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Abstract Book

ABSTRACTS

Listed alphabetically by first author's last name.

Acocella, Ryan*, and Anne Szklarski King's College, Wilkes-Barre, PA 18711. *Experimental and computational investigation of the isomerization of vicinal dibromides in conformationally rigid cyclohexane systems*. — Conformationally rigid cyclohexane systems containing vicinal bromine atoms can undergo a diatropic shift, or 1,2 interchange, when heated. This isomerization results in the rearrangement of the bromine atoms from the diaxial positions to the diequatorial positions. The goal of this project was to determine if this diaxial-diequatorial isomerization could be developed into an undergraduate laboratory experiment that would demonstrate the concept of kinetic and thermodynamic products. The first substrate investigated, 4-(*tert*-butyl)cyclohexene, was brominated to give a 9:1 ratio diastereomers, favoring the kinetic product. The kinetic product has the bromine atoms in the diaxial positions, whereas the thermodynamic product has both bromines in the equatorial position. The isomerization of 1,2-dibromo-4-(*tert*-butyl)cyclohexane was then completed under polar and nonpolar conditions by heating the substrate neat or in d_6-DMSO at various temperatures. The ratio of diequatorial to diaxial isomers for this simple substrate was monitored using gas chromatography/mass spectroscopy (GC/MS). The thermal equilibration ultimately resulted in a 1:1 ratio of isomers, indicating that the thermodynamic product was not significantly favored under these conditions. As a result, two additional substrates, cholesterol and a Diels–Alder adduct, were also investigated. Using the Spartan 2014 program, the three substrates were analyzed computationally in an effort to explain and predict the diastereomeric ratio for each substrate. The results of the isomerization reactions, the computational analysis, and the current status of the undergraduate laboratory experiment will be discussed. (**146**)

Acosta, Gabbrielle*, and Quyen Aoh Gannon University, Erie, PA 16541. *The Role of Ent3p in Put4p trafficking from the trans-golgi network to the plasma membrane*. — In cells, nitrogen is necessary for the production of many essential cellular products, such as proteins and nucleic acids. Often, nitrogen sources such as amino acids are imported from the extracellular media through transporters. For the brewer's yeast, *Saccharomyces cerevisiae*, a major source of nitrogen is the amino acid proline. Several studies suggest that the expression and transport of Put4p to the cell surface is regulated, much like the general amino acid permease Gap1p. Our preliminary data suggest that the deletion of clathrin adaptor *ENT3* reduces the growth rate of yeast grown in proline, suggesting that it regulates Put4p trafficking. In this study, we have tagged Put4 with Green Fluorescent Protein (GFP) and will determine if Ent3 is required for its trafficking to the cell surface. (**129**)

Ahmed, Gaser*, M. Dana Harriger, and Brad Engle Wilson College, Chambersburg, PA 17201. *Analysis of the effects of gluten proteins and low-gliadin wheat products on celiac disease in NOD-DQ8 mice*. — Celiac disease (CD) is an autoimmune disorder triggered by the ingestion of gliadin, a wheat gluten protein. Gluten is composed of gliadin and glutenin. According to Mayo Clinic data, 1% of adults in the U.S. have CD. Although there are medications that can suppress the symptoms, there are no cures for CD and a strict gluten-free diet is the only resort. Gliadin is the causal agent that triggers the immune response. The down-regulation of gliadins in wheat by RNAi (interference) provides low gliadin products, which may offer several more options for CD patients. This study was performed to determine the effects of gluten, gliadin, glutenin, and the low-gliadin products on the progression of CD plus ascertain if there is an intake threshold. The transgenic mouse model, NOD-DQ8, was utilized. Mice were exposed to different amounts of gluten, gliadin, and low-gliadin products by oral gavage. Blood samples were collected every two weeks from the tails, and the tissue transglutaminase tTG-IgA enzyme-linked immunosorbent assay (ELISA) was performed on the samples. Biopsies of the small intestine were collected for histological analysis of crypts, villi abnormalities, and the count of intraepithelial lymphocytes. Results of the study will provide further information about the immunotoxicity of gliadin, glutenin, and the safety of consumption of low-gliadin products, which may set the stage for application toward humans. (**78**)

Allen, Mia*, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The effects of chloroform and microbeads on zebrafish embryo development.* — Polyethylene beads (plastic microbeads) and trihalomethanes are persistent organic pollutants which are known to accumulate within the aquatic environment. Microbeads are present in a variety of personal care products such as: toothpaste, facial wash, and soap. Trihalomethanes are derivatives of chlorine which is used to sterilize drinking water. There are four different trihalomethanes which include: chloroform, bromodichloromethane, dibromochloromethane, and bromoform. It has been postulated that plastic microbeads and trihalomethanes combine to create a “toxic pill” for aquatic life. This research investigates the “toxic pill” theory. Zebrafish embryos were used as model organism for observing changes among different stages of embryonic development. Zebrafish embryos were subjected to four different experimental conditions: optimal water quality, water with added chloroform, water containing microbeads, and water containing microbeads infused with chloroform. Microscopic observations were recorded across 1 week of development and the occurrence of identifiable structures, malformations, hatchings, movements, free-swimmers, coagulation, and deaths were recorded and statistically compared between groups. Findings showed that specific embryonic stages were negatively affected by chloroform and exhibited malformations such as failure to complete the hatching phase, failure to detach from yolk, acquisition of a more curved/abnormal body structure, as well as a decreased survival rate compared to untreated control. This research suggests that zebrafish embryonic development is affected by chloroform and chloroform-infused microbeads. (**113**)

Alshahrani, Ahmed*, Christine Proctor, and M. Dana Harriger Wilson College, Chambersburg, PA 17201. *An epidemiological modeling approach to study the correlation between dromedary camels, Camelus Dromedarius and MERS-CoV*. — The Middle Eastern Coronavirus (MERS-CoV) is a coronavirus that emerged in Saudi Arabia in 2012, and has spread to 27 countries around the world. The largest outbreaks, approximately 80% of reported cases (1269), have occurred in Saudi Arabia. Like other coronaviruses, MERS-CoV affects the upper respiratory tract causing cough, fever, or breathing difficulties. In some studies, dromedary camels have been indicated as a potential host for the virus, with zoonotic transmission (animal to human) occurring. Aerosol transmission (human to human) has also been suggested to occur. To study the transmission, an SRI model was created to study the correlation between several risk factors (age, sex, population density, co-morbidity, contact to dromedary camels, exposure to infected cases, consumption of raw camel’s milk), and the transmission of MERS-CoV. The data for all 1269 reported MERS cases in Saudi Arabia were collected from the World Health Organization (WHO) and a follow up of the cases was conducted with Saudi Ministry of Health and Saudi International Health Regulations (IHR). Generalized linear models were used to evaluate which potential risk factors or combination of factors best explained the observed transmission rate. The study aims to identify which risk factor or a combination of risk factors are driving the transmission rate of MERS-CoV. Results from this study can be used to control or minimize the spread of the virus, and to avoid future outbreaks of MERS-CoV. (**5**)

Andre, Beverly*, Cynthia Surmacz, John Hranitz, Ibrahim Cakmak, and Selvi Cakmak Bloomsburg University, Bloomsburg, PA 17815. *Sublethal effects of acaracide treatments in Honey Bees*. — Honeybees (*Apis mellifera*) have experienced global declines, most pronounced in the USA and Europe, linked to Colony Collapse Disorder (CCD). While many factors may cause CCD, *Varroa* mites strongly influence hive health and persistence, directly and indirectly as an ectoparasite and disease vector. Beekeepers control infestations with acaracides, pesticides applied to bee hives to kill mites. Because sublethal stress (SLS) impairs bee performance and affects hive health, we hypothesized that acaracides cause SLS in honeybees. The intracellular chaperone heat shock protein 70 (HSP70) is an excellent biomarker for SLS in honeybees. This research, a collaboration between Bloomsburg University and the Beekeeping and Development Center in Bursa, Turkey, determined the levels of HSP70 (i.e., SLS) in honeybees pre- and post-treatment for mites with synthetic pesticides (coumaphos, an organophosphate and flumethrin, a pyrethroid) or natural (organic) pesticides (formic acid, thymol mix, and oxalic acid). Pesticides were applied by standard beekeeping practices at manufacturers' recommended dosages for treatments of *Varroa* infestations. Bee samples were collected pre- and post-treatment. HSP70 levels were measured by ELISA in tissues from homogenized head capsules. Among the synthetic pesticides, coumaphos did not affect HSP70 levels while flumethrin decreased the HSP70 levels, possibly associated with mite abatement. Among the natural pesticides, the thymol mix decreased HSP70 levels. The method of oxalic acid application affected sublethal stress levels; liquid oxalic acid treatment increased HSP70 levels, while steamed oxalic acid had no effect. Formic acid did not affect HSP70 levels. These findings suggest that the thymol mixture and flumethrin caused the least sublethal stress to bees and corroborates that bees are more sensitive to oxalic acid than formic acid, as natural acaracides. This research has the potential to inform beekeepers on the pesticide types and dosages that will control mite infestation while minimizing stress to the honeybees. (**52**)

Arnold, Lindsey*, Rachel Daley*, David Matlaga, and Matthew Persons Susquehanna University, Selinsgrove, PA 17870. *Variability in spider-beetle interactions across a Japanese knotweed-dominated riparian buffer*. — Invasive plant species can affect arthropod diversity within riparian buffer systems. Abiotic factors, such as light, moisture and ground cover may mediate intraguild interactions. Using pitfall traps, we sampled wolf spider and ground beetle diversity across a Japanese knotweed-dominated riparian buffer. We also baited traps with wolf spiders to determine if ground beetles avoided traps. Arthropods were sampled between June and November. We examined the effects of abiotic factors and chemical cues on substrate preferences among two common species: the wolf spider *Tigrosa helluo* and ground beetle *Pterostitchus melanariu*s. Using a series of substrate tests, *T. helluo* and *P. melanarius* were placed in containers with two substrate choices that varied in light levels, litter presence, or moisture mimicking field conditions. In addition, we tested soil substrate preferences for each species with and without conspecifics odor cues. Preliminary results of pitfall trap data suggest that diversity is lowest in the knotweed compared to adjacent vegetation. Ground spider and beetle diversity and abundance were reduced within knotweed. Substrate preference tests suggest that, while light and moisture levels had little effect on habitat preference, both species preferred litter over bare soil. Both spiders and beetles showed a significant preference for substrates with beetle odor cues when paired with spider cues, however this effect was not as strong when beetle or spider cues were paired with bare soil devoid of either cue. Given the size asymmetry of beetles and spiders, spiders likely represent a greater predation threat. Spider cues may represent a proximate mechanism for the competitive exclusion of beetles from preferred habitats. Odor-mediated exclusion through predation threat and abiotic structural changes by invasive plants species may structure ground arthropod communities among intraguild predators. (**47**)

Balasundram, Miriam*, and Anya Goldina Elizabethtown College, Elizabethtown, PA 17022. *Individual recognition in the crayfish genus Orconectes.* — The ability to distinguish neighbors from strangers is essential for conserving energy and minimizing aggression intensity in territorial animals. Unlike status recognition where recognition is based solely on individuals' social status, individual recognition is the ability to distinguish conspecifics based on unique characteristics. Status recognition has been shown in most vertebrate and some invertebrate species. In this study, we examined individual recognition in the crayfish *Orconectes rusticus* and *Orconectes obscurus*. All animals were socially isolated for 1 week. Following the isolation period two focal individuals were placed in a tank for a familiarization trial during which the winner of the interaction was considered dominant and loser a subordinate. Following the familiarization trial, each individual was paired with 3 opponents; 1) known opponent from the familiarization trial, 2) an unknown opponent of the same status as known opponent, and 3) a naïve individual, in three separate memory tests. The order of memory tests was randomized. Aggression intensity of 44 focal individuals exhibited during memory tests was compared to the initial aggression during familiarity trials. Preliminary analysis shows that once status is established, dominant individuals stay aggressive and maintain their status. Similarly, subordinates maintain low levels of aggression and stay subordinate in subsequent memory tests. Persistent winning and losing in dominant and subordinate focal individuals, respectively, indicates winner and loser effects. Dominant and subordinate individuals do not adjust aggression based on opponent type, suggesting that crayfish are not capable of individual recognition. We did not observe any difference in aggression, status establishment, or individual recognition between the two species. Future analysis will examine possible difference in fighting strategies between familiarity trials and memory tests in the two species. Our current findings are consistent with previous studies showing that while crustaceans exhibit robust winner and loser effects, they do not exhibit individual recognition. (**82**)

Banach, Christopher*, Alison Dyszel*, Serena Ngan*, Angeline Lonardi, Riley Slate, Thomas Basil, and Lara Goudsouzian DeSales University, Center Valley, Pennsylvania 18034. *Impact of ethanol on markers of heterochromatin maintenance and trinucleotide repeat expansion in Saccharomyces cerevisiae*. — Using three separate assays, our research examined ethanol's impacts on gene silencing via the Telomere Position Effect (TPE), trinucleotide repeat expansion, and chromosomal stability in *Saccharomyces cerevisiae*. Using a cell viability assay, we examined how ethanol influences gene expression through TPE. Our results show that *S. cerevisiae* grown in 5% ethanol undergoes increased silencing of a gene placed proximal to a modified telomere. Expansion of trinucleotide repeats is known to be a cause of several serious human diseases, such as Huntington's Disease and Fragile X Syndrome. We investigated the effect of ethanol on the level of CTG trinucleotide repeat expansion in the euchromatin of *S. cerevisiae*. Preliminary data indicates that ethanol in the growth medium causes increased levels of trinucleotide repeat expansion in *S. cerevisiae*. Genomic instability is a major cause behind many illnesses, including cancer. Using the *ADE3/8* color assay with a disomic strain of *S. cerevisae*, we investigated ethanol's impacts on chromosome loss in *S. cerevisiae*. Our work thus far shows that the presence of 5% ethanol in the growth medium increases chromosomal stability. (**130**)

Barr, Garrett* King's College, Wilkes-Barre, PA 18711. *Estimating the density of larval salamanders in fish and fishless streams and testing assumptions of mark-recapture techniques*. — Salamanders are an abundant and important component of northeastern and mid-Atlantic forests. Although their abundance and ecological roles in streams are less-studied, our understanding is increasing. Estimates of larval salamander density range from under 1 to over 100 m^{-2}, though most recent estimates (using mark-recapture and removal methods) do not address the impacts of fish. We estimated salamander density in fish and fishless streams in northeastern PA with mark-recapture using a Visible Implant Elastomer. Because of concerns that fish predation may bias estimates of salamander density, we also conducted laboratory and field experiments to test the effects of marking larval salamanders on fish predation. Our results confirm expectations that estimates of larval salamander density are higher in fishless streams. Contrary to expectations, laboratory and field experiments show that marked salamanders experience lower fish predation, suggesting that approaches to estimating salamander density should be further tested and refined to avoid biases. Future research should also investigate why marked salamanders experience lower predation rates. (**62**)

Belanger, Julie* King's College, Wilkes-Barre, PA 18711. *From inactivated virus vaccines to drug delivery: exploring creative uses for small hydrophobic molecules*. — Biological membranes, such as those found in cells and enveloped viruses, are comprised of lipid bilayers. These bilayers are known to have a hydrophilic surface that interacts with the aqueous environment, and an internal hydrophobic region, where the fatty acid tails of these lipids reside. It has been previously shown *in vitro* that hydrophobic naphthylenic compounds, such as napthylazides, selectively partition into this hydrophobic region. In the case of enveloped viruses such as influenza and HIV, the localization of these compounds within the membrane, along with UV irradiation, can be used to inactivate the viruses with preservation of surface epitopes. These inactivated virus preparations have been explored *in vivo* as novel vaccines for a variety of enveloped viruses. Similar partitioning of hydrophobic compounds can be used in simpler, non-infectious liposome-based systems that are more amenable to undergraduate research projects. In these systems, the interactions of hydrophobic compounds within a bilayer membrane comprised of egg phosphatidylcholine lipids is being explored toward applications in triggered drug release from liposomes. This presentation will explore the major findings of these areas of research, discussion of designing research for undergraduates using non-infectious materials, and a discussion of ongoing work. (**73**)

Bentkowski, Kristine, Vanessa Gomez*, Jane E. Huffman, and John Mischler East Stroudsburg University, East Stroudsburg, PA 18301. *High prevalence of Bartonella spp. among Pennsylvania Black Bears.* — Over the last decade tick-borne diseases have been increasing in the United States among human and wildlife populations. Confirmed cases of other tick-borne diseases have been noted along the northeast coast of the United States. Tick-borne diseases such as *Babesia* spp., *Bartonella* spp., and *Anaplasma phagocytophilum* are becoming more prevalent. In this study American black bears (*Ursus americanus*) were tested for tickborne pathogens transmitted by black legged ticks (*Ixodesscapularis*). Black bear samples were tested for the prevalence of *Babesia* spp., *Bartonella* spp., and *A. phagocytophilum* through PCR analysis. Results indicated that 69.3% (n=70/101) of bears tested were positive for *Bartonella* spp., and 1.99% (n=2/101) were positive for *A. phagocytophilum*, and 0.00% were positive for *Babesia* spp. No co-infections were detected amongst the black bear samples. This study is the first to document a high prevalence of *Bartonella* spp. in Pennsylvania black bear populations. (**3**)

