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General Meeting ABSTRACTS

Listed alphabetically by first author's last name.

Acheampong, Kwabena*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Exploring The Relationship Between Telomere Lengthening Pathways And Genetic Ancestry In African-American And European-American Patients with Non-Small Cell Lung Cancer*.- Background Lung cancer has the second-highest incidence rate and the highest cancer-related deaths among males and females in the US. Specifically, African Americans (AAs) have higher mortality rates and lower survival rates compared to European Americans (EAs) and other demographic groups. Determinants including, geographical, socio-political, behavioral, and biological determinants, contribute to understudied lung cancer disparities. The biological determinants that are investigated in this study are telomere lengthening network mechanisms and pathways and West African Ancestry. Hypothesis WAA is associated with clinically relevant non-canonical telomere lengthening and maintenance pathways in lung cancers from AA and EA patients. Methods Categorize NSCLC patients as high or low expressers based on median gene expression. Compare five-year disease-specific survival data by telomere length and high and low WAA. Conduct differential gene expression by WAA for all 2,093 genes. Results DAXX is significantly more expressed in Low WAA LUAD Patients. There were no other significant expression differences by ancestry. NSCLC patients with high WAA expressed slightly more canonical pathway genes and LUAD patients with low WAA expressed slightly more non-canonical pathway genes. Discussion Patients with high WAA may benefit from combinational drug chemotherapy that disrupts the non-canonical telomere lengthening pathway. Conclusion Significant differences in gene expression in the LUAD cohort saw patients with low WAA had higher DAXX expression than those with high WAA. NSCLC patients with high WAA had higher median expression of canonical pathway genes. NSCLC patients with low WAA had higher median expression of non-canonical pathway genes. There are 6 differentially expressed TMN genes by WAA in NSCLC patients. Future Directions To quantify and compare the impact of standard combination lung cancer chemotherapy drug response on telomere length (TL) in LUAD cell lines with high and low WAA. Calculate 5-year disease-specific patient survival based on TMN candidate gene expression. (**59**)

Amendano, Brigette*, Suzanne Spriggs, and Ian Cost Albright College, Reading, PA 19604. *A comparative analysis of the trigeminal nerve in the orbits of predatory birds*.- For many animals, touch is one of the most crucial senses as it allows an animal to assess its surroundings. It is also crucial for development and socialization. Remote touch is an essential part of avian survival as it allows them to identify prey and changes in pressure. Due to their dependence on remote touch for prey detection, birds are assumed to have a high number of mechanoreceptors, implying they have a complex trigeminal nerve system. The trigeminal nerve has three branches (V1, V2, and V3) that supply somatosensory information from the face and head. Birds from the families Apterygidae, Scolopacidae, Anatidae, and Threskiornithidae are probing birds known to have a sensitive bill tip organ supplied by the trigeminal nerve. In comparison to other birds that use vision, hearing, and other touch to identify prey resulting in less dependence of the trigeminal nerve. In this study, we compare the trigeminal nerve of predatory birds from the families Accipitridae and Tytonidae, and the passerine family Corvidae to each other as well as to birds from Apterygidae, Scolopacidae, Anatidae, and Threskiornithidae. We found branches V2 and V3 in the orbits using manual dissection and measured branch length and qualitatively evaluated complexity through the orbital region. Due to differences in somatosensory structures associated with this nerve we expected the nerve to be less complex in these predatory birds. It was found that birds from the raptorial families (Accipitridae, Tytonidae), and the songbird family Corvidae, demonstrated less complexity of the trigeminal nerve due to differences in foraging. More research must be done to identify definitive differences within the trigeminal nerve complexity between the families of these avians. (**90**)

Armstrong, Alexis*, Alexandra Kroznuskie, Ryan Stackhouse, Brennan Gerancher, Nidhi Kumar, Jared Franges, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Identifying novel antibiotics from soil bacteria*.- Antibiotic resistance is a major health concern due to misuse or improper use of antibiotics in the past. Many of these antibiotic resistant infections are caused by the ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species). Our study aims to identify novel antibiotics produced by bacteria from soil. Many bacteria in the soil naturally produce antibiotics. We have collected soil samples from several different locations around the Lehigh Valley and isolated bacterial colonies from those soil samples at either 25°C or 30°C to select for non-pathogenic bacteria. Once isolated, we tested the bacterial isolates for antibiotic production using microbes that are closely related to the ESKAPE pathogens. We have found multiple isolates that limit the ESKAPE relative and are characterizing them. Ongoing work will determine whether the antibiotics that are produced are novel. (**37**)

Assaf, Afaf*, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Biodiesel production from aquatic fern Azolla caroliniana via hydrothermal liquefaction*.- The use of biomass fuels is increasing in many developed countries, which helps reduce the overreliance on fossil fuels. Many studies have been conducted which demonstrate that the aquatic fern *Azolla* provides compounds that can be used for biofuel production. Researchers provided various data that support the type of compounds extracted are dependent on the extracting solvent, temperature, catalyst, etc. This project aims to characterize compounds present in *Azolla caroliniana* by comparing different extraction solvents at varying temperatures via hydrothermal liquefaction. The ultimate goal is to investigate methods utilized to achieve a maximum amount of biofuel compounds to be introduced to industrial usage. Extractions from the plant have been analyzed using gas chromatography mass spectometry. Based on our preliminary results, it appears that polar and nonpolar solvents are prone to influence the type of compounds extracted. In addition, running the reaction at higher temperature tends to alter the extracted compounds and affect their quantification. Specifically, methanol as an extraction solvent yields a large fraction of fatty acid methyl esters, which is the main component of biodiesel. This project has the potential to suggest a novel method to harness biomass energy. (**101**)

Bart, Alex*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *African American-enriched loss of heterozygosity on chromosome 3q24 impacts scramblase tumor suppressor genes in kidney cancer patients*.- Patients with renal cell carcinoma (RCC), the most common type of kidney cancer (85% cases), have the lowest survival in the U.S. compared to all other urologic cancers. The most frequent RCC subtype is clear cell RCC (ccRCC, 75% cases). African American (AA) ccRCC patients have worse survival than European Americans (EAs). There are environmental, lifestyle, and biological determinants of the racial disparity, with the tumor biology being the least understood. Genomic factors, like loss of heterozygosity (LOH), have been associated with poor cancer survival. LOH occurs when a heterozygous cell loses one of its alleles at a specific locus, which increases cancer susceptibility. Here we show a comparison of population-specific LOH in ccRCC patients that is associated with tumor suppressor and oncogenes. Our genome-wide analyses using the Partek Genomic Suite LOH Workflow revealed that AAs had significant LOH on chromosomes 1, 11, and X, which was not observed in EAs. Both populations had significant LOH on chromosome 3. Further region-specific analyses of chromosome 3 showed that AAs had significant LOH on the 3q region, while EAs exhibited significant LOH on 3p. Collectively, 306 genes in 10 AA-enriched chromosome regions were impacted by LOH. String v11.5 was used to determine known and predicted functional protein-protein interactions (PPI). Significant AA-PPI enrichment ($P = 0.0022$) revealed greater biological interactions than expected and molecular functions in scramblase activity ($P = 0.0382$). Scramblases are proapoptotic proteins and suspected tumor suppressors. We speculate LOH of scramblase genes can lead to loss of protein function, less apoptosis, greater disease progression, and decreased survival in AAs. Future work will explore the association between scramblase expression and ccRCC patient survival by race. (**10**)

Bell, Kiyah*, and Jeff Newman Lycoming College, Williamsport, PA 17701. *Isolation and characterization of carotenoids in Pedobacter and Roseopedobacter gen. nov.*.- *Pedobacter* is a genus in the *Bacteroidota* that usually produce pink or yellow carotenoids. Carotenoids are the most diverse and ubiquitous pigments found in nature, synthesized by plants, fungi, algae, and bacteria. They are a class of terpenoids with a linear, isoprene backbone, and their structure consists of an extended conjugated system. In this work, five previously identified *Pedobacter* strains were recovered from the Lycoming College Culture Collection (LCCC). The pigments were extracted with methanol to obtain spectroscopic characteristics by HPLC analysis. Compounds with a three-peaked spectrum, typical of carotenoids, plus a maximum absorbance around 480nm was commonly found in the pink strains, and 450nm was the peak wavelength found in the yellow strains. Phylogenetic analysis using the Genome Taxonomy Database (GTDB) and the RNA polymerase b-subunit (rpoB) tree revealed that the yellow *Pedobacter* strains and the pink *Pedobacter* strains each shared a common ancestor and formed separate clades on long branches. A computational genomic study, the Average Amino Acid Identity (AAI), suggested that organisms of different colors should be in distinct genera. After mining the genome for carotenoid biosynthetic genes using the Rapid Annotation using Subsystem Technology (RAST) website, we discovered that the pink species encode b-carotene ketolase, which the yellow species lack. The presence or absence of the b-carotene ketolase enzyme should allow the pink species to produce canthaxanthin and astaxanthin, pink carotenoids, yet the yellow species should produce b-carotene and zeaxanthin, yellow carotenoids. We conclude that the pink strains should be reclassified into a new genus, which we propose to call *Roseopedobacter,* due to their synthesis of pink carotenoids. In the future, we plan to optimize our LC-MS conditions to identify the carotenoids based on the molecular weight and fragmentation patterns. (**64**)

Best, Austin*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Characterization of Phytoplankton and Bacterioplankton Communities in the Eutrophic Raritan Bay*.- Raritan Bay, located between the states of New York and New Jersey, has a long history of cultural eutrophication and associated harmful algal blooms (HABs). Despite striking chemical and biological alterations occurring in Raritan Bay, publications in the early 1960s were the last to report consecutive measurements of both water quality parameters and plankton species composition in this system. While emerging research indicates that bacterial communities play important roles as HAB promotors, enhancers, and regulators, no research has been conducted in the Raritan Bay to understand the ecological relationship between the microbial community and HAB species. The objectives of this study were to characterize water quality trends and plankton composition in a eutrophic estuary and to further clarify the relationship among nutrients, bacteria, secondary consumers, and algal bloom generation in this system using ordination techniques. Monthly data on water quality, phytoplankton, and zooplankton were collected from April 2010–November 2021 and on bacterioplankton from August 2021 to November 2021 at six sampling sites. To build a spatial and temporal profile of the bacterial community, amplicon sequence analysis of the 16S rRNA gene, taken from extracted bacterial RNA, was employed. Results indicate that Raritan Bay continues to exhibit numerous symptoms of eutrophication, including high algal biomass, high turbidity, violations of the dissolved oxygen standard to protect fish health, and blooms of potentially harmful phytoplankton species. A total of 14 HAB species have been identified. Multivariate associated with high temperature, salinity, nitrate, and SRP and negatively associated with spring river discharge rates and total zooplankton abundance in Raritan Bay. After successful analysis of amplicon sequences, the final step will be to use Non-Metric Multidimensional Scaling (NMDS) to identify the bacterial species that are predominant during blooms and describe how does the microbial community change during a bloom. (**2**)

Branigan, Carter*, James Johnson*, and Jeff Newman Lycoming College, Williamsport, PA 17701. *Genomic comparisons between yellow and pink Pedobacter species*.- The genus Pedobacter includes both yellow and pink species, and the pink species are clustered into a distinct phylogenetic clade. The purpose of this study was to define differences in the sets of genes shared within each group that are not present in the other group. Full genome analysis using the Sequence-based comparison tool on the Rapid Annotation using Subsystems Technology (RAST) website identified orthologous genes for construction of venn diagrams and calculation of average amino acid identity (AAI) values. Our custom Venn Diagram Tool identified 589 unique coding sequences present in the pink strains that were absent in the yellow strains. There were 309 coding sequences shared by four representative yellow strains that were absent in the representative pink strain. These coding sequence differences are currently being evaluated to identify connections to phenotypic differences. AAI Matrices show the extent of differences between the two clusters of bacteria and support the separation of the pink strains into the novel genus *Rosepedobacter* gen. nov from the existing genus *Pedobacter*. (**32**)

Brown, Thomas*, Hannah Laughner*, Allison Mattern*, Joseph Colosi, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *A time-course comparison of bacterial communities in different soil environments using next-generation sequencing*.- Prokaryotes are, by far, the most abundant organisms in soil. They drive mineral cycles and are responsible for major characteristics of the soil ecosystem. Prokaryote biodiversity and function are greatly affected by physico/chemical characteristics of the soil such as texture, temperature, moisture, pH, mineral content, and vegetation. A better understanding of how external factors influence soil bacterial communities can further knowledge of how these communities form. Previously, we investigated the compositional differences between soil bacterial communities in adjacent lawn and meadow environments. Our work showed that the total number of operational taxonomic units (OTUs) was larger in the meadow environment, but the total number of bacteria was very similar for both environments. In this study, we wished to determine if changes in the outside environment, such as temperature and precipitation, might show differential effects on soil communities in the lawn and meadow environments. We hypothesized that the samples collected during the colder months would result in a lower microbial diversity than the samples collected during the warmer months, and that the meadow samples would show a higher microbial diversity than the lawn samples. We collected soil samples from each environment every month for six months and then extracted the mixed bacterial DNA from each sample. These samples were sequenced by massive parallel sequencing (next-generation sequencing). We analyzed the sequence data using the BaseSpace platform from Illumina. We found that the abundance of the microbial communities collected during the colder months was less than the samples collected during the warmer months. We also found that the diversity in the lawn samples was consistently less than that found in the meadow. (**30**)

Brown, Thomas*, Hannah Laughner*, Joseph Colosi, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Determining the impact of pollution from Bethlehem Steel on the microbial communities of nearby soil*.- The Bethlehem Steel Plant, located on the Lehigh River in Bethlehem, PA produced steel for over 150 years and was one of the largest producers of steel in the world until the 1970s. This manufacturing caused severe levels of pollution both above- and below-ground around the plant. Since stoppage of production, the area appears to have recovered from obvious pollution, with a return of abundant plant and animal life. We evaluated if the condition of the soil had likewise improved during this time. Soil microbial diversity has been shown to be a strong indicator of pollution. We indirectly investigated the presence of soil pollution in proximity to the Bethlehem Steel blast furnaces by using next generation sequencing of prokaryotes in nearby soil samples. If pollution lingers, we predicted that soil in close proximity to the blast furnace would have a significantly less diverse microbial population than a control sample of soil taken from across the river from the plant. We collected samples approximately 10m from the original blast furnace, as well as from underneath the tree line directly across the Lehigh River from the blast furnace as a control. We extracted the DNA and PCR-amplified the V3-V-4 region of the 16S ribosomal RNA gene. We mixed the amplicons with index primers before pooling the samples into one combined set for each location. The addition of the index primers allowed for the pooled samples to be demultiplexed and individual bacterial sequences to be identified. We analyzed the data using the Illumina Basespace platform and found that there was no significant difference in their microbial communities. We conclude that any remaining pollution surrounding the original blast furnace has not inhibited microbial diversity in the soil. (**63**)

Buckwalter, Silas*, Courtney Williams, and John Harms Messiah University, Mechanicsburg, PA 17055. *Correlating in vitro matrix deposition and COL1A expression with tumor fibrosis in human pancreatic cancer*.- Pancreatic cancer has a meager 5-year survival rate. The poor efficacy of chemotherapy has been attributed in part to the highly fibrotic collagen-rich tumor microenvironment. Our lab previously confirmed the gastrin receptor antagonist, proglumide, significantly decreases pancreatic tumor fibrosis *in vivo*. Our findings have also suggested the cancer cell, in addition to stromal cells, may be directly implicated in the elevated collagen synthesis. However, efforts to recapitulate proglumide inhibition *in vitro* have failed to demonstrate a decrease in the collagen mRNA expression or collagen matrix deposition when either myofibroblast-like pancreatic stellate cells or cancer cells were treated with proglumide. We therefore sought to test the fundamental hypothesis that *in vitro* matrix deposition and/or collagen (COL1A) expression correlate with *in vivo* tumor fibrosis. Utilizing a panel of four human pancreatic cancer cell lines, we employed Sirius Red/Fast Green staining to quantify collagen-specific and total matrix deposition relative to cell number. Masson’s Trichrome staining was used to quantify collagen fibrosis in a histological section derived from tumor xenografts of each cancer line. In these preliminary results, apparent differences among *in vitro* deposition were not statistically significant. High fibrosis in SW1990 tumor tissue was reflected in both COL1A expression and *in vitro* collagen deposition. PANC1 cells exhibited the least collagen staining in both contexts, but the highest COL1A expression. By contrast, high fibrosis in MiaPaca-2 was not reflected in either collagen RNA or deposition. However, heterogeneity of fibrotic distribution/regional density within tumors may require consideration. Further studies will be necessary to determine if these relationships are consistent and whether co-culture modeling will be necessary to address heterotypic communication between stromal and cancer cell compartments present in the tumor microenvironment. (**17**)

Bui, Theresa*, and Amy E. Faivre Cedar Crest College, Allentown, PA 18104. *The effects of leaf litter depth on seed germination of Oriental bittersweet (Celastrus orbiculatus)*.- *Celastrus orbiculatus*, or Oriental bittersweet, is a non-native, invasive plant species in many eastern forests in the United States. It displaces and competes with native plant species and changes natural forest habitats by climbing and sometimes girdling trees. Individual Oriental bittersweet plants produce a number of seeds. Thus, one way to reduce the presence of this species in forests is to understand more about the germination of its seeds. One factor that has been shown to affect its germination success is the depth of the leaf litter in the forest. For our study we collected seeds of Oriental bittersweet in November 2021 in a forest at Wildlands Conservancy in Emmaus, PA. After cold storing the seeds for almost two months, we set up germination trials in the Cedar Crest College greenhouse. The three conditions were no leaf litter, a shallow layer of leaf litter (1 Mg/ha), and a deep layer of leaf litter (16 Mg/ha). The leaf litter was sieved through a 15mm x 15mm grid before adding it to the pots. Each pot contained 12 seeds from six different plants. We ran two trials planted two weeks apart, with a total of 36 pots in each trial, 12 pots with seeds in each of the three conditions. We calculated and compared percent seedling germination among the three conditions. Knowing the effects of leaf litter on seed germination success may help in controlling seedling emergence and future spread of this invasive plant. (**89**)

Buia, Ainsley*, Nayab Baloch*, Macey Eberly, and Valbona Hoxha Lebanon Valley College, Annville, PA 17003. *The influence of alcohol after traumatic brain injury in Drosophila melanogaster*.-

Traumatic brain injury (mTBI) survivors, particularly those injured early in life are very likely to abuse drugs and alcohol later in life. Alcohol abuse following traumatic brain injury (TBI) is associated with poorer rehabilitation outcomes and a greatly increased chance of suffering future head trauma. This study, uses the fruit fly Drosophila melanogaster to investigate the role that alcohol sensitivity plays after traumatic brain injury period. We developed a HIT device that inflicts TBI in flies. Using this system, we tested how TBI affects alcohol sensitivity. Our results indicate that flies are very sensitive to the intoxicating levels of alcohol during the acute phase of post TBI. Furthermore alcohol exposure during the acute phase of TBI increases mortality rate. These effects decrease as time progresses, returning back to normal 48 hrs post TBI. Surprisingly our data suggests that the sedative effects of alcohol affect males and females differently. (**5**)

Caroland, Kailey*, John Hanson, and Jane Cavender Elizabethtown College, Elizabethtown, PA 17022. *Increased expression of SAM68 in SV40 transformed human diploid fibroblast cells and the effect on downstream splicing targets*.- Alternative splicing has emerged as a major player in cancer initiation and progression. The alteration of splicing factor profiles and the effect on their subsequent targets have been reported in several cancers. Comparing tumor samples and tumor cell lines to build protein profiles of specific isoforms has elucidated common alterations that may indicate the important drivers of tumorigenesis. However, when using primary tumors and tumor cell lines there is often not a matched control to directly compare the results. But employing the simian virus 40 (SV40) DNA tumor virus model, studies can be designed to investigate the isoform profiles before and after cellular transformation. For this study, human diploid fibroblasts immortalized with telomerase (HDF(tert)) were stably transfected with plasmid encoding the early region SV40 (HDF(tert+T)). Two clones were compared to the parental line, and it was found that the level of T-antigen was directly correlated to increased levels of the splicing factor SAM68. Increased levels of SAM68 and the subsequent downstream altered proteins has been implicated as a driver of, and is now a chemotherapeutic target for, lung colon and breast cancers. To elucidate the possible role of SAM68 in viral tumorigenesis, downstream splicing targets were assessed using RTPCR and Western blotting. We found no difference in the isoform ratios or levels of protein accumulation of the transcription factor TEF1, the apoptosis regulator BCLx, or bridging integrator BIN1. Interestingly, it was found that the SAM68 target SRSF1 (another splicing factor) showed increased levels of only the specific SRSF1-208 isoform in the transformed lines. Studies are ongoing to investigate the cellular localization and potential phosphorylation alterations of the SRSF1 protein. Additionally, the tyrosine kinase receptor RON implicated in the aggressive tumor phenotype of epithelial to mesenchymal transition (EMT) and a target of SRSF1 splicing, is currently under investigation. (**70**)

