secured successfully and so far has remained attached for more than two weeks. It also does not appear to interfere in any way with daily activities and movements made by the turtle. The techniques will be used next to attach radio transmitters to the carapaces of wild turtles living at Lacawac Sanctuary, located in the Poconos. Movements by different species of turtles will be compared to collect data such as the times of hibernation for winter and emergence in spring. (**56**)

Rudolph, Leah*, Jackie Brochu, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Modeling behaviorally mediated biological control of the spotted lanternfly*.- The spotted lanternfly is a global invasive insect pest. In native areas, 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. A recent modeling study established conditions for a collective biological control of invasive spotted lanternfly by social birds, specifically those that are sensitive to the lanternfly's potential toxicity. However, some recently observed lanternfly predators are not social, and some are not sensitive to its potential toxicity. Here, we introduce a generalized version of the previous model that incorporates all combinations of sociality and toxicity sensitivity. We establish conditions under which each predator can produce a robust biological control, establish how the social learning process proceeds for each, and quantify the relative speed and effectiveness of control across predator types. These models are a framework for studying the emergence of biological control by agents with any degree of sociality and toxicity sensitivity, including interactions between different types. Understanding how to facilitate the killing of lanternfly by diverse predators can inform management strategies for the lanternfly and similar invasive pests. (**80**)

Ruland, Dakota*, and Christopher Dolanc Mercyhurst University, Erie, PA 16546. *Comparing the growth response to tornadic canopy damage for three native tree species in Northwest Pennsylvania*.- With increasingly unpredictable weather patterns becoming more frequent, this research is important to landowners for various silvicultural reasons and those in agroforestry. There is not enough known about how northern temperate forests respond to severe wind damage. Tree-ring analysis was conducted on three eastern deciduous species, *Tsuga canadensis* (eastern hemlock*), Liriodendron tulipifera* (tulip tree), and *Quercus rubra* (red oak) to establish how tornadic canopy damage impacted each species growth based upon tree ring records. The area of study is in the path of the 1985 Albion, Pennsylvania tornado. The category F4 tornado left a 14-mile-long path was just one of dozens that tore through the region on May 31, 1985. This study is unique in design due to the lack of related research in the Northeastern part of the United States. It was hypothesized that all three species would show decreased growth upon crown loss and decreased photosynthetic capabilities. Cores were collected and processed from 30 trees, 10 for each species using standard dendrochronological methods and were measured to 0.01 mm precision using WinDENDRO to ensure accuracy. Ring records from the same species outside of the tornados path were collected and compared to sampling site cores to verify the uniqueness of indicator rings. Specimens were selected based on location along the tornados path as well as trees that exhibited candelabra growth. Candelabra growth was selected as an indicator as trees exhibit this type of crown growth when canopy is damaged. The results of the study have shown that *Tsuga canadensis* is showing growth release in some samples and growth suppression in others. Analysis so far indicates the growth releases are likely from the tree taking less damage and receiving more sunlight from the newly formed openings in the surrounding canopy. Analysis is ongoing and will be discussed. (**72**)

Safi, Sabeen*, Jonathan Jarrah*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Effects of aerosolized e-liquids on oral epithelial wound healing*.- Rising electronic cigarette (ECIG) use, particularly among youth, has raised concerns about oral health. Despite being marketed as safer than traditional cigarettes, emerging evidence suggests ECIGs may still cause harm. The oral cavity, as the first site of exposure, is especially vulnerable, with links to periodontal disease and impaired epithelial function and healing. While prior studies have shown that E-liquid flavorings can influence oral biological processes, many have not adequately modeled aerosolization, a critical component of vaping exposure. To address this limitation, this study builds on the work of Shamim et al. (2025) using a newly developed method of E-liquid aerosolization. Using the OKF6/TERT-2 oral epithelial cell line, this project focuses on wound-healing behavior as a measure of epithelial repair. A wound-healing assay was used to assess cell migration and wound-gap closure following exposure to aerosolized E-liquids, compared to media and air controls, and was quantified by quantitative image analysis. So far, we observe a delay in wound healing with ECIG aerosol exposure, with flavor-dependent differences in the extent of impairment, although data collection is ongoing. These findings suggest that flavored ECIG products may differentially impair oral epithelial repair, highlighting important implications for oral health and the regulation of vaping products. (**63**)

Schmidt, Drew, and Ann Yezerski King's College, Wilkes-Barre, PA 18711. *Hybrid bass*.- Both Largemouth Bass (*Micropterus salmoides*-LMB) and Smallmouth Bass (*Micropterus dolomieu*-SMB) are popular game fish that are commonly targeted by recreational anglers due to their widespread availability, strong fighting ability, and value as trophy fish. Within fishing communities, there have been many anecdotal reports of a so-called “meanmouth” bass that retains the bigger size of the LMB but puts up the fight of the SMB. Other bass hybrid species, such as Striped Bass and White Bass, have been reported. In this experiment, we followed up on our previous worked that successfully identified hybrids in some small New York ponds. This project aims to detect if the hybrid bass are capable of reproducing, which should not happen if the parents are two separate species. DNA extractions from fin clips were subjected to PCR for the genomic genes Sidkey and RAG-1 and then sequenced. Several Single Nucleotide Polymorphisms (SNP’s) were used to genotype individual fish. Hybrids should be heterozygous for SNP sites known to be conserved within each species. If the hybrids are successfully reproducing with each other or either parent species, they can be heterozygous at one site and homozygous at another. Pilot data has shown a few fish with this pattern, suggesting the ability to reproduce as a hybrid. (**125**)