Bertoline, Alaina*, and Jessica Schedlbauer West Chester University, West Chester, PA 19383. *Ecological integrity of edge and interior environments at West Chester University's Gordon Natural Area*. — Compared to forest interiors, forest edges are often degraded in habitat quality and ecological integrity because of edge effects. The recent clearing of a power line right-of-way in West Chester University's Gordon Natural Area (GNA), a protected eastern deciduous forest in southeastern Pennsylvania, has increased the forest area exposed to potentially harmful edge effects. A modified Rapid Upland Forest Assessment (RUFA) method was used to assess differences in ecological integrity between edge and interior environments of the GNA. This assessment was performed in five 50 m transects per environment and two 0-10 cm soil samples were collected per transect; ANOVA and cluster analysis were used to evaluate RUFA scores across growing environments, and ANOVA was also used to analyze soil pH data. Forest interior RUFA scores were almost two points higher than edge RUFA scores on average, a significant difference ($p < 0.05$) indicating lower ecological integrity in the edge environment. Interior transects scored higher in most RUFA metrics assessing forest structure and were the only transects with low presence or total absence of non-native plants. Unexpectedly, edge transects tended to score higher in measures of native forest composition. Significant differences between growing environments were also borne out by cluster analysis of RUFA scores that produced distinct clusters for the two growing environments. Soil pH was significantly higher ($p < 0.05$) and closer to neutral in the forest edge relative to the interior, which may promote plant growth and survival in the edge environment through increased nutrient availability. Overall, these findings suggest degraded environmental quality in both edge and interior environments, with worse conditions at the edge. Future management activities should focus on preventing the spread of non-native plant species into the forest interior and possibly reducing deer browsing pressure on understory plants. (**24**)

Bischer, Andrew*, and Abdalla Aldras East Stroudsburg University, East Stroudsburg, PA 18301. *The effects of artificial sweeteners and probiotics on the gut microbiome and immune system.* — The important role the microbiome plays in mammals is something that has been a key area of research in recent years. The microbiome plays an important role in both immune system development and health. Alterations to the composition of the microbiome have been found to be associated with diseases such as type 2 diabetes, obesity, Parkinson's, and irritable bowel syndrome. The effects of artificial sweeteners such as saccharin, sucralose, and aspartame on the microbiome have been an increasing area of research recently as their popularity continues to increase. As probiotics have become more popular as well, how they interact with the normal flora of the microbiome is also a focus of recent research. In this experiment, the three artificial sweeteners as well as a probiotic were fed to groups of mice. The large intestine contents were swabbed and cultured anaerobically to determine the effects on the gut microbiome diversity. Using ELISA on blood samples and tissue samples, cytokine and IgA levels were also studied and compared. The cytokines tested include tumor necrosis factor alpha, interleukin-2, and interferon gamma. The results indicate both sucralose and probiotics cause significant decreases in IgA levels in blood serum. Probiotics also caused a significant decrease in secretory IgA in the lumen of the small intestine. Sucralose was found to cause a significant decrease in IFN-γ in the Peyer's patches. (**127**)

Bischer, Andrew*, and Joshua Loomis East Stroudsburg University, East Stroudsburg, PA 18301. *Identification and characterization of a novel antibiotic-producing <u>Microbacterium</u> <u>sp.</u>* — Actinomycetes are Gram positive filamentous bacteria that are commonly found in soil. They are one of the most prominent antibiotic-producing bacteria in the world and include the genus *Streptomyces*. As the antibiotic resistance crisis grows and fewer companies are developing new antibiotics, universities must play a more important role in discovering and developing new antibiotics. The CDC estimates that 23,000 Americans die every year due to antibiotic resistante bacterial infections such as MRSA and multi-drug-resistant tuberculosis. In an attempt to identify a novel antibiotic-producing bacterium, soil samples were taken from different ecosystems throughout the eastern United States and screened for antibiotic-producing actinomycetes. One antibiotic-producer was isolated from an underwater sand sample off the coast of Key Largo, Florida. This species was found to inhibit the growth of all Gram positive bacteria that it was tested against, including a clinical strain of MRSA. It also inhibited the growth of *Mycobacterium smegmatis*. After sequencing the 16S rRNA gene, it was found to be of the genus *Microbacterium*. This is the only documented instance of a species of *Microbacterium* secreting an antimicrobial product. Due to the uniqueness of the colony and its antibiotic-secreting ability, we believe that we have a new species of *Microbacterium* that we have called *Microbacterium largo*. (**124**)

Blazaskie, Michael*, Atasha Rehrig, Grace Emmett, Andrea Nale, Jeff Stephens, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Expression of anchoring proteins and phosphatases correlates with cAMP levels in immortalized rat Schwann cell lines*. — Regulation of Schwann cell proliferation and myelination is orchestrated by a balance between mitogens and promyelinating factors secreted by neurons. *In vitro*, division of Schwann cells is promoted synergistically only when the heregulin/neuregulin family of growth factors and agents stimulating cAMP are added. While the role of cAMP and its effector, protein kinase-A, are well known in Schwann cell growth and differentiation, not much is known about the downstream signaling pathways. AKAPs are a family of proteins that anchor protein kinase-A and other signaling substrates such as phosphatases. This study was conducted to determine the relationship between endogenous levels of cAMP, the expression of AKAP150 and the phosphatase calcineurin, in mitogen-treated Schwan cell lines. Based on previous studies, it was hypothesized that cAMP levels will positively correlate with the expression of both AKAP150 and calcineurin in proliferating cells. Preliminary findings indicate that endogenous levels of cAMP significantly increased in Schwann cells treated with forskolin and heregulin + forskolin in comparison to other treatments. Immunoblot analysis of Schwann cells revealed an increase in the expression of calcineurin when treated with heregulin + forskolin or forskolin only in comparison to heregulin. In contrast, the levels of AKAP150 were decreased upon stimulation with both heregulin and forskolin in comparison to forskolin or heregulin only. Immunofluorescence experiments revealed that AKAP150 and calcineurin displayed an overlapping cytoplasmic staining pattern in forskolin-stimulated cells. Atomic force microscopy of proliferating Schwann cells exhibited a rounded topography under forskolin treatment. In conclusion, these observations suggest that synergistic activation of the cAMP pathway in Schwann cells along with heregulin correlates with an upregulation of calcineurin and downregulation of AKAP150. (**14**)

Breymeier, Corinne*, and Lisa Antoniacci Marywood University, Scranton, PA 18509. *Characterization of the Interaction between Mps3 and Cdc5 in Saccharomyces cerevisiae*. — Mps3 is a nuclear envelope protein identified in *Saccharomyces cerevisiae* and is involved in several chromosome functions such as sister chromatid cohesion, DNA damage repair, and telomere clustering. Mps3 is hypothesized to be involved in many of these processes through its association with several different chromatin associated proteins (Elg1, Htz1, Ctf18, Eco1). Recently our lab identified a physical interaction between Mps3 and the polo-like kinase Cdc5. Cdc5 functions in regulation of many essential cell pathways including several that Mps3 also functions. Our lab has generated a double mutant of Cdc5 and Mps3 to characterize the physical, genetic, and functional interaction of Mps3 and Cdc5. (**7**)

Broholm, Tessa*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Effect of local environment on abundance, reproductive effort and upland movement of woodland salamanders*. — Salamanders and other amphibians are disproportionately threatened due to habitat loss and fragmentation and other anthropogenic stressors. Threats to woodland salamanders in northeastern Pennsylvania and New Jersey have led to many habitat restoration projects that focus primarily on vernal breeding pool conditions and creation. However, both obligate vernal pool breeding salamanders and non-vernal pool breeding salamanders spend most of their lives in the woodland area surrounding pools. Therefore, it is important that future restoration projects consider how environmental factors in upland habitats affect the distribution and movement of both types of salamanders. The objective of this study was to investigate the impact of road proximity, canopy cover and soil pH on the reproductive effort and upland movement of salamanders. These parameters were compared between three isolated pools (> 1000 m from the nearest road) and two pools in a fragmented habitat (< 100 m from two roads) within a Pennsylvania state park. Preliminary results indicate that road proximity does not have a significant effect on vernal pool water chemistry, and salamander egg mass abundance was greater in the fragmented location. However, significantly more adult salamanders were found at cover board sites in upland habitat surrounding isolated pools. Results for salamanders correspond with results of a previous study on wood frogs in the same location in which wood frogs in the fragmented location were trapped at a lower frequency near roads than expected by chance. Together, these two studies indicate that the presence of roads may reduce the amount of upland habitat utilized by amphibians. Further investigation into soil pH, canopy coverage, and night migrations during this breeding season will provide additional information about salamander habitat preference. (**64**)

Brough, Carla, and Ondra Kielbasa* Alvernia University, Fleetwood, PA 19522. *Immunofluorescence and fusion index analysis of ethanol-treated C2C12 muscle cells in culture*. — Alcoholic myopathy affects 40-60% of long-term alcoholics and is more prevalent than other common alcohol-related diseases such as cirrhosis of the liver. A range of cellular and molecular mechanisms have been implicated in its pathogenesis, including decreased protein synthesis, altered gene expression profiles, misregulated signaling pathways, increased cell death, and increased oxidative stress. Despite the growing body of knowledge in this area, the process by which ethanol consumption leads to the development of myopathy in skeletal muscle is not well understood, and multiple factors are thought to contribute to disease progression. A key event in the formation of skeletal muscle is the fusion of myoblasts to form multinucleated muscle fibers. There are conflicting reports in the literature with regard to the effect that alcohol has on fusion of myoblasts during differentiation, with at least one study showing a negative effect and another showing no effect on this process. The purpose of this study was to address this discrepancy by assessing the effect of ethanol on the differentiation of C2C12 skeletal muscle cells in culture, utilizing the fusion index calculation as a measurement of differentiation. Our results demonstrate a significant reduction in the fusion of myoblasts to form multinucleated myotubes when treated with a physiologically relevant concentration of ethanol at the start of differentiation. These results are consistent with previously published evidence demonstrating that ethanol reduces the differentiation capability of skeletal muscle cells, in part by preventing fusion of myoblasts to form mature muscle fibers. In continuing studies, we are examining the expression of fusion-related proteins to determine if they are altered upon treatment with ethanol. (**77**)

Brown, Morgan*, Joseph Artemiou*, and Steve James Gettysburg College, Gettysburg, PA 17325. *Untangling defects in cell cycle control caused by a reciprocal translocation in the fungus Aspergillus nidulans*. — SR/RRM ribonucleoproteins function in a variety of nuclear processes, including mRNA transcription, export of mature mRNAs from nucleus to cytoplasm, and intron splicing, but were not known to be involved in control of the cell division cycle. We ascribed a previously unreported role in cell cycle regulation to a SR/RRM family protein, *snxA* (suppressor of nimX–Cdk1). *snxA* mutations specifically affect the G2-M transition of the cell cycle by suppressing defects in regulators of the CDK1 mitotic induction pathway. mRNA and protein expression are strongly down regulated in *snxA*1 and *snxA*2 mutants, suggesting that *snxA* acts by restraining the transition from G2 phase to mitosis (James *et al*., 2014. *GENETICS* 198: 617). We recently discovered the genetic basis for down-regulation of *snxA* expression in the *snxA* mutants: whole-genome sequencing revealed a reciprocal translocation in which part of the *snxA* locus on the right arm of Chromosome II was joined to a large uncharacterized gene on the left arm of Chromosome I. The Chromosome I breakpoint occurs within the fourth exon (out of five) in a novel GYF-domain gene, AN6228. GYF-containing proteins associate with proline-rich motifs in certain target proteins. In this study, we are determining the contribution of each disrupted gene, *snxA* and AN6228, in restraining mitotic induction. For example, a complete deletion of AN6228 revealed that a subset of traits formerly ascribed to the *snxA* locus may instead be attributed to defects in this GYF-domain protein. Currently, we are reconstructing the AN6228 partial disruption created by the translocation, in order to assess whether this disrupted allele may confer partial function and to more precisely characterize its contribution to the cell cycle. In addition, reciprocally translocated chromosomes often display strong recombinational suppression in the vicinity of translocation fusions. We are using linkage analysis to investigate this phenomenon in the translocation mutants. (**132**)

Burns, Jessica*, Elizabeth McGovern, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. *Species differences in bat emergence and foraging times in northeastern Pennsylvania*. — Different species of bats are known to feed on different types of insects and may begin foraging at different times after sunset, depending in part upon their preferred prey. We used acoustic monitoring data from 2 sites in the Delaware Water Gap National Recreation Area in northeastern Pennsylvania to compare the timing of early-night foraging activity for 5 different species of insectivorous bats. Bat echolocation calls were recorded as.wav files with an AR125 detector and calls were identified to species using the SonoBat 3 autoclassifier. We restricted our analyses to recordings made between 1 June and 15 July 2014 in an attempt to exclude migrating bats. We then compared the timing of bat activity during the first 3 hours after civil twilight to assess differences in early-night activity patterns between species. We used a Kruskal-Wallis test to compare the distribution of bat activity between species within this 3-hour period. Our preliminary analyses included echolocation calls from big brown bats (*Eptesicus fuscus*), eastern red bats (*Lasiurus borealis*), hoary bats (*Lasiurus cinereus*), silver-haired bats (*Lasionycteris noctivagans*), and unidentified *Myotis* spp.; sample sizes for tri-colored bats (*Perimyotis subflavus*) were too small to be included in our analyses. We found highly significant differences ($p < 0.001$) in median activity times between species in this 3-hour period, with hoary bats active earlier and eastern red bats active later than the other species. (**38**)

Cabrera Vicens, Brenda*, Kelly Perri, and Joyce Belcher Cabrini University, Radnor, PA 19087. *Testing the effects of prolactin on osteoblast differentiation*. — In this study, we investigated the effect of the hormone prolactin, or PRL, on the formation of bone using an osteoblast cell model for differentiation. If osteoblast differentiation is obstructed, then bones are more likely to become brittle. Bone disorders, such as osteoporosis, are very common so it is important to understand such disorders on the cellular level. There is little knowledge of how prolactin affects bones on the cellular level and whether it has a role in specific bone disorders. We hypothesized that osteoblast differentiation would increase as levels of prolactin increased. In this experiment, different dosages of prolactin were withheld or given to three different groups of osteoblasts: a control group, a low dosage group, and a high dosage group. These dosages were intended to mimic real-life physiological events in humans. For example, it is known that the high dosage level mimics the amount of prolactin that is secreted during early pregnancy. Since days 7, 14, and 21 are critical points in osteoblast growth cycle, different assay and stains were administered or performed on those days. The different assays and stains were biochemical assay, alkaline phosphatase assay, mineralization stains (Alizarin Red and Von Kossa) and calcium measurement assay. With the methods performed on the differentiating osteoblasts, it was proven that as the dosage of prolactin increased, so did osteoblast differentiation and mineralization (of calcium, phosphate and other minerals). In conclusion, this experiment has helped us to understand how prolactin can affect osteoblast differentiation, and possibly bone mass. More research will be conducted on other types of bone cells such as osteocytes, chondrocytes, and osteoclasts. (**79**)

Callerame, Deanna*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Optimization of set of template-primer DNAs for robust PCR reaction*. — The polymerase chain reaction (PCR) has been a commonly-used technique since it was invented in the 1980s. Although it is a basic laboratory procedure, there are a multitude of projects that involve the amplification of DNA for use in virology, forensics, and so on. Three components used in this process can be produced in-house as opposed to purchasing them commercially: template DNA (pUC 19 from *E. coli*), DNA polymerase (*Taq* DNA polymerase), and DNA ladder (used in gel electrophoresis). The expenses for running a PCR add up, so it is crucial that the reaction produces as much product as possible. By optimizing the PCR—altering primer concentration, changing magnesium concentration, and using different annealing temperatures—the amount of amplicon can be maximized. Once the PCR is running successfully, the product can be used as a control template-primer for the PCR reaction of which the success of molecular cloning and protein overexpression of the *Taq* DNA polymerase is reliant upon. (**172**)

Camarata, Tia*, and Andrew Samuelsen Albright College, Reading, PA 19604. *Designing a binary plasmid that allows inducible non-antibiotic elimination of the host bacterium*. — Antibiotic usage is not always a feasible method for controlling bacterial growth in a research setting. Specifically, the soil bacterium *Agrobacterium tumefaciens* is useful in genetically engineering plant tissue, but there are a limited number of antibiotics that effectively kill this species. Therefore, the goal of this project is to develop a method of engineering *Agrobacterium* with the potential to be eliminated without the use of antibiotics. We are currently in the process of synthesizing a plasmid that has three major components: a *pCambia* backbone, a rhamnose-inducible promoter, and the *E.coli* gene *hok*. pCambia was selected to be the backbone of the proposed synthesized plasmid because it is a binary vector and has been successful in previous plant transformation experiments. Binary vectors are useful because they have a broad host range origin of replication, meaning that they can be used in several species of bacteria with successful replication, namely *E. coli* and *Agrobacterium*. A rhamnose-inducible promoter was obtained that operates best in the presence of low levels of rhamnose and can be suppressed in a solution of 0.2% glucose. Hok is a host-killing peptide that degrades the plasma membranes of bacteria and is naturally present in *E.coli* and is used by the bacterial cell itself during apoptosis. Utilizing the *Hok* gene with a rhamnose-inducible promoter, bacterial death should be able to be controlled (provided the promoter is not leaky). Thus, the growth of an engineered strain of *Agrobacterium* will be controlled by simply changing the growth medium; the colonies will thrive in glucose but will be effectively killed off upon the introduction of rhamnose. This should allow elimination of the bacterium after it has delivered its genetic payload to the plant cell. (**173**)

Carson, Emily*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Identification of a novel genus in the <u>Bacillacecae</u>*. — A bacterial strain, designated EAC, was isolated from Loyalsock Creek and identified as a novel species within the family *Bacillaceae* during an undergraduate microbiology course in the spring of 2016. The bacteria were found to be closely related to *Bacillus luciferensis* and *Bacillus acidiceler*, with 16s rRNA sequence similarities of 98.86% and 98.73% respectively. The phenotypic comparisons of fatty acid composition, carbon utilization, growth sensitivity, and gene content showed that *Bacillus sp. EAC* had more similarities to *Bacillus luciferensis* and *Bacillus acidiceler* than to *Bacillus subtilis*, the *Bacillus* type species. The average amino acid identity (AAI) between *Bacillus sp. EAC* and the reference organisms, *Bacillus luciferensis* and *Bacillus acidiceler*, was 82%, less than the 95% species threshold. The average amino acid identity when comparing the two reference strains or *Bacillus sp. EAC* with *Bacillus subtilis* was 56%. This is substantially less than the 70-95% typically seen within most genera, suggesting that that these three organisms and *Bacillus subtilis* belong in different genera. Many other species in the family *Bacillaceae* have been initially misclassified into the genus *Bacillus* and later moved into new genera. As such, *Bacillus sp. EAC*, *Bacillus luciferensis*, and *Bacillus acidiceler* may belong in a novel genus separate from *Bacillus subtilis*. (**121**)