Castaneira, Ryan*, Daniel Morris, Josie Rice, Savannah Kreiser, and Nik Tsotakos Penn State University-Harrisburg, Middletown, PA 17057. *Alterations in the non-coding transcriptome of glucose-stressed human glomerular epithelial cells may indicate novel biomarkers associated with early diabetic kidney disease*.- Diabetic Kidney Disease is a slow, gradual complication of diabetes.Previous work on a podocyte-like cell line showed that phenotypic changes following exposure to high glucose, such as downregulation of podocalyxin and nephrin, are gradual and irreversible. Along with protein-coding genes, several long non-coding RNAs (lncRNA), such as MEG3, MEG8, and H19 are dysregulated in human glomerular epithelial cells (HGEC) chronically cultured in high glucose levels. In the present study, we aim to identify lncRNAs that are dysregulated shortly after exposure of the cells to high glucose, prior to the complete loss of podocalyxin and nephrin. Through a qPCR array, we've identified approximated 20 upregulated and 20 downregulated non-coding RNA's in HGEC that were exposed to high glucose for 2 weeks. In the literature, several of these lncRNAs have been connected to essential transcriptional processes, such as chromatin remodeling, and cellular growth and viability. Future research will determine whether any of these molecules could be used as biomarkers for early kidney injury. (**24**)

Chang, Musea*, and Robert Kurt Lafayette College, Easton, PA 18042. *Targeting altered metabolism in tumor associated macrophages*.- Part of the innate immune system, macrophages serve a critical role in the tumor microenvironment. These tumor associated macrophages (TAM) can have both pro- or anti-tumor effects. Previously, we found that these TAM demonstrated increased expression of three genes associated with altered metabolism: *glut1, ampk* and *pkm2*. This study focused on whether targeting altered metabolism in macrophages would impact expression of these genes and tumor progression. For this purpose, we focused on inhibitors of lactate dehydrogenase (FX-11), eIF2 (ISRIB), AMPK (Compound C), and GCN2 (GCN2-IN1). Initial studies focused on identifying concentrations of these inhibitors that would not impact the viability of the macrophages or tumor cells. We identified that 200nm, 10uM and 750nM of ISRIB, FX-11, and GCN2-IN1 respectively would not kill the macrophages or the EMT6, 4T1 or 168 breast cancer cell lines. We could not identify a dose of Compound C that would not kill the tumor cells or macrophages that was near the compound's IC50. To determine whether the metabolic inhibitors would impact *glut1, ampk* and *pkm2* expression, bone marrow-derived macrophages were incubated with tumor cells in the presence or absence of the inhibitors, and qRT-PCR was used to follow *glut1, ampk* and *pkm2* gene expression. The data showed that targeting eIF2 with ISRIB consistently decreased expression of all three genes when the macrophages were co-cultured with the EMT6, but not the 4T1 tumor cells. Current studies are evaluating whether the metabolic inhibitors can impact tumor progression. For this purpose, BALB/c mice will be given the EMT6, 4T1 or 168 tumor cell lines, and an inhibitor or control (DMSO) will be delivered into the tumor sites. Tumor volumes and survival will be followed over time. For the 4T1 tumor bearing mice the number of lung metastasis will also be quantified. (**73**)

Chau, Phuong*, and Ian Cost Albright College, Reading, PA 19604. *Comparing Dental Measurement in North American Bats with Corresponding Diets*.- Bats possess canines, incisors, premolars and molars, which are specialized to enable chewing and crushing of food items. These teeth are found on both the upper and the lower jaws despite their differences in sizes. Previous studies indicates that diet influences the shape and number of teeth.This project aims to explore the comparative anatomy of bat teeth with distinct aspects to determine the impact of dental morphology and its contributors toward the variation in mammals with different diets. We hypothesize that there is a correlation between tooth measurements of bat species specimen and their corresponding diets. Using digital calipers and microscope, the study measured 46 skulls from 28 bat species. Diets, common names, living locations, sexes, and dental formulas for each species were collected from the literature. The analysis of recorded data was done using Excel (organization of data and graphics) and RStudio (statistical analysis). The results support our hypothesis as there are significant differences among teeth measurement and their correspond diets. These important points of the research will help in further study of the influence of gravitational force on teeth alignment other morphological aspects associate with related dental issues. Further studies are necessary to understand how diet influences the arrangement of teeth in these mammals. (**104**)

Cook, Brandi*, Adam Cooke, and Deborah Austin Wilson College, Chambersburg, PA 17201. *An evaluation of <u>Salmonella</u> spp. and <u>Escherichia</u> <u>coli</u> in feline commercial raw meat-based diet and kibble*.- Feeding a raw meat-based diet (RMBD) has become increasingly popular amongst pet owners. There is debate about whether pet owners should feed felines a commercial RMBD because of the potential for higher bacterial levels. Although cats have a gut microbiome to help aid in the homeostatic balance of bacteria, the entrance of bacteria through the diet can cause bacteria dysbiosis, causing vomiting, diarrhea, weight loss, and blood in the stool, which may lead to gastrointestinal diseases such as inflammatory bowel disease (IBD). The symptoms of IBD are acute at first but may worsen over time if not treated after diagnosis. Therefore, it is important to understand whether some foods are more likely to introduce larger quantities of bacteria into the feline diet than others. This study quantified the amount of *Salmonella* spp. and *Escherichia coli* in various cat foods. The samples varied based on lot number, flavor, manufacturer, and type of food

– commercial RMBD or kibble. The foods were homogenized in phosphate-buffered saline, serially diluted, plated on selective media for each bacterium, and incubated for growth. Samples were plated on Brilliant Green agar, modified, to determine the number of *Salmonella* spp*.* present. Samples were also plated on MacConkey Sorbitol agar to determine the number of *E. coli* present. While there were no statistically significant differences in *Salmonella* spp. among the food tested, there was a statistically significant difference in the amount of *E. coli* among the foods. A single lot of one brand of RMBD showed a statistically significant lower amount of *E. coli* compared to the other lots. There were no other statistical differences in amounts of *E. coli* in the remaining comparison groups. By analyzing additional foods we can better understand how bacteria is introduced via diet and reduce the risk of gastrointestinal diseases in felines. (**29**)

Crocker, Amanda*, Grace Tulevech*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Spotted lanternfly infestation is associated with tree of heaven presence in the US*.- The spotted lanternfly, *Lycorma delicatula*, has established itself as a harmful invasive species in a number of locations worldwide. The insect's occupancy in Asia and growing presence in North America pose a significant threat for global invasion in the near future. Currently, methods including mid-winter chipping of eggs, insecticides, and egg parasites are being utilized as mechanisms to destroy lanternflies. It has been proposed to target the tree of heaven, *Ailanthus altissima,* to mitigate lanternfly spread since it is one of the most preferable host plants. While there is a colloquial consensus that the spotted lanternfly prefers, and quite possibly depends on, the tree of heaven, this has not been studied quantitatively. It is not completely understood whether or not manipulating the invasive tree of heaven will lessen lanternfly spread, due to the variety of plants the lanternfly can sustain itself on. In North America, predictions have shown that the pest could expand its range to a majority of the United States. Here we collected data at the county level to test the hypothesis that there is an association between reported lanternfly infestation and reported tree of heaven presence. Analysis of a 160 county region defined by the current US infestation found a positive association between the lanternfly infestation status and the reported tree of heaven presence ($p = 0.013$), suggesting that worldwide lanternfly mitigation efforts involving the tree of heaven may be worth further investigation and implementation. (**91**)

Dardis, Jackson*, Darci Ott, Victor Witkofski*, and Diane Bridge Elizabethtown College, Elizabethtown, PA 17022. *Characterizing ferroptosis in the model invertebrate Hydra vulgaris*.- Ferroptosis is a form of regulated cell death distinct from apoptosis. It occurs in diverse animals and in plants, but has not been documented in *Hydra*, an invertebrate genus used for studies of stem cell biology and aging. To characterize ferroptosis in *Hydra*, we treated *Hydra vulgaris* with the ferroptosis-inducing compound diethyl maleate (DEM) and the ferroptosis inhibitor Liproxstatin-1 (Lip-1). DEM caused cell death of ectodermal epithelial cells in *Hydra vulgaris*, and Lip-1 blocked its effects, providing evidence that it is possible to induce ferroptosis in *Hydra vulgaris*. We have designed and tested PCR primers to detect changes in expression in the gene CHAC1, which can show increased expression during ferroptosis in mammals. Planned experiments include investigating whether ferroptosis occurs during heat shock in *Hydra vulgaris* and in the heat-sensitive species *Hydra oligactis*. (**16**)

Davila, Dayana*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Phenotypic and genomic characterization and comparison of two novel Pedobacters recovered from a freshwater creek in Central Pennsylvania*.- This study is one of many in the microbiology field that is trying to not only identify and characterize novel organisms, but to push forward for a more effective taxonomic method. The microbiology field has been trying to combat the issue of "catch-all" groups, in which these novel species are placed in a genus due to its similarity to an existing organism in a genus although it could be vastly different from the type species. These "catch-all" groups cause genera to be very broad and not specific the way that it is intended to be. A narrowing of taxonomy will help better characterize the constant novel species being identified and help with the understanding of microbial organisms, their functions, their main characteristics, and possible harms or benefits. In this study we investigate the Pedobacter genus and compare two novel pink–pigmented species, Pedobacter sp. AJM and Pedobacter sp. R20-19, to 3 other species in this genus, Pedobacter heparinusT DSM 2366, Pedobacter psychrotolerans DSM 103236, and Pedobacter petrophilus LMG 29686. Members of this genus are characterized as rod-shaped, gram-negative, non-spore forming, non-flagellated, aerobic, and yellow, pink, or unpigmented (Margesin et al., 2003). This study further investigates the genetic similarities between the pink and yellow pigmented species in the genus and test the possibility of a genus split. Genomic comparisons between yellow and pink pigmented species were made using the sequence–based comparison tool on The SEED Viewer (Overbeek et al., 2014). We explored the unique genes in these two species, such as the prevention-host-death and oligosaccharide flippase, which is not found in any other Pedobacter species aside from R20-19. (**33**)

Davila, Juan*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Phenotypic and genomic characterization of a novel Pedobacter recovered from a freshwater creek in Northcentral Pennsylvania*.- The importance of studying novel microorganisms and documenting their genomic and phenotypic characteristics is to see what makes each organism unique and if any of their genes can be used to further science and potentially be useful for society. A bacterial strain designated MC2016-14 was isolated from a freshwater creek and the 16S rRNA gene sequence identified it as a novel *Pedobacter* species. Members of this genus are rod-shaped, gram-negative, non-spore forming, non-flagellated, aerobic and yellow, pink or unpigmented (Margesin et al., 2003). The genome of the novel strain was sequenced at the Microbial Genome Sequencing Center (MiGS) (Pittsburgh). The *Pedobacter* sp. MC2016-14 16S rRNA gene was most similar to that of *Pedobacter ginsengisoli* Gsoil 104T with a percent identity of 97.86%. The rpoB gene was 88.5% identical to that ortholog from *Pedobacter cryconitis* DSM 14825T. The highest Average Nucleotide Identity (ANI) value was 72.3% with *Pedobacter lusitanus* NL19T. The highest average amino acid identity (AAI) value was 68.9% relative to *Pedobacter duraquae* DSM 19034T which is below the 74% threshold for a new genus (Saeedi, et al.,2021). One unique feature found in the genome of MC2016-14 was that it has 16 copies of the gliding motility protein (gld) found in operons that consist of the fused ABC transporter permease protein (gldF) and substrate-binding protein (gldG). Along with the operon having ABC transporter ATP-binding protein (gldA). This unique feature was rarely seen in *Pedobacter* type strains whose genomes were reviewed to check for the presence of the gldFG fused gene and the gldA gene. Based on this genomic data, it is concluded that strain MC2016-14 is a novel species in a novel genus. The next steps are to acquire the closest relatives and conduct comparative phenotypic studies. (**27**)

Dempsey, Chris*, Michelle Kuns, and Greg Andraso Gannon University, Erie, PA 16541. *A five year (2016-2021) summary of water quality, zooplankton, and fish community changes in Presque Isle Bay, Erie Pennsylvania*.- Monitoring water quality in aquatic ecosystems is critical to our understanding of how they change over time. Located in Erie, PA, Presque Isle Bay (PIB) is a unique body of water that provides ecological, economic, and recreational benefits. Since October 2016, we have collected monthly water quality, plankton, and fish community data in PIB. Sampling in most years extends from May through November and occurs near the middle of each month. Water quality data includes temperature, dissolved oxygen, specific conductivity, pH, photosynthetically active radiation (PAR), secchi disk, and dissolved organic carbon. Zooplankton are sampled in duplicate vertical tows using a 153 micron net with an 18cm opening. After preservation, samples are identified to family. Fish are sampled using a semi-balloon bottom trawl for 10 minutes (approximately 0.70 km). All fish are identified to species level, and body length of several species is recorded. Water quality data depicts a seasonal pattern with no noticeable change over the last five years. Plankton samples tend to be dominated by *Daphniidae* and *Bosminidae*. Seasonal data suggests a peak in zooplankton abundance in early summer and a swift decline through the rest of the year. Although we have collected 20 species of fish belonging to 11 families, the catch has been dominated by four species: yellow perch (63%), white perch (18%), round goby (7%), and spottail shiner (6%). Across sample dates, species richness has ranged from 3 to 14. The Shannon diversity index is generally low (<1.50), due to low richness, and the catch being dominated by a few species. Our data suggests a seasonal, but stable aquatic environment with predictable changes in water quality and the fish community on an annual basis over the last five years. (**3**)

Dempster, Ruth-Ann*, Keyanna Safforld, and Christopher Kavanau East Stroudsburg University, East Stroudsburg, PA 18301. *Use of cylindrical topology self-organizing maps for reference-free rotational image alignment and classification*.- One of the great unsolved problems of molecular imaging of biological molecules is finding a technology to bring electron micrographs into a reference-free rotational alignment. We circumvented the dependence of subjective user- or computer-generated external or internal reference images used by other so-called “reference-free” techniques. Alignment is performed using an unsupervised self-organizing map configured on the surface of cylindrical arrays of artificial neurons. Although alternative alignment protocols often depend on an expert to adjust many ad hoc parameters, the technology described here instead achieves the minimization of one objectively calculated target function by varying only two free parameters. Because these self-organizing maps preserve the topological properties of the input images, the relative azimuths of dataset images are obtained directly from the array’s intrinsic cylindrical coordinate system by noting each mapped dataset image’s respective azimuthal coordinate placement around the cylinder. The technique was successfully tested on simulated data including 2-dimensional regular polygons. (**75**)

Dias, Kathlyn*, and André Walther Cedar Crest College, Allentown, PA 18104. *Identification of Replicatin Protein A phosphorylation dependent protein-protein interactions via Yeast Two Hybrid system*.- Dysfunction in proteins involved in DNA repair, replication, and recombination is linked to human cancers. Human Replication Protein A (RPA) is a highly conserved heterotrimeric ssDNA binding protein which participates in many of these pathways involving DNA and is homologous with RPA (encoded by the RFA genes) in the highly studied eukaryotic model organism, *Saccharomyces cerevisiae*. The RPA protein is composed of three subunits (70kDa, 32kDa, and 14kDa, encoded in yeast by the *RFA1*, *RFA2*, and *RFA3* genes, respectively), and the 32kDa subunit is phosphorylated in a cell-cycle and DNA damage dependent manner, suggesting that phosphorylation of RPA may regulate its function. This study attempts to identify protein interactions with RPA’s 32kDa subunit when either constitutively phosphorylated or dephosphorylated. Since RPA interacts physically with other proteins, a Yeast Two Hybrid Assay will be used to determine protein interactions in *Saccharomyces cerevisiae*. The system utilizes the *ADE2* reporter gene with five RPA variant-Gal4 binding domain fusion proteins mated against unknown cDNA yeast library protein-Gal4 activating domain fusion proteins. The RPA variants individually consist of wild type subunits of the 70kDa, 32kDa, and 14kDa along with two genetically modified subunits: hyperphosphorylated 32kDa and dephosphorylated 32kDa. Ten phosphorylation-dependent protein interactions with RPA have been identified through Y2H. Proteins found to have a phosphorylation-dependent interaction with RPA can potentially be utilized in cancer research and in further understanding DNA repair, replication, and recombination. (**54**)

Esposito, Abigail*, and Robert Kurt Lafayette College, Easton, PA 18042. *Studying the impact of lactate on the metabolic stress response in macrophages*.- Previously, we reported that macrophages at early tumor sites have a mixed phenotype with production of pro- and anti-inflammatory cytokines, decreased production of reactive oxygen species, a decrease in the ATP production rate, and a higher dependence on oxidative phosphorylation for ATP production. Since these macrophages could not be clearly defined as M1 or M2 we set out to characterize them further focusing on their metabolism. We observed an increase in the expression of genes associated with altered metabolism such as *ampk*, *glut1*, and *pkm2* in macrophages from the tumor microenvironment of BALB/c mice bearing the 4T1, 168 and EMT6 murine breast cancer cell lines.