Schultz, Sarah*, Michael Harrel, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Interactions between DPPC multilamellar vesicles and N-phenyl-1-napthylamine*.- Understanding molecular interactions within lipid bilayers is important in fields like drug delivery and in vitro cell assays. Herein, interactions between 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC) multilamellar vesicles (MLVs) and a hydrophobic fluorescence probe N-phenyl-1-napthylamine (NPN) were studied using fluorescence spectroscopy at an excitation of 340 nm. DPPC MLV samples with and without cholesterol were also observed to see the effect on the gathered emission data. Varying mole ratios of NPN:DPPC (in MLVs) using 20mM and 40mM NPN in DMSO were tested and also compared to DPPC in organic solution, without MLV formation. The fluorescence emission of NPN varied slightly with the mole ratio (NPN:DPPC) added, but was not affected by the amount of DMSO. The added cholesterol had a marked effect on the emission, suggesting close interactions between the cholesterol and NPN in the bilayer. The liposome samples without cholesterol had a higher emission than the respective liposome samples containing cholesterol suggesting the NPN was in a more hydrophobic environment. This is in contrast with the DPPC non-MLV solution samples, where it was also found that the amount of DMSO only impacted the treated lipid samples not the treated MLV samples. Additional testing through Dynamic Light Scattering (DLS) was done on liposomal samples to confirm the presence of MLV's. Ongoing research will be done to test the effects in small unilamellar vesicles made using ultrasound, with sizes less than 100nm. (**119**)

Selesky, Kara*, Angelena Donovan*, Joy Haddad, Olivia Shuster, Christopher Stobart, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Mānuka honey demonstrates antiviral activity toward both coronaviruses and Respiratory Syncytia Virus*.- Mānuka honey is produced from the *Leptospermum scoparium* tree in New Zealand. It is known for its healing and antimicrobial, anti-inflammatory, and antioxidant properties. The Unique Mānuka Factor (UMF) is an internationally recognized system of certifying the quality of mānuka honey to validate its potency, authenticity, shelf life, and freshness. Researchers have identified 2,300+ components that contribute to its taste and health benefits. During the winter months, there is a rise in respiratory infections caused by a wide range of viruses. Common respiratory infections are caused by several viruses in the coronaviridae family, and Respiratory Syncytia Virus, a virus in the pneumoviridae family. Coronaviruses have positive-sense single-stranded RNA genomes, and RSV has a negative sense single-stranded RNA genome. While these viruses do not have the same genome type, both infect the respiratory track and cause similar cytopathic effects of cell-cell fusion to make syncytia. We wanted to test whether mānuka honey has inhibitory effects on these viruses. In collaboration with Cafe Buzzstop in New Zealand, we obtained samples of mānuka honey with varying unique mānuka factors (UMF5, 10, 15, 20, and 25). To test antiviral activity in RSV, we cotreated cells with RSV and different concentrations of each of the UMF amounts. At 24h post infection, fluorescence focus units were calculated when virus production peaks. For MHV, we used reporter chimeric viruses containing firefly luciferase (FFL) and nsp5 genes from OC43 (O5) and HKU1 (H5) along with the wildtype (M5) virus. For this assay, viral replication was measured at 12 h.p.i by measuring FFL activity. Mānuka honey greatly inhibited both MHV and RSV virus replication in the co-treatment assays. Further experiments will test the effects of mānuka honey on the kinetics of virus replication. (**10**)

Selesky, Kara*, Angelena Donovan*, Kiomara Quinones*, Olivia Shuster*, Joy Haddad, Christopher Stobart, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Mānuka honey demonstrates antimicrobial activity*.- Antimicrobial resistance is a major healthcare challenge that is a threat to public health and safety. Mānuka honey has become popular as it is known for its use in home remedies for its healing and antimicrobial, anti-inflammatory, and antioxidant properties. Mānuka honey is produced from the Leptospermum scoparium tree in New Zealand. Mānuka honey is graded with the Unique Mānuka Factor (UMF), an internationally recognized system of certifying the quality of mānuka honey to validate its potency, authenticity, shelf life, and freshness. Researchers have identified 2,300+ components that contribute to its taste and health benefits. We wanted to test if mānuka honey has antimicroicrobial properties against bacteria, fungi, and viruses. We are testing the antibacterial effects against Staphylococcus aureus, Pseudomonas aeruginosa, Shigella flexneri, Escherichia coli, and Streptococcus pyogenes, and its antifungal effects on Candida albicans. For the bacteria and fungus, we are testing inhibition of microbes using disk diffusion assays, colony forming units, and O.D. 600 readings. We are also testing antiviral activity on coronaviruses using chimeric mouse hepatitis viruses (MHV) to test several common coronaviruses and measure viral replication with firefly luciferase luminescence. We tested the antiviral properties of mānuka honey against 3 reporter viruses including wild type MHV-FFL (M5), and chimeric MHV-HKU1-FFL (H5), and MHV-OC43-FFL (O5) by replacing the MHV nsp5 gene with nsp5 genes from human coronaviruses HKU1 and OC43. Antiviral activity was measured using a virus inhibition assay and growth curve analysis. Preliminary data suggest that mānuka honey has antimicrobial effects on specific bacteria as well as the three MHV strains tested. (**25**)

Shane, Joseph*, Lizzy Minetola*, and Cole Pearson* Shippensburg University, Shippensburg, PA 17257. *Teaching at the interface of science and religion*.- This presentation is divided into two parts. First, the content, pedagogy, and assessments associated with an undergraduate, interdisciplinary honors seminar on science and religion are described. The seminar is structured around five major themes: (a) philosophy of science, religion, and their interactions, (b) historical and contemporary case studies, (c) evolution in the United States as a necessary case study with particular emphasis on the Scopes "Monkey" trial from 1925, (d) comparative religion and science, and (e) contemporary issues at the intersection of science and religion. Second, the course instructor will describe the results of a recent sabbatical leave project with the Dialogue on Science, Ethics, and Religion (DoSER) program within the American Association for the Advancement of Science (AAAS). (**6**)