Carwell, Shanna*, and Deanne Garver Marywood University, Scranton, PA 18509. *Characterization of phthalates as contaminants in unscheduled alcohol samples from the Baltic region*. — Unscheduled alcohol, also known as non-commercial alcohol, is unregulated and could be the cause of many health risks. These alcohol samples are often contaminated with dangerous chemicals, such as methanol, aldehydes, ketones and heavy metals. Phthalates are a group of aromatic diesters that are commonly used to soften and increase flexibility in plastics. The phthalates in plastic containers can be extracted into the alcoholic beverages during the production and cooling processes. Phthalates in food and beverages are regulated around the world, but unscheduled alcohol samples are not routinely assayed for these compounds, which puts consumers at risk. We evaluated a variety of unscheduled alcohol samples from Latvia and Estonia for the presence of diethyl phthalate, dibutyl phthalate, di-isobutyl phthalate, n-butylbenzyl phthalate and diethylhexyl phthalate. They were assayed by LC-MS (tandem liquid chromatography-mass spectrometry) after hexane extraction clean up and concentration. LC-MS is an analytical technique that combines the physical separation of liquid chromatography with mass analysis. Samples contained varying amounts of the phthalate contaminants. Research sponsored by: International Association for Responsible Drinking (**143**)

Chambers, Morgan*, and Jodi Yorty Elizabethtown College, Elizabethtown, PA 17022. *Investigating the connection between apoptosis and the corticosterone-induced loss of splenic dendritic cells in mice*. — Dendritic cells (DCs) are vital components of the immune system that have the unique capability of linking the innate and adaptive immune system by recognizing a variety of antigens and initiating an immune response. Glucocorticoids, such as corticosterone (CORT), regulate DC activity. Prior to this study, preliminary data showed that elevated levels of CORT in mice led to splenic DC loss, which could occur in a number of ways, one being apoptosis. There is much controversy in the literature regarding the ability of CORT to induce apoptosis in DCs. Thus, this study investigated the mechanism of the loss of classical splenic DCs in C57BL/6 mice, following administration of CORT in their drinking water as well as changes in anti-apoptotic protein expression in DC lines in vitro. Mice were exposed to 150 µg/mL CORT in their drinking water for 12 hours. Following spleen processing, flow cytometry was used to quantitatively characterize DCs by cell-surface proteins and assess apoptosis with Annexin-V staining. There was no significant increase in apoptosis or necrosis in the spleens of mice treated with CORT, despite visual reduction in size. In vitro experiments using bone marrow-derived dendritic cells (BMDCs), from C57BL/6 mice exposed to CORT, demonstrated no change in expression of anti-apoptotic proteins Bcl-xL and Bcl-2. Therefore, other reasons for splenic DC loss, such as migration out of the spleen, may be investigated in the future. (**159**)

Chern, Kacie*, Jane Huffman, and Abdalla Aldras East Stroudsburg University, East Stroudsburg, PA 18301. *Local prevalence and strain diversity of Borrelia burgdorferi in Peromyscus leucopus and Ixodes scapularis*. — Lyme disease is now the most common vector-borne disease in the United States. Lyme disease victims experience extremely varied severity of symptoms, ranging from barely any symptoms at all to lifelong suffering and neurological damage. The first aim of this investigation is to compare multiple collection seasons to determine prevalence of *Borrelia burgdorferi,* the etiologic agent of Lyme disease, in *Ixodes scapularis* (blacklegged ticks), the vector of *B. burgdorferi*, and *Peromyscus leucopus* (white-footed mice), the predominant reservoir host of the bacterium in the northeast. The polymerase chain reaction (PCR) was be used to compare urinary bladder, spleen, heart, and ear biopsy samples from *P. leucopus* for the presence of *B. burgdorferi*. Additionally, it has been established that certain clinical strains in broader genotypic categories are associated with differing symptomatology in humans and in mice. The present study is further investigating these strains seeking to determine whether certain strains have proclivities for one tissue or another in mice in the environment. Samples have been collected during 2014, 2015, and 2016 from the same geographic area in northern New Jersey and select sites in northeast Pennsylvania and are currently in testing. (**4**)

Christopher, Thomas*, and Deanne Garver Marywood University, Scranton, PA 18509. *The antimicrobial effect of thymol on biofilm proliferation in hydroponic lettuce farming*. — There are many well-documented benefits to hydroponic farming versus traditional farming methods, including reduced farming space, a controlled growing environment, and no use of harmful pesticides. One of the challenges associated with hydroponic farming is combating the bacterial biofilm that accumulates at the bottom of the reservoir supplying water and nutrients to the system. While not comprised of pathogenic bacteria, this biofilm contains bacteria that can have a deleterious effect upon the development of the crops. Currently, methods to eliminate biofilm include ozonation, copper ionization, and sodium hypochlorite, among others. It is the objective of this research to utilize natural products which can be added to the hydroponic system in order to prevent biofilm adherence and growth. A biofilm sample was obtained from a local farmer and through DNA analysis; four bacterial species were isolated in the biofilm sample: *Bacillus thuringiensis, Pseudomonas aeruginosa, Bacillus amyloliquefaciens,* and *Pigmentiphaga daeguensis*. Thymol, the major component of the essential oil of thyme, was used to evaluate antimicrobial activity against all four strains of bacteria in the biofilm. A concentration effect has been established and proof of concept studies are in progress to demonstrate the effect of thymol on improved growth and health of lettuce plants. (**102**)

Cirilo, Joseph*, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *The Colloidal Enigma: N-phenyl-1-naphthylamine (NPN) and dimethylsulfoxide (DMSO) Colloid Formation in Water*. — Colloids can be found in everyday life, from milk and whipped cream, to jelly and muddy water. Typically, a colloid is a substance suspended in solution, made up of two or more immiscible components. The goal of this research project was to gain a better understanding of colloids that are created in metastable systems comprised of small molecules that have been used *in vitro* to study biological membranes. Colloids that were created and characterized were formed when N-phenyl-1-naphthylamine(NPN) dissolved in dimethyl sulfoxide (DMSO), or acetone, and then added to water. NPN is soluble in DMSO, but not water. DMSO, however, is soluble in water, a property which would seemingly prevent the formation of such colloidal suspensions, the DMSO dissolving in the water and the NPN crystallizing out. Fluorescence microscopy and particle sizing were used to characterize the colloids that formed. NPN is a hydrophobic fluorophore that fluoresces when exposed to light of wavelength about 350nm. It then loses its ability to fluoresce under light, after periods of prolonged light exposure (wavelength 420-460 nm) Particle-sizing using a light-scattering detector indicated that the average size of the colloids ranged from 375-458 nm in radius. Turbidity measurements were done using a fluorimeter, by comparing to turbidity standards. The suspension, itself, appears to be a white cloudy mixture. When observed under a microscope, the individual spheres of the colloids can be seen. This may lead to implications in drug-delivery research, as the small colloids may be able to either pass through or integrate with cell membranes, bringing with them another compound. Further research would include integration of radical scavengers to reduce the photo-bleaching of the colloids, therefore allowing them to be better observed and tracked when placed in the presence of cells. (**140**)

Cobb Irvin, Tracie*, Victoria Gould, and Lara LaDage Penn State University-Altoona, Altoona, PA 16601. *Assessing spatial learning and memory in small squamate reptiles*. — Clinical research has leveraged a variety of paradigms to assess cognitive decline, commonly targeting spatial learning and memory abilities. However, interest in the cognitive processes of nonmodel species, typically within an ecological context, has also become an emerging field of study. In particular, interest in the cognitive processes in reptiles is growing although experimental studies on reptilian cognition are sparse. The few reptilian studies that have experimentally tested for spatial learning and memory have used rodent paradigms modified for use in reptiles. However, ecologically important aspects of the physiology and behavior of this taxonomic group must be taken into account when testing for spatially based cognition. Here, we describe modifications of the dry land Barnes maze and associated testing protocol that can improve performance when probing for spatial learning and memory ability in small squamate reptiles. The described paradigm and procedures were successfully used with male side-blotched lizards (*Uta stansburiana*), demonstrating that spatial learning and memory can be assessed in this taxonomic group with an ecologically relevant apparatus and protocol. (**169**)

Coleman, Alyssa*, and Matthew Persons Susquehanna University, Selinsgrove, PA 17870. *Octopamine effects on wolf spider courtship and mating interactions: more sex or more cannibalism?* — The biogenic amine and neurohormone octopamine (OA) serves as an invertebrate homolog of norepinephrine. A number of octopaminergic insecticides have been developed for crop pests but the impact of these OA-active compounds have been poorly studied among non-target species like spiders. The wolf spider *Pardosa milvina* is an economically and ecologically important ground predator and biocontrol agent in agricultural systems throughout the United States. Previous studies have shown that male wolf spiders with elevated endogenous levels of octopamine show coercive mating tactics compared to low-OA males, suggesting that OA-based insecticides may have negative effects on non-target species in agricultural systems. We compared the effect of ingested octopamine on the courtship, mating, and sexual aggression behavior of both males and females of the wolf spider *Pardosa milvina*. We dehydrated male and female spiders prior to dosing males alone, females alone, both sexes, or neither with a 2 mg/ml concentration of OA and water solution among random pairs of unmated spiders. Additionally we ran a set of spiders that were not withheld water to control for the effects of dehydration. We then measured male courtship duration and intensity, male aggression levels, and female receptivity and aggression across all five treatments. We also measured the frequency of mating success and sexual cannibalism across groups. Preliminary results suggest that OA generally decreased male courtship intensity toward females when females were not also dosed with OA while females dosed with OA did not show elevated aggression. Male mating success was generally lower in OA-treated males but OA showed little effect on male cannibalism. We found no significant effect of dehydration on male and female courtship and mating behaviors, indicating that ingestion is a viable method for dosing spiders with OA. (**46**)

Collins, Crystal*, and Kara Mosovsky Moravian College, Bethlehem, PA 18018. *Antibiotic Tolerance: distinguishing between classical resistance and persistence in a macrophage infection model*. — *Burkholderia pseudomallei* is a facultative intracellular bacterial pathogen that causes the deadly disease melioidosis. Melioidosis is difficult to treat because *B. pseudomallei* is inherently antibiotic resistant. In previous studies, we found that a combination of ceftazidime and INF-γ synergistically reduced the intracellular bacteria in macrophages infected with either *B. pseudomallei* or the related *B. thailandensis*. However, the remaining bacteria are antibiotic tolerant, which could still pose a threat to the host. Using pre-established methods to distinguish between antibiotic resistance and persistance, we have determined that the remaining bacteria are persister cells. Further characterizing these dormant, slow-growing, antibiotic tolerant cells, can potentially lead to future treatments against this fatal disease. (**105**)

Cooney, Dan*, and Quyen Aoh Gannon University, Erie, PA 16541. *The role of SCAMP3 in Amyloid Precursor Protein trafficking*. — Alzheimer’s disease is a neurodegenerative disease associated with loss of memory and cognitive function. The formation of extracellular plaques containing aggregated β-amyloid peptide is related to the proteolytic processing of the amyloid precursor protein (APP). APP is cleaved into two parts, one of which is β-amyloid protein which, in mutant forms, is associated with Alzheimer's pathology. APP can be ubiquitylated in a manner that promotes its sorting into multivesicular bodies and degradation in the lysosome. Current research indicates that the endosomal sorting complexes required for transport (ESCRTs) target APP to be degraded in lysosomes. Disruption of ESCRT function leads to accumulation of β-amyloid. Secretory carrier membrane protein 3 (SCAMP3) interacts with ESCRT proteins to transport and sorting of membrane proteins, therefore SCAMP3 may regulate APP trafficking. We developed a protocol for transfecting APP into HeLa cell line using Mirus Trans-IT X2 lipofection reagent. Optimal transfection was obtained using a low cell density and a low concentration of transfection reagent. We are currently optimizing the protocol for fluorescence microscopy to detect APP in lysosomes and endosomes. (**12**)

Corpus, Larry* Misericordia University, Dallas, PA 18612. *Littoral zone diversity of larval caddisflies (Trichoptera) from Meadows Pond, Dallas, Pennsylvania*. — The diversity of aquatic macroinvertebrates is usually less in ponds than in streams. Reasons given for the lower diversity exhibited in lentic waters include fewer habitats, warmer and less oxygenated water, increased predation, less allochthonous nutrient production and availability, and increased pollution. In order to investigate this difference in diversity, the littoral zone of a small pond at The Meadows nursing and rehabilitation center in Dallas, PA, was sampled monthly from August 2015 to July 2016 in order to: 1) establish a reference collection of identified organisms to use for future comparison; and 2) to determine whether any differences existed in macroinvertebrate diversity and abundance between vegetated and non-vegetated shoreline regions. Samples were made using a modified 4.9 m long extensible swimming pool pole with an attached 1.0 mm-mesh aquatic dip net. Thus far 5,029 specimens have been sorted and identified. The gastropod families Physidae, Lymnaeidae, and Valvatidae predominate all other species and are present in both vegetated and non-vegetated sites. Larval chironomids (Diptera: Chironomidae), while not as numerous as the gastropods, are the predominant insect in open littoral areas, and *Eurylophella* sp. (Ephemeroptera: Ephemerellidae) are the best represented insect in vegetated littoral sites. The caddisflies are represented by five genera in two families, including *Agraylea* sp., *Oxyethira* sp., and *Dibusa* sp. (Trichoptera: Hydroptilidae), and *Nectopsyche* sp. and *Mystacides* sp. (Trichoptera: Leptoceridae). The hydroptilids are silk case makers, often using algae in their cases, and the leptocerids often have sticks protruding from the openings of their cases. Given the size of the pond and the other aquatic macroinvertebrates that have been collected, the diversity of the trichopterans is considered to be quite good. (**43**)

Custer, Brittany*, and Debra Wohl Elizabethtown College, Elizabethtown, PA 17022. *Do genetics, environment, and lifestyle all affect the oral microbiome? A comparative study of the oral microbiome between Amish, non-Amish, and twins.* — Monozygotic twins, also known as identical twins, share great genetic overlap and often share similarities in environment and lifestyle choices. To understand the oral microbiome, we examined monozygotic twins compared with others of similar and differing community, environment, and lifestyle choices. Oral microbiomes are known as communities of microorganisms inside of the oral cavity that can be commensal, symbiotic, or pathogenic. Saliva samples were collected from six non-Amish females and twelve Amish females, including one pair of monozygotic twins, all between the ages of thirty and sixty years. Community DNA was extracted and the V4 region of the 16S gene was amplified and sequenced. Sequenced DNA was trimmed at 252 base pairs and Phred scores above thirty were obtained indicating high quality sequence data. Based on published literature of the oral microbiome, it was predicted that all of the samples, regardless of population (i.e., Amish and non-Amish), would have a similar core set of organisms in the oral microbiome. We predict, however, that community composition of the microbiome will differ significantly between the Amish and non-Amish populations due to differences in genetics, environment, and lifestyles. Because the Amish monozygotic twins share the largest overlap in genetics, environment, and lifestyle, we predict their microbiomes will share the greatest similarities. These predicted results may support our understanding of how environment and genetics affect microbial composition; however, more studies need to be done to fully determine the cause of such results.   (**111**)

Davis, Kaleb*, and Christopher Brey Marywood University, Scranton, PA 18509. *Double-stranded RNA klf-3 microinjected into Caenorhabditis elegans klf-2 mutant: effects on morphology and fecundity*. — The nematode *Caenorhabditis elegans* is a model organism used to study gene interactions. Krüppel-like Factors (*klf*) are transcription factors that are important in fat regulation. Deregulation of *klf*’s results in abnormal fat accumulation that can result in obesity and diabetes in humans. *C. elegans* is an ideal model to study *klf*’s because while humans have 17 *klf* genes, *C. elegans* have only 3. The purpose of this study was to examine the interaction between *klf-2* and *klf-3* in the form of a double mutant. These double mutants were created by microinjecting *klf-3* dsRNA into a *klf-2* (*ok1043*) mutant. Progeny at the L4 stage of microinjected worms were individually transferred to plates to be examined for fecundity and morphological differences. Fecundity was studied by counting eggs laid by progeny and returning after 24 hours to count how many eggs had hatched. Morphological studies were performed by examining double mutant progeny under a compound light microscope with focus on the reproductive region. Results will be presented at the meeting. (**161**)

Decker, Macy*, Sara Goodson, and Christopher Brey Marywood University, Scranton, PA 18509. *Examining klf-1 expression pattern in the intestine of Caenorhabditis elegans*. — Krüppel-like transcription factors (*klfs)* are one of the most common transcription factors found in all living organisms. One of their key roles is in regulating fat metabolism. When fat metabolism is deregulated, this causes obesity, which leads to type 2 diabetes. In humans, there are 17 *klf* genes, whereas in *Caenorhabditis elegans* there are only three, making it the ideal model organism to study this gene family. In this study, we focused on the specific gene *klf-1* and its *gfp* expression pattern in the worm's intestine. Preliminary tests have shown the expression of vector pHZ337 of *klf-1* is within the first 500 bp of the promoter, starting at the ATG start site. In deletion construct pMD337.395 which covered 370bp of the promoter starting at the 5' start codon ATG, expression had ceased. The alteration between pHZ337 and pMD337.395 is ca.130bp of the promoter. The differences between expression and no expression leads us to speculate that the 130bp are required for expression of *klf-1*. Thus, we are targeting the 130bp of the *klf-1* promoter to gain a greater understanding of *klf-1*expression. After the 130 bp of the promoter is amplified, it will be cloned and microinjected into *C. elegans* to determine whether or not this region of the promoter is critical to *klf-1* expression in the worm's intestine. (**74**)