Since it has been established that tumor cells experience an increase in glycolysis and therefore an increase in lactate production, which is referred to as the Warburg Effect, this study focused on whether lactate was able to induce expression of *ampk*, *glut1*, and *pkm2* in macrophages and whether this was associated with a metabolic stress response in macrophages in the tumor microenvironments. We found that lactate was able to induce expression of *ampk*, *glut1*, and *pkm2* in bone marrow-derived macrophages. Next, western blots were used to determine whether lactate treated macrophages were undergoing a metabolic stress response. For this purpose we screened expression of ATF4, eIF2, phosphorylated eIF2, and GCN2 which are associated with a metabolic stress response. We found lactate did not induce expression of ATF4 or eIF2, eIF2 was not phosphorylated by lactate treatment, but there was a slight increase in the expression of GCN2. These data imply that a metabolic stress response was not induced by treating bone marrow-derived macrophages with lactate. The next phase of this study is to analyze these proteins in tumor associated macrophages to determine whether a metabolic stress response is present in macrophages at early tumor sites. (**72**)

Finniff, Bridget*, and Angela Hess Bloomsburg University, Bloomsburg, PA 17815. *The Mechanisms Involved in the Development of Vemurafenib Resistance in Human Melanoma Cells*.- Cutaneous melanoma may not be the most common skin cancer; however, it is the deadliest. For patients with metastatic melanoma the survival rates drop to just 15%. Vemurafenib inhibits a specific mutation in B-Raf (V600E) found in the many metastatic melanomas. Although vemurafenib is somewhat effective in treating melanoma, resistance to the drug occurs at a frequent rate. Resistance to vemurafenib has recently been associated with increased EphA2 expression. EphA2 expression is associated with aggressive forms of melanoma and increased melanoma plasticity as characterized by vasculogenic mimicry (VM). This study explored the mechanisms involved in the development of resistance to vemurafenib by investigating changes in EphA2 expression and vasculogenic mimicry in resistant and non-resistant cells. The data collected so far demonstrate that A375P vemurafenib resistant (VR) cell line was partially resistant to vemurafenib and expression levels of EphA2 were slightly higher in the resistant cell line when compared with the non-resistant cell line. These experiments benefit cancer research because it aims to shed light on the mechanisms associated with vemurafenib resistance and provide insight into the development of new therapeutic approaches for the treatment of melanoma. (**56**)

Franges, Jared*, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Testing antiviral activity of baicalin against the mouse hepatitis virus protease*.- To date, there are seven known human coronaviruses (HCoVs) that cause disease. HCoV-HKU1, HCoV-OC43, HCoV-NL63, and HCoV-229E each cause the common cold. In the past twenty years, SARS-CoV 1, MERS-CoV, and SARS-CoV 2 have emerged into the human population and can cause severe lower respiratory symptoms and death. Treatments for these emerging viruses have been very limited until recently with the COVID pandemic. One of the drug targets for CoVs is the protease (3CLpro, Mpro, nsp5). It has been shown that components of the Chinese traditional patent medicine used to treat acute respiratory infections (composed of three herbal remedies) have antiviral activity against the SARS-CoV 2 3CLpro. It has not been tested whether these components have antiviral activity against the human coronaviruses that cause the common cold. In this study, we are testing the antiviral activity of one of these compounds, baicalin on the 3CLpro of mouse hepatitis virus (MHV, a model CoV), HCoV-OC43, and HCoV-HKU1. We are using chimeric CoVs that express the nsp5 protease from either HCoV-OC43 or HCoV-HKU1 in place of the MHV nsp5 in the MHV genome to test for antiviral activity. The project will determine whether the active ingredients in the herbal remedies have antiviral activity against the proteases from multiple human CoVs. (**35**)

Franzone, Katherine*, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining the role of Replication Protein A in the cellular response to chemotherapeutic drugs in Saccharomyces cerevisiae*.- According to the American Cancer Society, in 2022 there will be around 1.9 million new cancer cases diagnosed and over 609,00 people are expected to die from cancer-related causes in the United States alone. Current chemotherapeutic cancer treatments are non-specific and target actively dividing cells. This leads to damage in the patient's healthy cells, leading to unwanted side effects and decreasing the efficiency of the treatment. An increase in specificity of chemotherapeutic drugs would greatly reduce the death of healthy cells by treatment. To better understand the impacts of the DNA damage caused by chemotherapeutic drugs and how eukaryotic cells response to this stress, our project focuses on analyzing the effects of chemotherapeutic agents in the baker's yeast *Saccharomyces cerevisiae,* which has been used extensively as a model for human cells. Specifically, we have been analyzing the function of Replication Protein A (RPA), which is a highly conserved protein involved in DNA replication and repair in both humans and yeast. To dissect the function of RPA, our lab has previously generated strains that contain various mutations in the yeast RPA homolog, RFA, along with different known repair genes, and we have been examining the sensitivity of these yeast strains to DNA damage using spot assays to look at the survival of yeast on media (YEPD) with various concentrations of the chemotherapeutic agents campothecin and hydroxyurea. The differences in growth and survival rates of the various strains in the spot assays have allowed for preliminary conclusions to be drawn about the importance the various regions in RPA have in the cellular response to DNA damage caused by chemotherapeutic drugs. A clearer picture of RPA's role in DNA repair and its interactions with other genes will allow for a better understanding of the underlying causes of cancer and more specific chemotherapeutic drugs. (**48**)

Fritz, Everett*, Julia Kobusky*, Allie Shulskie*, Alana Andreoli, Cheyenne Jenner, and Kenneth Klemow Wilkes University, Wilkes-Barre, PA 18766. *Five-year assessment of the effectiveness of the Forestry Reclamation Approach on an anthracite mine in northeastern Pennsylvania*.- In spring 2017, a five-acre section of an anthracite mine previously reclaimed with grasses and forbs was recontoured and replanted with 5000 tree seedlings, following the Forest Reclamation Approach (FRA). The site was located in the Avondale section of Plymouth, PA, 8.8 km west of Wilkes-Barre. The property represents the northernmost FRA site in the United States. Beginning in fall, 2017, the success of the reforestation effort was monitored within forty-two 10m x 10m permanent quadrats arrayed throughout the site. Survival and growth of all woody plants were assessed annually within some or all of the plots depending on the year. Complete censuses were made in 2018 and 202l. Within each quadrat, seedlings were given specific X and Y coordinates for future reference. Data collected for each seedling within each quadrat included survival, height, microtopographic location, and predation status. The data were then compiled to analyze growth rates of species between microtopographic location of seedlings with their survival, growth rates, and predation. Plots typically contained 10-25 saplings. *Pinus strobus* and *Populus tremuloides* were the dominant species encountered, while the *Castanea* and *Quercus* species had fewer individuals, reflecting initial planting patterns. Survival of all species exceeded 90%, and individuals of all species showed appreciable growth. In particular, many individuals of *P. tremuloides* grew from <0.3 m tall in 2018 to >2 m tall in 2021, effectively converting the site from a rocky meadow to a tall shrubland. In addition to the success of the planted species, we observed plots into which other species – particularly *Robinia pseudoacacia* and *Rhus typhina* colonized – often in stem densities too high to record. Thus, after five years, the FRA conducted at the Avondale site appears successful, indicating that it is a viable reclamation strategy to use in the anthracite coal fields of northeastern Pennsylvania. (**93**)

Giletto, Martha*, and Austen Barnett DeSales University, Center Valley, PA 18034. *Examining the evolution of epidermal growth factor (EGF) pathway ligands in insects*.- The EGF pathway is a highly conserved and ubiquitously used cell signaling cascade in the development of many animals. In the highly studied Drosophila melanogaster, four ligands (vein, gurken, spitz, and keren) are used to activate the pathway while one ligand (argos) is used to repress activation of the EGF pathway. An arthropod centered phylogenetic analysis showed that the genes which encode the ligands Vein and Argos were present in the last common ancestor of all arthropods. However, this analysis showed the genes encoding Gurken evolved in the last common ancestor of the Diptera, the clade which includes flies. In continuation of this research, evidence was provided showing the orthologues of spitz and keren are the result of multiple independent gene duplication events. In an attempt to determine the ancestral role of the spitz/keren gene during insect development, we used RNAi targeting the orthologues of the genes in two separate lineages, Orthoptera and Hemiptera. These lineages are represented by the cricket Gryllus bimaculatus and the milkweed bug Oncopeltus fasciatus respectively. (**108**)

Gilla, Trisha*, and Frank Varriale King's College, Wilkes-Barre, PA 18711. *A comparison of dental microwear between two cusps from M1 tooth of <u>Mesodma</u> (Mammalia: Multituberculata)*.- Dental microwear analysis on extinct species can play an important role in determining their way of life and aid in evolutionary discoveries. Dental microwear is seen as scratches and pits on the tooth under the microscope. The current study was undertaken to compare microwear between two cusps (cusps 1 and 2) from M1 tooth in the multituberculate genus *Mesodma*. We hypothesized that there will be no significant differences between the cusps since they are both from the same tooth and under the same influence by occlusion with the lower 4th premolar. Eight specimens of teeth from the Raymond Alf Museum were examined for microwear. After digitizing the microwear using Microwear Version 4.02, lengths and widths of scratches were tested for normality via a Shapiro-Wilk test in PAST Version 4.09. Both the lengths and widths of scratches from two cusps were not normally distributed ($p < 0.05$). Therefore, a Mann Whitney test was used to compare the lengths and widths of scratches on the cusps. The lengths of scratches showed significant differences on 5 out of the 8 specimens ($p < 0.05$). In addition, the widths of the scratches showed significant differences on 6 out of the 8 specimens ($p < 0.05$). These preliminary results suggest that the dental microwear between cusps 1 and 2 may be different. Contrary to our expectations, the differences between cusps could be due to the small changes in tooth formation which can cause differences in size and shape in cusps. In addition, the two cusps might not be in opposing areas, which can show wear caused by attrition during mastication. Furthermore, there is a greater significant difference in the widths of the scratches, which could be due to the differences in pressure of the jaw as food was impressed between each cusp in *Mesodma.* (**103**)

Gorecki, Shannon*, Abigail Stocker*, 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 (2-hydroxyethyl), bis (6-hydroxoyhexyl), and bis (7-hydroxyheptyl) 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. The antioxidant properties were measured and compared with standard antioxidants using a FRAP assay kit. (**96**)

Greenberg, Samantha*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Exploring the relationship between ClearCode34 gene expression, race, and genetic ancestry as risk factors for racial disparities in renal cell carcinoma survival*.- Kidney cancer is a top ten cancer in incidence in the United States. Renal cell carcinoma (RCC) is the most common type (85%), while clear cell RCC (ccRCC) is the most common subtype (80%). African American (AAs) notably have lower ccRCC survival rates than European Americans (EAs). Certain genomic/transcriptomic factors have been identified as risk factors for ccRCC survival, and may drive this disparity. A gene expression profile called ClearCode34 was previously developed to distinguish between two subtypes of ccRCC, ccA and ccB. Patients with the ccB subtype are known to have lower rates of survival, higher rates of metastasis, and increased tumor size/grade. Genetic ancestry has been linked to lower survival for AA patients with other urologic cancers. Here we show that AA and EA ccRCC patients have different ccA/ccB subtype frequencies differentiated by both self-reported race and West African Ancestry (WAA). mRNA expression, survival data, and self-reported race were downloaded from The Cancer Genome Atlas (TCGA) Firehose Legacy cohort on cBioPortal as a discovery cohort. Genetic ancestry was calculated using STRUCTURE from The Cancer Genetic Ancestry Atlas to group patients with >70% and <70% WAA. Prediction Analysis of Microarray (PAM) in R was used to classify the ClearCode34 subtypes. GraphPad Prism analyzed survival data by comparing across subtypes and races or ancestry groupings. AAs and high WAA patients had significantly higher percentages of ccB-typed tumors. ccB-typed patients showed worse 5-year disease-specific survival rates than ccA-typed. However, these differences were not signficant between self-reported races and WAA groupings. Future directions include pathway analysis via Gene Set Enrichment Analysis (GSEA) to identify novel targets in AAs and EAs using a precision medicine approach. All significant findings will be validated in a Cooperative Human Tissue Network/Geisinger cohort. (**9**)

Greenwood, Kate*, Gabriel Castro*, Alexia Williams*, and Brian Gray York College of Pennsylvania, York, PA 17405. *Exploring differential circRNA expression in a model T cell line*.- Circular RNAs (circRNA) are covalently-bonded, closed-loop RNA structures with the ability to serve as potential biomarkers for various human pathologies, due to their presence and function within human immune cells. Several circRNAs have been identified in human peripheral blood mononuclear cells (PBMCs) showing differential expression patterns in disease states such as asthma, sepsis and lupus, suggesting a relationship between circRNAs and the immune response. Three circRNAs, hsa_circ_0049224, hsa_circ_005519 and hsa_circ_VMA21, were chosen from literature to determine their presence in T cells and investigate their genetic response. In order to assess the functionality of the experimental system, three other circRNAs associated with cell development were chosen from York College of Pennsylvania's primer library maintained by Dr. Sean Georgi. Selected circRNAs were hsa_PDE4B, hsa_circ_BANP and hsa_circ_HIPK3. These circRNAs were known to be present in T cells, the cell model chosen for this research. Jurkat T cells were chemically activated and/or suppressed with PMA/ionomycin and dexamethasone. The Jurkats were treated with dexamethasone to chemically suppress T cell activation, and/or phorbol myristic acid and ionomycin to chemically activate the T cells. In Jurkats after 24 hours of chemical treatment, none of the immunological circRNAs were expressed, no matter the treatment regimen. In contrast, we observed variable expression of hsa_circ_PDE4B with chemical treatments, and saw that Jurkats appeared to produce a variety of isoforms of hsa_circ_PDE4B in addition to the expected small circRNA product. These results suggest that the treatment may have induced alternative circRNA splicing, which may play a role in the immune response not previously documented. (**43**)

Grenier, Jazzlyn*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Expression of circPDE4B in human cell lines and chicken (Gallus gallus) retinal development*.- Circular RNA (circRNA) is a recently discovered genetic material where the 5' and 3' ends of one or more exons are covalently bound together. CircRNAs have been found to regulate gene expression and are tied to roles in neurodevelopment and retinal function. One circRNA, circPDE4B, is expressed in human retinal cells and regulates cellular proliferation in alveolar epithelial cells. However, the expression pattern of the linear and circular forms of PDE4B have never been studied across retinal development and in many human cell lines. The purpose of this study was to determine the expression of circPDE4B and PDE4B in multiple human cell lines and throughout the development of chicken (*Gallus gallus*) retina. PCR results showed that circPDE4B was expressed in HEK-293 (human embryonic kidney) cells, but not in U-87 (glioblastoma) cells, MDA-435 (melanoma) cells, or MCF-7 (breast cancer) cells while the linear form was expressed in each of the cell lines. This indicates that circPDE4B could have a role in HEK-293 cells. qPCR results showed that circPDE4B expression increased across chicken retinal development, indicating it may have a role in retinal development. However, the expression pattern was similar between the linear and circular forms of PDE4B, so there is likely no preferential splicing occurring from the linear to the circular form of the gene. Future research could aim to determine the function of circPDE4B in HEK-293 cells and developing chicken retinal cells. (**106**)

Guevin, Daniel*, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Development of a cell-based vaccine against pancreatic cancer*.- Pancreatic cancer is one of the deadliest and most rapidly proliferating cancers which makes it a prime target for treatment by immunization. An altered form of the cholecystokinin receptor (CCK2i4svR) that includes 69 amino acids in the third intracellular loop encoded by a retained intron (IV) is expressed by many aggressive pancreatic tumors. Our aim is to develop a vaccine that will activate host adaptive immunity to recognize this novel protein. We have engineered a tumor cell-based vaccine in which immortalized syngeneic cells express a derivative of the Simian virus 40 Large Tumor antigen protein (SV40 T ag) that contains a 20 amino acid insert corresponding to a unique sequence found in the CCK2i4svR pancreatic-cancer associated growth factor receptor. Immunization of mice with a synthetic peptide corresponding to the 20mer insert did induce peptide-specific CD4+ T cells in previous studies. C57Bl/6 mice were injected with the tumor vaccine cells (4A-1) or similar cells (B6/WT-19) that expressed unaltered SV40 T ag to elicit T cell responses against epitopes within the SV40 T ag and the CCK2i4svR sequence. An ELISPOT assay was used to detect epitope peptide-specific T cell responses in red cell-depleted splenic lymphocytes prepared from the animals. Target peptides included a known CD4+ epitope from SV40 T ag, the 20mer from CCK2i4svR, and a control HBV epitope. CCK2i4svR-specific responses were detected, but frequencies were inconsistent. We are currently testing whether immunity elicited by this vaccine can control the growth of orthotopically implanted murine pancreatic cancer Panco2 cells engineered to co-express the human CCK2i4svR variant. Groups of mice were immunized twice with either 4A-1 or B6/WT-19 cells before orthotopic implantation of the engineered tumor cells and proglumide therapy. Tumor progression/burden and immune status (ELISPOT) were monitored at 4 weeks. Tumor architecture and leukocyte infiltration will be assessed by immunohistochemistry and staining. (**57**)

Hanna, Donna*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *An interdisciplinary approach for establishing baseline conditions prior to dam removal in Bushkill Creek, PA*.- The proposed removal of four small dams in Easton, PA along the Bushkill Creek, a tributary of the Delaware River, has provided a valuable opportunity for baseline monitoring and establishment of reference conditions using historical information. One important principle in ecological restoration practice is to develop reference models for planning and communicating a shared vision of project targets. Reference models are best developed using multiple sources of information. Given that we are in the site assessment phase of the Bushkill Creek restoration project, the objective of this research was to establish a reference model and baseline inventory by collecting information on past and current conditions at the site. Monitoring data were collected from sites approximately 35 m upstream and downstream of dams and free-flowing reference sites located approximately 5 km upstream of all dams. Historical texts were used to understand the social significance of the dams and detect the type and degree of threats that have caused degradation in Bushkill Creek. Baseline monitoring results indicate that oxygen levels, macroinvertebrate diversity, and proportion of sensitive taxa are significantly lower upstream and downstream of dams in comparison with reference model reaches. The strong correlation between water quality and macroinvertebrates in this system implies that removal of the dams would lead to improvements in water quality, biotic integrity, and resilience in lower Bushkill Creek. Historical information on previous uses of the dams and their social significance to the Easton community can be used as a baseline to guide additional research for restoration of the human-ecosystem relationship in the Bushkill Creek. (**84**)

Hanson, John*, Kimberly Manning, and Jane Cavender Elizabethtown College, Elizabethtown, PA 17022. *SV40 T-antigen sensitization of human cells to erastin and cisplatin-induced death: apoptosis or ferroptosis?*.- Regulated cell death (RCD) is a necessary process for tissue regeneration, immune responses, and maintenance of proper homeostasis. RCD has been expanded to include processes such as apoptosis, necroptosis, pyroptosis and ferroptosis. The role of ferroptosis in cancer is an emerging area of study that has potential for anti-tumor therapies. Ferroptosis is an iron-dependent RCD that involves lipid peroxidation. Chemotherapeutics, such as cisplatin, have been shown to activate both apoptosis and ferroptosis in certain cell lines, thus providing a therapeutic target for combinatorial treatments. Since it is estimated that 15% of tumors are virally induced, elucidating the mechanisms of ferroptosis can provide targets for virally-induced cancer growth. This study aimed to extend the literature surrounding the sensitization of cells to apoptosis by SV40 T-antigen to include the oncoprotein's effect on ferroptosis. Specifically, human diploid fibroblasts cells, and clonal lines transformed with SV40 T-antigen were treated with the ferroptosis inducer erastin, or with the apoptosis-inducing chemotherapeutic, cisplatin. After drug treatment, apoptosis was monitored by cleaved caspase 3, and ferroptosis was indicated by the upregulation ASCL4 and/or CHAC1. ACSL4, Acyl-CoA synthetase long-chain family member 4, is essential for the increase of polyunsaturated fatty acid (PUFA) in the lipid membrane, which upon oxidation drives ferroptosis. CHAC1, ChaC glutathione-specific gamma-glutamylcyclotransferase 1 catalyzes the destruction of the ferroptosis inhibitor glutathione. Data has confirmed cleaved caspase 3 in cisplatin treated cells, indicative of apoptosis; however, preliminary studies have not detected increases in CHAC1 or ACSL4 RNA expression. With respect to CHAC1, it is possible that erastin inhibition of the xc- transporter, which exchanges intracellular glutamate for extracellular cystine, is complete. Thus, without cystine there is no production of the antioxidant glutathione, negating the need for CHAC1. Experiments are underway to confirm ASCL4 expression in erastin-treated cells to determine if HDF undergo the intrinsic ferroptosis pathway. (**71**)

Harlow, Gracie*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *A test of the enemy release hypothesis in the New Zealand mud snail, Potamopyrgus antipodarum*.- The New Zealand Mud Snail, *Potamopyrgus antipodarum*, has become a world-wide invader. One of the leading hypotheses for why some invasive species are so successful is the enemy release hypothesis which states that invasive species have the ability to outcompete native species because they are less susceptible to natural parasites and predators of their invaded regions. The purpose of this study was to determine if the New Zealand mud snail is released from its parasitic enemies in locations in the mid-Atlantic region of the United States. We sampled at least 200 New Zealand mud snails from each of the Little Gunpowder Falls River in Maryland and two populations from Spring Creek watershed in Centre County, PA. Each snail was measured and dissected to determine if they were brooding. If brooding, the number of offspring produced was recorded. Native snails from one site in Spring Creek were also collected and were subjected to bright light to induce cercarial emergence giving a crude infection rate. The results of this study yielded no natural parasites in the invasive New Zealand mud snails. These results suggest that New Zealand mud snails have escaped parasitism in its invaded range in the mid-Atlantic region of the United States. (**79**)

Hertel, Austin, Madison Heeter*, Mara Bestram, Ross Gibson, Gwendolyn Ciletti-Dougherty, and Steven Mauro Gannon University, Erie, PA 16541. *Genomic surveillance of Sars-CoV-2 variants enhances mitigation strategies and reveals viral evolution in a university campus context*.- Upon its discovery in December 2019, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has been responsible for millions of deaths globally having since been declared a worldwide pandemic by the World Health Organization (WHO). Similar to other RNA viruses, SARS-CoV-2 has an enhanced ability to consistently mutate, resulting in the proliferation of several variants of concern (VOCs) as classified by the WHO. The increased transmissibility, virulence, and decreased effectiveness of public health measures attributed to VOCs highlight the importance of genomic surveillance of SARS-CoV-2 in tracing the spread of mutants and elucidating the emergence of novel variants. Gannon University, located in Erie, PA. has undertaken surveillance for SARS-CoV-2 VOCs utilizing RT-qPCR and Next Generation Sequencing (NGS) to continually monitor their prevalence in those infected within the campus population. Like many industries, higher education has been negatively impacted by the COVID-19 pandemic. The results of this study provide insights into the impact of SARS-CoV-2 VOCs in a university campus environment and viral evolution in a distinct population. These findings have led to enhanced risk-aversion strategies at Gannon University to mitigate the impact of emerging SARS-CoV-2 VOCs. Furthermore, our results illustrate the potential for localized genomic surveillance to reduce the burden of a public health crisis in similar industries and in the general population. (**65**)