Shults, Jessica*, Karlee Kelly*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Investigating how RPA phosphorylation influences DNA adaptation and DNA repair in* *<u>Saccharomyces cerevisiae</u>*.- Cancer is the second leading cause of death in the United States and is caused by DNA mutations that interfere with genes that regulate normal cell growth and division. Many current chemotherapy treatments cause DNA damage that kills actively dividing cancerous cells by overwhelming DNA damage recognition and repair pathways, but this often leads to harmful side effects in actively dividing normal cells. Therefore, understanding how cells recognize and repair DNA damage is vital for developing future cancer therapies that could better target only cancerous cells. The baker's yeast *Saccharomyces cerevisiae* is a valuable eukaryotic model for studying DNA damage and repair because of its genetic flexibility, fast growth, ease of genetic modification, and high level of homology in repair pathways with human cells. One highly conserved protein is the single-stranded DNA-binding protein Replication Protein A (RPA) that is vital for DNA replication, repair, and DNA damage cell cycle checkpoints. RPA can be phosphorylated, suggesting a role in regulating its function. In this study, we examine the cellular response to DNA double-strand breaks and DNA-damaging agents in yeast that contain mutations that affect RPA phosphorylation. We hypothesize that RPA phosphorylation plays a role in regulating cell cycle checkpoints and DNA repair pathways. We use yeasts with an inducible DNA double-stranded-break system, allowing us to control the timing of DNA damage and whether the damage is repairable. In yeast where the damage is not repairable, we are examining cell cycle checkpoint progression by videomicroscopy, while in yeast where the damage is repairable, we are examining DNA repair using either cell viability assays or qPCR analysis of genomic DNA. Studying these pathways in baker's yeast can provide insights into DNA-damaging cancer treatments and how genome instability contributes to cancer and its treatment. (**129**)

Simmons, Emma*, Sarah Simmons*, and Jeffrey Simmons Mount St. Mary's University, Emmitsburg, MD 21727. *The integration of electrically conductive textile technology and unique algorithms in the acquisition and analysis of critical pulmonary data*.- We conducted tests to determine the viability of electrically conductive textiles as a novel method for detecting thoracic cavity expansion. This fabric was then used to develop a wearable device that measures human respiratory rate. Existing respiratory monitors have several drawbacks, including high-cost, low accuracy, non-continual measurement, and discomfort. Our goal was to develop a device that would be low-cost; comparably accurate to medical devices; collect real-time and longitudinal data; and be discreet, durable, and comfortable. We hypothesized that the use of conductive textiles as a non-invasive biosensor in conjunction with a microcontroller would meet these requirements. Several silver-based conductive textiles were evaluated for elasticity, dimensional stability, and changes in electrical resistance under strain. After identifying the fabric that produced the greatest voltage change when stretched, we programmed a microcontroller to measure, record, and analyze the sensor output. The Alpha Prototype integrated the conductive fabric sensor into a cotton chest strap connected to the microcontroller system. To evaluate performance, we conducted two trials with human subjects performing physical activities. During these activities, the Alpha Prototype successfully detected respiratory rate changes corresponding to activity level. To improve comfort and usability, we developed a Beta Prototype by integrating the biosensor directly into a shirt. Two additional trials reassessed functionality and validated accuracy against established measurement methods. Respiratory rates recorded by the Beta Prototype were compared with readings from a commercial spirometer and manual breath counts. The device demonstrated strong correlation with both the spirometer ($r^2 = 0.97$) and manual counts ($r^2 = 0.99$). Across all four trials, prototype measurements were accurate and comparable to conventional respiratory monitoring methods. The final design was low-cost, discreet, and comfortable for continuous respiration monitoring, with potential for long-term respiratory tracking in pulmonary patients. (**71**)

Skuza, Natalie P*, Alex Krupka, and Whitney Leach DeSales University, Center Valley, PA 18034. *A low-cost, open-source imaging system for behavioral assays in Nematostella vectensis*.- Behavioral assays in aquatic invertebrate model systems often require specialized imaging platforms that limit accessibility in undergraduate teaching and research laboratories. The starlet sea anemone, Nematostella vectensis, has emerged as a powerful model for studying behavior and circadian biology, yet standardized, low-cost approaches for long-term behavioral recording remain limited. Here, we describe a modular and inexpensive imaging system for continuous and time-lapse behavioral recording of N. vectensis under controlled light:dark conditions. The system integrates a Raspberry Pi 4B, Raspberry Pi Camera Module v2, and a custom-built LED ring light capable of both white and infrared illumination, allowing observation across a 12:12 h light:dark cycle without introducing visible light during dark periods. The total cost of the system is under USD $100 and can be assembled using readily available components. This setup enables reproducible behavioral assays in wet laboratory environments and lowers technical barriers for undergraduate neuroscience and organismal biology research. (**27**)