DeWitt, Carolyn*, and Linda Kennedy Mansfield University, Mansfield, PA 16933. *Measuring variation in the macroinvertebrate population of a headwater stream: May-September 2016*. — The presence and/or absence of specific macroinvertebrate species has been widely used as a surrogate for determining water quality in Pennsylvania (Hussain 2012). Mansfield University students are beginning a long term macroinvertebrate study of regional streams. However, before using one-time sample collections to investigate local water quality we must first determine the natural seasonal variation for individual species and the overall macroinvertebrate population structure. To this end, macroinvertebrates were collected from Mill Creek, a 3rd order tributary to the Tioga River, located in the headwaters of the Susquehanna River watershed. To date three population samples have been collected from the same location on Mill Creek (May, July, and September of 2016). Field methods, laboratory methods and specimen identification and analysis followed the Pennsylvania Department of Environmental Protection's protocol for freshwater wadeable streams (PADEP). Noticeable differences from May to July include a 29% decrease in Mayfly populations, a 69% decrease in stonefly populations, a 1007% increase in water penny populations and a 39% increase in non-biting midges. Analysis is currently ongoing. Hussain, Q. A. (2012). Macroinvertebrates in streams: A review of some ecological factors. *International Journal of Fisheries and Aquaculture, 4*(7):114-123. PADEP. 2015. *An Index of Biotic Integrity for Benthic Macroinvertebrate Communities in Pennsylvania's Wadeable, Freestone, Riffle-Run Streams*. Pennsylvania Department of Environmental Protection, Bureau of Clean Water, Harrisburg, PA. (**92**)

Dile, Tracy*, Andrea Nagy, and Christine Proctor Wilson College, Chambersburg, PA 17201. *Effects of apiary practices on colony collapse disorder in the European Honey Bee, Apis mellifera*. — Nearly 90% of all flowering species of plants need help from animal pollinators for reproduction. *Apis mellifera*, or the European honey bee, is the most utilized pollinator in commercial crop production, responsible for 80% of commercial crop pollination. Their estimated agricultural economic contribution via assisted fertilization worldwide is greater than $200 billion annually. Without the service of honey bees, manual pollination by humans would be very costly, and have a detrimental economic impact to agriculture. Large populations of adult bees are disappearing, leaving behind stores of honey, brood, and most surprisingly, their queen. Named

Colony Collapse Disorder in 2006, researchers have yet to determine a cause for this phenomenon. Theories have included cell phone towers, bacterial and viral diseases, as well as neonicotinoid pesticides, yet none of these theories individually have yielded a positive correlation. This study analyzed USDA colony loss data from commercial apiaries across the Unite States from January 2015 to March 2016. Commercial apiaries were defined as operations with 5 or more colonies. Generalized linear models were used to assess what factor or combination of factors best explained percent colony loss in 2015. Factors analyzed included: apiary type (honey production vs. pollination services), queen replacement, parasite infestation, bacterial and fungal infections, pesticide exposure, extreme weather, monthly temperatures, and hive destruction. The data from this study took a multi-impact approach and is a crucial first step in focusing future research investigating CCD. (**1**)

Dillee, Melody*, Jonathan Matejcek*, Georgina D. VanNorden, and Joshua Slee DeSales University, Center Valley, PA 18034. *Cofilin localization in bovine aortic endothelial cells in response to cell stress*. — Actin filaments have been shown to reorganize into stress fibers following treatment with various forms of cellular stressors, including both mechanical and chemical cell stressors. Cofilin, a member of the actin depolymerizing factor family of proteins, is required for the reorganization of actin filaments. We propose that cofilin is, in part, responsible for the reorganization of actin filaments into stress fibers under these conditions. Previous immunofluorescence microscopy of cofilin indicates that phosphorylated cofilin (serine-3) increases in the nucleus and decreases in the cytoplasm during fluid shear stress (FSS), a mechanical stress experienced by vascular endothelial cells. In addition, when placed under conditions that cause cell stress, such as treatment with dimethyl sulfoxide (DMSO), cofilin becomes dephosphorylated and locates primarily to the cytoplasm, suggesting that it could facilitate the changes in actin structure. Continued research will investigate the localization of cofilin in bovine aortic endothelial cells (BAOECs) under various forms of cellular stress. (**171**)

Doran, Taylor*, Molly Schnaubelt*, Stephanie Barr*, and André Walther Cedar Crest College, Allentown, PA 18104. *Identification of genetic markers to rapidly genotype strains of yeast used in beer production.* — Beer making involves the fermentation of sugars extracted from malted grains using different species of brewing yeasts. There are many species of brewing yeasts used in beer production, but two of the most commonly used are the top fermenting yeasts species *Saccharomyces cerevisiae* used in the brewing of ales, and the bottom fermenting yeasts species *Saccharomyces pastorianus* used in the brewing of lagers. Different yeast strains lead to different flavors, alcohol contents, and color profiles, so it is important to use monocultures of the proper yeast strain to obtain the desired beer. Contamination of fermentation tanks by other brewing strains or wild yeast strains not normally used in the brewing process can lead to undesirable beer outcomes. The problem of contamination is particularly relevant in large breweries that use fermentation tanks for different kinds of beers. Current methods to identify yeast contamination use biochemical and metabolic tests that may take up to a week to obtain results, at which time large volumes of beer may have been tainted by the contaminating yeast. Our research focuses on developing a rapid molecular analysis tools to genetically identify beer yeasts using techniques such Short Tandem Repeat PCR with gel analysis, HRM-qPCR, or capillary electrophoresis. After analyzing the results of our repeated genomic DNA isolation and identification tests, we have developed a protocol which is more streamlined than any currently available methods available to identify the difference between their beer strains and any contaminants. Thus far, we have identified three loci which we can amplify and use to distinguish different species of beer yeasts. We continue to search for more prominent distinguishing loci that we can use to enhance and further develop our current protocol method for future use by large-scale brewers. (**109**)

Durnin, Brook*, and Chad Freed Widener University, Chester, PA 19013. *Spatial analysis of the hydrology and ecology of the Tarkhill Creek Watershed in Pike County, Pennsylvania*. — The Tarkhill Creek is a first order stream in the Delaware River watershed in the Pocono Mountains of Pennsylvania. It is one of three streams that discharges into Pecks Pond in Pike county which ultimately flows to the Little and Big Bushkill Creeks. Of the three streams it is the only one that supports a native brook trout population. Pecks Pond is a lake that was created in the early 1900's by logging and then damming the Little Bushkill Creek. During this study Pecks Pond, a 300-acre lake, was drained to support the replacement of the dam. So changes in the first order stream dynamics have been quantified using sensors in the stream and the hydrology of the surrounding forest was monitored using sensors in each of the land cover habitats. All of the data was spatially analyzed in a geographic information system. Understanding the hydrology and ecology of this watershed will ultimately lead to a better understanding of Upper Delaware River watershed dynamics. (**118**)

Durnin, Brooke *, Matt Bell, Ryan Petrin and Dr. Itzick Vatnick Widener University, Chester, PA 19013. *Black Spot Disease Does Not Affect the Physiological Performance of Rhinichthys atratulus.* — Black spot disease is common among fish in the northeast USA . *Uvulifer amabloplilis* is a trematode that causes black spot disease in fish. This organism follows a complex life cycle that begins with a bird host and passes through snails ending up infecting fish. We tested the swimming ability of Blacknose Dace minnows infected with black spot disease and examined the relationship between the degree of infection and body size. Blacknose Dace (*Rhinichthys atratulus)* were captured in Ridley Creek at Ridley Creek State Park. Most of the captured fish had black spot disease present on their bodies. The fish were placed in a swimming flume where they swam at different speeds until they exceed their capacity to keep up with the current speed. We found the percentage of parasites present was not correlated with either the body length or body mass that. Additionally, Black Spot disease does not appear to hinder their swimming ability. **(17)**

Egberts, Carly*, and Anya Goldina Elizabethtown College, Elizabethtown, PA 17022. *Inquiry based activities for teaching about invasive species in grades seven and eight*. — The topics of biodiversity and invasive species are not taught in depth in secondary curriculum. We developed a unit about invasive species focusing on the local invasive crayfish species *Orconectes rusticus*. This comprehensive unit incorporates multiple components of Pennsylvania Environment and Ecology standards and includes many engaging activities. Students start by using basic observation skills to identify native and invasive crayfish species using a dichotomous key. The unit then focuses on inquiry-based activities to examine the impacts of invasive species on ecosystems and the traits that allow invasive species to outcompete native species. These activities include being in charge of a National Park and determining how to fix the various invasive species problems located in their park, as well as researching various traits of invasive species to then create their own species. The unit closes with an activity examining animal behavior, specifically agonistic behavior between *Orconectes rusticus* crayfish. The students are able to observe two crayfish fighting and score them. This knowledge is applied in observing and scoring their own live crayfish interaction. By incorporating the activities developed in this unit, students will develop an understanding about the impacts of invasive species on the environment and biodiversity, as well as the importance of preventing the expansion of invasive species. (**89**)

Emmett, Grace*, and Jeffrey Stephens Misericordia University, Dallas, PA 18612. *AFM imaging of human chromosomes*. — This study was undertaken to determine if human chromosome banding can be detected by atomic force microscopy (AFM). The AFM, was designed by physicists to measure rigidity of metals, but could also take images by scanning across a micron sized sample in tapping mode. More recently discovered, the AFM can also be used as a tool for measuring the size, topography, and amplitude of organelles, cells, and proteins while imaging. Using the AFM for biological matter has developed in the last decade for genetics and molecular research with chromosomes being successfully scanned in contact mode. The AFM produces 256x256pixel images with a scanning speed of 5 microns/second. The banding patterns under the AFM can detect the same patterns as an electrophoresis, suggesting that the AFM can be a new tool for genetics research. (**139**)

Eplett, Sarah*, and Ryan Colyer Cabrini University, Radnor, PA 19087. *Development of a custom detection and acquisition system able to perform fluorescence lifetime imaging*. — We present a custom detection and acquisition system integrating optical components, a prototype photon detector, and custom electronics. This microscope uses a laser to excite fluorophores in order to count individual photons using compressive sensing and lifetime imaging. Compressive sensing consists of using multiple mirrors and a point detector in order to produce an image. Lifetime imaging refers to the amount of time it takes for the electron in a fluorophore to return to the ground state after being excited by the laser. Our method propagates fluorescence lifetime imaging through compressive sensing so that full image acquisition can be performed efficiently using a single point detector. A major component of this project involved the design of a custom electronic circuit using a field-programmable gate array (FPGA) to acquire fluorescence lifetime information for each photon detected. The FPGA circuit design is based on the principle of tagging the arrival time of each photon, allowing them to be reassigned to compressive sensing frames. Then software will be used to reassemble these into fluorescence lifetime images. A custom detection path is also being developed making use of lenses, mirrors, filters, and a custom photon detector. This project is expected to lead to a novel and cost-effective design for efficiently acquiring fluorescence lifetime images under low light conditions which are favorable for biological samples. (**151**)

Evans, Tiara*, Richard Jackson, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Development of a qualitative method for detection of intravenous methadone abuse.* — Methadone is a synthetic opioid drug commonly used to treat addition and mitigate the withdrawal symptoms commonly experienced by recovering heroin addicts. Disaccharides such as sucrose and lactose are used as adjuvants in the production of methadone which is intended to be taken orally. When methadone is consumed/abused intravenously, the adjuvant disaccharides will appear in urine due to their complex structure and the inability of the human body to break them down outside of the digestive tract into monosaccharides. Using sucrose and lactose as markers in urine, scientists have been able to determine the method of consumption of methadone, orally (which is the intended route of administration) or intravenously (abusive route of administration) in patients. Based on this information, research was conducted to utilize a series of qualitative tests in the hopes of designing a cheaper and more resourceful detection method than the current costly and time-consuming method of HPLC detection. Presumptive tests, such as Barfoed's and Seliwanoff's tests, both exploit the ability of reducing sugars to undergo oxidation-reduction reactions to produce a colored product. A qualitative test scheme was designed and tested to be able to distinguish between solutions containing only lactose, only sucrose, or a mixture of lactose and sucrose. The detection limits of each individual oxidation-reduction reaction to produce a visible colored product was determined, and the limitations of a qualitative test for methadone urinalysis was identified. (**149**)

Fallone, Jenna*, Thomas Christopher, and Deanne Garver Marywood University, Scranton, PA 18509. *Potential treatment of acne using active antimicrobial compounds found in essential oils*. — *Propionibacterium acnes*, a bacterium that thrives within the pores of our skin, is one of the leading causes of Acne Vulgaris, a medical condition that plagues most adolescents and many adults. Recent studies have demonstrated that *P. acnes* is becoming more resistant to modern antibiotics, as with many other infectious bacteria. There has been an ongoing race among researchers to discover or develop new novel antimicrobial compounds, as the risk of bacterial resistance has been rapidly rising. Compounds obtained from nature have been utilized extensively, taking advantage of various plants to treat numerous diseases. The use of essential oils from plants has increased dramatically, with new scientific studies which prove the beneficial characteristics of many plants in nature. In this study, the major component of the essential oil of lavender, named linalool, was evaluated to determine if it has the capability to inhibit the growth of *P. acnes*. (**101**)

Felt, Kristen*, Makayla Lagerman*, Ryan Doan, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *Behavior of a Sex Trivalent in Metaphase I and Anaphase I*. — Failure to correctly position chromosomes during cell division can lead to incorrect chromosome distribution. Incorrect chromosome distribution can be catastrophic both for the cell and the organism that the cell inhabits. We are studying chromosome positioning in meiosis I by studying the position of a sex trivalent. Typically, homologous autosomes connect to form a bivalent, which forms a bipolar attachment to the spindle by metaphase I. In anaphase I, homologues separate to opposite poles. Often, partner sex chromosomes like the X and Y chromosomes in humans behave similarly. However, in some cases, there are multiple sex chromosomes. The cellar spider *Pholcus phalangioides* is one such case. *P. phalangioides* has X_1, X_2, and Y sex chromosomes, and males combine the X_1, X_2, and Y chromosomes together to form a sex trivalent, in which the Y chromosome faces one spindle pole while the X_1 and X_2 chromosomes face the opposite pole. With one attachment site opposing two attachment sites, one might assume that spindle forces would be unbalanced, but the sex trivalent aligns with all of the autosomes on the metaphase plate. We use time-lapse phase-contrast microscopy, laser ablation, and immunofluorescence to study the alignment of the sex trivalent on the metaphase plate, attempting to gauge how forces are balanced in this odd system. (**134**)

Francisco, Sarah*, and Steven James Gettysburg College, Gettysburg, PA 17325. *Genetic and biochemical analysis of Aspergillus nidulans SET2, a histone H3K36 trimethyltransferase that controls mRNA levels of the snxA shuttling mRNA-binding protein*. — *Aspergillus nidulans snxA* (suppressor of *nimX*-cdc2) encodes an ortholog of the budding yeast Hrb1/Gbp2 SR/RRM proteins. Hrb1 and its paralog Gbp2 regulate mRNA export and prevent the export of defective mRNAs. We discovered a previously unreported role for *snxA* in cell cycle regulation, in which *snxA*1 and *snxA*2 mutations specifically suppress the heat-sensitivity of mutations in regulators of the CDK1 mitotic induction pathway (James et al., 2014. GENETICS 198: 617-633). By themselves, recessive *snxA*1 and *snxA*2 mutations exhibit strong cold-sensitive lethality, and at the permissive temperature for growth, *snxA* mRNA and protein expression are strongly repressed. These defects are phenocopied by a *snxA* deletion (D*snxA*), indicating that *snxA* acts normally by antagonizing the CDK1 mitotic induction pathway to restrain the G2/M transition. To further understand *snxA* function, we generated suppressors of *snxA* cold-sensitivity, and discovered that loss of the *set*2 Histone H3-Lysine36 methyltransferase strongly rescued *snxA*2 but only weakly suppressed *snxA*1. qPCR analysis revealed the underlying mechanism of suppression: *set2* mutants restored full transcriptional proficiency to *snxA*1 and *snxA*2. These phenotypes were largely mirrored in a non-methylatable Histone H3-K36L mutant, indicating that methylation of Histone H3 at Lysine-36 acts to repress transcription at the *snxA* locus. These observations are in line with known *set2* functions in preventing excessive and cryptic transcription of active genes. In this study, we used immunoblotting to characterize SET2 biochemical activity. As expected, global H3K36 trimethylation is abolished in *set*2 deletion strains (D*set2* and D*set2 snxA*2). Interestingly, preliminary results suggest that H3-K4 trimethylation, a mark of active gene expression, is increased in D*set2* mutants. In order to better understand the reasons for differing suppression of *snxA*1 versus *snxA*2 by *set2* mutants, we are examining (1) *set2* mRNA and protein levels and (2) levels of H3-K4 trimethylation in *snxA*1 and *snxA*2 mutants. (**133**)

Frantz, Devin*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Characterization of Flavobacterium franzi AED, isolated from a freshwater creek.* — A Gram-negative, rod-shaped, yellow pigmented bacterial strain, designated AED, was isolated from the Loyalsock Creek in Montoursville PA as part of an undergraduate Microbiology course. Growth was observed at temperatures 4-30 °C and optimal pH of 5-8.; 16S rRNA sequence analysis revealed that the closest matches to AED were *Flavobacterium reichenbachii* and *Flavobacterium glaciei*. The 16S data showed that the closest match had a percent value of 98.3 which is below the 98.6% that dictates a novel species. Genome sequencing of AED and the reference strains was accomplished along with DNA-DNA Hybridization (eDDH), Average Nucleotide Identity (ANI), and Average Amino Identity (AAI). eDDH was accomplished with Genome-to-Genome-Distance Calculator and this revealed that the closest match was *Flavobacterium glaciei* with a 25.2 GGDC value. With phenotypic and genotypic data, strain AED represents a novel species of the genus *Flavobacterium* with a proposed name of *Flavobacterium franzi*. (**122**)