Holzinger, Shealyn*, Kathryn Sarachan, and Adam Cooke Wilson College, Chambersburg, PA 17201. *The effectiveness of sulfuretin as an antifungal chemical compound compared to clotrimazole on Trichophyton rubrum*.- Topical fungal infections are among the most prevalent and widespread diseases faced by humankind in today’s world. Current treatments usually include either topical creams or ingestible pills, yet the former are often ineffective and the latter result in unwanted side effects. This prompts a search for alternative antifungal chemicals that are both effective and safe to use. Recent research has indicated that aurones might possess antifungal capabilities, but no research indicates how aurones compare to standard antifungals. This research sought to compare an aurone (sulfuretin) to a common antifungal (clotrimazole) and compare their fungistatic and fungicidal abilities. Three different experimental tests were conducted: a Minimum Inhibitory Concentration (MIC) Assay and a Disk Diffusion Assay (DDA) were used to determine fungistatic ability, and a Minimum Fungicidal Concentration (MFC) Assay was used to determine fungicidal ability. The MIC and DDA revealed that sulfuretin possessed little to no inhibitory ability, and the MFC revealed that neither clotrimazole nor sulfuretin possessed fungicidal activity. In summation, these results showed that sulfuretin does not possess any fungistatic activity comparable to clotrimazole, nor did sulfuretin display the fungicidal activity clotrimazole lacks. Therefore sulfuretin would not make a good alternative to standard antifungal options used currently. While sulfuretin did not possess any antifungal properties, other aurones may. Further experimentation involving different aurone species is required in order to better understand the overall antifungal properties of the chemical group. (**61**)

Howells, Joshua*, Kathryn Sarachan, and Brad Engle Wilson College, Chambersburg, PA 17201. *Effects of post-treatment Lyme disease syndrome and potential causes*.- Lyme Disease is caused by the bite of either *Ixodes scapularis* or *Ixodes pacificus*, black-legged ticks found in North America. Their bite infects the host with the bacterium *Borrelia burgdorferi*. Individuals infected by *B. burgdorferi* experience symptoms of fatigue, musculoskeletal pain, a target-shaped rash at the site of the bite, and in severe cases migraines. Every year Lyme Disease affects 476,000 people nationwide and 10-15% of them will develop Post-Treatment Lyme Disease Syndrome (PTLDS). PTLDS is defined as prolonged symptoms, including joint pain, fatigue, and neurocognitive problems, for at least 6 months following the initial antibiotic treatment for Lyme Disease. PTLDS is estimated to affect over 2,000,000 individuals in the United States. No specific PTLDS biomarker has been found, making diagnosis and specific causes difficult to determine. Here, a correlation was sought between age of onset, antibiotics given, certain symptoms of initial Lyme, and time between infection and treatment of Lyme Disease with the diagnosis of PTLDS. Thirty surveys were received from twenty-two Lyme Disease patient who developed a PTLDS diagnosis and eight who completely recovered without further symptoms. Experimental factors were compared using t-tests. Preliminary analysis indicated that the presence of a rash was a statistically significant predictor of the development of PTLDS. Further research with a larger sample size is indicated to confirm these results. (**68**)

Jaber, Khoula*, Sydney Jones*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *FabI G93V substitution as one mechanism for triclosan resistance*.- The overuse of antibiotics and antimicrobials creates a selective pressure that encourages the growth of bacteria strains with genetic mutations conveying drug resistance. This is a growing concern in clinical settings where physicians seek to decrease infection. The use of triclosan, an antimicrobial added to a wide range of health and consumer products (e.g., hand sanitizers, soaps, toothpaste), was called into question and ultimately determined to be not generally recognized as safe and effective (GRAS/GRAE), and thus banned from use in products regulated by the US Food and Drug Administration (FDA). This significantly reduced its use in consumer products, yet its demonstrated accumulation in our environment. Thus, there is ongoing concern for bacterial resistance and studies are needed to better understand the genetic alterations that allow the growth of resistant bacteria. Triclosan targets the FabI enzyme in lipid biosynthesis and inhibits its NADH reductase activity, leaving the enzyme nonfunctional. A *fabI* gene mutation in *Escherichia coli* resistant strains has been identified, coding for a G93V or G93S substitution that alters the triclosan target site on FabI, blocking it from binding to inactivate the enzyme (Heath et al 1999). We have noted that this same mutation arises in laboratory-exposed strains of other bacteria species responsible for clinical infections (*Cronobacter muytjensii*, *Escherichia coli*, *Enterobacter cloacae*, and *Klebsiella aerogenes*) and have developed a PCR-RFLP assay that can be used to rapidly identify the underlying genetic mutation. Furthermore, we have noted the existence of strains with varied levels of resistance that do not contain this specific mutation, suggesting the presence of additional resistance mechanisms. We seek to further assess those strains, exploring other mechanisms of resistance such as *fabI* gene duplication, *fabI* gene overexpression, and efflux pump upregulation. (**49**)

Johnston, Madeline*, Brittany Hayden, and Jennifer Ness-Myers Messiah University, Mechanicsburg, PA 17055. *Establishing a developmental chemical hypoxia model in Danio rerio*.- Oligodendrocytes produce and maintain myelin in the central nervous system (CNS), enabling neurons to transmit axonal signals rapidly via saltatory conduction. During development, oligodendrocyte precursor cells (OPCs) respond to multiple environmental signals and intrinsic timing to initiate myelination. In the event of tissue injury, the myelination program is disrupted and results in a ‘maturation arrest’ and consequent defects in CNS myelin. Oxygen deprivation (hypoxia) during prenatal development is a common cause of white matter injury, which leads to cognitive and functional impairment. It is the purpose of this study to develop a new method of inducing hypoxia in developing zebrafish as a model for oligodendorocyte injury. Sodium sulfite is an oxygen-scavenger that can be used in aqueous solutions to reduce dissolved oxygen levels. Consequently, the solution parameters of sodium sulfite were evaluated for pH and dissolved oxygen (DO) stability over time. Additionally, zebrafish larvae at three days post-fertilization (dpf) were subjected to sodium sulfite-induced hypoxia at various concentrations and durations. Following hypoxia and a recovery period of 24 hours, RNA analysis of gene expression was performed via qPCR to detect changes in myelin gene expression. (**95**)

Johnston, Natalie*, and John Harms Messiah University, Mechanicsburg, PA 17055. *Optimization of a novel qRT-PCR assay for relative quantification of CCK2R splice variants in pancreatic cancer*.- Pancreatic ductal adenocarcinoma (PDAC) is a particularly aggressive cancer and its behavior is driven in part by the hormone, gastrin, via its preferential receptor, CCK2R. A splice variant of CCK2R, called CCK2i4svR, encodes a hyperactive receptor associated with elevated tumor growth, and arises from failure to splice the 4th intron. To test the hypothesis that relative abundance of CCK2R and CCK2i4svR expression will present prognostic value, we developed a novel SYBR Green qRT-PCR assay capable of differentiating the variant transcripts. Employed against RNA isolated from patient samples representing both PDAC and normal pancreas, primer-dimer and occasional non-specific amplification were observed in samples with low or no receptor expression. We hypothesized primer modifications and annealing/extension temperature optimization would eliminate these artifacts in no-template conditions. Analyses demonstrate that primer-dimer artifacts were heterodimeric. Artifact frequency was significantly reduced by slight modifications to each of three reverse primers while redesign of the shared forward primer significantly compromised selectivity against contaminating genomic DNA. Having validated the new primer combinations using no-template and plasmid-based qPCR, qRT-PCR analysis of a panel of control RNAs and low-expression samples is ongoing. (**50**)

Joyce, Isabella*, and Austen Barnett DeSales University, Center Valley, PA 18034. *Interrogating the roles of eye genes in an eyeless arachnid*.- Paleontological and neontological studies suggest that the last common ancestor of extant arachnids possessed at least three pairs of eyes. This character state is relatively stable, and exemplified in modern spiders. Non-arachnid arthropods possess a myriad of diverse visual systems. However, underlying this diversity is the observation that most studied arthropods utilize a conserved set of genes, termed retinal determination genes, to pattern their eyes during embryonic development. Eye loss is common amongst animals in cave or soil ecosystems. The mite *Archegozetes longisetosus* is a tropical, soil dwelling arachnid that has lost its eyes. Paradoxically, many of the conserved retinal determination genes are retained in its genome. Furthermore, RNAseq data suggest that these genes are actively transcribed during embryogenesis. To elucidate the role of these eye-patterning gene in an eyeless arachnid, we utilize *in situ* hybridizations to follow their expression patterns during embryogenesis. (**107**)

Justice, Rachel*, Lindsey Welch, and André Walther Cedar Crest College, Allentown, PA 18104. *Creating biodiesel using mutant versions of the oleaginous yeast, Cryptococcus neoformans*.- Fossil fuels are a main contributor to climate change as most people use them in their vehicles. Biodiesel, typically made from plants, is a much safer source of renewable energy that will not increase global climate change as it is carbon neutral. Yeast is a promising alternative to plants in the production of biodiesel. Not much information is known about most of the oleaginous yeasts currently being used to produce biodiesel. *Cryptococcus neoformans* is an oleaginous yeast that has its entire genome mapped out. In this research, oils were extracted from yeast using hydrothermal liquefaction and converted into fatty acid methyl esters, the main component of biodiesel, through an optimized series of reactions. In five strains tested, when looking at the top three fatty acid methyl esters produced, an average of 74.3% of the fatty acid methyl esters were unsaturated and 17.5% were saturated. The composition of the biodiesel is being compared to *Rhodotorula glutinis,* a similar oleaginous yeast strain. This research will demonstrate the reliability and consistency of hydrothermal liquefaction in the process of biodiesel production. The results from this research could propose a new type of yeast, *Cryptococcus neoformans*, to be used in the production of biodiesel. (**100**)

Keller, Caleb*, and Meda Higa York College of Pennsylvania, York, PA 17405. *The detection of SARS-CoV-2 RNA in wastewater to estimate COVID-19 occurrence at York College of Pennsylvania*.- COVID-19 is a contagious upper respiratory disease caused by the virus SARS-CoV-2, that has been classified as an international public health emergency. To mitigate the spread of COVID-19 at York College of Pennsylvania (YCP) during the spring 2021 semester, rapid antigen tests were used to detect the presence of virus in symptomatic individuals. Though somewhat effective, this strategy was less sensitive when compared to PCR virus detection methods and lacked the ability to sample the campus community widely and often. Because virus sheds into the feces of infected individuals, wastewater samples can be used to not only detect the scale of COVID-19 spread in a college community, but to track COVID-19 spread as well. The Wastewater Based Epidemiology (WBE) approach has proved to be effective in the past by providing early warnings of outbreaks of pathogenic viruses such as influenza. In this study, COVID-19 was detected by extracting SARS-CoV-2 RNA from wastewater samples via PEG 6000 precipitation and viral RNA extraction. A SuperScript® III First-Strand Synthesis System for RT-PCR was performed to visualize SARS-CoV-2 RNA presence via gel electrophoresis. RT-qPCR was performed to quantify SARS-CoV-2 RNA. This study recognized methodology optimization that may be beneficial to other researchers attempting to trace virus spread via WBE. Our study displayed the scale of COVID-19 outbreak in the YCP student population by indicating specific locations on campus where more individuals were infected with COVID-19 within a respective timeframe. We were also able to develop and optimize a WBE methodology for YCP to use for future outbreaks of any disease. If used in conjunction with college administration and YCP Health Services, this approach could help combat disease spread within the college community by quickly identifying groups or locations on campus in need of further testing. (**41**)

King, Erin*, and Ann Yezerski King's College, Wilkes-Barre, PA 18711. *Molecular genetic evidence for the existence of a hybrid cross between Largemouth bass, Micropterus salmoides, and Smallmouth bass, Micropterus dolomieui*.- Hybridization causes alleles to move from one gene pool of a species to another, causing issues with extinction, competition, and fitness of the ecosystem. Recently, a pond microecosystem near Afton, New York was found to have unusual looking bass that seemed to be hybrids between Largemouth bass (*Micropterus salmoides*) and Smallmouth bass (*Micropterus dolomieu*) which has rarely been reported in the literature. For this study, seventy-two bass fin clip samples were obtained and subjected to genetic testing by three different approaches. In this pilot study, the autosomal Recombination Activating Gene (*RAG1*) was used to assess evidence of heterozygosity. The mitochondrial *cytb* gene was used to determine the species of the mother. Finally, microsatellites will be used in the future to determine exact paternity and maternity to better refine the population structure. The results of the *RAG1* and *cytb* genes suggested that the genetic make-up of these fish is not as simple as a single hybridization event. Further data from additional genes in addition to phenotypic measurements using ImageJ will hopefully not only answer questions about the species' origins of these fish, but also serve as a foundation for ecological studies on the effects of hybridization. (**20**)

Kleb, Sarah*, and Jodi Lancaster Elizabethtown College, Elizabethtown, PA 17022. *The effect of Poly(I:C) and IFN-α on the immune system as Observed through IL-12 production in dendritic cells*.- Activation of dendritic cells (DCs) through toll-like receptor (TLR) agonists causes release of cytokines. DC2.4 cells are immature murine DCs derived from the bone marrow that express TLRs, including TLR3. The response of DC2.4 cells to varying doses and times of the TLR3 agonist, poly(I:C), were conducted. In contrast to previously studied MuTu DCs, DC2.4 cells produced little to no interleukin-12 (IL-12) after 12-hour exposure to doses from 1-1000 μg/mL poly(I:C). This was surprising because literature suggests that the expression of TLR3 dramatically increases when DCs are maturing, which should occur upon poly(I:C) exposure. Once fully mature, DCs receive inflammatory signals to reduce TLR3 expression. Treatment of DCs with interferon-a (IFN-α) has been found to enhance IL-12 production by increasing TLR3 expression. DC2.4s exposed to IFN-α prior to poly(I:C) treatment also failed to produce IL-12. Experiments using lipopolysaccharide (LPS) confirmed that the cells can make IL-12 through activation of the TLR4 pathway. Ongoing studies are investigating the functionality of the TLR3 pathway in the cells. Luciferase assays with IFN-β plasmids are being conducted to confirm the presence of a functional TLR3. Western blotting and immunofluorescence are also being explored to qualitatively determine whether the DC2.4 cell line expresses TLR3, as reported in literature. Analysis of TLR3 levels and production of IL-12 by DC2.4s allows for greater understanding of how different lab-derived lines of DCs exhibit responses to TLR agonists. Additionally, the maturation status of the lab's DC2.4 cells is being considered. (**66**)

Klopp, Elijah*, M. Dana Harriger, Sonny Bleicher, and Katherine Mertes Wilson College, Chambersburg, PA 17201. *Use of camera collars to monitor reintroduction risks to Oryx dammah, scimitar- horned oryx*.- The scimitar-horned oryx (*Oryx dammah*) is a species of oryx that is extinct in the wild primarily due to human disturbance, over-hunting, drought, and livestock overgrazing. Present reintroduction efforts of captive raised oryx have been successful to the enclosed Ouadi Rimé-Ouadi Achim Game Reserve in the African republic of Chad. This region is within the native habitat of scimitar oryx, spanning between the savannah habitat of the Sahel, and the Saharan Desert. Successful reintroduction will depend on monitoring for potential risks such as disease transmission, predation, and resource depletion. This study evaluates one of the most comprehensive methods to monitor large game species with camera collars. Three focal oryx (a breeding male and two females) were fitted with collars at the Fossil Rim Wildlife Center in Glen Rose, Texas between April and May, 2019. A total of 78 captured videos for each individual were uploaded and analyzed using Behavioral Observation Interactive Software (BORIS). Using this software, we compared the interactions of the focal animals with a list of cohabitating species at Fossil Rim. The two females, one older and one younger, were more social than the male. The older female encountered more, and spent more time with, both conspecifics and other species than the younger one. All three oryx spent significantly more time with conspecifics (including an Arabian oryx) than with competitors or humans. The results of this study, supported by field observations, demonstrates that camera collars are a useful tool for monitoring risk encounters and social behaviors of captive oryx and would be effective for the monitoring of oryx into a reintroduced environment. (**7**)

Kowalski, Rae Ann*, Jared Fagan*, Colin Olson, Zachary Buchman, Nicole Schwab, Jenna Kunst, Rajinikanth Mohan, and Michael Foulk Mercyhurst University, Erie, PA 16546. *Metagenomic analysis of contaminated soils near Erie Coke Corporation in Erie, PA*.- Legacy industrial activities of the last century left an indelible mark on surrounding communities. In downtown Erie, PA, the Erie Coke plant produced coke products for the steel industry for the better part of the last century. We hypothesized that this intensive industrial activity resulted in contamination of soils near the plant, changing their microbial community. Samples were collected near the fence line of the plant. To test the impact on nearby neighborhoods, samples were collected in the median of a roadway near the plant. A control sample was collected from a remote site. Two biological replicates were collected at each site. Chemical analysis revealed that the Erie Coke and nearby neighborhood samples contained elevated levels of polycyclic aromatic hydrocarbons (PAHs) compared the control. Interestingly, the roadway median sample contained more PAHs than the Erie Coke sample. This could be due to the additional contamination from automobiles using the roadway. To investigate the microbial community structure, DNA was prepared from the samples and sent for Illumina sequencing. Preliminary analysis revealed that the bacterial communities in the three samples were substantially similar, but with subtle differences. The samples were dominated by Proteobacteria and Actinobacteria, with other domains contributing less than 1% to the community structure. Both contaminated soils exhibited a moderate shift from the Proteobacteria to Actinobacteria with the Erie Coke sample showing a larger shift. Within the Proteobacteria, alphaproteobacteria were depleted and both betaproteobacteria and gammaproteobacteria were increased relative to the control sample. Further analysis will be devoted to understanding the effect on the changed microbial community on the most prominent biochemical pathways present in the samples. (**28**)

Kumar, Nidhi*, Brennan Gerancher, Jared Franges, and Dia Beachboard DeSales University, Center Valley, PA 18034. *Coronavirus cleavage of host proteins using the nsp5 protease*.- Innate immunity is the first line of defense against viruses. When an RNA virus enters the host cell, it can be detected by RIG-I-like receptors in the host cell cytoplasm. The receptors will then signal to the nucleus to induce antiviral genes. To successfully replicate, viruses must either avoid being detected or block the induction of the antiviral genes. We know that Coronaviruses are detected by the host cell but that the antiviral genes are not induced. One of the ways viruses can evade the detection pathway is use viral proteases to cleave the proteins in the signaling cascade. We use the model coronavirus mouse hepatis virus (MHV) for these studies. We hypothesize that the MHV main protease, nsp5, is cleaving host proteins to block the induction of antiviral genes. We have performed *in silico* protease digests of proteins within these signaling pathways and identified 5 candidate proteins that could be cleaved by MHV nsp5. We are cloning these genes from mouse cells and tagging them. This will allow us to easily detect cleavage products. Ongoing work will then determine whether these proteins are cleaved by the virus protease and the outcome of that cleavage on innate immune signaling and virus replication. (**36**)