Smith, Alysse*, Debra Wohl, and Elizabeth Newell Elizabethtown College, Elizabethtown, PA 17022. *Establishing reliable DNA extraction methods for microbial analysis of embalmed cadaveric tissues*.- Extracting microbial DNA from cadaveric tissues holds significant potential for microbiological research that would be prohibitively invasive in living patients, yet embalmed tissues present unique challenges for DNA recovery. This study investigated and optimized DNA extraction protocols specifically for cadaveric tissues, addressing critical considerations for medical and microbiological research applications. Three distinct extraction methods were employed on stool and gastrointestinal tissue samples, specifically from the cardiac sphincter, greater curvature, pyloric sphincter, and proximal duodenum, across four cadaveric donors. The protocols tested included a phenol-chloroform extraction, the Qiagen QIAamp® BiOstic® Bacteremia DNA Kit, and the New England BioLabs Monarch® Spin gDNA Extraction Kit. NanoDrop spectrophotometry indicated that sufficient DNA concentrations were yielded by the Monarch extraction kit. Illumina sequencing of the 16S V4 region was then completed to assess DNA extraction quality and community dynamics and composition. Sequencing results indicate that all samples contain evidence of Bacteria, Archaea, and Eukarya, with Bacteria identified as the dominant domain. At the phylum level, Pseudomonadota, Bacteroidota, and Proteobacteria emerged as the most dominant taxa across samples; however, deeper analysis of their relative abundances, functional implications, genus-level composition, and overall characterization is still underway. If sequencing yields significantly distinguishable results, findings may reveal microbial composition variation along the GI tract, potentially informing more effective GI-related diagnostic approaches than current methods. However, regardless of the depth achievable for microbial classification, this research provides valuable procedural insights for embalmed tissue DNA extraction, including optimal protocols, necessary modifications beyond traditional methods, realistic limitations, and observed pitfalls. This work establishes foundational considerations for using cadaveric specimens in microbial studies with medical implications. Even inconclusive sequencing results underscore the need for continued protocol development to establish consistent extraction methods for embalmed tissues, advancing the field’s capacity for post-mortem microbiological research and understanding. (**85**)

Snider, Eric*, and Mahita Kadmiel Allegheny College, Meadville, PA 16335. *Measuring the effects of glucocorticoids and mineralocorticoids on human corneal epithelial integrity in the presence or knockdown of the glucocorticoid receptor*.- Corneal epithelial cells are important to protect the cornea from the external environment. These cells form a tight barrier, which can be lost over time due to a variety of different factors including age, diabetes and chronic stress. Glucocorticoids (GC) can be used as a way to treat the thinning of the epithelium. However the molecular mechanisms by which these GC work are an area of current research. This study investigates the effects of macrophage secreted proteins, and their effect on the epithelial integrity, in Human Corneal Epithelial (HCET) cells. Our previous data indicates that Human Corneal Epithelial (HCET) cells when treated with dexamethasone (DEX) - a synthetic glucocorticoid, increases epithelial resistance in a glucocorticoid receptor (GR) dependent manner, when compared to Aldosterone (ALDO), a canonical ligand of the mineralocorticoid receptor, and a combination of both DEX and ALDO. However when the drugs were added to the secretome of monocyte-derived macrophages for 24 hours we found interesting results which suggested a crosstalk between glucocorticoids and mineralocorticoids. When HCET cells were treated with macrophage secretome (conditioned media), we observed that the ALDO treated group had the highest epithelial resistance when compared to other treatments. To further investigate the mechanism of ALDO-mediated increase in epithelial resistance, we propose to perform SDS-PAGE and western blot analysis on the HCET cells grown in conditioned and unconditioned media. Additionally, we intend to perform immunostaining to examine tight junction proteins (TJP) expressed by HCET cells in response to the macrophage secretome. This study could provide significant insight for the development of new ways to promote epithelial integrity via steroid-based therapy. (**106**)

Sokol, Amanda, and Ann Yezerski King's College, Wilkes-Barre, PA 18711. *How the SLC6A3 gene, which is associated with dyslexia, may influence college major choice*.- Dyslexia is a common learning disability associated with difficulties in reading and language processing. Dyslexia has been linked to several genetic loci involved in brain development and cognitive function. *SLC6A3* is a particular gene related to dyslexia that encodes the dopamine transporter responsible for regulating dopamine levels in the synapse. Dopamine signaling plays an important role in attention and motivation when it comes to learning, which suggests a possible contribution to choice in academic choices after high school. This study looks at the relationship of *SLC6A3* alleles associated with dyslexia traits and the choices made about academic futures after highs school by comparing student genotypes to college major choice. DNA samples were collected from currently enrolled college students using a non-invasive buccal swab. Participants completed a survey about their academic major choice and any history of dyslexia related symptoms or diagnosis. Target regions of the *SLC6A3* gene were amplified using PCR, followed by a nested PCR to increase specificity. These amplified DNA fragments were either genotyped via restriction fragment length polymorphism or direct sequencing. Statistical analysis was used to search for associations based on several academic choices including attending college, major choice, and success within the Physician Assistant major. (**120**)

Speakman-Viggiano, Samantha*, Emily Davis, Grace Wright, Francesca Giardini, Vaughn Shirey, and Stephen Mason Immaculata University, Immaculata, PA 19345. *Fire effects on heath (Ericaceae) leaf structural defenses*.- Anthropogenic climate change is increasing the size, frequency, and severity of wildfires, leading to cascading effects throughout terrestrial ecosystems, particularly during plant succession. Although fires consume aboveground biomass, post-fire environments are characterized by increased light availability, reduced plant competition, and pulses of soil nutrients that promote rapid plant regrowth. However, it remains unclear whether this vigorous growth results in leaves that are more or less structurally defended against herbivores. We hypothesized that leaves from post-fire sites would exhibit higher leaf mass per area (LMA) than leaves from unburned sites. In 2018, 1,550 heath (Ericaceae) leaves were collected across three burned sites and two unburned control sites in the New Jersey Pinelands National Reserve. For each leaf, we measured dry mass and leaf area to calculate LMA and used a t-test to compare LMA between burned and unburned sites. Leaves from burned sites had significantly higher LMA than those from unburned sites ($p < 0.001$), supporting our hypothesis. Our findings suggest that fire can increase plant structural defense during succession, with potential consequences for herbivore interactions and broader trophic dynamics, thereby helping inform conservation management decisions. (**92**)