Frey, Tiffany*, Colton Ryan, Marie Pizzorno, and Adam Hersperger Albright College, Reading, PA 19604. *Ectromelia virus accumulates less free double-stranded RNA compared to vaccinia virus*. — Most orthopoxviruses, including vaccinia virus (VACV), contain genes in the E3L and K3L families. The protein products of these genes (termed E3 and K3, respectively) have been previously shown to combat PKR, a host defense pathway. Interestingly, ectromelia virus (ECTV) contains an E3L orthologue but does not possess an intact K3L gene. In this study, we attempted to gain insight into how ECTV can still efficiently evade PKR despite lacking K3L. We employed the “J2” monoclonal antibody to detect dsRNA, which activates PKR, within cells using immunofluorescence and flow cytometry. Relative to VACV, ECTV accumulated significantly less dsRNA in BSC1 cells. The dsRNA detected in VACV-infected cells was unbound by E3, a viral gene product known to inhibit the PKR and RNase L anti-viral pathways by binding to dsRNA. We found no difference between dsRNA levels in ECTV and VACV-infected cells until later time points post-infection (after 8-12 hours). Thus, it appears that E3 shielded dsRNA from detection for a limited amount of time. If sufficient dsRNA was produced, a threshold was crossed by which additional dsRNA cannot be sequestered by the available pool of E3. Indeed, we failed to detect the activation of the RNase L pathway in ECTV-infected cells at any time post-infection. Conversely, RNase L was activated at later times in the replication cycle of VACV, which correlated with the presence of detectable dsRNA using J2. The mechanism by which ECTV seems to generate less free dsRNA is likely related to its protracted replication cycle relative to VACV. Viral gene expression as measured via real-time PCR showed that late gene expression of ECTV is delayed and of lower abundance compared to VACV during the early stages of infection. Therefore, by slowing down its replication cycle, ECTV may be better able to manage the effects of generating dsRNA. (**103**)

Garcia, Cecelia*, and Wendy Boehmler York College of Pennsylvania, York, PA 17405. *Identification and characterization of phosphodiesterase 10A (PDE10A) in zebrafish (Danio rerio).* — Phosphodiesterase 10A (PDE10A) plays the critical role of regulating cAMP and cGMP within the striatum, a section of the brain thought to be responsible for cognitive thought and motor control. Parkinson’s Disease and schizophrenia have been linked to mutations in PDE10A and symptoms can be relieved though the use of PDE10A inhibitors. We wanted to investigate whether PDE10A plays a role in neurodevelopment as other genes involved in neurodegenerative disease have been shown to underlie the mechanisms of neural development. Zebrafish, an organism commonly used to study neurological and developmental disorders in humans, possess a predicted mRNA sequence for PDE10A. Using a reverse transcriptase polymerase chain reaction strategy, we have determined that PDE10A is highly conserved with the human orthologue and the gene is expressed during the embryological stage of zebrafish development. It will be of interest to determine the spatio-temporal expression of the gene throughout development using whole-mount *in situ* hybridization to gain insight into the role it may play in brain development. (**165**)

Garman, Brittany*, Angela Belli, and Cynthia Walter Saint Vincent College, Latrobe, PA 15650. *Meadow management and Rudbeckia hirta: effects of burning and mowing on plant diversity*. — Implementing common meadow management techniques can allow for lush, vivacious growth of native plants and shrubs in already existing meadows in western Pennsylvania. At Winnie Palmer Nature Reserve at Saint Vincent College in Latrobe, Pennsylvania, the meadows were slowly decreasing in plant diversity over the years. This decline specifically affected the beautiful flowering plant, Black-eyed Susans, *Rudbeckia hirta,* previously planted on the reserve, but absent in recent years. To solve this problem, two meadow management techniques (single cut alone and prescribed burning with cut) were executed in 2015 to compare to control, unaltered plots. All plots were measured, flagged, and mapped to ensure similar size parameters. The main plots per treatment were 80 meters x 15 meters and replicate plots per treatment were 15 meters x 6 meters. Also, plant species abundance surveying was conducted and soil samples were collected and analyzed before and a year after the prescribed burn to chemically and quantifiably see a difference. The Burn/Cut and Cut plots appeared to be dramatically more diverse in 2016. After a two-factor ANOVA with replication was performed focusing on how management techniques altered species richness between 2015 and 2016, the effect of management was almost statistically significant (p=0.09). The Burn/Cut and Cut plots had an average of 2+ species while the Control plot had an average of 1-2 species. The two meadow management techniques allowed for the re-growth of *R. hirta* in only the Cut and Burn/Cut plots throughout the entire nature reserve while contributing to an overall increase in diversity in these target plots in the meadows at the reserve. Future work should include annual burns and cuts to increase species diversity and density. (**28**)

Garrigan, Emily*, Tracie Young, and Bridgette Hagerty York College of Pennsylvania, York, PA 17405. *The cost of the outdoor cat and dog: rehabilitation of wildlife in southern Pennsylvania*. — Invasive species pose a threat to native wildlife species worldwide. Through predation, competition, disturbance, hybridization, and disease transmission, invasive mammals interrupt natural ecosystem functions. Domestic dogs and cats affect wild populations of mammal, avian, and reptile species. Wildlife rehabilitation centers accept wild animals as patients for treatment after they have had contact with a domestic animal with the goal of releasing them back in to the environment. Our objective was to evaluate the impacts of domestic cats and dogs on small mammals and birds located in south central Pennsylvania. Survival of patients admitted to Raven Ridge Wildlife Center in Lancaster County, PA between July 2015 and June 2016 was analyzed based on species, type of incident, location, and season. Survival of patients who had been attacked by cats was significantly lower than prey species admitted for any other reason. Cats and dogs impacted 23 species, including three rabies vector species. Eastern Cottontails accounted for a majority of cat and dog attacks. Moreover, no admitted avian species survived a dog or cat attack on any occasion. Birthing seasons (March-August) for many species showed increased attacks by both dogs and cats with most attacks occurring in urban areas. These attacks cost Raven Ridge Wildlife Center an estimated $7,557 in one year. Through the nature of rehabilitation, and with biases occurring on the rescuer level, this study was not a comprehensive assessment of the problem in Pennsylvania. Wildlife rehabilitators should focus on reducing the likelihood of these attacks through public outreach. Both cat and dog attacks occurred near locations identified as important breeding habitat for threatened or endangered birds, making prevention of these events a priority. (**29**)

Gartley, Shamus*, and Frank Varriale King's College, Wilkes-Barre, PA 18711. *Testing the effect of dentine hardness on microwear in the saurolophine hadrosaur Kritosaurus navajovius (Dinosauria, Ornithischia).* — Recent work on the material properties of dentine in hadrosaurian (duck-billed) dinosaurs has uncovered the presence of three types that are of differing hardness. Hard mantle dentine (HMD) is the most resistant to wear and located near the periphery of dental occlusal surfaces. Orthodentine (OD) is deep to, and softer than HMD. The interior most occlusal surface is composed of vasodentine (VD) which has greater softness than either HMD or OD. If not controlled for, dentine hardness variability could introduce error when microwear from different teeth of the same individual or among individuals is compared. To investigate the influence of dentine hardness we examined teeth in a nearly complete left dentary of *Kritosaurus navajovius*. We sought to test the effect of differences in dentine by quantifying and comparing length and width of microwear striations between dentine types within teeth. We predict that lengths should show the least difference as these features are an indicator of time spent in occlusion and not closely related to hardness. In contrast, widths should be significantly different as softer dentine can be more easily gouged than harder types. Four teeth were examined at alveolar positions 9, 10, 13 and 22. As expected, striation length showed the least difference among dentine types. Significant difference was found between HMD and OD at position 22, whereas OD and VD were different at position 10. Length differences were not found among dentine types on the remaining teeth. Width showed more difference among hardness. In post-hoc comparisons two teeth showed significant differences of HMD vs VD in one and OD vs VD in another tooth. A difference between HMD vs OD was found only on one tooth. When differences are present they are often between wider scratches of the soft VD compared to more narrow scratches in HMD and OD. (**58**)

Gleich, Samantha*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Interactive effects of iron enrichment and acidification on coastal phytoplankton assemblages*. — The composition of marine phytoplankton assemblages is influenced by complex ecosystem interactions, and certain environmental conditions may favor growth of harmful phytoplankton species and lead to formation of harmful algal blooms (HABs). HABs, which are increasing in frequency worldwide, are fast-growing phytoplankton assemblages that cause harm through the production of toxins or oxygen depletion. Marine ecologists have some understanding of the role of nutrient enrichment in generating HABs, but they know very little about how nutrients interact with ocean acidification to create change in phytoplankton species composition. Coastal ecosystems can be acidified via atmospheric carbon dioxide fluxes and by microbial degradation of organic matter, and studies suggest that nutrient enrichment, HAB formation, oxygen depletion, and acidification are linked in nature. Therefore, the first objective of this study was to statistically analyze a 7-year environmental monitoring dataset to examine the relationship between seawater pH and DO concentration in the Raritan Bay, an estuary with a long history of water quality degradation and HABs. The second objective was to use a series of in situ microcosm experiments to evaluate the interactive effects of iron enrichment and acidification on phytoplankton abundance, species composition, and individual HAB species. Iron was chosen for this study because pulses of iron have been associated with HABs in other coastal ecosystems and acidification alters iron solubility. Results indicate that a positive correlation exists between pH and DO concentration over time, indicating that HAB formation and acidification may be linked in Raritan Bay. Iron enrichment and acidification in microcosms led to a significant increase in certain HAB species, including the potentially harmful raphidophyte, Heterosigma akashiwo. This study provides insight regarding environmental conditions leading to bloom formation and may contribute to more accurate HAB forecasting. (**116**)

Goodson, Sara*, and Deanne Garver Marywood University, Scranton, PA 18509. *Anti-inflammatory effects of ellagitannins and anthocyanins in berry leaf teas*. — Recent studies have demonstrated that flavonoids, such as ellagitannins and anthocyanins, possess anti-inflammatory properties. Raspberry leaves are known to contain both classes of compounds. In this study, raspberry leaves from multiple sources were extracted with ethanol or hot water. These extracts were analyzed by a liquid chromatography-mass spectrometry method using electrospray ionization. In addition, blueberry leaves, which are rich in anthocyanins, were also evaluated using these methods. The relative amounts of these compounds were determined in both raspberry and blueberry extracts to determine which plant source provides the most anti-inflammatory compounds. The goal of this study is to determine whether flavonoids and anthocyanins from these leaves may be used as a natural alternative to anti-inflammatory medicines, which have potential dose-limiting undesired side effects. The results of these studies will help in the design of a clinical trial in inflammatory tendinitis and arthritis, since tea brewed from raspberry leaves has been anecdotally reported to provide relief from inflammatory pain. (**142**)

Graff, Adrian*, and Wendy Boehmler York College of Pennsylvania, York, PA 17405. *Effects of road salts on endocrine gene expression in zebrafish (Danio rerio).* — Tyler Run Creek in York County, Pennsylvania experiences alarmingly high levels of salinity due to excessive use of road salt during the winter months. High salinity has been shown to impair the endocrine system in fish which controls growth, development, reproduction, and ability to fight off disease. Three key endocrine genes (parathyroid hormone, growth hormone, and atrial natriuretic peptide) were investigated in this study after exposing zebrafish embryos to salinity levels compared to those in Tyler Run. Using a quantitative PCR strategy, we found that there was no change in endocrine gene expression in salt treatment groups compared to control. It will be of interest to determine if chronic exposure to salinity and the treatment of embryos at different developmental time points causes alterations in the expression level of these genes. (**87**)

Grant, Sarah*, and Ryan Colyer Cabrini University, Radnor, PA 19087. *Development of a novel fluorescence lifetime imaging technique using compressive sensing*. — We present the development of a new method for fluorescence lifetime imaging microscopy which combines the advantages of phasor analysis and compressive sensing. Compressive sensing is an imaging technique where the desired image is sampled using a mirror array and a point detector. Each mirror in the array corresponds to a pixel of the image and can be oriented to control whether or not the light from the corresponding pixel reaches the detector. In this way, data for larger portions of the image can be collected using a single point detector and fewer measurements are needed. Measurements are taken with various randomly generated mirror patterns and then used to reconstruct the image using L1 minimization algorithms. In fluorescence lifetime imaging, the lifetimes of fluorescence emitters are used to create an image which reveals biochemically relevant information such as binding processes, aggregation, and conformational changes. Using a sine and cosine summation, fluorescence lifetime data can be represented as phasors and presented on a phasor plot. The application of compressive sensing to fluorescence lifetime imaging provides an efficient way to perform wide-field fluorescence lifetime acquisition with a single point detector and low levels of photodamage to biological samples. Because large portions of the image can be measured at once, this enables rapid acquisition even with low levels of illumination. We show simulation results which characterize this new method. (**152**)

Grant, Sarah*, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087-3698. *Using flow cytometry and Click-iT® Plus EdU Alexa Fluor® 488 to study mitogen-induced DNA synthesis in Coelomocytes of the invertebrate Eisenia hortensis*. — Mitogens induce mitosis and facilitate the study of the molecular mechanisms of cell proliferation and to understand different cellular responses including the immune response to foreign components and DNA mutation. This study tested whether mitogens known to stimulate vertebrate cells also stimulate coelomocytes (leukocytes) of the invertebrate *Eisenia hortensis* (earthworm). Coelomocytes carry out innate immune defense functions to protect the coelomic cavity during infection and include chloragocytes, hyaline amoebocytes, and granular amoebocytes. Four mitogens (pokeweed mitogen, phytohemagglutinin, concanavalin A, and a mixture of phorbol-12-myristate-13-acetate and ionomycin) were used *in vitro* to stimulate coelomocytes. Newly synthesized DNA was labeled with the nucleotide analog 5-ethynyl-2’-deoxyuridine (EdU). Incorporated Edu was quantified by flow cytometric analysis using an azide dye which binds to incorporated Edu. Preliminary results confirm that concanavalin A induces DNA synthesis in a dose-dependent manner suggesting that growth factor-induced pathways that stimulate cell proliferation in invertebrates may use evolutionarily conserved biochemical signaling pathways used by vertebrate species. Further testing with ConA is ongoing to verify inter-assay reproducibility over a wider range of concentrations, incubation times, and temperatures with the ultimate goal of identifying the receptors and downstream effector molecules that mediate the signaling associated with DNA synthesis in this invertebrate model. (**76**)

Grant, Sarah*, Jessica Mastrando, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087. *Using flow cytometry for the analysis of macroautophagy in the earthworm in response to polycyclic aromatic hydrocarbons*. — Macroautophagy, a process used by cells to degrade their cellular components, can be used by cells as a survival mechanism. The degradation process involves the lysosomal machinery and provides macromolecules which are released back into the cell and can be used as nutrients when materials are not available in the environment. Removing these cellular components can also be useful when organelles are damaged or present in excessive amounts to help prevent unregulated growth or cell death. One form of cellular damage is inflicted by polycyclic aromatic hydrocarbons (PAHs) which are carcinogenic, teratogenic, genotoxic, and immunotoxic. PAHs are toxic compounds generated from the use of petroleum products which bioaccumulate and persist in the soil because they have high lipophilicity and are resistant to degradation. In this study, coelomocytes extracted from the earthworm *Eisenia hortensis* were exposed *in vitro* to one of two PAHs, 7,12 dimethylbenz[a]antracene (DMBA) or pyrene. Earthworms were selected because of their risk of PAH exposure in soils due to airborne fallout. After PAH treatment, the levels of macroautophagy were measured using a fluorescent dye that is specific for the double membrane structures that make up the autophagolysosomes, hallmarks of macroautophagy. Flow cytometry provided the platform for fluorescence detection. It was hypothesized that PAHs would cause cell-damage-induced macroautophagy in earthworm coelomocytes, making it possible for earthworms to be used as bioindicators of contaminated soils. Our preliminary results do not show a reproducible correlation between *in vitro* exposure to PAHs and increases in macroautophagy compared to controls. Future studies could investigate responses to PAHs using an *in vivo* model combined with longer-term exposure regimens. (**30**)

Gromiller, Lewis*, Sean Freidhof*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Does fish odor influence the emergence behavior of the invasive New Zealand mud snail.* — The New Zealand mud snail, *Potamopyrgus antipodarum*, is a world-wide invasive species that has had established populations in North America for over three decades. Previous work has determined that behavior may play a role in invasion success of the species. In North America there are at least three clones, two of which appear to be invasive (US1 and US2). Previous work has also determined that the species is capable of detecting and responding to chemical cues from potential fish predators. Here we compare the emergence behavior of different invasive populations of the New Zealand mud snail in the presence and absence of fish chemical cues from blacknose dace and zebrafish. To measure emergence behavior, snails were removed from water for ten seconds and then placed in a petri dish filled with water and the time that it took for the snail to emerge from the shell and to right itself (start moving along the bottom) was noted. The snails were exposed to each of three treatments, plain water, water taken from a fish tank that held blacknose dace, and water taken from a fish tank that held zebrafish. Results will be discussed. (**56**)

Grubb, Austin*, and Jack Holt Susquehanna University, Selinsgrove, PA 17870. *A study of diatom communities in the upper main stem of the Susquehanna River during various late-summer discharge regimes, 2014-2016*. — The upper main stem of the Susquehanna River is formed by the confluence of the West and North Branches; each chemically and physically distinctive. The upper main stem retains the signatures of the two branches due to weak lateral mixing, which are referred to as the West Branch plume (WBP) and the North Branch plume (NBP). Characterization of the diatom communities requires samples taken from sites that occur in the plumes of both branches. Since 2009, we have monitored the upper main stem at an established transect that straddles Byers Island near Shamokin Dam, PA and below the Adam T. Bower inflatable dam at Sunbury, PA. From 2014-2016 the upper main stem experienced similar low flow regimes in September but different regimes in August: high (2014), moderate (2015), and low (2016). Diatom biofilm samples were taken from stones in WBP and NBP sites and examined by scanning electron microscopy. The Pollution Tolerance Index and Shannon Diversity Index values showed little variation between WBP and NBP (2.6-3.0, 2.0-2.9, respectively). We found the greatest species richness in the diatom communities during 2014 (53 species), a higher discharge year, while years 2015 and 2016 were somewhat comparable (47 and 44, respectively). All biofilm communities were dominated by *Achnanthidium minutissium* every year*.* In 2014 and 2016, WBP was dominated by *Ach. deflexum* and *Gomphoneis clevei*. The dominant species in NBP varied each year: in 2014, *Gomphoneis clevei* and *Cocconeis placentula*; in 2015, *Gomphonema exiguum, Gomphonema minutum*, and *Rhoicosphenia abbreviata*; and in 2016, *Cymbella affinis*. Despite similarities in community metrics and some dominant taxa, the Proportional Bray-Curtis similarity values between the three years was 58% for WBP, 30% for NBP, and 48% between WBP and NBP. Taxa richness was consistently lower with low discharge, but there was no clear relationship with the other indices. (**83**)