Landry, Alianna*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *The expression of linear and circBANP in developing chicken (Gallus gallus) retinal tissue and human cell lines*.- Cancer is a devastating disease that affects many people around the world. Although there are many treatments available, which are dependent on factors such as stage and type of cancer, there is no cure for most forms of the disease. One important way to take a step forward in treatment is to fully understand all the components of the disease, including novel genetic elements, such as circRNAs. circRNAs are a fairly recent discovery, and are generated as a result of joining the 3' and 5' ends of an RNA molecule. Although the functions of some circRNAs have been determined, the function of most circRNAs is still unknown. One circRNA, circBANP, has been found in several types of cancers. In order to further understand circBANP expression in other cancers, as well as in normal development, this study analyzed the expression of linear and circBANP throughout embryonic development of the chicken (Gallus gallus) retina, as well as determined the expression of linear and circBANP in various human cancer cell lines. To analyze the change in expression of linear and circBANP in the developing retinal cells, qPCR was used. Additionally, gel electrophoresis of PCR reactions of linear and circBANP in human embryonic kidney cells (HEK-293), glioblastoma (U 87), melanoma (MDA 435), and breast cancer (MCF 7) cell lines were also performed to determine whether the genes were expressed. The results showed that linear BANP decreased as development progressed, whereas circBANP did not have any significant changes in expression. Gel electrophoresis also concluded that linear and circBANP are expressed in HEK-293, U 87, MDA 435, and MCF 7 human cell lines. These results provide promising potential starting points for further research in which the function of circBANP could be determined in chicken retinal development as well as in the tested human cell lines. (**105**)

Lopez-Soliz, Maurice*, Ashly Ramos*, Stephanie Soto Mangandi*, Joseph Tetreault, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Development of a naturally derived hydroponic nutrient solution from recirculating aquaculture system effluent using batch vermifilter reactors*.- Population growth, decreasing farmable land, and water scarcity have increased demand for decentralized, safe, and healthy fresh food. Recirculating aquaculture systems (RAS) provides location-independent, intensive seafood production in food deserts. Commercial RAS success is currently limited by the production of nutrient-dense effluent that requires costly waste treatment to prevent polluting natural waterways. Prior research has identified that the effluent contains all essential plant nutrients and could be reutilized as a hydroponic nutrient solution. If an efficient treatment method to remove organic matter (OM) and mineralize particulate-bound nutrients is developed, this can transform the effluent into a value-added commodity for resale. Vermifiltration utilizes earthworm metabolic processes in conjunction with microbial communities to break down wastes and has been shown to remove OM and mineralize solids in other agricultural industries. This research characterizes the degree of solids reduction, nutrient mineralization, and OM removal in RAS effluent achieved by pilot-scaled vermifilter batch reactors for reuse as a naturally derived hydroponic nutrient solution. Results presented include the reduction rate of total suspended solids (TSS), chemical oxygen demand (COD) concentrations and total nutrient mass mineralization for all essential plant macro and micro-nutrients. Vermifilter effectiveness is determined by TSS and COD reduction rate and total nutrient mineralization compared to an aerobic microbial control. This research provides foundational data for developing a nutrient economy in the RAS and hydroponic industries to support a closed-loop, integrated, and intensive farming system for increased food security. (**85**)

Madden, Ellen*, Mia Krevh*, and Quyen Aoh Gannon University, Erie, PA 16541. *The Role of trans-Golgi Network and Endosomal Adaptors in Growth of Saccharomyces cerevisiae*.- In the yeast *Saccharomyces cerevisiae*, trafficking of a variety of proteins between the cell surface, *trans*-Golgi network (TGN), endosomes, and vacuole is regulated by clathrin adaptors. In this study, we focused on the role of the TGN-endosomal clathrin adaptors Gga1, Gga2, AP-1, Ent3, and Ent5 on the nitrogen-regulated growth of *S. cerevisiae*. Evidence suggests that the trafficking of the major amino acid and nitrogen permeases used for cell growth are regulated by these clathrin adaptors. We hypothesized that distinct combinations of adaptors may regulate nitrogen permease trafficking under different nitrogen conditions, leading to distinct effects on cell growth. To discern the role of clathrin adaptors in nitrogen-regulated growth, we have constructed various single, double, and triple clathrin adaptor deletion mutants and tested their effects on growth in preferred and non-preferred nitrogen sources. Growth assays were performed in 96 well plates and growth curves were plotted to visualize the differences in growth rate in mutant vs. wild-type cells. Our results show that the single deletion of either *ent3, ent5,* or *apl2* (AP-1 subunit) did not impact cell growth in preferred or non-preferred nitrogen sources. Double deletions of *ent3* and *ent5* but not *apl2* with *ent3* or *ent5* had reduced growth in cells in both preferred and nonpreferred nitrogen sources. A triple deletion of *ent3*, *ent5*, and *apl2* had the greatest growth defect in both preferred and nonpreferred nitrogen sources. These results suggest that Ent3 and Ent5 are functionally redundant and complementary to AP-1 function, and that cell growth requires AP-1 and Ent3 or Ent5. Moreover, these clathrin adaptors' role in cell growth is not linked to their function in regulating specific nitrogen permeases and suggests a more general function in cellular processes that may affect metabolism and/or cell cycle regulation. (**42**)

Marks, James*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Comparing active DNA demethylation in lung cancer patients with high and low west african ancestry*.- Lung cancer remains the leading cause of cancer-related death in the United States. Across all racial demographics, African Americans (AAs) have the highest lung cancer mortality. Studies have shown distinct DNA methylation patterns in AAs with cancer, highlighting a potential biological factor that influences disproportionate lung cancer mortality rates. AA-specific hypermethylation has been identified in many cancer types including prostate, bladder, and head and neck cancers. Active DNA demethylation pathways, like those involving the TET family of proteins, may play a role in the dysregulation of DNA methylation. Additionally, West African Ancestry (WAA) is a biological determinant that has been associated with survival and aggressive tumor biology. Active DNA demethylation varies between lung cancer patients with high and low WAA. Using cBioPortal, clinical, demographic, and Illumina mRNA-sequencing data for active DNA demethylation enzymes from patient samples were downloaded. STRUCTURE data for global genetic ancestry were downloaded from The Cancer Genetic Ancestry Atlas (TCGAA) and merged with other data. Differential gene expression analyses were performed by race and by genetic ancestry status as high WAA (>78%) or low WAA(<78%) based on the median WAA of the AA cohort. Disease-specific survival by expression stratified by WAA ancestry was calculated using GraphPad Prism 9.0. AA patients in the cohort had higher median expression of *TET2* and *SMUG1*. *SMUG1* and *TDG* had higher median expression in individuals with high WAA. Patients with high WAA had worse disease-specific survival across all analyses when compared to individuals with low WAA. Genes involved in DNA demethylation show differential expression across race and WAA status. Further, individuals with high WAA had worse disease specific-survival. A future direction is to explore the functional relationship between WAA and active DNA demethylation pathway inhibition in lung cancer cell lines with high and low WAA. (**12**)

Marrero, Zee*, Jeanne R. Berk, and Audrey J. Ettinger Cedar Crest College, Allentown, PA 18104. *The effect of lighting conditions on the ability to consistently determine presumptive drug test results*.- Presumptive drug testing is a way to rapidly test for the presence of specific chemical groups in unknown chemical compounds. It is used in forensic science to establish a putative identity of a drug at a crime scene. These tests are often performed outside the laboratory by law enforcement officials. Therefore, it is important to establish whether test results can be read consistently outside the lab. Color perception may vary across individuals, lighting conditions, and sample concentrations, and sample identity may be most difficult to determine for compounds yielding products of similar color. We chose aspirin, chlorpromazine, and doxepin for testing using the same presumptive drug test, the Marquis reagent, because these compounds yield similar colored products. Photographs of the reactions were taken under identical lighting conditions and then were systematically altered using editing software (Lightroom) to simulate different lighting conditions. Human subjects were shown the edited photographs and asked to compare them in several formats to test their ability to differentiate between presumptive test results. The same photos were compared using two smartphone applications to determine their ability to distinguish between them. In this analysis, L*A*B* values were used to calculate the color measurement from each application and a threshold was set for determining if the perceived value was correct in comparison to our directly measured color value. The results showed that lighting conditions have a strong influence over the ability of a smartphone camera to differentiate which chemical compound is being displayed. This suggests that smartphone apps may not be able to identify the results of a presumptive drug test accurately and consistently. Additional color identification technology may be required for accurate assessment of presumptive chemical tests in the field. Human trials will show if the human eye can distinguish between the edited photos more effectively. (**109**)

Martin, Ciara*, Coby Rush*, Carl Tyce*, and Alexander Krupka* DeSales University, Center Valley, PA 18034. *Development of a novel low-cost apparatus for assessing thermal nociception in the rat*.- The purpose of this project is to develop an affordable, accessible, and reliable apparatus for precisely assessing the tail-flick nociceptive response in laboratory rats. A response is invoked via infrared laser stimulation and measured by the experimenter or through an automated detector designed using off-the-shelf electronics (Arduino Uno) An infrared laser provides a transient noxious stimulus, and the apparatus was designed using simple construction materials, including custom designed 3D printed components. This results in a design with greatly reduced costs, precise materials, and easy distribution/sharing. We selected an 820 nm infrared laser diode for our design, chosen because it produces a near-infrared wavelength beam of low intensity capable of activating both Aδ and C thermal nociceptors. Further, by marking the tail with an opaque black dye (India Ink) and focusing the laser at this point we can achieve a more salient stimulus at lower power (60-150mW) improving safety for the rodent and experimenters. We hope this project will make thermal nociception assessment cheaper and more widely available, especially to institutions with limited research budgets. By creating an apparatus and procedure that is both affordable and accessible, the ability to test stress in rodents becomes accessible to smaller laboratories with lower funding. It also makes nociception testing in rodents more reliable than alternative methods by establishing constant parameters, as well as utilizing electronic timing. Furthermore, the low cost of this apparatus makes it accessible to many teaching environments, allowing students to get hands-on experience with high-tech equipment and exposure to other STEM concepts such as circuitry, 3d printing, and more. By designing this affordable, accessible, and accurate system, researchers have new ways to analyze stress on laboratory rodents. (**111**)

Mason, Stephen*, Vaughn Shirey, Lauren Ponisio, and Jon Gelhaus Immaculata University, Immaculata, PA 19345. *Responses from bees, butterflies, and ground beetles to different fire and site characteristics: A global meta-analysis*.- Climate change in concert with fire suppression is increasing the size, severity and frequency of fires globally. At the same time, insects, an exceptionally biodiverse group that provide essential ecosystem services such as pollination and decomposition, are declining precipitously. We know little, however, about the fire mechanisms that contribute to insect decline. To understand if there is a larger global signature of fire on insect communities, we conducted a global systematic search and meta-analyses on the pyroentomology literature for butterflies (Lepidoptera: Rhopalocera), bees (Hymenoptera: Apoidea), and ground beetles (Coleoptera: Carabidae) and report how each taxa's richness and abundance response to overall fire, 16 different fire and site characteristics, as well as fire combined with forest/grassland management treatments. Across 100 studies and 445 effects, we found that bee biodiversity increased after fire and fire in combination with forest/grassland management treatments. In contrast, fire had no significant positive or negative effect on ground beetle and butterfly biodiversity. Furthermore, we did not find any fire and site characteristics that decreased richness across our taxa. Surprisingly, we found that only 7% of the studies quantified fire severity, which likely explains the inconsistent results within the pyroentomology literature. We conclude that further consideration of fire mechanisms will advance our understanding of how insects respond to fires. Our findings on how each taxa's richness and abundance respond to each fire and site characteristic will create a stronger foundation to help scientists and conservation managers make better decisions and predictions to achieve their research and management goals. This presentation will focus on our recent pyroentomology publication found here: https://doi.org/10.1016/j.biocon.2021.109265 (**8**)

Masters, Ashlynn*, and Cynthia Keler Delaware Valley University, Doylestown, PA 18901. *The evolution of resistance: how quickly do bacteria evolve antibiotic resistance?*.- Bacteria can evolve resistance to antibiotics through both mutations in their genome and lateral gene transfer. In this experiment, antibiotic resistance was observed through the development of mutations after continued exposure to antibiotics. Three different species of bacteria (*Pseudomonas aeruginosa, Staphylococcus aureus*, and MRSA) were tested against five different antibiotics (Penicillin, Daptomycin, Ciprofloxacin, Sulfamethoxazole/Trimethoprim, and Tetracycline) using the standardized Kirby-Bauer Disk Diffusion Method. The colonies growing closest to the disc were then transferred and subjected to another round of exposure to the antibiotic. This process was repeated for 8 to 15 rounds of exposure. The *Pseudomonas aeruginosa* developed resistance to all of the antibiotics except for ciprofloxacin, the MRSA developed resistance to only penicillin, and the *Staphylococcus aureus* did not become resistant to any of the five antibiotics tested. (**25**)

Matthews, Mikayla*, John Minora, and Christopher Brey Marywood University, Scranton, PA 18509. *Chemotaxis as a novel paradigm for assessment of mutant behavior*.- Chemotaxis has long since been a vehicle through which biologists have studied traits of genetically ideal organisms, such as the nematode *Caenorhabditis elegans.* The use of a chemotaxis assay technique, which measures an organism's ability to sense and travel towards food odor sources, can be used to monitor and experiment with different chemotaxis rates of organisms and their mutant strains. This assay can be used for a wide array of different studies. The most recent and most interesting types of investigation utilizing chemotaxis assays have been experiments into the genetics behind chematosensory functions, and even the inheritance of these genes. In order to pursue more advanced experiments such as this in Marywood's lab, we first wanted to establish a scale by which the mutant strains of *C. elegans* in this lab could be measured for chemotaxis. Wild type N2 strains were assayed for their rate of travel towards a known attractant odor, diacetyl. Also tested were a mutant strain that is deficient in its ability to sense diacetyl, and a mutant which phenotypically displays deformed morphology that impacts its locomotive ability. Finally, there is a mutant strain that Marywood's lab is focused on, *klf-3*, which was also assayed; this is a mutation which saddles the organism with increased body fat with a high homology to the human *klf* family of genes whose mutations can cause diabetes and obesity. We hypothesize that these mutant worms which are stricken with obesity, will still display a high chemotaxis rate similar to that of wild-type N2 worms, rather than a lower chemotaxis rate as displayed by the mutant control strains. (**23**)

Mazza, Samantha*, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087. *Flow cytometric and microscopic analyses of antimicrobial properties exhibited by protein extracts purified from Eisenia hortensis*.- Antimicrobial resistance has become a major issue in recent years due to the liberal and improper use of antibiotics leading to antibiotic and antimicrobial resistance. Alternative antimicrobial therapies are thus in need of discovery and development to combat this issue, including but not limited to, invertebrate sources. Earthworms lack adaptive immunity, but have been able to survive and mount efficient non-specific defense responses against pathogens due to elements of their robust innate immune system including cellular responses such as phagocytosis by coelomocytes, and chemical responses mediated by lysozyme, antimicrobial peptides, and agglutinating components found in the coelomic fluid. This study used flow cytometry and microscopic methodologies to investigate the antimicrobial effects of a crude protein extract isolated from the earthworm *Eisenia hortensis.* Both cell morphology and viability of the bacterium *Bacillus megaterium* were examined. Using the cell viability dye propidium iodide (PI), preliminary flow cytometry results obtained from duplicate experiments showed significant cell killing ($p < 0.05$) occurred when *B. megaterium* was treated with either a high (2.5 mg/ml) or a low (1.25 mg/ml) concentration of extract for 2 hr. The high concentration exhibited cytotoxicity between 26-37%, whereas the low concentration showed killing between 19-38% in assays A and B, respectively. Fluorescence and phase contrast microscopy revealed that following exposure to the extract for 4.5 hr, bacterial cells exhibited noticeable differences in light refraction, substantive clumping, and high levels of PI uptake compared to untreated controls. Future studies aim to focus on purification of the specific protein(s) responsible for the observed cytotoxic effects in the antimicrobial earthworm extract. (**26**)

Minton, Russell*, and Kathryn Perez Gannon University, Erie, PA 16541. *Microbial associations with Metcalf's Tryonia, Tryonia metcalfi (Gastropoda: Cochliopidae), an imperiled ciénega endemic*.- The Chihuahuan Desert ciénegas are a hotspot for imperiled organisms including freshwater springsnails and bacteria. Many of these taxa are endemic to the desert and to the individual waterbodies where they occur. Efforts to conserve diversity in these threatened areas must account for the life history of the organisms, but also interactions between organisms including microbes. We documented the microbial assemblage associated with *Tryonia metcalfi*, a critically imperiled freshwater snail endemic to a ciénega system in western Texas. We identified 14 bacterial families in our snail samples and determined a core assemblage of 19 bacterial taxa, four of which represented novel lineages, that are likely dependent on the snail. Future conservation efforts involving *T. metcalfi* and its environment should therefore consider the microbial diversity associated with both the snail and the ciénega. (**77**)

Mitchell, Michaela*, Collin Olson, Nicole Schwab, Jenna Kunst, Zach Buchman, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *Analysis of polycyclic aromatic hydrocarbon pollution in Erie*.- The Erie Coke plant near Lake Erie has been a source of toxic chemical waste for many decades. Now that the plant has been shuttered, we explored possible lingering effects of the toxic compounds- primarily polycyclic aromatic hydrocarbons (PAH) at various land and water sites near the Erie Coke plant using Gas Chromatography- Mass Spectrometry. We found that the significantly high levels of chemicals-including benzo-ene compounds, chrysene, fluoranthene, naphthalene, phenanthrene and pyrene- were found in the immediate vicinity of the plant and much less contamination was detected in the land areas nearby. However the lakeshore near the Coke plant showed substantially high levels of some of these compounds suggesting a potential threat of exposure to humans and wildlife. We also discuss data which explains one possible mechanism of reduction of the toxic residues within the community. (**83**)

Monostra, Megan*, and Vinayak Mathur Cabrini University, Radnor, PA 19087. *Identification of horizontal gene transfer between Caudovirales bacteriophages and bacteria for the hemolysin-coregulated protein*.- This study seeks to investigate the genetic phenomenon of horizontal gene transfer (HGT), specifically involving interactions between bacteriophages and their host bacteria. From a biological perspective, this type of horizontal gene transfer occurs when bacteriophages attach themselves to a bacterial cell and inject it with a vector such as a plasmid that integrates into the host genome. In this study we developed and utilized an analysis pipeline written in Python that automatically identifies instances of HGT between phage and bacteria. We focused on the hemolysin coregulated protein (Hcp) that is part of the bacterial type VI secretion system and has a role in bacteriophage tail tube formation. A total of 53 Hcp protein sequences in Caudovirales bacteriophages were retrieved from NCBI. A majority of these belonged to the Myoviridae family of Caudovirales bacteriophages. 29 out of the 53 sequences showed evidence of HGT with bacterial pairs. Phylogenetic analysis of the Myoviridae phages indicated a clade organization that supports the pattern of horizontally acquired genes. The results provide evidence of extensive horizontal gene transfer between bacteria and bacteriophages pairs. Further analysis of the results will help us in understanding the functional role of HGT and the evolutionary dynamics of this study system. (**19**)

Morrill, Kayla*, Riley Moore*, Katie Hollen, Alexandra Gates, and Diane Bridge Elizabethtown College, Elizabethtown, PA 17022. *A survey of Hydra species in selected south central Pennsylvania lakes, and differences between species in dispersal-related behavior*.- Species of the genus *Hydra* are freshwater invertebrates present in lentic ecosystems around the world. Research on the phylogeny and biogeography of the genus has identified four species groups. However, relatively little work has been done on *Hydra* ecology during the last forty years, even though the freshwater habitats where *Hydra* are found are often substantially impacted by human activities. Our project aimed to characterize the distribution of *Hydra* species in selected lakes in south central Pennsylvania. We sampled six lakes within Lancaster and Dauphin counties. Based on preliminary sampling of a lake on the Elizabethtown campus, we hypothesized that the species *H. oligactis* and *H. vulgaris* would be present in all locations. Plant material was gathered from lake bottoms near shore and examined for *Hydra* using stereoscopic microscopes. *Hydra* species were identified based on bud morphology and structure of nematocysts, and detection probabilities for each species were estimated using the program MARK. *Hydra* were found from all four species groups and at all six locations, although the lakes varied in size, dissolved oxygen levels, and whether an inflowing stream was present. *Hydra* are often found attached to aquatic plants or other substrates but can also float at the water surface. In culture, floating occurs in response to low food availability. We established clonal cultures of the four species collected and determined the fraction of animals floating during a period of seven days without food. Four replicates of 20 animals each were monitored for the species *H. oligactis*, *H. vulgaris*, *H. viridissima*, and *H. hymenae*. *H. hymenae* showed a significantly lower rate of floating than representatives of the other species. This difference has potential implications for dispersal of these different species. (**4**)