Strömbom, Daniel* Lafayette College, Easton, PA 18042. *From coursework to publication and back: Integrating quantitative teaching and research in undergraduate biology*.- Many areas of modern biology rely heavily on quantitative reasoning and modeling, yet undergraduate biology curricula often provide limited exposure to these approaches. To address this gap, our department implemented a curriculum that integrates quantitative training throughout the biology major. Central to this effort is a required introductory course in Quantitative Biology that introduces students to basic mathematical and computational modeling and quantitative analysis of biological systems. The course serves as an entry point to additional coursework in biostatistics, mathematical modeling, applied computational modeling, and bioinformatics, and prepares students for independent research projects involving quantitative approaches. Over the past several years, this structure has produced multiple undergraduate research projects that have resulted in peer-reviewed publications across several areas of biology. In turn, examples and results from these projects are incorporated back into coursework, creating a feedback loop between teaching and research. This presentation will briefly outline the curriculum and illustrate how early exposure to quantitative modeling can lead undergraduate biology students from introductory coursework to publishable research. (**5**)

Tarutis, Jr., William* Lackawanna College, Scranton, PA 18509. *Dehydration increases leaf light attenuation in young deciduous trees*.- Understory leaves of ten deciduous tree species spanning the successional range were collected in July 2025 from juvenile and sapling trees at the edge of a developing forest in Hanover Township, Luzerne County, Pennsylvania to assess the effects of dehydration on the attenuation of photosynthetically active radiation (PAR) with respect to relative water content (RWC) and specific leaf area (SLA). Leaves were hydrated overnight to full turgor and allowed to dry over several days under controlled laboratory conditions. Leaf PAR transmittance using a full-spectrum light source was periodically measured at 1-nm intervals with a Sekonic C-7000 spectrometer. Mass-specific attenuation coefficients (*kmass*) calculated using the Beer–Lambert law increased linearly as RWC declined, with proportionally greater increases in the green (550 nm) and far-red (700-750 nm) spectral regions. Dehydration effects vary with tree successional status, consistent with differences in leaf thickness and internal structure associated with SLA, despite high phenotypic plasticity in juvenile and sapling trees. These findings suggest that leaf optical responses to hydration state can provide insight into leaf structure, water status, and light capture within leaf economics frameworks. (**78**)

Tarutis, Jr., William* Lackawanna College, Scranton, PA 18509. *Light attenuation efficiency of deciduous tree leaves in relation to successional status: integrating optics with structure*.- The efficiency of leaf light attenuation by trees was assessed over the range of photosynthetically active radiation (PAR) by combining Beer-Lambert Law transmittance (T) with specific leaf area (SLA). This metric, *kmass*, represents a mass-specific attenuation coefficient defined as $-\ln(T)$ x SLA. Understory leaves of ten deciduous tree species spanning the successional range were collected on three dates during the 2025 growing season from juvenile and sapling trees at the edge of a developing forest in Hanover Township, Luzerne County, Pennsylvania. Leaf PAR transmittance was measured at 1-nm intervals with a Sekonic C-7000 spectrometer within 1.5 hours of solar noon under clear skies to minimize light spectral variations. One-sided leaf surface area and oven-dry mass were measured in the laboratory to obtain SLA. Linear mixed models of PAR transmittance show significant ($p<0.05$) date and SLA effects on $-\ln(T)$, but not species, suggesting high phenotypic plasticity in juveniles and saplings. However, species was significant when compared to *kmass*, with species groupings loosely separating along successional lines. Trait-space trajectory plots of $-\ln(T)$ versus SLA show seasonal shifts toward greater attenuation and lower SLA. These results suggest that combining leaf optics and structure into *kmass* provides an integrative functional trait for assessing leaf-level light capture. (**13**)

Tomov, Sophie*, Stephanie Yacoub*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *The effects of electronic cigarettes on Streptococcus gordonii and Streptococcus intermedius adherence to human epithelial cell*.- E-cigarette (E-cig) use has risen sharply since their introduction in 2007, exposing users to aerosolized mixtures called E-liquids (E-liqs) that can alter respiratory physiology. While the respiratory consequences of vaping have been previously studied, its impact on oral host–microbial interactions remains less understood, despite the oral cavity being the first point of contact during E-liquid use. Streptococcus intermedius and Streptococcus gordonii are key oral commensal species that contribute to oral microbial homeostasis and inhibits colonization by pathogens such as Porphyromonas gingivalis. Because epithelial adherence is essential for its protective function, we investigated whether exposure to direct or aerosolized E-liquids affects S. intermedius or S. gordonii adhesion to oral epithelial cells. Using OKF6/TERT-2 cells as a model for the human oral mucosa, bacterial adherence was quantified following treatment with flavored E-liquids delivered either directly into culture media or through media bubbled with aerosolized E-liquids. This work contributes to the growing understanding of how E-cig exposure influences the oral microbiome. (**12**)

Tran, Thuy-Tien*, Jiangyue Zhang, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Analysis of Vitamin C antioxidant activity*.- This is a continuous study of Vitamin C (Ascorbic Acid) antioxidant activity using High-Performance Liquid Chromatography (HPLC) and Saccharomyces cerevisiae. 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 and fresh Vitamin C supplement brands used were 21st Century (2020) and Nature Made (2022). 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. Based on ANOVA analysis, no significant difference was observed ($p = 0.54$) for the antioxidant activity between expired and fresh categories, as well as between brands. Further research is being conducted utilizing Saccharomyces cerevisiae as the model organism to determine if Vitamin C supplements have a protective effect for mitochondrial DNA against oxidative damage (8-oxoguanine). Qualitative preliminary results indicate that Vitamin C does have some protective effect on yeast against hydrogen peroxide oxidative damage. (**105**)