Grunmeier, Orvil*, Dustin Bendas*, David Matlaga, and Alissa Packer Susquehanna University, Selinsgrove, PA 17870. *The impact of induced plant stress on goldenrod galling insect success*. — Tall Goldenrod (*Solidago altissima*) provides a habitat for two highly specialized parasites- the goldenrod gall fly (*Eurosta solidaginis*) and the goldenrod gall moth (*Gnorimoschema gallaesolidaginis*). The larvae of both species burrow into the stems of the plant and take advantage of the goldenrod's resources to form ball and spindle galls respectively. Galling insect success is therefore dependent on the health and viability of the goldenrod shoots. The goal of this study is to investigate the relationship between shoot size and gall size for both gall types. We predict larger shoots will host larger galls of either type because they have higher photosynthetic output and therefore more resources available for the gall. Also, we predict that gall size will be an effective proxy for larval development. We sampled 208 gall infested shoots, 104 of each type of gall, and measured height of the shoot, height of the gall on the shoot, and diameters of both the galls and the shoots. To investigate how plant stress may impact larval development, we subjected the plants to varying degrees of defoliation zero defoliation, 1/3 of leaves removed, 2/3 of leaves removed, and total defoliation (N = 26 per treatment). We found that defoliated plants have a higher mortality rate than intact plants, indicating that defoliation may inhibit resource allocation to the galling insect. We expect that the larvae on shoots with greater defoliation will be less successful than those on intact shoots, as measured by the presence of an exit hole marking the end of their larval development. This study will shed light on how plant resource availability affects parasitic insect development. (**48**)

Habbershon, Ethan*, and Douglas Glazier Juniata College, Huntingdon, PA 16652. *What causes the temperature-size rule? A study of two aquatic crustaceans with different body-size responses to temperature*. — The temperature-size rule (TSR) states that ectotherms should grow to a larger adult size in cold versus warm environments. Approximately 83% of all studied ectothermic species exhibit the TSR (Atkinson 1994), though the reduction in adult size with increasing temperature is on average 10 times greater in aquatic versus terrestrial animal species (–5.0% °C^{-1} vs. –0.5% °C^{-1}: Forster et al. 2012). Despite the general significance of the TSR, debates continue about the mechanism(s) causing it. Therefore, the purpose of our research has been to test hypothetical mechanisms proposed in the literature to explain the TSR, by using two sexually dimorphic aquatic crustacean species: *Lirceus brachyurus* (Isopoda), which shows the TSR, and *Gammarus minus* (Amphipoda), which does not. We tested for the TSR by comparing mean body sizes of sexually mature (amplexing) males and females of several populations of each species that have naturally lived for many generations in freshwater springs with different, relatively constant water temperatures. These natural comparisons contrast with most TSR studies that have examined relatively short-term, single-generation effects of temperature in the laboratory. Natural comparisons are useful because they permit the study of adaptive (genotypic) responses to different temperatures, and not merely phenotypically plastic responses as seen in the laboratory. So far, our results contradict the size-fecundity hypothesis (Arendt 2011), and provide mixed support for the oxygen-limitation hypothesis (Hoefnagel and Verberk 2015). Interspecific differences in thermal sensitivity of oxygen supply and demand have been examined by using inter and intra-population comparisons of the body-mass scaling of gill surface area and metabolic (oxygen consumption) rate. We have also begun to investigate how temperature affects the cell sizes and relative rates of growth and sexual maturation in our two test species. (**61**)

Hake, Sean*, Dan Ressler, and Jon Niles Susquehanna University, Selinsgrove, PA 17870. *Prioritizing Brook Trout Sampling in Unnamed Tributaries Using a Network Model*. — Pennsylvania has 62,750 streams and only 8000 of those have been sampled for fish populations. Our main objective is to prioritize which streams should be sampled to find populations of Brook Trout. A network model approach is used to map Brook Trout habitat that allows for a visualization of connectivity between suitable habitats. A network model is a tool that can calculate pathways or routes based on minimizing costs associated with each network path. The network model has three major components; restrictions, starting points and costs. We are attempting to model brook trout habitat and potential movement of fish within a stream network using network model. We start with the known population from a field survey and assign travel costs within each stream network segment based on the probability of brook trout populations in that segment. We have developed additional cost equations that add greater cost as a function of the number of coal mine sites on the PA DEP mine inventory database, and the number of oil and gas wells on the PA DEP oil and gas well database. We added physical barriers to the network model where we calculate a stream and road intersection as a culvert. It was found in the study that the network model seems to be an effective visualization tool for estimating brook trout habitat and potentially linked populations. This study illustrates suitable Brook Trout habitat while visualizing the connectivity of pathways for fish travel in unnamed tributaries. (**97**)

Hannum, Courtney*, Zachary High*, and David Andrew Lycoming College, Williamsport, PA 17701. *Quantitative Genetic Analysis of Grooming Behavior in the Fruit Fly Drosophila melanogaster*. — Grooming is an innate behavior exhibited by nearly every type of animal with articulated limbs. In many organisms, proper initiation and maintenance of grooming contributes significantly to an individual's fitness, allowing the organism to find resources and attract mates. In the fruit fly, *Drosophila melanogaster*, grooming has long been recognized as an innate behavior subject to variability between individuals. These observations indicate that grooming behaviors can be characterized as quantitative traits, or quantifiable traits with continuous variation in a population. This project tests the hypothesis that natural variation in grooming behavior is driven by genetic variation in fly populations, and, by extension, that specific genetic variants of small effect contribute additively to the expression of this complex behavior. We utilized a subset of the *Drosophila* Genetic Reference Panel (DGRP), a population of ~200 inbred fly lines, to study genetic influences in grooming. This resource allows for relatively straightforward whole genome association mapping of loci associated with the quantitative traits being studied. This pilot project sought to examine grooming in a select subset of the DGRP in order to establish grooming as a quantitative trait and examine preliminary differences in populations in various grooming metrics, including total grooming time, grooming bout length, and the number of grooming bouts in a specified time. We recorded behavior from more than 750 animals from 35 DGRP lines and scored them for grooming behaviors using freely available video annotation software. There is a continual gradation of all grooming metrics analyzed across the different DGRP lines, suggesting that these traits have genetic components influencing their differential expression between lines. Whole genome association analysis, although preliminary, points to several genomic regions of slight effect on grooming, including several known nervous system genes. Among the most promising genes influencing grooming are the locomotor rhythm regulator *dyschronic* (*dysc*) and the metabotropic glutamate receptor gene *mangetout* (*mtt*). Continuations of this study will focus on extending phenotypic classification of grooming to all ~200 DGRP lines using automated behavior scoring software and detailed genetic analysis of these preliminary association loci. (**42**)

Harutyunyan, Anna*, M. Dana Harriger, and Deborah Austin Wilson College, Chambersburg, PA 17201. *Synthesis and effects of Fe-AZT and Pd-AZT on viability of human hepatocytes and hepatocellular carcinoma cells*. — Hepatocellular carcinoma (HCC) is the fifth most common cancer and third most common cause of cancer mortality around the world. HCC is difficult to treat due to early metastasis and progression, therefore developing and testing new anticancer agents that target HCC cells is critical. Several studies have demonstrated that azidothymidine (AZT) has antitumor activity and induces apoptosis in malignant cells. AZT and other thymidine derivatives are phosphorylated intracellularly and are integrated into the cell's DNA, which terminates the phosphate-sugar backbone, thus damaging the DNA and inducing apoptosis. An organometallic complex of platinum (Pt) AZT has previously demonstrated to be more effective in tumor suppression than pure AZT. Several organometallic complexes of AZT have been synthesized and shown to have antimicrobial activity, however their anticancer properties were not tested. In this study, an attempt was made to synthesize organometallic complexes of AZT with divalent palladium (Pd^{2+}) and trivalent iron (Fe^{3+}). The structure and mass to charge ratio of Fe-AZT complex were confirmed by IR spectroscopy and mass spectrometry. The optimal conditions of Pd-AZT complexation are being determined. The apoptosis-inducing ability of the Fe-AZT is being assessed and compared to that of AZT by treating HCC cells (HepG2) and normal human hepatocytes (THLE-2) with several concentrations of Fe-AZT and AZT. The viability of both cell lines is being quantified by 3-(4,5-Dimethylthiazol-2-Yl)-2,5-Diphenyltetrazolium Bromide (MTT) assay. The efficacy of both complexes in inducing apoptosis will be compared by two-way ANOVA and Tukey's post-hoc test. Due to higher thymidine turnover in malignant cells, it is anticipated that HepG2 cell line will be more sensitive to Fe-AZT toxicity than THLE-2 cell line. (**10**)

Healy, Michael*, and Amy Parente Mercyhurst University, Erie, PA 16546. *Utilizing a wireless sensor network to monitor water quality in Presque Isle Bay*. — Wireless sensor networks (WSNs) have become a large part of a technologically–based society and have a multitude of uses ranging from cell phone communication and militarized functions to environmental and habitat research. The wireless sensor network to be used for studying Presque Isle Bay's water quality will be composed of Vernier-brand products, readily available commercially. There are three main stations for this wireless sensor network consisting of the data monitoring or remote nodes, gateway nodes, and the monitoring station. Four parameters will be monitored, including pH, temperature, conductivity, and dissolved oxygen. Each utilizes a separate probe, which will eventually be housed in a waterproof casing to allow their introduction into the environment. This assembly, termed a remote node, will be attached to a buoy located within Presque Isle Bay. The ultimate goal is to relay the signal from the remote node back to the monitoring station using a wireless sensor network. (**96**)

Hearne, William*, and Isaac VonRue King's College, Wilkes-Barre, PA 18711. *Investigation of the thermoreversible gelation of polycaprolactone and its multiple melting points*. — Polycaprolactone

(PCL) is a polymer of special interest because of its possible application as a drug delivery system. This research was focused on the thermoreversible gelation of PCL dissolved in acetonitrile, specifically focusing on the multiple melting points observed at annealing temperatures around 3°C and below. PCL sample 5-7-15 was dissolved in acetonitrile with the mass fraction of PCL in solution being 0.198. Tests were conducted with differential scanning calorimetry (DSC) in order to measure the transition temperature from gel to solution. Varying the annealing temperature yields different numbers of melting peaks for PCL gel from a singular melting peak to four distinct melting peaks. The peaks at lower temperatures are believed to be poorly formed lamellae which melt first and then allow for partial recrystallization. Peaks observed at higher points are believed to be lamella that are well formed and take more energy to melt as a result. Samples that were annealed at temperatures higher than 3°C showed a single endothermic peak while annealing temperatures from 2°C – (-5)°C showed the emergence of up to four endothermic peaks. Below -5°C the melting peaks smoothed out into two distinct peaks. While the proportions of poorly formed and well-formed lamella changed with the annealing temperature, the total enthalpy remained the same. (**148**)

Henry, Marquise*, Brenna Gormally, and Michael Romero Elizabethtown College, Elizabethtown, PA 17022. *Effects of chronic stress on metabolic and immune responses in House Sparrows*. — Stress activates the hypothalamus-pituitary axis increasing corticosterone levels. A stressor can be considered anything that challenges an animal's ability to maintain homeostasis, such as predators or changes in weather. Prolonged stress inhibits immune function and decreases metabolic rate. The reactive scope model provides a context to understand stress by separating responses to stress into four levels; predictive homeostasis, reactive homeostasis, homeostatic overload, and homeostatic failure. Homeostatic overload refers to the point where exposure to stressful stimuli inhibits the individual from being able to maintain homeostasis, leading to system damage. This model predicts that exposure to multiple, repeated stressful stimuli can cause an animal to enter homeostatic overload quicker than exposure to a single stressor. To test this hypothesis, we compared immune and metabolic responses of house sparrows (*Passer domesticus*) exposed to an acute and chronic stressors. Individuals were exposed to eight days of stressors. The first four days were considered exposure to acute stress. The following four days were considered chronic stress. At the end of each stress treatment, blood and uric acid samples were collected. We observed immune function by measuring the ability of collected plasma to kill *Escherichia coli*. While exposure to acute stress increased microbial killing capacity, chronic stress caused a decrease in microbial killing capacity, supporting the reactive scope. The presence of uric acid decreased after an acute stressor and remained near that level after the chronic stressor. The decrease in microbial killing capacity and decrease in uric acid concentrations support the depression in immune function and metabolic rate predicted by the reactive scope model. (**70**)

Hernandez, Erika*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Assessment of the biological effects of estrogenic contamination in a sewage-impacted urban estuary*. — Environmental estrogens are aquatic contaminants of emerging concern (CECs) that can cause developmental and reproductive abnormalities in aquatic organisms. Because most wastewater treatment plants are not designed to remove CECs, they are an important source of environmental estrogens in rivers and estuaries. The first objective of this research was to monitor estrogenic activity within Raritan Bay, an estuary located between the states of New York and New Jersey, using a yeast estrogen screen method. Estrogenic activity will also be determined before and after treatment at the Middlesex County wastewater treatment plant (WWTP), which is the second-largest plant in the state of New Jersey that outfalls directly into Raritan Bay. For the purposes of this study, "estrogenic activity" refers to the expression of an estrogen-responsive gene in a recombinant yeast strain, and the expression is dependent on the concentration of estrogenic compounds (i.e., ligands) in the water. Raritan Bay is ideal for investigating the effects of estrogenic hormones because one of the primary water pollution problems in this system results from combined sewer overflows following storms. The second objective was to determine the effect of environmentally relevant levels of estrogenic compounds on copepod mortality, growth rate, and reproduction. Results indicate biologically relevant levels of estrogenic activity and the greatest amount of activity in Raritan Bay downstream of the WWTP outfall. Toxicity assays will provide valuable information about the impact of estrogenic compounds on aquatic invertebrates, which serve as an essential component of this aquatic ecosystem. (**115**)

Hoffman, Anthony*, Katheryn Yomes*, and Christopher Taylor Mercyhurst University, Erie, PA 16546. *Progress towards a catalytic method for generating imine nucleophiles.* — Substituted amines and imines are key functional groups in a variety of applications, ranging from drug discovery to materials research. While there are many versatile reactions that use imine electrophiles to create highly functionalized amines, there are few effective 'umpolung' reactions for these functional groups in which imines or imine precursors can act as effective nucleophiles. Such reactions would provide complementary synthetic routes to complex amines, and would be useful tools for the construction of biologically active molecules. In this study, we describe our exploration of new strategies for catalytically generating imine derivatives that act as nucleophiles. We have successfully synthesized several complex imines in order to test the catalytic cycle on intramolecular systems with a range of electronics. This presentation will include a discussion of the synthesis of these precursors and our ongoing efforts to develop a complete and functioning catalytic cycle. (**147**)

Hoffman, Justin*, Joshua Reeder, Russell Leinbach, Kaitlin Leffler, and Karen Campbell Albright College, Reading, PA 19604. *Monitoring bat activity in Pennsylvania's National Parks: captures and acoustic monitoring*. — In 2014, we conducted surveys at Valley Forge National Historic Park (VAFO) and Hopewell Furnace National Historic Site (HOFU) through a cooperative agreement between Albright College and the United States National Parks Service. This survey was modelled after the pre-White-nose syndrome study performed by Dr. James Hart in 2005. Both studies used mist netting and yielded data which suggested the particular impact of White-nose syndrome on the six hibernating bat species native to southeastern Pennsylvania, in particular *M. lucifugus*. The 2005 data suggests a high density of *M. lucifugus* with a total of 25 captures between both sites. The 2014 data indicates a decrease in the density of *M. lugifugus* with a total of 1 capture. The total number of captures between both studies has no significant variation, however, the species composition differs between the studies. The 2004 study revealed a large quantity of *M. lugifugus* and *M. septentrionalis* while the 2014 study yielded a large quantity of *E. fuscus* and *L. Borealis* indicating the impact of WNS on the populations. In 2015, we augmented the 2014 study through the use of stationary recording and driving transects. By implementing all three techniques, we were able to use the driving transects to guide our mist netting and stationary recordings. This study yielded similar data to the 2014 study with respects to the mist netting. The major difference was the absence of any *M. lugifugus* or *M. septentrionalis*. The echolocation recordings however did indicate the presence of a *Myotis* genus. As a continuation of the 2015 study, this summer we have been performing driving transects at both VAFO and HOFU to furthermore aid the National Park Service in the development of future management plans for the parks and the species which inhabit them. (**37**)

Hunter, Tracy*, Stephen Madigosky, and Itzick Vatnick Widener University, Chester, PA 19013. *Evaluation of the thermal properties of a primary rainforest at the Amazon Conservatory of Tropical Studies (ACTS) Iquitos, Peru*. — The variation of both spatial and temporal temperature profiles within an undisturbed primary rainforest environment is currently not well understood. Clearly, the extreme vertical stature along with the complex horizontal attributes of the forest makes this a very dynamic and difficult system to assess. Consequently, we sought to ascertain the differences in thermal profiles both vertically and horizontally over a well-defined area at the Amazon Conservatory of Tropical Studies (ACTS) in northeast Peru. To accomplish such, a series of data loggers were vertically and horizontally deployed throughout a well-defined area of primary forest located at the ACTS. Ibutton data loggers were programed to acquire data every 20 minutes over a 7-day period in July 2016. Weather events were also monitored during this interval in order to compare this information with data obtained from data loggers. Results indicate that the temperature profiles within the forest are thermally stratified, cyclical, and are impacted by light to heavy rainfall events. This was especially apparent when rainfall events occurred during daylight hours. In this instance, evaporative processes helped to cool all reaches of the forest canopy, typically causing temperature drops of between 0.5-4 degrees C. Loggers strung horizontally high within the canopy (~26 m) revealed only slight variation that can be attributed to intermittent light flecking received throughout the canopy. The fine variation exhibited over the duration of this study is a result of the towering nature of the forest canopy along with the complex architectural and topographic variations detected at the study site. These are important features that help to define the dynamic nature of this tropical forest. (**22**)