Mukherjee, Sohini*, and David Andrew* Lycoming College, Williamsport, PA 17701. *Parameter optimization of EthoVision XT® for automated quantification of spontaneous grooming behaviors in Drosophila melanogaster*.- Neurodevelopmental disorders such as Fragile X syndrome (FXS) are central areas of research due to their high prevalence and severe health and behavioral consequences. Understanding the genetic and cellular causes of intellectual disorders like FXS can help researchers bridge the gap between the causes of genetic diseases and treatments. In humans, FXS occurs due to a loss of function mutation in the *FMR1* gene. *Drosophila* that are mutant for the *FMR1* ortholog, *drosophila mental retardation 1* (*dfmr1*), are used as a model for FXS and have been shown to exhibit human-like repetitive behaviors in the form of excessive grooming. Quantifying excess grooming is typically done by manually scoring methods. The process is time consuming and subject to scorer bias. We have been developing an automated scoring method that relies on EthoVision® software. Initially, we built a dataset of manually-scored videos to use as a benchmark for comparing automated scores and performed an interrater reliability test to ensure the identification of grooming bouts among different scorers. Grooming bout identification was typically consistent regarding the percentage of time identified as grooming, but the grooming bout lengths and number often varied between scorers. We are currently focusing on identifying the optimal parameter settings of EthoVision® software to generate automated grooming scores most similar to manual scores. We have worked with an array of activity and movement setting threshold, which the software uses to identify grooming motions. Our results have shown that an activity setting of 16 along with a movement threshold of 0.05 cm/s and an activity threshold of 0.10yields the best set of automated scores that are comparable to manual scores. We plan on implementing these best-fit settings on a larger data set of manually scored videos to verify the utility of this method. (**110**)

Munoz, Valerie*, Erica Spiess, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. *Acoustic analysis of changes in bat community composition along the Upper Delaware River from 2009-2020*.- In recent years, North American bats have faced several major threats including the rise of White-nose Syndrome (WNS, *Pseudogymnoascus destructans*), an invasive fungal disease. This invasive fungus has caused major declines in bat populations due to its disruption of hibernation and negative influences on physiology, which often result in death. Massive mortality of hibernating bats from WNS has had considerable effects on the species composition of the bats in many areas of eastern North America. There has been an increase in monitoring efforts to understand the effects that WNS has had on bat populations, and to assess shifts in species composition. Students from East Stroudsburg University have been conducting acoustic monitoring of bat populations in the Upper Delaware Scenic and Recreational River Corridor since 2009. Recordings of bat echolocation calls were made using a Binary Acoustic Technology AR125 detector. For this study, we analyzed acoustic data collected at the historic Zane Grey Mansion in Lackawaxen, PA. We compared the bat species composition from summer nights in 2009, 2012, 2014, and 2020. The echolocation calls were analyzed using the SonoBat 4 autoclassifier and then manually vetted to confirm species identifications. We found a number of differences in the species recorded over this time period, including loss of diversity over time. The decline seen in our data is similar to results of other studies of bat communities in eastern North America where WNS has hit bat populations the hardest. (**94**)

Newman, Thalia*, Annarose Taylor*, Liew Chun Wai, and Robert Kurt Lafayette College, Easton, PA 18042. *The roles of lipopolysaccharide and flagellin in the TLR4 and TLR5 signaling cascades*.- Toll-like receptor (TLR) signaling pathways are essential to our ability to initiate an innate immune response. TLR signaling leads to activation of NFκB, a transcription factor that regulates inflammatory responses. Using a computational model of the TLR4 and TLR5 signaling pathways, we analyzed how different levels of the TLR4 agonist lipopolysaccharide (LPS) and TLR5 agonist flagellin (FLA) influenced NFκB activation. Our initial research focused on the analysis of data from a single signaling cascade; when TLR4 was triggered with LPS alone. From the computational data produced by the model, we observed that moderately high levels of LPS were associated with higher RNA levels, which we used as a marker of NFκB activation. LPS levels that were on the lower or higher end of the spectrum resulted in lower RNA levels, indicating that a threshold point existed where LPS was no longer inducing the TLR4 signaling pathway. After looking at TLR4 signaling alone we analyzed the effects of the signaling when the model was triggered with LPS and FLA at the same time; the dual signaling model. RNA output was shown to increase as FLA increased and decrease as LPS increased. Both variables were shown to play a significant role on the RNA levels, with the FLA appearing to show a more statistically significant association with RNA output. While the first 50,000 timesteps of the dual modeling data were consistent with the experimental data for 2-72 hours, we lacked experimental data beyond this point and were unable to determine the validity of the model over a longer period of time. For this reason, we conducted experiments to gather information about how LPS levels affected NFκB through a six-day period. Future analysis is focused on the addition of the TLR3 cascade and how modifying Irak4 levels affects NFκB activation. (**15**)

Nguyen, Tiffany*, Bianca Caresosa*, and Ronald Kaltreider York College of Pennsylvania, York, PA 17405. *Roscovitine and Antimetabolites Inhibition of CDK5 Activates a Potential PI3K Involvement in Cancer Progression and Aggression*.- The PI3K/AKT/mTOR pathway is one of the most commonly mutated pathways found in cancer. Cyclin-dependent kinase 5 (CDK5), an essential kinase within this pathway that mediates several biological processes, is upregulated in many cancers. Studies have shown that decreasing CDK5 reduces the aggressiveness of various cancers. However, little is known about the upstream factors that regulate this kinase, such as PI3K and protein kinase B (AKT) . Recent studies have shown combining a CDK5 inhibitor (Roscovitine, RSV) with chemotherapeutic drugs like temozolomide (TMZ) and doxorubicin (DXR) targets cancer in a synergistic manner to induce apoptosis and decrease cellular proliferation. Our study was designed to determine the cancer-suppressing effects of RSV when combined with the antimetabolite (methotrexate, MTX) within three human cancer cell lines (U87, HT29, and MCF-7). Using this *in vitro* model, we performed a cytotoxicity assay to determine the LD50 of each antimetabolite. Using the calculated LD50 value, we then measured gene expression of PI3K and AKT (qRT-PCR) under combination treatments with RSV. The LD50 for MTX from each cell line was determined for each cell type (U87: 6.038 µM; HT29: 1.001 µM; MCF-7: 1.200 µM). MTX was then combined with a low (1.0 µM) or high (20 µM) dose of RSV and gene expression was determined. We found that there was a decrease in PI3K and AKT expression when treated with MTX/RSV in all three cancers. Our work suggests that RSV improved the therapeutic activity of multiple conventional chemotherapeutic drugs, namely MTX. The combination of RSV and antimetabolite is a potential therapeutic possibility in multiple cancers associated with CDK5 overexpression. (**44**)

Odoemena, Sofia*, and Leslie Rieck Lycoming College, Williamsport, PA 17701. *Coliform Trends in Urban Streams Receiving Stormwater within Lycoming County MS4 Area*.- The Lycoming College Clean Water Institute (CWI) has been assessing the water quality of the urban streams and studying the stormwater outfalls within the Lycoming County MS4 region since 2015. A Municipal Separate Storm Sewer System (MS4) is a conveyance owned by a public entity which is designed to collect stormwater runoff. Stormwater run-off has been shown to be an important pathway carrying bacteria from urbanized areas to nearby surface waters, frequently accompanied by excess nutrient loads and other contaminants. As a result, the US EPA requires municipalities with MS4s to comply with many regulations to reduce the quantity and improve the quality of urban stormwater runoff, one of which is the implementation of best management practices (BMPs), which are structures or practices meant to divert, detain, infiltrate, or retain stormwater or otherwise improve its quality. Several MS4 permittees within Lycoming County are in the process of implementing BMPs with the goal of reducing sediment and nutrient loads transported to the West Branch of the Susquehanna River and, eventually, the Chesapeake Bay. To support these efforts, the CWI has complied a baseline dataset of fecal coliform data to allow for post-BMP implementation monitoring. Here, we present these baseline data for the stream site of Millers run and Bull run, highlight notable trends, and discuss the potential management implications of these current conditions. (**78**)

Ordoñez, Catalina*, Mikyung Jang, and Quyen Aoh Gannon University, Erie, PA 16541. *The Role of SCAMP3 in CXCR4 Trafficking*.- The CXC-Chemokine Receptor Type 4, CXCR4 is a G-protein coupled receptor that helps regulate cell growth and division, differentiation, and migration. CXCR4 can be overexpressed when its trafficking to the lysosome is decreased. Overexpression of CXCR4 is associated with metastasis in cancer and promotes HIV infection. When bound to its CXCL12, CXCR4 is ubiquitylated and downregulated via endocytosis. At the early endosomes, CXCR4 is ubiquitylated by the ubiquitin ligase ITCH and then sorted into multivesicular bodies by the ubiquitin adaptor proteins Hrs and Tsg101. Degradation of CXCR4 occurs in the lysosomes. This project is interested in whether Secretory Carrier Membrane Protein (SCAMP) 3, which interacts with Hrs and Tsg101, regulates CXCR4 trafficking. RNA interference will be used to knockdown SCAMP3 and CXCR4's localization relative to markers of the early endosome and lysosomes will be monitored through indirect immunofluorescence. Control immunofluorescence assays were performed with pulse chase time of 5, 15, 30, and 60 minutes to examine CXCR4 localization. We have found that CXCR4 accumulates in large compartment, indicative of lysosomes at 60 minutes or later. We are currently working to optimize the assay to accurately measure colocalization with both endosomal and lyosomal markers. (**18**)

Ortiz Fernandez, Destiny*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Somatic copy number variation in African Americans and European Americans with renal cell carcinoma*.- Renal cell carcinoma (RCC) is the deadliest of all urologic cancers in the US. RCC survival is highly dependent on subtype, with the two most common being clear cell RCC (ccRCC) and papillary RCC (pRCC). African Americans (AA) have lower survival rates when compared to their European

American (EA) counterparts for every subtype (ccRCC 67.1 vs 72.6, pRCC 80.5 vs 87.5). RCC survival disparities may be accredited to population differences in novel genomic factors, like West African ancestry (WAA) and somatic copy number variations (SCNVs).RCC patients with high WAA have varying SCNV and survival patterns that differ from patients with low WAA. An ancestrally diverse human reference genome was assembled using AA and EA 1000 Genomes Project study participants with African and European genetic ancestries. To investigate the association between WAA and RCC tumor biology, ccRCC and pRCC patients were categorized by >70% (high) and <70% (low) WAA with The Cancer Genetic Ancestry Atlas. Differential analysis of SCNV, gene expression, and disease-free survival were performed. Some self-reported AAs were clustered into the low WAA RCC patient subgroup based on genetic ancestry. Ancestry-enriched SCNVs were identified on chromosomes 7, 12, and 19 in ccRCC patients, and chromosome 12 in pRCC patients. Individuals with low WAA and low expression of an *SFSWAP* isoform (an RNA binding protein) had better survival than those with low WAA and high *SFSWAP* isoform expression. Genetic ancestry is associated with population differences in RCC tumor biology. WAA can serve as a potential prognostic factor and may guide therapeutic options, thus leading to reduced RCC survival disparities. (**13**)

Osei-Gyening, Isaiah*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Comparing the association between genetic ancestry, DNA methylation, and patient survival in African Americans and European Americans with lung cancer*.- Lung cancer is the second most common cancer in the US and the leading cause of cancer-related death. African Americans (AAs) have higher mortality rates when compared to European Americans (EAs). Most AAs have >70% West African ancestry (WAA). Genetic ancestry may share a relationship with DNA methylation and patient survival for lung cancer patients. I hypothesize that Lung cancer patients with high and low WAA (>70% vs <70%) have different DNA methylation patterns in distinct regions of the genome that show a relationship with survival. Download genetic ancestry from TCGAA and categorize patients by WAA. Then download the Illumina 450K DNA methylation array from the NCI GDC Legacy Portal and compare the differential methylated (DM) genomic regions by WAA using the PGS Methylation Workflow. Integrate normalized Illumina mRNA-sequencing data for DM genes by WAA. A total of 43 out of 485,512 CpG probes had statistically significant DNA methylation differences by WAA (FC = +/- 2, P + FDR = ≤0.05), corresponding to 31 genes. Patients with >70% WAA had hypermethylation at distinct regions of the genome (promoter, intronic, intergenic, 5' and 3' UTRs) for both coding and non-coding genes. FDA-approved DNA methylation inhibitors DAC may be used to reverse high WAA-specific hypermethylation of tumor suppressor genes. Genetic Ancestry and DNA methylation may lead to population-specific gene methylation panels and potentially reduce lung cancer health disparities. (**11**)

Panetta, Sydnie*, and Susan Cronin Immaculata University, Immaculata, PA 19345. *The compost project*.- Composting is the process of organic waste being broken down by the use of microorganisms and other decomposers. The purpose of the experiment was to identify the fungal organisms present in the compost bins present on Immaculata's campus. Samples were taken from the both compost bins located on Immaculata's campus. This was done by using a soil corer. The samples were swabbed and plated on Yeast Extract Peptone Dextrose agar with Pen/Strep. This specific agar is used to promote the growth of fungi while preventing the growth of bacteria. The plates were incubated at 32°C for two-three days. After the incubation period, DNA was extracted from the fungi samples. A PCR was performed then a Gel Electrophoresis was performed to see if there were any bands present. Bands indicate possible sequences. These samples that showed bands were sent out for sequencing. When the sequencing was finished, the DNA sequences were sent out in a database called *NCBI Blast*. Three fungal organisms were identified: *Candida sake, Rhizopus delmar,* and *Geotrichum candidum.* By identifying some of the fungal organisms, this will help demonstrate a better understanding of how these organisms play a part in the breakdown of the brown and green matter in compost. (**34**)

Petrick, Hayden*, and Christopher Dolanc Mercyhurst University, Erie, PA 16546. *Effects of Diameter and Crown Class on Ash (Fraxinus spp.) Mortality from Agrilus planipennis (Emerald Ash Borer) in Northwestern Pennsylvania*.- The emerald ash borer (*Agrilus planipennis*; EAB) is an invasive jewel beetle species whose larvae mature and consume the cambium of host ash trees (*Fraxinus* spp.), which results in observable and quantitative dieback of host canopy. However, dieback has been observed to be reduced in young ash trees, and the purpose of this study is to determine why they remain unaffected. Mortality and canopy dieback of pumpkin ash (*Fraxinus profunda*) trees with differing diameters and crown classes were analyzed using the combined data of two permanent plots in Erie, Pennsylvania. These two plots were established in 2016 before EAB infestation, and annual censuses reoccur every summer. Collected data include visible crown class, diameter at breast height (dbh), canopy dieback (ash rating), and mortality. The smallest trees (3.2 – 11.7 cm dbh) had a lower mortality rate (27%) than the largest trees (12 – 48.7 cm dbh) with 73% mortality. The overtopped crown class (n=50) had the lowest mortality rate (26%) while the intermediate (n=22) and dominant/codominant (n=32) crown classes had higher mortality rates (63.6% and 78.1% respectively). 83% of all trees in this study showed severe canopy dieback, but 17% of trees have smaller diameters and are in the overtopped crown class. Both diameter and crown class appear to be correlated with mortality and canopy dieback. Trees of smaller diameter and overtopped crown class had less dieback and mortality than trees of larger diameter and intermediate or dominant/codominant crown class. Over the census years, no change in the number of ash seedlings has been observed and they appear to be unaffected by the EAB wave. This observation and the results of this study suggest that the future of the cohort of young ash is promising. (**87**)

Pezak, Corey*, James Murray, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *The search for a more specific histone deacetylase Inhibitor*.- SAHA (Vorinostat) is a histone deacetylase inhibitor (HDAi) currently FDA-approved for the treatment of cutaneous T-cell lymphoma after the failure of other treatments. Because SAHA inhibits a number of different histone deacetylases, it has some side effects, including fatigue, diarrhea, nausea, thrombocytopenia, dehydration, and pulmonary embolism. The goal of this project is to identify SAHA-derived compounds that have greater specificity than SAHA. As a first screen, we have tested these putative HDAis for their ability to reduce growth of *Saccharomyces cerevisiae* in liquid culture. Cultures were treated with three different concentrations of each compound and growth was monitored by spectrophotometry. We have found one compound (JKM [3-278]) that reduces yeast growth rate by 77% at millimolar concentrations. JKM [3-278] We continue to screen putative HDAis using our yeast growth assay as well as more directly measuring histone acetylation. We are also further testing JKM [3-278] against particular histone deacetylases to better understand its specificity. (**45**)

Prematta, Spencer R.*, and Jeffrey P. Thompson York College of Pennsylvania, York, PA 17405. *Loop-mediated isothermal amplification (LAMP) assay development for the detection of Frog Virus 3 (FV3)*.- Ranavirus is a genus of double-stranded DNA viruses that target ectothermic hosts. This virus genus has caused massive die-off events in amphibians, reptiles, and other aquatic animals. Frog Virus 3 (FV3), the type species of Ranavirus, has been found to affect frogs and other amphibians greatly and has been a culprit of recently observed population decline. FV3 causes edema, skin-sloughing, and is associated with high fatality in tadpoles and frogs. Currently, there are several tests available for the detection of FV3 in a sample. However, methods associated with these tests limit their usage as these protocols are time-consuming and require expensive instruments that may not be readily available. A recent study was successful in developing a Loop-mediated isothermal amplification (LAMP) assay for the detection of the Largemouth bass ranavirus. In this study, we sought to develop a LAMP assay for the rapid detection of the Major Capsid Protein (MCP) gene that is present within FV3. This was performed through the designing of LAMP primers using both software and hand design methods. LAMP reactions were carried out using New England Bio Labs' LAMP 2x MasterMix with UDG and the associated protocols. A large array of troubleshooting methods based upon previous literature were attempted for the development of this assay. This includes the addition of dimethyl sulfoxide, pullulan, guanidine chloride, several primer sets, and a manual LAMP hot start. In spite of these optimization efforts, this study was unable to achieve consistent colorimetric results that aligned with the identity of the controls. The techniques used to improve this detection method can serve to further develop convenient LAMP assays specific to FV3 and provide an increased understanding of LAMP technology. (**52**)

Rager, Sydnie*, Kaitlyn Stroscio, Olivia Pericak, Zach Buchman, Colin Olson, Christina Judy, and Rajinikanth Mohan Mercyhurst University, Erie, PA 16546. *A transcription factor involved in growth repression is a positive regulator of senescence in plants*.- Shortening of day length or photoperiod, such as that observed during the Fall season, triggers molecular and physiological changes in plants that results in senescence. We are using the model plant *Arabidopsis* to understand the molecular basis of dark-induced senescence (DIS). DIS is largely controlled by the plant hormone, ethylene that is commonly associated with fruit ripening. Ethylene is synthesized from S-adenosyl methionine through the formation of the intermediate ACC. We found that treatment of plants with ACC promoted senescence- even without darkness- only in plants overexpressing a transcription factor TEM1, but not wild type. We also observed that the increased senescence in these plants is associated with increased gene expression, suggesting that the transcription factor may regulate senescence gene expression directly or indirectly. Studying the dynamics of TEM1 protein and identifying TEM1 target gene expression will reveal how this novel pathway activates senescence in plants. (**88**)

Romano, Giulia*, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Novel presumptive tests for drugs of abuse using chemiluminescence*.- Benzodiazepines are often used for treatment of insomnia, convulsions, and many psychiatric disorders. The widespread use of this class of drugs has raised concern about recreational benzodiazepine abuse. This highlights the importance of chemical detection and concentration determination of the benzodiazepine drugs within a human system. Although there are many different approaches to detection, this proposal outlines a novel presumptive testing method using chemiluminescence. The proposed chemiluminescent method offers high sensitivity, a broad linear dynamic range, and quick, simple sample analysis. A comparative study was designed to analyze three azepine drugs, carbamazepine, clonazepam, and diazepam. The chemiluminescent reagents to be discussed are tris(2,2'-bipyridyl dichlororuthenium (II) hexahydrate (Ru(bipy)3Cl2•6 H2O) with cerium (IV) sulfate, known as Method A, and n- bromosuccinimide (NBS), known as Method B. Chemiluminescence was detected using a Berthold Technologies Lumat3 tube luminometer. Method A was more sensitive for carbamazepine and clonazepam, while method B was more sensitive toward diazepam. These drugs were detected in concentration ranges of 1.1 to 0.275mM. The results from this work suggest novel presumptive tests for these drugs of concern. These methods require minimal sample preparation, offer a rapid screening process, and facilitate the detection of these compounds in biologically relevant concentrations. (**98**)