Trinh, Ngan*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Metagenomic analysis of the microbial community in a freshwater aquarium containing American eels (Anguilla rostrata)*.- The American eel (*Anguilla rostrata*) is a catadromous fish found in Atlantic coastal rivers and streams of North America and in the Sargasso Sea. It has a long snake-like body with yellowish-brown to dark skin and can grow up to about 4-5 feet in length. Unlike most freshwater fish in North America, American eels spawn in the ocean and migrate into freshwater to grow and mature. In aquarium environments, microorganisms such as bacteria, fungi, and parasites may be present and some can act as pathogens. These microorganisms can affect eel health and may become a problem in eel culture systems. Therefore, identifying microbial communities present in freshwater eel tanks is important for understanding the environment of the organisms. In this study, environmental DNA (eDNA) was isolated from water collected from eel tanks in the Lycoming College biology lab. PCR amplification targeting bacterial 16S rRNA and fungal ITS regions was performed. The amplicons were then barcoded and sequenced with the Oxford Nanopore Flongle. Sequencing data were analyzed using the EPI2ME metagenomics workflow to identify archaeal, bacterial, and fungal organisms present in the sample. The sequencing results showed that bacterial organisms were the most abundant in the eel tank samples. The most abundant Bacteria detected included *Klebsiella pneumoniae, Bacillus velezensis, Salmonella enterica, Serratia symbiotica, Escherichia coli, Mycetocola zhujimingii, Candidatus Planktophila sulfonica, Streptomyces sp. NBC_01167, Piscinibacter gummiphilus,* and *Cutibacterium acnes*. The most abundant fungi were *Vishniacozyma victoriae, Raffaelea scolytodis,* and *Tremella mesenterica*. These results describe the microbial communities detected from eDNA in the freshwater eel tank environment. (**52**)

Turnow, Ava*, and Isis Rivera-Walsh Messiah University, Mechanicsburg, PA 17055. *CRISPR-mediated knockout of MAST3 in THP-1 cells*.- In recent years, CRISPR technology has been evolving rapidly and continues to be used in innovative ways. Originally observed in bacteria as a primitive immune system, CRISPR allows for a targeted sequence to be cut out of the genome and replaced with the desired sequence. CRISPR has exciting implications in medicine, as it could be beneficial in treating genetic diseases or in knockout (KO) of targeted genes to be studied. One of these genes is the MAST3 gene, identified as a susceptibility gene for inflammatory bowel disease (IBD). MAST3 has been implicated in regulating NF-κB, a crucial transcription factor in inflammatory and immune responses, but the exact mechanism is unknown. Overexpression of MAST3 has been shown to stimulate NF-κB while reducing gene expression leads to decreased TLR4-stimulated activity of NF-κB. The purpose of this study is to establish CRISPR within a human macrophage culture, in order to knock down MAST3 expression, and study the subsequent effects of the KO on the inflammatory response via the NF-κB pathway. Protein of THP-1 cell lysates before or after treatment with LPS (bacterial lipopolysaccharide) will be quantified via Braford Assay, then western blots will be performed to detect endogenous MAST3 and IκB-α, a vital protein in the NF-κB pathway. In-vitro Cas9 digestions will be run to assess the efficacy of sgRNA generated from CRISPR vector plasmids for MAST3 and IKKβ, a known activator of NF-kB, used as a positive control. After transfection via electroporation is confirmed, the effects of the CRISPR KO will be evaluated via Western Blot of the target proteins and ELISAs of inflammatory cytokines. Implementing CRISPR in a macrophage cell line and studying MAST3 KO will allow us to study the impact of gene expression on inflammation, providing insights into the future of IBD treatment. (**96**)

Turrell, Remy*, and Andrea Nerozzi Wyoming Seminary Upper School, Kingston, PA 18704. *Food preferences of Tetrahymena*.- Tetrahymena is a unicellular eukaryote that primarily ingests food particles using phagocytosis, which is facilitated by its cilia and cytoskeleton. The purpose of this experiment is to determine if Tetrahymena would selectively ingest live versus dead particles, as a preliminary step to an investigation on the effect of microplastics on this freshwater microscopic heterotroph. To assess optimal feeding conditions, the Tetrahymena was presented with 1% India ink (carbon particles, c.2μm), a substance known to be ingested by the organism. The vacuoles in 20 Tetrahymena were assessed using a light microscope for all experimental conditions. The mean number of vacuoles containing particles, and the standard error were determined for each trial. The mean number of vacuoles in each cell containing ink at 4 hrs (25.15, ±2.78 SE) and 2 days (19.60, ±3.08 SE) were not significantly different. The optimal feeding temperature was determined to be 20°C. The Tetrahymena was then presented with India ink as well as living Escherichia coli, a prokaryote that is similar in size to the India ink particles (c.2 μm). The number of vacuoles per cell containing ink and E.coli were similar, 21.3±2.75, and 17.5±3.62 respectively. This data suggests that Tetrahymena is an indiscriminate eater, as Tetrahymena ingested both living and dead particles, and will likely ingest other non-living particles. This project will be furthered by studying more of Tetrahymena's feeding preferences, specifically with regard to microplastics, a common pollutant in aquatic ecosystems. (**44**)