Januszkiewicz, Eric* East Stroudsburg University, East Stroudsburg, PA 18301. *Optimization of a Multiplex PCR Analysis for Crotalus horridus*. — Multiplex PCR analysis allows for the amplification of multiple loci at one time and is highly useful for genetic studies, particularly for monitoring species populations such as for the timber rattlesnake. Timber Rattlesnakes (*Crotalis horridus*) have experienced habitat loss, population fragmentation, and extirpation throughout their range in the Northeastern United States. Information regarding the genetic variation of this species can be used for conservation management efforts. A multiplex of nine primers was designed for genotyping populations of *C. horridus* to evaluate genetic variation. DNA was extracted from shed skins, tissue samples, blood, and scale clippings. From thirty-two samples, 93% of the loci were amplified with a mean of 8.7 alleles per locus. The mean polymorphic information content was 0.67, indicating this multiplex can be used for future analysis of *C. horridus* populations. (**68**)

Jenkins, Carson*, and Jeffrey Thompson York College of Pennsylvania, York, PA 17405. *The impact of N-glycosylation on the binding affinity of IL-13 to the receptor IL-13Rα-2*. — It has been shown that the cell surface receptor IL-13Rα-2 is overexpressed on the surface of human glioblastoma multiforme (GBM) cells, the most common and aggressive form of brain cancer. Many studies have demonstrated the effectiveness of GBM therapies using IL-13Rα-2 as a target. IL-13Rα-2 is a glycoprotein with four potential sites of *N*-glycosylation, and while it has been shown that total deglycosylation inhibits its ability to bind to IL-13, it is unknown which of these glycosylation sites plays the greatest role. In order to determine this, four mutant forms of IL-13Rα-2 were created such that each was not glycosylated at one of the four potential glycosylation sites and those IL-13Rα-2 mutant genes were transfected into separate human embryonic kidney IL-13 sensor cell lines. After treatment with the IL-13 ligand, a SEAP reporter assay was performed on the different cell lines to determine the effect of this deglycosylation on IL-13 binding to IL-13Rα-2. It was determined that deglycosylation of amino acid numbers 290 and 299 affects this receptor's ability to bind to IL-13, giving a better understanding of what aspects of IL-13Rα-2 govern its affinity for the ligand. This knowledge allows for the potential development of more advanced and more effective methods of IL-13Rα-2 targeted GBM therapies. (**155**)

Jones, Alexandra*, Rob Kulathinal, and Craig Stanley Temple University, Philadelphia, PA 19119. *Functional genomic landscape in Drosophila provides evidence for pervasive adaptation on sexually selected male traits*. — Male reproduction contains among the most rapidly evolving traits across sexual taxa. However, whether these highly diverged traits and their underlying genes are the result of adaptive (e.g., sexual selection) or neutral processes remains unknown. Here, we study the functional landscape of genome-wide adaptation across protein-coding genes involved in various aspects of male and female reproduction using two deeply sequenced populations of *Drosophila melanogaster.* Protein-coding genes were functionally assigned to reproductive classes based on their tissue expression, annotated ontological class, and sex-biased expression. For each functional class, the total number of synonymous and non-synonymous polymorphic and fixed sites were compared to the sibling species, *Drosophila simulans*. We find that male reproductive classes are generally more diverged between species, with genes involved in sperm development evolving the most rapidly. In general, male genes are enriched for signals of positive selection (gamma, *Ns*) at significantly higher levels compared to both female and non-reproductive gene classes. Male genes, particularly those expressed in sperm development, are also highly differentiated between recently diverged populations and appear to be more prone to gene gain/loss across global populations. Our novel findings direct our attention to sperm competition and gamete selection as an important driving force in rapid male evolution at the molecular level. (**66**)

Jones, Carli*, and Robert Kurt Lafayette College, Easton, PA 18042. *Studying the interaction of the immune response to Echinostoma caproni and murine mammary carcinoma*. — While scientists have characterized the immune responses to a plethora of infections, until recent years there had been relatively little research on polymicrobial diseases, which can be thought of as concurrent immune challenges within an organism. While polymicrobial diseases are generally thought to involve viruses, bacteria, fungi, and parasites, one can also include cancer as another category of immune challenge. In this study we investigated whether tumor-bearing mice would be adversely affected by a parasitic infection, and likewise whether a parasitic infection would be amplified by the presence of a tumor. In order to address these questions, mice received either the 4T1 murine mammary carcinoma, infection with *Echinostoma caproni*, or both immune challenges. With respect to health and disease burden, the overall health of the mice with single or double infections did not differ, and the double infection did not impact worm burden compared to the *E. caproni* only group. There was, however, a higher tumor volume over time in the double infection group compared to the tumor only group, although there was a great deal of variability in the tumor sizes. In studying the immune parameters, we found that the tumors caused an increase in the total number of splenocytes regardless of whether the mice had a concurrent parasitic infection. Taking a closer look at the splenocytes, we found that the amount of macrophages in the spleen increased over time in the double infection group, whereas in mice with a single immune challenge this cell population decreased over time. There were also more lymphocytes in the double infection group compared to the 4T1 only group. Infection with *E. caproni* alone influenced the macrophage and lymphocyte populations. Ongoing studies are investigating further differences in macrophages and lymphocytes from the single or double immune challenged mice using quantitative real time PCR. (**9**)

Kable, Brianna*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Characterizing the expression of Runx1t1 throughout retinal development in chicken (Gallus gallus)*. — Our understanding of the molecular mechanisms responsible for neurogenesis in the nervous system is still incomplete. The vertebrate retina provides an ideal model to study the mechanisms of cell fate determination because of its structural simplicity and conserved development. This study looks at a previously-unstudied transcription factor in the retina known as Runx1t1 and proposes a possible function in the development of retinal progenitor cells (RPCs) to their specific cell types. Using qPCR to analyze the expression of Runx1t1, we find that expression increases significantly throughout retinal development, suggesting a role in the regulation of the later stages. (**15**)

Kaltreider, Tara*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Characterization of a novel species of Rugamonas*. — In the Spring of 2016, a novel microbe was isolated from the Loyalsock Creek in Pennsylvania. Bacterial strain TLK was identified in the

Lycoming College microbiology class as a potentially novel species in the genus *Rugamonas*. There is only one species currently in the genus *Rugamonas* and that is *Rugamonas rubra* MOM 28/2/79. To be able to classify the potentially novel species, reference organisms *Rugamonas rubra* CCM 3730, *Duganella* sp. LCCC 1032, *Duganella zoogloeoides* HSV, and *Duganella phyllosphaerae* CCM 7824 were studied in parallel with bacterial strain TLK for phenotypic and genomic comparisons. Strain TLK is gram negative with colonies that are cream or white in color. It is able to grow at temperatures between 4°C and 30°C, the optimal temperature is 22°C. Strain TLK is salt sensitive and cannot grow on media above a 0.5% NaCl concentration. It is able to grow at a pH between 4 and 11. *R.* sp. TLK has enough distinct characteristics to be a novel species, including 1,334 unique genes that differentiate the organism from *R. rubra* ATCC 43154, *D. zoogloeoides* ATCC 25935, and *D. phyllosphaerae* T54. There are 354 shared genes between strain TLK and *R. rubra* ATCC 43154. Strain TLK had average amino acid identity, average nucleotide identity, and DNA-DNA hybridization values below the species thresholds as well as a high sensitivity to salts, resistance to certain antibiotics, the ability to use D-salicin, L-serine, D-galacturonic acid, L-galacturonic acid lactone, and glucuronaminde. Based on the genomic and phenotypic characteristics, strain TLK is concluded to be a novel species of *Rugamonas*. (**123**)

Kanaparthi, Jay*, Stephen Madigosky*, and Itzick Vatnick Widener University, Chester, PA 19013. *A seventeen-year profile of rainfall and tropical forest phenology in the upper Amazon Basin (Iquitos, Peru)*. — Long-term data sets that investigate microclimatic variation along with associated biotic cycles in tropical forests are rare and are currently highly sought after. Data of this nature is becoming valuable because it helps researchers precisely evaluate the impacts of climatic change on a local and regional level. It is for this reason that we, along with other Peruvian collaborators, have compiled a long-term data set that spans several decades that not only evaluates the dynamic nature of rainforests, but also addresses how plant cycles are affected by subtle variation in forests that do not show distinct seasonal cyclical patterns. We analyzed monthly rainfall data and correlated this with fruiting and flowering data to better understand the interplay between these variables. Of particular interest are the distinct rainfall patterns that are revealed when considered over several decades. Although this forest is considered an “everwet” forest, we disagree with this characterization owing to the distinct seasonality that we have observed. Our results also indicate that there are patterns exhibited in tree species with regard to both flowering and fruiting episodes and that these are somewhat predictable. Additionally, some of these can be positively correlated with rainfall patterns. While somewhat variable, there are correlations that suggest that many species favor an extended dry period before initiating flowering. Lastly, we clustered species of trees that share similar seasonal fruiting and flowering intervals to identify potential predictability of these annual cycles among different species. (**60**)

Kanaskie, Caroline*, Yueli Liang*, Cheyenne Moore, and Carol Loeffler* Dickinson College, Carlisle, PA 17013. *Hemlock woolly adelgid abundance and hemlock health in hilltop vs. valley sites*. — Eastern hemlocks (*Tsuga canadensis* (L.) Carr.) are valuable forest trees in the northeastern United States and adjacent Canada, providing shelter for birds and other wildlife as well as temperature moderation via shading for forest streams. However, hemlocks are experiencing widespread mortality and may soon be eliminated over much of their range due to infestation by an invasive insect, the Hemlock Woolly Adelgid (HWA, *Adelges tsuga* Annand). We compared adelgid abundance and hemlock health (crown density, crown ratio, amount of new growth per twig) on ten or more trees in each of sixteen sites that were located in eight pairs of a high-elevation hemlock stand on a rocky hillside and a lower elevation stand in a stream valley nearby. In early results (winter of 2013-14), hemlocks in the eight high rocky hillside sites had significantly greater adelgid levels and significantly poorer health by all measures than did hemlocks in the eight paired stream valley sites. This poster reports continuation of these observations over three more years, with supplemental analysis of soil nutrient levels and foliar chemistry using samples collected in fall of

2016 at each site. Our questions were as follows: 1) Do high elevation hemlock trees continue to suffer higher adelgid attack and to show poorer condition and growth over a period of several years than do hemlock trees in low elevation stream valleys? 2) Do soil chemistry and/or foliar chemistry differ between ridge and stream valley sites? 3) Do any significant differences in soil chemistry and/or foliar chemistry shed light on the differences in adelgid abundance and hemlock health in the high ridge sites vs. lower stream valley sites? Analyses are ongoing and results will be discussed, along with the implications of differences in results between the two habitats for management strategies to help protect this important forest tree. (**45**)

Kelleher, James*, Emily Wolcott, and Darl Swartz Delaware Valley University, Doylestown, PA 18901. *A novel avian sexing assay using fecal DNA*. — Many groups of birds are difficult to consistently sex, due to a lack of sex-specific characteristics in plumage or external anatomy. Methods include internal anatomy, behavioral observations, and drawing blood for DNA testing. These methods are either extremely difficult, detrimental to the bird, or both. Reliable and noninvasive methods of sexing would be valuable for wildlife professionals and in the pet and agricultural industries. Our goal was to determine if DNA isolated from fecal samples can be used in a novel qPCR assay to reliably determine avian sex across a range of species. Samples were gathered from native Pennsylvania species at a local wildlife rehabilitator, largely from Passerine birds. As none of these species have published genomes, sequences from closely related species were aligned to locate highly conserved sequences for a general avian gene and a female-specific gene on the W chromosome. Primers were designed for both genes, and three sets of assays were run: a dilution series on known male and female tissue samples, a set of tissue samples from 11 birds, and a set of fecal samples from 24 birds. Results from these assays were mixed. During the tissue runs, the general gene amplified in House Finch *(Haemorhous mexicanus)* samples, but not in American Robin *(Turdus migratorius)* samples. The female-unique gene was amplified in every sample, including males and blanks and was independent of [DNA], implying significant issues with the sequence itself. Results from the fecal samples suggest that the DNA is too degraded to acquire meaningful data. Only one sample amplified at all for the general gene. These results suggest that fecal DNA is inadequate for use in avian sexing, and that feathers are a more effective and minimally invasive source of DNA. Additional W-chromosome genomic sequencing is needed to better characterize specific species and design primers. (**41**)

Kerney, Dayshia*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Chryseobacterium greenlandense is a latter heterotypic synonym of Chryseobacterium aquaticum*. — Several novel and reference *Chryseobacterium* genomes were sequenced and analyzed using a variety of metrics. Two species, *Chryseobacterium greenlandense* and *Chryseobacterium aquaticum* were unusually similar. The 16S rRNA sequences were 99.24% identical. The average nucleotide identity (ANI) of 96.24 is higher than the 95-96% species threshold. The average amino acid identity (AAI) of 95.94 is higher than the 95% species threshold. The DNA-DNA hybridization was estimated using the Genome-Genome Distance Calculator at the DSMZ website. This metric, which has a species threshold of 70%, was calculated between 71.1% and 74.9% using all three methods. Together, these results suggest that two strains are members of the same species. Given the rules of priority, *C. greenlandense* should be considered a latter heterotypic synonym of *C. aquaticum*. Phenotypic analysis revealed a few minor difference in antibiotic sensitivity and carbon source utilization. (**107**)

Kimmel, Mallory*, and Jennifer Elick Susquehanna University, Selinsgrove, PA 17870. *The Effect of rainfall intensity on the mobility of legacy sediments*. — Analyses and comparison of suspended sediment loads with corresponding precipitation events (Fall 2016), were inconclusive due to erratic weather associated with an El Niño year. Low precipitation amounts, short duration storm events, and storms evaluated as low intensity limited data collection. Issues related to stream flow and an

El Niño weather pattern resulted in a modified methodology and procedure in sample treatment. In this study, following the peak of storm events, 500 mL water samples were collected from several sites along the creek, including tributaries flowing into Middle Creek and downstream from a legacy sediment source. Filtered samples were oven dried, weighed and compared to unfiltered paper weights. Following several storm events with negative sediment loads, the amount of water collected was increased to 4L. Additionally, the filters were air dried. Positive suspended loads were obtained after these modifications, however, the low amount of data collected is inconclusive. The original objectives in this study were to (1) determine if sediment transported along a small section of Middle Creek (Snyder County, PA) were from a legacy sediment source, (2) identify the intensity of storm necessary to increase suspended sediment load, and (3) compare storm event duration, intensity, and the total sediment loads. Middle Creek flows through legacy sediments deposited between 1833-1992. Legacy sediments are important to study because they threaten lowland aquatic ecosystems by transporting abundant organics, dissolved nutrients, and suspended sediments which may result in algal blooms and the burial of benthic communities. This study recommends future analyses of suspended sediment load from Middle Creek be conducted during intervals unaffected by El Niño, possibly during the summer months, when high energy thunderstorms pass through Central PA. Also, this study recommends X-ray analysis of sediment from tributaries flowing into Middle Creek and the legacy sediment source. (**90**)

King, Carli*, Megan Young*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Division of the Genus Pedobacter*. — While studying several novel pink-pigmented bacterial species discovered in a Microbiology course, we sequenced the genomes of the novel organisms and the closest validly published species, which were classified in the genus *Pedobacter*. The genus *Pedobacter* was established in 1998 within the family *Sphingobacteriaceae*, comprised of *Pedobacter heparinus, Pedobacter piscium, Pedobacter africanus, and Pedobacter saltans. Pedobacter saltans* was reclassified into the genus *Pseudopedobacter* in 2014 based on its similarity to the newly described *Pseudopedobacter beijingensis.* Different genera within most families and phyla have average amino acid identity (AAI) values between 50 and 70%. Sequenced genomes within the genus *Pedobacter* were compared to *P. heparinus,* the type species of the *Pedobacter* genus. Yellow or non-pigmented strains had AAI values above 70%, while pink pigmented strains had values below 70% when compared to *P. heparinus.* The pink *Pedobacter* species were phylogenetically coherent with AAI values above 78% and can be phenotypically distinguished from the *P. heparinus* clade based on pigmentation. We propose that the genus *Pedobacter* be further divided into two separate genera, *Pedobacter* and *Lycobacter* with *Lycobacter fisheri* BMA the type species of the new genus. (**106**)

Kish-Levine, Samantha*, and Carol Loeffler* Dickinson College, Carlisle, PA 17013. *Effects of expanding deer populations on understory vegetation and invasive species*. — Over the last 40 years, overpopulation of white-tailed deer *(Odocoileus virginianus* Zimmerman) at Florence Jones Reineman Wildlife Sanctuary in Perry Co., PA has led to elimination of most understory woody vegetation other than heavily browsed, slowly growing thorny shrubs *(Rubus* spp., *Berberis thunbergii* DC, and others). This opening of the understory has allowed the invasive species Japanese stiltgrass (*Microstegium vimineum* (Trin.) A. Camus) to become increasingly dominant in the ground vegetation, spreading and thickening as the canopy slowly loses adult trees. In 1992, nine fenced exclosures designed to keep out deer were set up at different locations around the sanctuary in order to study patterns of forest recovery given an absence of deer. Shrubs recovered quickly in some locations and trees or a mix of trees and shrubs eventually dominated the fenced plots. In 2012, nine additional exclosures were set up near each of the existing exclosures and control plots to see if recovery of woody plants would still occur given the greater prevalence of stiltgrass (from less than 5% coverage in the 1990s to 50% or greater coverage in shadier parts of the forest by 2012). In each exclosure, the number of species and percent cover of each was determined in three permanent 1m^2 quadrats as in the earlier study. These species were then sorted into broader categories (e.g., trees, shrubs, forbs, stiltgrass, other grasses, ferns). The most striking results over four years were that shrubs, especially *Rubus* species, increased in number and in percent cover in several of the new fenced plots, though not yet to the levels in older fenced plots; whereas stiltgrass percent cover is decreasing in those plots. Shading and fern cover appeared to retard shrub recovery in certain plots. Tree cover in new fenced plots still resembles that in control plots. (**54**)