Rotondo, Julianna*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Chromatin Protects DNA from Alkylation Damage*.- DNA is constantly being damaged by both internal and external factors, which can lead to mutation and possibly cell death. Chromatin, the complex of proteins and DNA that makes up eukaryotic chromosomes, has been shown to limit what proteins can access the DNA. We hypothesized that it may also protect the DNA from damaging agents. We investigated whether altering the structure of chromatin would affect the sensitivity of *Saccharomyces cerevisiae* to a series of DNA alkylating agents. Opening the chromatin over the amino acid biosynthetic genes with sulfometuron methyl seemed to increase the sensitivity of those genes to alkylation damage. Increasing chromatin compaction by arresting cells in metaphase with Nocodazole had a small protective effect against alkylation damage. We also found that the size of the damaging agent affected chromatin's protective ability. It appears that the larger the damaging agent, the more chromatin was able to protect the DNA of the yeast cells. Altering chromatin state could be used in the future to help make tumor cells more sensitive to DNA damaging chemotherapies or help people who are going to be exposed to damaging agents such as UV light and some carcinogens. (**21**)

Saar, Lily*, Kiyah Bell, Dayana Davila, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Comparison of AutoMLST, GTDB, rpoB, and 16s trees in evaluating the position of novel Pedobacter species, as well as known Pedobacter species, in a potential reclassification*.- This analysis is a portion of a larger project on the reclassification of the *Pedobacter* genus of bacteria. This involves creating a new genus for the pink *Pedobacter* species, as well as incorporating several species previously classified in the genus *Pedobacter* into the existing genus *Nubsella*. Phylogenetic trees were constructed using the genomes of novel bacterial species isolated from a freshwater creek in Lycoming County, as well as close relatives in order to visualize the relationships among current members of the *Pedobacter* genus. Trees were created using the 16S rRNA gene, the rpoB gene, a set of 77 concatenated proteins (AutoMLST=Automatic MultiLocus Sequence Typing) and a set of 120 proteins (GTDB=Genome Taxonomy Database). The different trees are compared in the context of their ease of construction, resolution, timeliness, and other factors to determine which tree would be the most appropriate to accurately illustrate the evolutionary relationships among the organisms. (**39**)

Sands, Autumn*, Daniel Strömbom, Amanda Crocker, Grace Tulevech, Kelly Ward, and Cameron Cloud Lafayette College, Easton, PA 18042. *Modeling the local spread of the Spotted Lanternfly in the US*.- The invasive spotted lanternfly (*Lycorma delicatula*) has recently spread from its native range to several other countries, and modeling studies forecast that it may become a global invasive pest. In particular, since its confirmed presence in the United States in 2014 it has established itself as a major invasive pest in the Mid-Atlantic region, where it is threatening both naturally occurring and commercially important farmed plants. Quarantine zones have been introduced to contain the infestation, but the spread to new areas continues, and at present the pathways and drivers of spread are not well understood. In particular, several human activity related factors have been proposed to contribute to the spread, however, quantitative evidence in support of most of these are lacking, and no mechanistic model for the local spread of the spotted lanternfly in the US, or elsewhere, can be found in the literature. Here we collect data and use statistical methods to test whether a number of such factors are associated with spotted lanternfly infestation at the county level. We find that primary interstate highway presence, national park presence, number of garden centers, and population are associated with infestation. We then introduce a mechanistic local spread model based on the factors found to be associated with infestation, assess its accuracy in a smaller region, and then use it to forecast the future spread in a larger region. Given that our model is truly minimal and mechanistic our findings may be instrumental in informing management and further modeling efforts related to the current spotted lanternfly infestation in the US, and potentially for current and future invasions elsewhere globally. (**92**)

Shah, Raivat*, Emily Luo*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Impacts of e-liquids upon macrophage phagocytosis of Escherichia coli*.- In the past decade, the use of aerosol-releasing electronic-cigarette devices (ECIGs) has exponentially risen in popularity. ECIGs vaporize flavored e-liquids into an aerosol which is then inhaled by the user. Macrophages are white blood cells responsible for phagocytosis, a cell-ingesting mechanism, of pathogenic microbes and play a role in maintaining homeostasis. *Escherichia coli,* a Gram-negative species of bacteria, can be used as a model organism to evaluate macrophage phagocytic efficacy following exposure to flavored e-liquids. Hence, the purpose of this study is to determine the immunological impacts of e-liquids -/+ flavors on macrophage growth and phagocytosis using *E. coli.* First, the THP-1 human monocyte cell line, a precursor to macrophages, is grown with RPMI at

37°C, 5% CO_2 (standard conditions) -/+ flavored e-liquids and cell counts evaluated over several days via trypan blue exclusion. In parallel, THP-1 cells are stimulated and differentiated to M0 macrophages with 200 nM phorbol 12-myristate 13-acetate. M0 macrophages are then polarized to M1 macrophages with lipopolysaccharide and Interferon-gamma while simultaneously exposed to flavorless and flavored e-liquids at a final concentration of 1% (v/v) along with untreated control cells. Treated and control M1 macrophages are incubated with GFP+ *E. coli* at an MOI of 100. Following incubation, samples are processed for confocal microscopy analysis. In addition, M1 macrophages are washed and incubated with RPMI antibiotic media to kill extracellular bacteria. M1 macrophages are then washed and lysed with sterile water. Lysates are serially diluted and plated on agar for *E. coli* CFU counts. We predict that e-liquids -/+ flavors will decrease M1 macrophage phagocytosis of *E. coli* compared to control. This study may indicate that flavored e-liquids negatively modulate host M1 macrophage phagocytic efficacy, thereby decreasing immune function against pathogenic infection. This study may inform the broader public of the detrimental implications of vaping upon overall immune health. (**38**)

Shrestha, Adina*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Identifying Population-Specific UGT and CYP mRNA Isoform Expression upon Menthol Exposure in Lung Cancer Among African Americans and European Americans*.- Background Lung cancer is the leading cause of cancer-related deaths in the U.S. Approximately 85% of lung cancer patients have non-small cell lung cancer (NSCLC) consisting of lung adenocarcinoma (LUAD) and lung squamous cell carcinoma (LUSC). African Americans (AAs) have a higher mortality rate compared with European Americans (EAs), despite smoking less. When AAs do smoke, most select menthol cigarettes. Cytochrome P450 (*CYP*) and uridine diphosphate (UDP)-glucuronosyltransferase (*UGT*) break down menthol and other tobacco carcinogens. Not much is known about how population-specific expression of *CYPs* and *UGTs* impact aggressive lung tumor biology. Hypothesis Population-specific *CYPs* and *UGTs* mRNA expressions impact aggressive lung tumor biology. Methods The Broad GDAC Firehose was used to download normalized mRNA-seq and clinical data (LUAD *n*=50 AAs, 342 EAs; LUSC *n*=24 AAs, 274 EAs in The Cancer Genome Atlas (TCGA)). The TCGA Splicing Variants Database (TSVdb) was used to access *UGT* and *CYP* mRNA isoform data by race. Performed differential expression (DE) on *UGT* and *CYP* genes and isoforms using Excel (two-sample t-test assuming unequal variances, *P*=0.05). Results 10/20 *UGTs* and 15/55 *CYPs* are DE by race and 9 *UGT* and 15 *CYP* mRNA isoforms are DE by race. 6/14 *UGT* mRNA isoforms are DE in survival by race. 11/22 *CYP* mRNA isoforms are DE in survival by race. Conclusion AAs have lower expression of *UGT* and *CYP* mRNAs and mRNA isoforms that break down carcinogens which may help to explain the high incidence of lung cancer in AAs. AAs overall had better 5-year survival than EAs among LUAD patients, especially by high-expressors of both short and long isoforms. In the future, AA and EA lung cancer cell lines will be exposed to menthol cigarette smoke to determine population-specific drug responses to chemotherapy agents. (**58**)

Silva, Nicole*, Zahaira Velasco*, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining growth rate and capsule formation in mutant strains of the oleaginous yeast Cryptococcus neoformans to be used in biodiesel production*.- The burning of fossil fuels leads to the release of the greenhouse gas carbon dioxide (CO_2) which is a main contributor to climate change. Research is to find fuels that are renewable and more carbon neutral to replace the burning of fossil fuel has led to the promising option of biodiesel that can be made from lipids in biological matter that can be chemically converted into fatty acid methyl esters, the main component of biodiesel. While there has been active research on generating biodiesel from plants oils and animal fats, these sources can be expensive and are better served as sources of food. A potential alternative are oleaginous yeasts which are naturally oily yeasts that can convert sugars into large quantities of lipids. While a number of oleaginous yeasts have been studied in the production of biodiesel, the lack of molecular tools to study and manipulate these yeast make them unappealing. The oleaginous yeast *Cryptococcus neoformans* has been extensively studied since it is linked to infections in immunocompromised individuals of extensive genetic engineering tools have been developed in this organism. In addition *C. neoformans* can feed on cellulose and wood sugars, making it more carbon neutral. Our lab is examining mutant strains of *C. neoformans* that lack the virulence factor found in its capsule as a safe and genetically malleable system to develop biofuel. We have shown that *C. neoformans* biomass can be converted to biodiesel containing methyl esters of stearic acid, oleic acid, linoleic acid, and palmitic acid. We are examining the growth rates of strains of *C. neoformans* containing mutations that may affect capsule formation and measuring capsule size of these strains by staining with India ink staining. Our research should allow us to identify the strains of *C. neoformans* that are optimum for biodiesel production. (**55**)

Skirboll, Sydney*, and Jeffrey Thompson York College of Pennsylvania, York, PA 17405. *Novel CRISPR-Cas9 visualization system for the functional removal of IL13α1 receptor and analysis of cell behavioral changes*.- Glioblastoma is the most prevalent form of brain cancer, and over 95% of patients die within five years of receiving a diagnosis. Current treatments are often unsuccessful and damage non-cancerous tissues. Therefore, therapies that specifically target GBM tumors while sparing healthy cells are promising for improving patient outcomes. IL13 receptors have been identified as potential targets due to their overexpression in GBM and association with resistance to chemotherapy drugs. These receptors also control or regulate the JAK/STAT pathway in which alterations cause increased cellular proliferation. In this research, a CRISPR-Cas9 knockout of IL13 receptor α1 was performed in HEK293 cytokine reporter cells, designed to produce secreted embryonic alkaline phosphatase (SEAP) as a detectable product of the JAK/STAT pathway. A two-step transfection method with a novel “redlight/greenlight” CRISPR-Cas9 system was used. In this procedure, cells expressed mCherry following the first transfection for easy visualization of Cas9 coexpression. After the second transfection, GFP fluorescence indicated the expression of the second plasmid. It contained an anti-IL13Rα1 sgRNA to knock out the receptor and an anti-Cas9 sgRNA to simultaneously stop Cas9 and mCherry expression. Following the CRISPR-Cas9 edit, the function of the JAK/STAT pathway was assessed with a SEAP assay after the addition of cytokine ligands. IL13 activation of the pathway was significantly hindered ($p\text{-value}<0.0001$) in cells treated with anti-IL13Rα1 sgRNA compared to control cells. These results are promising for the potential use of the “redlight/greenlight” system for future CRISPR-Cas9 gene-editing experiments. Through this easy-to-visualize CRISPR-Cas9 system, information regarding the function of IL13 receptors as well as any protein can be gained more quickly and efficiently. (**53**)

Slifka, Jacob*, Brad Engle, and Sonny Bleicher Wilson College, Chambersburg, PA 17201. *Quantifying the contact-independent inhibitory effect of cinnamon bark oil on the fungal pathogen Pseudogymnoascus destructans*.- The invasive fungus, *Pseudogymnoascus destructans* (*P.d.*) is the vector for white nose syndrome, a condition that has been decimating bat populations across North America since 2006. Some volatile organic compounds (VOCs) show the ability to inhibit fungal growth while also having the capacity to penetrate porous material, such as the soil found in caves (hibernaculum) where *P.d* grows. We designed two experiments to determine if the VOC cinnamon bark oil (CBO) could be used as an inhibitor for this fungus. We additionally investigated whether CBO has detrimental effects on endemic cave fungi. We used i-plates as environmental/growth chambers placing known concentrations (ppm) of CBO placed on one side and colony forming units (CFUs) of fungi on the other. Two weeks of fungal growth, quantified using CFU counts, showed the CBO minimum inhibitory concentration (MIC) for *P.d.* was at 50ppm, or lower, with CBO also inhibiting three endemic *Pseudogymnoascus* species of fungi. Despite the effectiveness of CBO suppressing the growth of *P.d.,* the suppression of other fungi present in the hibernaculum makes CBO a risky treatment to utilize in natural environments. (**62**)

Terry, Madeline*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *How important are the different DNA double strand break repair pathways?*.- While DNA is subject to many different types of damage, double-strand breaks are one of the most dangerous for the cell. To deal with double-strand breaks, the cell contains four different repair pathways: homologous recombination (HR), nonhomologous end joining (NHEJ), alteranative end joining (alt-EJ), and single strand annealing (SSA). The goal of this research is to understand the relative use of each pathway in *Saccharomyces cerevisiae* and how they affect DNA integrity. We analyzed the frequency and type of 5-FOA resistance causing mutations in URA3 in wild type yeast and yeast missing critical components of HR or NHEJ. We hypothesized that loss of NHEJ would lead to fewer mutations, due to the fact that HR carries out accurate break repair. So far we found that our two wild type strains have mutation frequencies of 0.0002107 and 0.001133. These frequencies will later be used in comparison with our mutant strains. Our two wild type strains were also sent for sequencing. We determined that our wild type 1 strain appears to have less mutations than wild type 2, the difference being one point mutation to multiple point mutations and possible deletions. Understanding these repair pathways and how repair can lead to mutations can help us better predict cell viability and even a cell's risk of cancer or apoptosis. (**46**)

Tulevech, Grace*, and Daniel Strömbom Lafayette College, Easton, PA 18042. *Collective motion from attraction and burst-and-glide dynamics*.- Moving animal groups exhibit a range of fascinating behaviors. The standard explanation for how these groups form and function is that the individual animals interact via attraction, repulsion and alignment, where alignment is proposed to drive the collective motion. However, it has been shown both experimentally and theoretically that alignment interactions are not required to induce group level alignment. In particular, via the use of self-propelled particle models it has been established that asynchrony in positional update induce group level alignment (aka polarization) in combination with attraction alone. However, the exact type of asynchrony that has been shown to induce polarization in combination with attraction is unlikely to be operating in real world animal groups. So, for this combination to be a biologically plausible explanation for the collective motion we observe in nature, a more realistic type of asynchrony is required. Here we introduce two previously unreported asynchronous update schemes, burst-and-glide and burst-and-stop, and show via simulation that they also induce polarization in combination with attraction alone. Given that burst-and-glide/stop dynamics is readily observed in a wide array of social animals, in particular fish, relying on these to explain collective motion in animal groups that exhibit burst-and-glide dynamics is preferable to previously published explanations. And may contribute to a better understanding of how moving animal groups form and function more broadly. (**6**)

Tulio, Dominic*, and Kelly Orlando Immaculata University, Immaculata, PA 19345. *Identification of key amino acid substitutions between members of the Candida glabrata PMU gene family, and their role in conferring phosphatase activity*.- Phosphate is an essential nutrient that the yeast species, *Candida glabrata,* uses in various cellular processes. These single celled organisms need to be able to cut off phosphates from organic molecules in their environment and take them into the cell. *C. glabrata* has a three gene family consisting of *CgPMU1, CgPMU2,* and *CgPMU3,* all of which encode enzymes with some phosphatase activity against a few phosphate-containing compounds. *CgPMU2* encodes an enzyme that is upregulated when the cell is starved of phosphate and is able to cleave phosphate off of a wide range of organic compounds in the external environment (Orkwis *et al*., 2010). The proteins expressed by this three-gene family are approximately 75% identical in amino acid sequence. In a previous paper, Orlando *et al*. was able to determine that the novel amino acid changes that conferred the broad-range phosphatase activity on CgPmu2 protein were generally found toward the C-terminal end of the protein (Orlando *et al*., 2015). In that paper, they were able to identify a number of individual amino acids that seem to confer phosphatase activity on CgPmu2. However, when they combined all of their identified point mutations onto a *CgPMU1* background gene, they were not able to fully replicate the strong, broad-range phosphatase activity of the full-length CgPmu2. Therefore, our plan is to identify additional differences in amino acid sequences in the C-terminus of CgPmu2 that contribute to its phosphatase activity. Once we create these mutants we will test their phosphatase activity as compared to the mutants from Orlando *et al* and with full length CgPmu2. (**51**)

Vargas, Shaylene*, Brad Engle, and Kathryn Sarachan Wilson College, Chambersburg, PA 17201. *The combinatorial effects of lumefantrine and tetrandrine on the radiation sensitivity of U-87 glioblastoma cells*.- Glioblastoma is the most common and aggressive malignant brain tumor with a 15-month median patient survival time. Although radiotherapy and temozolomide (TMZ) treatment are often prescribed as life-prolonging therapy, glioblastoma cells are known to show significant resistance to both radiation and chemotherapy. Lumefantrine, an antimalarial drug, has been found to reverse the radiation/TMZ resistance of glioblastoma cells and tetrandrine, a phytochemical, has been found to increase glioblastoma cell sensitivity to radiation. The primary purpose of this study was to determine the combinatorial effects of tetrandrine and lumefantrine on the radiation sensitivity of U-87 glioblastoma cells. Glioblastoma cells were plated in 96 well plates, incubated for 24 hours, treated with various concentrations and combinations of lumefantrine and tetrandrine, exposed to UVC radiation or not. There were 12 treatment conditions, including the control, DMSO, and the MTT blank, with 16 replications per treatment condition. Results were quantified using an MTT cell viability assay. Preliminary results produced several notable findings, compared with the control (no drug or radiation treatment), 1) the vehicle for the drugs, DMSO, showed a reduced cell viability; 2) there was no apparent difference in cell viability, following radiation treatment; 3) lumefantrine when used independently, resulted in a trend of dose dependent decrease in cell viability; and 4) the combination treatments appeared to have a proliferative effect on the cells. Overall, the results of this study are inconclusive with respect to the combinatorial effect of lumefantrine and tetrandrine on the radiation sensitivity of U-87 glioblastoma cells. Further studies will be necessary to determine the potential therapeutic value of lumefantrine and tetrandrine used in combination with radiation for the treatment of glioblastoma. (**14**)

Velazco, Lily*, Hunter Zondory, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Generation of neutralizing monoclonal antibodies against bacteriophage T4*.- Antibodies protect by various mechanisms, but induction of antibodies that block infection by binding to pathogen surface structures is a goal of current vaccines. Past Messiah University Microbiology courses included experiences wherein students blocked infection of *Escherichia coli* B by bacteriophage T4 using polyclonal T4-specific goat antiserum. Unfortunately, the polyclonal serum is no longer available. We have undertaken to generate mouse monoclonal antibodies that neutralize phage T4 to use in the same laboratory experiences. Our strategy was to immunize Balb/c mice with concentrated T4 suspensions from which endotoxin (lipopolysaccharide) had been depleted by gentle organic extraction. Mice were injected twice over a two week period with ~ 1.6 – 3.5 x 1010 pfu of T4r+ phage. Serum was prepared from blood collected by cheek vein puncture and assessed for T4-neutalizing activity in a 96-well plate scale-screening assay. Briefly, small amounts of *E. coli* B and T4 were combined in each well. Ongoing infection by T4 limited the density of bacterial growth in a well when measured at 6 – 8 hours. The presence of neutralizing antibody prevented infection, and instead allowed the bacteria to grow to near-saturation. Use of serially diluted serum samples allowed relative neutralizing titers to be determined. This presentation will describe development of the 96 well plate-scale screening assay and how it was further adapted to tolerate the presence of antibiotic that will be in supernatants of hybridoma cultures (Gentamicin, or the mixture of Penicillin and Streptomycin). Exponentially growing *E. coli* B cells were transformed with plasmids encoding ampicillin and either gentamicin or streptomycin resistance. Infection by T4 was confirmed in the presence of the relevant antibiotic, as well as the ability of each transformant to proliferate if T4 was neutralized by goat antisera under similar conditions. Production and screening of hybridomas is in progress. (**69**)