Updegrove, Madelyn*, Corinne O'Connor, and Jenny Hayden Cedar Crest College, Allentown, PA 18104. *The regulation of DNA repair by lysine acetylation in Mycobacteria*.- Tuberculosis is a lung infection that kills up to 2 million people worldwide annually. *Mycobacterium tuberculosis*, the bacterium that causes tuberculosis disease, has a pathway that may potentially help with its virulence and persistence: lysine acetylation. Lysine acetylation is a post-translational modification that regulates metabolism and gene expression via protein activity. Deacetylases take acetyl groups off of lysine side chains while acetyltransferases put the acetyl groups onto lysines. Lysine acetylation has been shown to be important for stress response in *M. tuberculosis*. We use *Mycobacterium smegmatis* as a model organism to better understand *M. tuberculosis*. In this study, we're investigating if DNA repair pathways are regulated by lysine acetylation in *M. smegmatis*. UV exposure was utilized to cause DNA damage in mutant *M. smegmatis* strains that do not have either deacetylases or an acetyltransferase. This approach allows us to study the role of lysine acetylation in DNA repair. We hypothesize that the wild type will have more efficient DNA repair than one of the mutant strains that lack the three deacetylases found in *M. smegmatis.* Understanding how lysine acetylation regulates DNA repair pathways in mycobacteria can provide insights into mechanisms that help bacteria survive under stress. Potentially, lysine acetylation could be a novel drug target for treating tuberculosis disease. Since antibiotic resistance in *M. tuberculosis* is an increasing problem, there is a dire need for new treatments for this global health problem. (**40**)

Vana, Aurora*, Luis Cabo-Perez, and Joe Adserias-Garriga Mercyhurst University, Erie, PA 16546. *Assessing population affinity misclassification rates in FORDISC using cranial and post-cranial measurements*.- In forensic anthropology, the construction of a biological profile is integral to the identification of human remains, which includes estimating sex, age, stature, and population affinity. Population affinity estimation is frequently performed using FORDISC, a computer program that uses multivariate discriminant function, which compares cranial or post-cranial measurements from an unknown individual to reference samples of known population groups. Although both cranial and post-cranial data can be used, cranial measurements are considered more accurate because cranial morphology reflects population specific traits more reliably than post-cranial morphology. This study examines whether misclassification rates differ between cranial and post-cranial measurements, and whether certain population affinity groups are more likely to be misclassified. Using an initial sample of forty white individuals, cranial and post-cranial measurements were entered into FORDISC, and the resulting classification, posterior probability, and f-typicality values were recorded for each case to compare the effectiveness of the two measurement sets. (**86**)

Ventura, Caitlyn*, Cora Zilinski*, Avery Pelusak, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *A genetic screen for modifiers of rpoS expression*.- The rapid rise of antibiotic resistance in bacteria is a major public health threat, making once-treatable infections harder to manage. *rpoS* is a sigma factor which regulates the expression of numerous stress response genes, including those which respond to antibiotic stress. Sigma factors help bacterial RNA polymerase bind to gene promoters and initiate transcription. However, the regulation of *rpoS* itself remains poorly understood. In this study, we sought to identify the genetic factors influencing *rpoS* expression. We constructed an *E. coli* genomic library and transformed it into a strain containing a *rpoS-lacZ* fusion. We screened for plasmids which altered *lacZ* expression levels and confirmed their phenotypes by performing a beta-galactosidase assay and qPCR analysis of *rpoS* gene expression. We sequenced the plasmid inserts to identify the genes. Our screen yielded two genes, *yggW* and *dksA*, which have not been previously characterized as regulators of *rpoS* levels. Further studies will focus on validating these genes and exploring their potential in enhancing the effectiveness of current antibiotic treatments. (**22**)

Wenger, Heidi*, Hannah Annunziata*, and Valbona Hoxha Lebanon Valley College, Annville, PA 17003. *The effect of traumatic brain injury on survivorship and locomotor performance*.- Traumatic brain injury (TBI) is a major neurological condition that can impair survival and motor function, yet the effects of mild TBI and the role of genetic susceptibility remain incompletely understood. In this study, we used *Drosophila melanogaster* as a model system to examine the impact of mild TBI on survivorship and locomotor activity, and to assess the influence of Tau dysfunction and cannabidiol (CBD) treatment. Our findings show that mild TBI does not significantly affect survivorship in wild-type flies, suggesting that low-level injury alone may be insufficient to induce overt lethality. In contrast, flies carrying mutations in the Tau gene display increased sensitivity to TBI, as evidenced by reduced survival and impaired locomotor performance in a negative geotaxis (climbing) assay. These results indicate that Tau dysfunction exacerbates vulnerability to neural injury, supporting a link between neurodegenerative pathways and trauma susceptibility. We further evaluated the potential therapeutic effects of CBD following TBI. However, CBD treatment did not improve survivorship or locomotor deficits in either wild-type or Tau mutant flies. Overall, our results demonstrate that genetic background, particularly Tau-related pathology, plays a critical role in modulating TBI outcomes, while CBD does not confer measurable protective or curative effects in this model. These findings highlight the importance of considering genetic susceptibility in TBI research and therapeutic development. (**134**)

Wiegand, Sydney*, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Characterization of cold tolerant bacteria isolated from fourteen beaches along the Atlantic coast*.- Bacteria living in marine environments must be able to tolerate certain conditions such as low temperatures and saline environments. There is limited research on the culturable microbes from the ocean, as well as the mechanisms that marine bacteria use to survive. In this study, we cultured bacteria from 14 beaches along the Atlantic coast of the United States and characterized their tolerance mechanisms. Plating undiluted sea water and incubating at 4°C, we found over 50 isolates and found surprisingly similar bacteria in numerous beaches across the coast. Using 16s ribosomal RNA sequencing, we identified Pseudomonas , Pseudoalteromonas , and Cobetia as the most common genera across all of the beaches. The common presence of a certain species of bacteria indicates that the species may have tolerance mechanisms suitable for the average marine environment. Future directions include exploring the cold and salt tolerance mechanisms of each species and looking for a correlation between mechanism type and environment. (**83**)

Wingert, Maegan*, and Debra Wohl Elizabethtown College, Elizabethtown, PA 17022. *Effect of microbial diversity on glucose metabolism in C. elegans*.- Diets high in glucose are associated with metabolic dysfunction, acceleration of aging, and increased risk for obesity and diabetes. Glucose has been shown to detrimentally effect the physiology of *Caenorhabditis elegans* through decreases in lifespan. The gut microbiome has an important role in host physiology, yet most laboratory settings feed *C. elegans* a monoculture of *E. coli*, which does not reflect the diverse microbial community present in their natural environment. This study investigated whether a microbiome of 12 bacterial species native to the *C. elegans* natural diet can protect against the detrimental effects of elevated glucose levels. Worms were maintained on NGM plates containing varying concentrations of glucose (0%, 0.1%, 0.5%, and 1.0%) and either a standard OP50 *E. coli* diet or the diverse 12-species community. Growth, lifespan, and reproductive output assays were conducted to evaluate physiological changes. High glucose concentrations significantly reduced worm growth and reproductive output compared to the control ($p=0.001$ and $p<0.001$, respectively). Worms fed with the diverse microbial community had an increase in growth and reproductive output relative to the control ($p<0.001$ and $p<0.001$, respectively). Differences in bacterial composition were observed across the different glucose concentrations suggesting shifts in species composition. Molecular analyses are planned to identify differences in bacterial composition between the glucose concentrations to determine if this is a contributing factor to the changes observed in worm growth and reproduction. The results suggest that microbiome diversity may protect against the negative impacts of glucose in *C. elegans*, which emphasizes the importance of host-microbe interactions in overall health. (**67**)

Zelaya, Diego*, Bridget Shaver, Ava Severino, and Robert Kurt Lafayette College, Easton, PA 18042. *An experimental approach to studying anti-tumor activation of bone marrow-derived macrophages and macrophages within murine mouse mammary fat pads*.- Macrophages are immune cells that can influence cancer progression, metastasis, and treatment outcomes. This study investigated how to optimize the anti-tumor activation of bone marrow–derived macrophages (BMDMs) and mammary fat pad macrophages. Toll-like receptor (TLR) agonists were used to stimulate macrophages and induce an immune response. BMDMs were treated with the TLR agonists flagellin, lipopolysaccharide (LPS), and R848 under single (flagellin), dual (LPS and flagellin), and triple (LPS, flagellin, and R848) stimulation conditions. After stimulation, quantitative PCR (qPCR) was used to measure Il1, Il6, Tnfa, Il12, Il18, Ccl5, Cxcl9, Cxcl10, Cxcl11, and Ccr7. Results showed that gene expression was generally highest under triple stimulation conditions compared to dual or single stimulation conditions. Additional experiments compared high and low agonist concentrations demonstrating that both dose and number of agonists influence the strength of macrophage activation. Nitrite, IL-12, and ROS production also increased following the triple agonist treatment. Similar experiments were conducted to determine whether macrophages resident in the mouse mammary fat pads could also be activated by TLR agonist treatment. However, insufficient macrophage recruitment may have limited the ability to detect pro-inflammatory factors by qPCR. To address this, the chemokine CCL2, which is a well-known macrophage recruiter, is being injected into the mammary fat pads at different concentrations to recruit macrophages to this site, and it seems to be efficient as there tends to be more cells collected from the fat pads when CCL2 is delivered. Future experiments will combine TLR agonist stimulation with enhanced macrophage recruitment in order to determine whether anti-tumor macrophages can be activated in vivo. (**102**)

Zeok, Paige*, Jacob Wagers, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Updated identification of microbial strains over 10 years old from the Lycoming College Culture Collection using Nanopore sequencing*.- The microbial culture collection at Lycoming College has accumulated over 1000 strains of bacteria and fungi identified by students in Microbiology and other courses during the past 20 years. Earlier identification strategies relied on a single Sanger sequencing read of the PCR-amplified 16S rRNA gene followed by a BLAST search of NCBI GenBank. If the identification suggested that the organism was a novel species, additional primers could be used to assemble the nearly complete 16S rRNA gene sequence for submission to GenBank. We recently purchased a third generation Oxford Nanopore MinION DNA sequencer, which allows up to 96 barcoded samples to be sequenced at once on an inexpensive “Flongle” flow cell. In this study, frozen cultures were recovered from our culture collection in the -80°C freezer and grown on nutrient agar plates at 22°C for 2-3 days. A single, well-isolated colony from each recovery plate was transferred to new patch plates to assess growth on different media and at different temperatures; and to sterile water for use in PCR. The cells suspended in water were passed through two freeze and thaw cycles and used as a template for 16S rRNA gene amplification with “universal” 27f and 1492r primers. The PCR products were barcoded and sequenced on a Flongle and the reads were assembled into consensus sequences using ONT’s EPI2ME amplicon workflow and BLASTed against the NCBI 16S rRNA and core nucleotide databases for identification. The new data and older identifications were consistent in most cases though there were two instances in which strains were switched while making permanent cultures. In other cases, strains originally identified as being novel species could now be assigned to more recently described species. Other strains are still novel species candidates (<99.5% identical 16S rRNA) and will have their genomes sequenced. (**48**)

Zhu, Cindy*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Synthesis of three putrescine analogs as possible antioxidants*.- This investigation will involve the synthesis of several putrescine analogs produced using 100% ethanol as the solvent. These nucleophilic substitution reactions with alkyl alcohol halides will produce bis(3-hydroxypropyl), bis(4-hydroxybutyl), and bis(5-hydroxypentyl) putrescine. In this study, 100% ethanol was used as the reaction solvent this allowed for yields of the polyamine analogs to proceed in a greener solvent. There are many advantages for using alcohols over traditional volatile organic solvents in synthetic reactions. Alcohols are preferred solvents as they are more environmentally friendly, can be reclaimed or recycled, and reactions are run at lower temperatures. It was also found, in this work that the use of 100% ethanol increased the product yield dramatically over other more toxic alcohol solvents used for previous studies in our laboratory. The analog products were analyzed using FT-IR and FT-NMR. (**60**)