Villeda, Blanca*, Adam Cooke, M. Dana Harriger, and Deborah Austin Wilson College, Chambersburg, PA 17201. *A comparative study of primary land use and microplastic concentrations of sediment in the Conococheague Creek*.- Plastics are ubiquitous today due to their wide range of applications and affordability. Microplastics, plastic debris less than 5 mm in length, are known to be ingested by different freshwater organisms. Once ingested, microplastics can obstruct the organism's digestive system and clog their feeding appendages. This study investigated whether microplastics are present in the Conococheague Creek and whether there is a correlation between primary land usage and microplastic concentrations in the Conococheague. The Conococheague is a tributary of the Potomac River, which flows into the Chesapeake Bay. It is also the source of drinking water for the Borough of Chambersburg. Four areas of study along a 20-mile reach were chosen based on the land use the creek is flowing through: the headwater of the creek, a recreational area, an agricultural area, and an urban area. Three sediment samples were collected from each site. Microplastics were separated from sediment based on density using zinc chloride (specific gravity 1.6 g/ml) stained with rose bengal dye and identified by stereomicroscopy. Observed microplastics were classified based on their shape: fragments, films, fibers, and other. Microplastics were present in all samples, but there was no statistical difference between the average number of microplastics per dry weight between the four sites. The most abundant type of microplastic in all samples was microfibers. However, there is a trend in the composition of microplastics among the samples. The urban site had the most diverse composition of microplastics, followed by the agricultural site, the recreational site and finally the pristine site. This study indicates that microplastic contamination occurs at multiple locations along this reach of the Conococheague Creek. Further studies could elucidate points of contamination along the creek and whether the microplastics are affecting the organisms in this aquatic habitat. (**86**)

Vyas, Khushali*, and André Walther Cedar Crest College, Allentown, PA 18104. *Examining the mechanism of Replication Protein A regulation of telomere length in Saccharomyces cerevisiae using a PCR amplification-based protocol*.- Many proteins affect the function of telomerase and therefore the length of telomeres in eukaryotic organisms. One such protein is Replication Protein A (RPA) which is a highly conserved, heterotrimeric, single-stranded DNA binding protein that is essential for many DNA maintenance pathways including telomere maintenance. RPA is phosphorylated in a cell-cycle dependent manner and in response to DNA damage, suggesting that phosphorylation may play a vital role in regulating its function. We hypothesized that phosphorylation may regulate RPA functions in telomere synthesis, and our lab has previously shown that mutations in RPA that effect phosphorylation cause changes in telomere length in the baker's yeast *Saccharomyces cerevisiae* (*S. cerevisiae*). However, the mechanism for RPA phosphorylation's regulation of telomere synthesis is unclear. As a result, we have been measuring telomere length of various *S. cerevisiae* mutants such as TEL1, EST1, and RIF1 mutants and those with phosphorylated and dephosphorylated states of RPA. After isolating genomic DNA from *S. cerevisiae,* the telomere sequences were tailed with a specific DNA sequence, amplified using Endpoint Polymerase Chain Reaction (PCR), and measured through gel electrophoresis. We are currently analyzing the telomere lengths of *S. cerevisiae* mutants and seeing positive and negative effects on telomere length caused by the addition of different mutations. We have confirmed our Endpoint PCR protocol using a control and have been able to verify our protocol in terms of amplifying telomere lengths. We have also started to confirm our results through Southern Blot Hybridization. By comparing telomere lengths of RPA phosphorylated mutants to known telomere synthesis mutants, we will have a better understanding of the role RPA phosphorylation plays in regulating telomere synthesis. Since the abnormal regulation of telomere synthesis is required for cancer cell formation and cancer progression, our research may provide insights into novel treatment targets for cancer. (**74**)

Wallace, Kaylee*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *The effect of heat stress on invasive New Zealand mud snail mortality*.- The New Zealand mud snail (*Potamopyrgus antipodarum*) is among the most globally widespread aquatic invaders, occurring in at least 40 countries and 6 continents. The species is easily spread unintentionally attached to clothing and gear that comes in contact with water containing the snail. Finding methods to decontaminate gear is important to reduce the possibility of spread. The purpose of this study was to test the effect of heat stress on *P. antipodarum* mortality. Using a warm water bath, we tested four different water temperatures (50°C, 45°C, 35°C, and 25°C) at different time intervals to assess mortality. We found that both increased temperature and exposure time resulted in higher mortality with complete mortality after five minutes at 50°C or 10 minutes at 45°C. Thus soaking gear in semi-hot water for a short time period may be a suitable way to decontaminate materials. (**81**)

Watson, Talia*, Lindsey Welch, and Audra Bratis Cedar Crest College, Allentown, PA 18104. *Selective oxidation of naphthol derivatives with metal acetylacetonate catalysts*.- While amidst a pandemic, it is of grave importance that novel treatments for diseases are being found. Naphthoquinones are a promising alternative to some antibiotics as they have significant pharmacological properties. The typical catalyst used to synthesize naphthoquinones is hexavalent chromium which has many unfavorable qualities. Metal acetylacetonate catalysts are a safer alternative while being composed of earth-abundant metals such as iron, cobalt, and vanadium. The synthesis of 5-hydroxy-1,4-naphthoquinone (juglone) and 1,4-naphthoquinone were achieved via oxidation of 1-naphthol with tris(acetylacetonato) cobalt (III), tris(acetylacetonato) iron (III), and bis(acetylacetonato) oxovanadium (IV) catalysts. Products of oxidation reactions were characterized with infrared spectroscopy and gas chromatography/mass spectrometry. Other starting naphthyl compounds including 1-bromo-2-naphthol, 2,7- and 2,3-dihydroxynaphthalene were tested, but there was no naphthoquinone product formation. In addition to the successful oxidation of 1-naphthol, oxidation of 1,5-dihydroxynaphthalene and 4-chloro-1-naphthol were also investigated with promising conversion to naphthoquinones. This presentation will communicate the effect of catalyst on the selectivity toward each product. Based on the findings presented, the synthesis of naphthoquinones using this novel approach with metal acetylacetonate catalysts was successful for a variety of naphthol starting compounds. (**99**)

Whittington, Jacob*, M. Dana Harriger, Tonia Hess-Kling, and Rebecca Thomas Wilson College, Chambersburg, PA 17201. *Analysis on the outcomes of physical therapy on patients with shoulder injuries in different age groups*.- The shoulder is one of the most commonly injured joints in the human body. In 2006, the American Academy of Orthopaedic Surgeons (AAOS) reported that roughly 7.5 million Americans received medical care for shoulder issues. Since 2012, more recent studies indicate increasing incidence of patients with shoulder complaints of up to 29.3 per 1000 individuals. Fractures, dislocations, frozen shoulder, and rotator cuff tears are a few common shoulder injuries that occur due to its unique anatomical design. Physical therapy targets and works to improve the healing process as well as improve function of an injured joint by increasing mobility, decreasing pain, and reestablishing function. Due to the commonality of shoulder injuries, it is vital to analyze the effects that physical therapy has on patients with shoulder injuries. This study investigated whether a younger population of patients (18-45 years old) responded better to physical therapy by developing more mobility and strength along with decreased pain in the shoulder joint after injury in comparison to an intermediate (45-60 years old) and older population of patients (61+ years old). Under the guidelines of Health Insurance Portability and Accountability Act (HIPAA) and Institutional Review Board (IRB) approval, data was collected from patient files undergoing treatment for shoulder injuries at Somerset Physical Therapy. Data included age, gender, body mass index (BMI), upper extremity functionality index (UEFI), and number of clinical visits. Data is being analyzed to determine if age can be a predictor of outcomes. A comparison of interest includes examination of BMI as it relates to the number of visits needed for the younger population vs. the intermediate and older population. Preliminary data suggests that a younger population of patients who undergo physical therapy for shoulder injuries have better outcomes than an intermediate and older population of patients. (**67**)

Wilson, Emily*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Effect of road proximity and habitat fragmentation on the dispersal and genetic diversity of the wood frog (Rana sylvatica) in natural and created vernal pools*.- Habitat fragmentation by roads is a threat to the regional viability of vernal-pool breeding amphibians. Habitat connectivity determines the geographic limits of a population because it is necessary for the dispersal of organisms away from their site of origin, which leads to the exchange of genetic material. The North American wood frog (*Lithobates sylvaticus*) is often used as an indicator species of environmental quality because of its dependence on vernal pools. Wood frogs are a highly philopatric species that breed in vernal pools and hibernate and forage in upland forest. Previous studies have demonstrated that road proximity is correlated with differences in population structure. One study in Jacobsburg State Park, PA investigated the effect of road proximity on the upland movement of wood frogs by comparing results between a fragmented site, which is <100 m from two roads, and an unfragmented site where the nearest road is greater than 1000 m away. Wood frogs at the unfragmented site were uniformly abundant in traps around the vernal pools, whereas there was evidence of significant non-uniform orientation in wood frog movement at the pools in the fragmented site. Wood frogs were significantly more abundant in traps further away from roads at the fragmented site, indicating that the presence of roads may be reducing the amount of upland habitat utilized by adult wood frogs. An important next step is to compare genetic diversity as a measure of gene flow in wood frog populations between the isolated and fragmented sites using microsatellite DNA markers. Our results demonstrate the importance of habitat connectivity for the regional viability of amphibian populations and help inform conservation efforts. (**1**)

Wolfe, Calista*, M. Dana Harriger, Adam Cooke, and Deb Austin Wilson College, Chambersburg, PA 17201. *The comparative effects of a raw based diet versus a kibble diet on the reduction of dental calculus in dogs*.- Periodontal disease (PD) is one of the most prevalent oral diseases found in dogs. PD is an inflammatory disease that results from infection of the gums, bone, and tissues surrounding and supporting the teeth. PD develops from excessive dental calculus buildup (DCB), the hardening of dental plaque, saliva, bacteria, and minerals. There are two stages of gum disease, gingivitis, and periodontitis. Without treatment, gingivitis will progress to PD. The high percentage of dogs affected by PD renders it necessary to determine whether a dog's diet has an impact on the reduction of established DCB. This study contained two groups of whippets that were fed different diets. The control group was fed the same kibble diet the test subjects were already consuming. The treatment group was fed a commercially available raw based diet (RBD). The amount of DCB on the test subject's teeth was measured using a visual assessment scale that displays the stages of PD. Photos of the test subject's teeth and gums were taken every Tuesday and Friday for five weeks, then organized into grades of PD dependent upon the amounts of DCB present on the surface of the test subject's teeth. Statistical analyses were performed to determine whether there were significant differences between grade of PD and type of diet fed as well as any differences between DCB of the control group compared to the treatment group. Results of this study do not indicate a correlation between diet and reduction of established DCB within the parameters of the study design. Further analysis is required to better understand the impact of diet on PD in canines. (**102**)

Wolfinger, Madison*, Khushali Vyas*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Optimizing a PCR-based technique to measure telomerase regulation in the yeast Saccharomyces cerevisiae*.- Organisms with linear chromosomes must the address the end-replication problem that prevents the DNA replication machinery from replicating DNA at chromosomal ends, resulting in the loss of potentially important DNA with each cellular division. To overcome this problem, cells attach non-coding, repeated DNA sequences known as telomeres that can be partially shortened without the cell losing DNA from important genes located near DNA ends. Telomeres are synthesized at the end of the chromosome by a ribonucleoprotein called telomerase that has a reverse transcriptase activity that allows it to synthesize DNA from an internally contained RNA template. In most normal somatic cells, telomerase expression is inactive, but in cancer cells telomerase expression is often upregulated, causing telomeres to maintain their length even though they are rapidly dividing and supporting the formation of tumors. The model organism *Saccharomyces cerevisiae* is a yeast has been extensively used as a model for the function and regulation of human telomeres. Many proteins affect the function of telomerase, including the highly conserved, single-stranded DNA binding protein Replication Protein A (RPA) that plays a role in DNA replication, the cell cycle, and DNA repair. Phosphorylation of RPA can change its function in repair and replication, and may affect telomere synthesis. To understand the role of RPA phosphorylation in regulating telomere synthesis we examined telomere length in yeast strains with or without genetic mutations that regulate RPA phosphorylation. Following isolation of genomic DNA from yeast strains, the chromosome ends were amplified using PCR targeted at telomeric regions, and telomeres were analyzed by gel electrophoresis. We will present data suggesting that RPA phosphorylation may regulate the length of telomere lengths in yeast. A better understanding of how normal cells regulate telomere synthesis will provide insights into how malignant cells activate telomerase, and potential therapeutic targets to kill cancer cells. (**47**)

Wong, Felicia*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Effects of virgin coconut oil on oral commensal bacterial species Streptococcus oralis*.- Virgin Coconut Oil (VCO) is an oil product extracted from coconuts that preserves all the natural values of the coconut. VCO's main components are Medium Chain Fatty Acids, lauric acid, and lactic acid. These VCO components have been shown to have antibacterial effects, including inhibiting the growth of bacteria or killing them. The oral cavity (mouth) is a place in the body that houses a multitude of microbes, including commensal and pathogenic bacteria species. The aim of this study is to evaluate the effects of different concentrations of VCO on the growth of oral commensal bacterial species *Streptococcus oralis* utilizing a 24 hour growth curve. The highest concentration of VCO (12%) exhibited the strongest growth inhibitory impact on *S. oralis,* which is comparable to the 5% hydrogen peroxide control. As the concentration of VCO decreased, the strength of bacterial growth inhibition also decreased, thus allowing bacterial growth. With the 0.375% and 0.18% VCO concentrations, the growth of *S. oralis* is very similar to the BHI control. VCO presents a dose-dependent inhibitory effect on *S. oralis* bacteria, as greater concentrations of VCO yield greater bacteria growth inhibition. Future studies will assess the impact of VCO on other species of oral bacteria, commensals and pathogens, to determine a VCO concentration range that can selectively inhibit the growth of pathogenic bacteria while allowing oral commensal bacteria to continue growing. Oral pathogenic bacteria cause negative oral and dental manifestations, such as dental caries (cavities), periodontal (gum) disease, and abscesses. Therefore, the introduction of VCO into the field of dentistry would be important. The implementation of VCO (at a specific concentration) could be considered as part of oral treatments, or in the diet of patients as a means to promote oral health. (**60**)

Wright, Kara*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *The effect of the pesticide malathion on the mortality of the invasive New Zealand mud snail*.- Invasive species may be at an advantage if they can tolerate pollution better than native species. The invasive New Zealand mud snail, *Potamopyrgus antipodarum,* tolerates a wide range of ecological conditions. The purpose of this experiment was to determine the tolerance of this species to a commonly used pesticide. Laboratory studies were conducted on four adult populations of the invasive New Zealand Mud Snail, to assess mortality rates from different concentrations of a malathion pesticide. We used concentrations of 0 (control), 10, 25, 50, 100, 250, and 500 [mg/L] on snail populations from Spring Creek, PA (PA001 and PA009), the Gunpowder Falls River in Maryland (GFMD), and the Musconetcong River in New Jersey (MR). Logistic regression analysis was performed on the collected data showing a significant increase in mortality from an increase in the malathion concentration. We also found significant differences between populations in mortality. Overall, the GFMD population survived at a higher rate than other populations with Spring Creek populations appearing most susceptible to the pesticide. In comparing the survival rate to other studies, it appears that *P. antipodarum* shows similar susceptibility to malathion as other aquatic snail species. (**80**)

Wynings, Rachel*, Alyson Grindall, Nathan Hendel, Nicole Wartella, and William Biggers Wilkes University, Wilkes-Barre, PA 18766. *Effects of Microcystis aeruginosa on the Reproduction and Development of Capitella teleta*.- Cyanobacterial Harmful Algal Blooms (CHABs) that occur in freshwater and marine ecosystems are well known in causing toxicity to both marine invertebrates and vertebrates. We have investigated the effects of *Microcystis aeruginosa*, a cyanobacteria that causes CHABs and produces toxic microcystins, on the survival, growth, and reproduction of the polychaete annelid *Capitella teleta*. This polychaete is viewed to be an opportunistic organism since it tolerates organic pollution loading, high hydrogen sulfide levels, and low oxygen levels very well and therefore becomes a dominant species. Our laboratory results indicate that the presence of *Microcystis aeruginosa* in the water surprisingly is not toxic to *Capitella*, as juvenile worms of *C. teleta* were found to consume the *Microcystis* cyanobacteria without apparent toxicity as evidenced by fecal pellets, and also exhibited an increased growth rate when supplied with both *Microcystis* and Tetramin compared with control cultures grown with just Tetramin. When provided with just *Microcystis* as a food source however, females were found to reabsorb their eggs without completing larval development. These results indicate that *Microcystis* algal blooms may be beneficial to the growth and development of this hardy polychaete species in the marine environment instead of being toxic. (**76**)

Zarilla, Alexandria*, Daniel Oar*, Joshua Nel*, and Quyen Aoh Gannon University, Erie, PA 16541. *Secretory carrier membrane protein 3's (SCAMP3) role in β-amyloid production and secretion*.- Alzheimer's disease is a neurodegenerative disease associated with loss of memory and cognitive function. The aggregation of extracellular plaques containing β-amyloid is related to the processing of the amyloid precursor protein (APP). When endocytosed to the early endosome, APP will either be degraded by the lysosome or sent back to the *trans*-Golgi network. Degradation of APP is regulated by endosomal sorting complexes required for transport (ESCRTs). Disruption of ESCRT function leads to accumulation of β-amyloid. The secretory carrier membrane protein 3 (SCAMP3) interacts and opposes the function of the ESCRT proteins. In this study, we have found that expression of APP-EGFP in H4 neuroglioma colocalizes with SCAMP3. Interestingly, APP-EGFP and SCAMP3 are found in the trans-Golgi Network in transiently transfected cells and in the late endosome/lysosome in stably transfected cells. These results suggest that SCAMP3 has a role in regulating APP trafficking in the TGN-endolysosomal system. We hypothesize then that SCAMP3 may regulate APP trafficking by promoting or inhibiting trafficking of APP to the lysosome and propose to examine SCAMP's effects using RNA interference in both an immunofluorescence and biochemical ELISA assays. (**40**)

Zondory, Hunter*, Lily Velazco*, and Lawrence Mylin Messiah University, Mechanicsburg, PA 17055. *Generating neutralizing monoclonal antibodies against bacteriophage T4: designing a screening assay*.- Antibodies protect by various mechanisms, but induction of antibodies that block infection by binding to pathogen surface structures is a goal of current vaccines. Past Messiah University Microbiology courses included experiences wherein students blocked infection of *Escherichia coli* B by bacteriophage T4 using polyclonal T4-specific goat antiserum. Unfortunately, the polyclonal serum is no longer available. We have undertaken to generate mouse monoclonal antibodies that neutralize phage T4 to use in the same laboratory experiences. Our strategy was to immunize Balb/c mice with concentrated T4 suspensions from which endotoxin (lipopolysaccharide) had been depleted by gentle organic extraction. Mice were injected twice over a two week period with ~ 1.6 – 3.5 x 1010 pfu of T4r+ phage. Serum was prepared from blood collected by cheek vein puncture and assessed for T4-neutalizing activity in a 96-well plate scale-screening assay. Briefly, small amounts of *E. coli* B and T4 were combined in each well. Ongoing infection by T4 limited the density of bacterial growth in a well when measured at 6 – 8 hours. The presence of neutralizing antibody prevented infection, and instead allowed the bacteria to grow to near-saturation. Use of serially diluted serum samples allowed relative neutralizing titers to be determined. This presentation will describe development of the 96 well plate-scale screening assay and how it was further adapted to tolerate the presence of antibiotic that will be in supernatants of hybridoma cultures (Gentamicin, or the mixture of Penicillin and Streptomycin). Exponentially growing *E. coli* B cells were transformed with plasmids encoding ampicillin and either gentamicin or streptomycin resistance. Infection by T4 was confirmed in the presence of the relevant antibiotic, as well as the ability of each transformant to proliferate if T4 was neutralized by goat antisera under similar conditions. Production and screening of hybridomas is in progress. (**31**)