Kraycer, Paul* Marywood University, Scranton, PA 18509. *Caenorhabditis elegans krüppel-like transcription factor family genetic analysis: examining klf-2 and klf-3 interaction.* —The free-living nematode *Caenorhabditis elegans* is a model organism that contain genes in the Krüppel-like Transcription Factor family (*klf*) that are homologues to *klfs* found in humans. *klf*s are important in the storage of lipids in the intestines of *C. elegans* and play a major part in the formation of adipose cells. Their control over adipose cells causes them to be linked to predisposition to obesity and type-2 diabetes in humans. Studies have shown that the *klf*-2 and *klf*-3 genes are both important in the storage and utilization of fatty acids within the intestine by promoting fatty acid ß-oxidation, however little research has been done examining the interaction between these two transcription factors. Preliminary tests suggests that *klf*-3(RB1603) mutants mate at an inefficient rate. Thus, In order to study the interaction between these gene we performed RNA interference via microinjection on *klf*-3(RB1603) mutants in order to knock out the *klf-2* gene. The F1 generation of these worms will be visibly screened using light microscopy for any changes in morphology. Similarly, they will screened for the amount of progeny produced for the extent of sterility. Finally the worms will be stained with Oil Red O-stain to examine any differences in fat accumulation. (**75**)

Kriebel, Devon*, Grace Cadigan*, Sebastian Moreno, Jeffrey Stratford, and Michael Steele Wilkes University, Wilkes-Barre, PA 18766. *Animal-mediated seed dispersal across an urban-rural gradient.* — The effects of urbanization on species richness are well established, yet we understand very little of the consequence of urbanization on plant-animal interactions and related ecological processes. Oaks and their seed dispersers are an ideal system to study the effects of plant-animal interactions in anthropogenic-dominated landscapes. Our study investigated the caching and dispersal of pin oak (*Quercus palustris*) and red oak (*Q. rubra*) acorns by small mammals throughout rural, urban, and suburban sites in northeastern Pennsylvania. We presented 75 tagged acorns of both species in 27 different exclosures in 2015 and again at 25 exclosures at the same locations in 2016 that prevented access by other acorn consumers, such as deer, turkey, and blue jays, but allowed access by rodents (squirrels, chipmunks and field mice). In 2015, caching rate was significantly higher in suburban sites vs. rural and urban sites and significantly fewer acorns were eaten at suburban sites than the other two sites. We observed no significant difference in caching distance throughout the gradient. In 2016, we observed higher caching rates in urban and suburban sites vs. rural sites, and higher rates of seed predation at rural sites compared to the other two. We suggest that different assemblages of rodents as well as variation in the availability of alternative foods likely contributed to the outcome of these results. (**25**)

Kruszynski, Catherine*, Kallie Hinspeter, and Amy Danowitz* Mercyhurst University, Erie, PA 16546. *Design and synthesis of a triazole-based small molecule library for the inhibition of bacterial quorum sensing*. — As the efficacy of traditional antibiotics is diminishing, it is becoming increasingly important to find novel bacterial systems to target for antibiotic development. One system that by be targeted is the bacterial quorum sensing system. In this system, bacteria use small molecule signals to communicate with one another and induce group behaviors. It is thought that inhibition of bacterial quorum sensing may be possible using synthetic small molecules. Such inhibition would cause bacteria to be unable to participate in group behaviors such as biofilm formation and infection. The research presented here focuses on the design and synthesis of a focused library of adamantyl-derived triazoles which will be tested for their ability to inhibit quorum sensing in *Vibrio fischeri.* The traizole scaffold was chosen because of its ease of synthesis and structural similarity to native quorum sensing molecules. Herein, we will describe the design and synthesis of an initial triazole-based library as well as early data regarding the ability of these molecules to inhibit quorum sensing in *Vibrio fischeri*. (**100**)

Kurey, Caitlin*, Kuntal Patel*, and Mary Lynn Grayeski Marywood University, Scranton, PA 18509. *Enhanced luminol chemiluminescence with silver and gold nanoparticles*. — The effect of silver and gold nanoparticles on the chemiluminescent reaction of oxidation of luminol by hydrogen peroxide is evaluated for potential development of improved analytical measurements. Both gold and silver strongly enhance the chemiluminescence with as much as 10% increase in intensity observed with both types of nanoparticles. Addition of gold nanoparticles results in higher relative light emission. This enhancement can be explained due to a catalytic effect. This effect is examined in the presence of various metal ions for changes in chemiluminescence intensity and kinetics. Enhancement is observed in the presence of cobalt, iron, and copper. The highest intensity is obtained with cobalt. Kinetic characteristics will be discussed as they relate to analytical measurement implications. (**144**)

Kutz, Dylan*, Michael Bilger, and Jack Holt Susquehanna University, Selinsgrove, PA 17870. *Sensitive Streams: Seasonal assessments of benthic macroinvertebrate community assemblage at five headwater streams in central Pennsylvania*. — This was the end of the second year of a survey of five headwater streams in Bald Eagle State Forest (Little Weikert, Green Gap, Lick, Coral and Henstep Run), each of which forms a separate cut on Penns Creek Mountain. The study sites are shaded by a mixed forest of hemlock and birch with a substrate of small boulders, cobble, and sand. Because of the uniform geology, hydrology, and land use, the chemical and physical properties of the streams are very similar. Conductivity (11-29 µs/cm) and buffering capacity (57.37-304 µeq/L) are low, pH varied between 4.85 and 6.84, but the average pH remained below 6.5. We sampled each stream for benthic macroinvertebrates (BMI) using the PADEP six kick method within a one-hundred-meter reach each season, beginning in the summer of 2015 and continuing through the present day. From the five sites our preliminary findings indicate a relatively diverse community with the number of families ranging from 9-23 per sample. Some of the dominant families included are Hydropsychidae, Elmidae, Ephemerellidae and Leuctridae, but each family was dominant in different streams during different seasons. Compared to samples taken during the summer of 2015, we saw a higher Proportional Bray-Curtis similarity in communities between streams during 2016 (24%-55% and 36%-80%, respectively). Bray-Curtis similarity in communities between streams sampled during the fall of 2016 were slightly lower than those observed during the fall of 2015 (31%-74% and 37%-62%, respectively). The Bray-Curtis similarity of each stream compared to itself from 2015-2016, however, were considerably lower from year to year (22%-52%). The Hilsenhoff Biotic Index for each site ranged from 2.8-5.1, which was between the very good/good range for the water quality of a stream. The overall Shannon Diversity Index (SDI) for fall and summer of 2016 was 1.3-2.5, which was comparable to these seasons in 2015 (1.5-2.7). Identification and analyses of samples collected during the winter and spring of each year are ongoing. (**84**)

Lansberry, Seth* Lycoming College, Williamsport, PA 17701. *Individual and population health for two Eastern Hellbender meta-populations in a tributary of the West Branch of the Susquehanna River*. — Two meta-populations of the Eastern Hellbender salamander (*Cryptobranchus a. alleganiensis*), in a single tributary of the West Branch of the Susquehanna River, were surveyed for overall population health and for individual health parameters during August 2016. The overall objective was to establish baseline health conditions in a watershed where shale gas extraction ongoing and is expected to expand. Captured individuals were sexed, measured for length and weight, then assessed for external indicators of health, including evidence of infection, presence of parasites, open sores, healed wounds, scarring, loss of eyes, toes, limbs, and portions of the tail. Skin swabs were taken to test for the presence of chytrid fungus (*Batrachochytrium dendrobatidis*) infection and nearly 40% of individuals were shown to be infected. Blood was collected from the caudal vein of thirty-six individuals. The whole blood was centrifuged to generate plasma samples that were submitted to an independent lab for analysis of 13 blood chemistry parameters. Microhematocrits were taken by micro-centrifuging whole blood collected in capillary tubes. Blood smears were created and dried in the field, and later fixed and stained for determining white blood cell differentials, and to facilitate counts of micronuclei and the number of blood parasites (we focused on trypanosomes). No blood parasites were observed. Total body length/mass ratios were calculated to assess general health and to compare the results to similar measures taken during a study of the two meta-populations three years earlier. The results of this study show no obvious decline in individual or population health in the two meta-populations despite significant declines and local extinctions in eastern hellbender populations throughout the Susquehanna River watershed. (**32**)

Laplante, Michelle*, and John Cigliano Cedar Crest College, Allentown, PA 18104. *The combined effects of ocean acidification and global warming on prey detection in the minnow, Fundulus heteroclitus.* — Since the industrial revolution, anthropogenic carbon dioxide has been vigorously pumped into the atmosphere, causing global warming. Approximately 30% of this carbon dioxide has been absorbed into the oceans, causing a decrease in pH, known as ocean acidification. The oceans also are warmed by global warming causing a dual threat to marine organisms. Recent studies have shown that lower pH can have an effect on the physiology and behavior of tropical fish. The purpose of this study was to determine how the combined effects of global warming and ocean acidification affect the prey location ability of a temperate marine fish, the minnow *Fundulus heteroclitus.* Minnows were maintained for 1 months under four different conditions: (1) normal conditions (pH 8.2, 13°C), (2) decreased pH (pH 7.7), (3) increased temperature (18°C), and combined effects of increased temperature and decreased pH. Normal conditions are the average current conditions experienced by the fish and ocean acidification and warming conditions were based on the worst-case projections for the year 2100 of the International Panel on Climate Change (IPCC). The ability to detect prey cues was tested using a two- choice flume. Trials are complete and data are being analyzed; results will be discussed. Future directions of this project will include looking at the long-term effects and then determining if effects, once observed, are reversible. (**80**)

Latham, Nicholas*, Angeline Lonardi*, Riley Slate*, Alison Dyszel, Serena Ngan, Rachel Jesiolowski, Ellen Weidel, and Lara Goudsouzian DeSales University, Center Valley, Pennsylvania 18034. *Temperature effects on TPE, trinucleotide repeat stability, and chromosome loss in Saccharomyces cerevisiae*. — We investigated the influence of temperature on the genetic stability of Saccharomyces cerevisiae through the observation of the telomere position effect, trinucleotide repeat expansion and chromosome loss. Previous research has shown that genes placed adjacent to an S. cerevisiae telomere exhibit reversible transcriptional repression, a phenomenon known as the Telomere Position Effect (TPE). This specific alteration of genetic expression is not observed when the same genes are distanced from the telomeric heterochromatin. Using a cell viability assay, we investigated the ability of an S. cerevisiae telomere to silence the URA3 gene at a modified telomere via TPE at three different temperatures. We found that expression of URA3 was low at 23°C and 30°C relative to expression at 37°C. Our findings are consistent with previous studies which indicated that high temperatures diminish telomere length. Trinucleotide repeats are sequences of DNA composed of a repetitive pattern of three nucleotides. Though trinucleotide repeats exist naturally, expansion of these genomic sequences is known to be a cause of several serious human diseases, such as Huntington's Disease and Fragile X Syndrome. We investigated the relative levels of CTG trinucleotide repeat expansion in the euchromatin of S. cerevisiae grown at 23°C, 30°C, and 37°C. Preliminary quantitative data suggests that temperature affects expansion of CTG trinucleotide repeats in S. cerevisiae. Using an ADE3/8 color assay and a disome strain of S. cerevisiae, we examined the impact of temperature on chromosome loss. Our data indicate a correlation between high temperature and chromosomal instability. (**131**)

Leinbach, Russ*, Justin Hoffman, Joshua Reeder, and Karen Campbell Albright College, Reading, PA 19604. *The bats of Costa Rica.* — Costa Rica is a country rich in biodiversity and as a result is a favored ecotourism destination. Albright College was recently the recipient of a property in the southwestern region of Costa Rica to be used for class trips to do ecological research and teaching. The seminal trip was conducted in January 2017, involving twelve students and two professors. Part of the work conducted involved a survey of the bat populations at the property. Previous research by others has identified over 110 species of bats in Costa Rica, and we were interested to learn what would be found at Albright's field station. We conducted traditional surveys of bat populations using mist nets to capture flying bats. This approach allows direct observation of active individuals, and allows for positive identification of species through specific anatomical measurements. We employed single-tire mist nets at four sites around the property, placed along potential bat flight corridors. The nets were placed before sunset, and remained up for approximately 3 hours each night, until visual and acoustic bat activity, measured by a handheld acoustic receiver, had diminished. The survey was conducted over eight consecutive nights, with the locations of the two mist nets changed each night. A total of eighteen bats were captured, including *Desmodus rotundus*, the common vampire bat, two *Artibeus sp.* and *Phyllostomus haustatus*, the greater spear-nosed Bat. To our knowledge, this survey is the first of its kind to be conducted on this property and has provided a baseline of what species could be encountered in future visits. The Albright College Science Department intends to continue doing surveys of this type in future years, and so this study provides a good basis for comparison. (**36**)

Levri, Edward, and Rebecca Luft* Penn State University-Altoona, Altoona, PA 16601. *The invasive New Zealand mud snail in central Pennsylvania*. — The world-wide invader, the New Zealand mud snail (*Potamopyrgus antipodarum*) has established populations in the American west and in the Great Lakes region of North America. In the summer of 2013, the species was found in a high quality trout stream, Spring Creek, in Centre County, Pennsylvania. The goals of this study were to 1) determine the geographic distribution of the invader in central PA, 2) determine it rate of range expansion, 3) determine what clonal genotype(s) exist in PA, and 4) determine if the PA population differs in behavior from other invasive New Zealand mud snail populations. We found that the snail appears to be thus far limited to the Spring Creek watershed, although it has slightly expanded its range and increased its abundances at several locations within that watershed in the past three years. The genotype of the PA population matches the most common clone in the US west. The PA population behaves most similarly to its matching genotype in the western US, but some differences in behavior exist. (**67**)

Levri, James*, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *The relationship between water chemistry and the abundance of the invasive New Zealand mud snail in central Pennsylvania*. — The New Zealand mud snail (*Potamopyrgus antipodarum*) is an invasive species inhabiting much of the western US and the Great Lakes region of North America. Recently a population was discovered in Spring Creek in Centre County, Pennsylvania. The goal of this study was to determine the relationship between three water chemical variables and the abundance of the snail. Calcium concentration, conductivity, and pH were measured at 20 locations in Spring Creek and its tributaries where the New Zealand mud snail has been found or in a location between known sites where the snail exists. Relative abundance estimates were made in June-July of 2016.

Measurements of the chemical variables were made in June-July of 2016 and then again in December of 2016. We then utilized regression analysis to determine if a relationship exists between the three variables and the abundances of the snail. We found that conductivity significantly positively correlated with abundance in both the summer and winter while calcium concentration only positively correlated in the winter. pH did not significantly correlate with abundance, but the pH values were above 7 at all locations resulting in suitable conditions for the snail. (**57**)

Loh, Samantha*, Laura Spence, and Laura Scales Susquehanna University, Selinsgrove, PA 17870. *Feeding ecology of barn owls (Tyto alba; Scopoli, 1769) in central Pennsylvania*. — Barn owls are nocturnal predators known for requiring large portions of open land to hunt and roost while breeding. Due to the amount of prey needed to sustain each owl, a minimum distance of 1-2 km that probably allows them to avoid competition typically separates breeding pairs in central Pennsylvania. We noticed, however, what seems to be a "nest cluster" in Union County, Pennsylvania separated by a distance of less than 0.5 km. With no published data explaining this natural event, we decided to follow what prey items are available year-round with monthly live trapping of small mammals, and to analyze consumed fauna from the owl regurgitates of all the individuals in the cluster (3 nests). Our 18 month-long live trapping of small mammals suggests a high density but low diversity of prey items consisting of only *Peromyscus leucopus* (93%) and *Blarina brevicauda* (7%). Our preliminary data from owl regurgitate analysis portrays a diverse fauna of small mammals and birds as prey items, made of voles (72.8%), insectivores (16.2%), mice (10.6%), and birds (0.4%). Within the voles, 100% were *Microtus pennsylvanicus*; within the insectivores, we have found *Blarina brevicauda* (86%), *Condylura cristata* (9.3%), and *Sorex cinereus* (4.6%); and within the mice, we have found *Peromyscus leucopus* (46.4%), *Zapus hudsonicus* (21.4%), *Mus musculus* (10.7%), *Rattus norvegicus* (10.7%), and probably a hybrid of *Microtus* spp. (10.7%). Our owl regurgitate data has a similar distribution of prey items as previous studies conducted in the Eastern Deciduous Forest. In these studies, *M. pennsylvanicus* composed the majority of the prey items (up to 80%), followed by *B. brevicauda* (up to 20%). By comparing the diversity of the owl regurgitate within our cluster with values and analyses from other nests, combined with the results of our live trapping, we speculate on plausible explanations for this phenomenon. (**39**)

Long, Hailey*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Expression of THRA Over the Course of Retinal Development in Chicken (Gallus gallus) embryos and the impacts of Thyroid Hormone on THRA expression*. — The retina is the light sensitive portion in the eye in vertebrates. While the anatomy and function of the retina is well-understood, the molecular mechanisms underlying its development are not yet fully understood. For this research, I focused on determining when Thra (thyroid hormone receptor A) is expressed during development of the retina in chicken embryos through quantitative PCR. Then, the levels of Thra were evaluated without thyroid hormone present, by first utilizing cell culture to simulate a scenario with no thyroid hormone and then finally performing qPCR on the cultured retinas. The results of these experiments suggest that Thra is equally present over the course of development and that thyroid hormone has no impact on expression of Thra. (**156**)

Love, Esther*, Lisa Iacaruso, and Cynthia Walter Saint Vincent College, Latrobe, PA 15650. *The effects of high molecular weight cranberry extract and thieves oil on Streptococcus mutans*. — The most prevalent carcinogenic agent responsible for causing dental caries is *Streptococcus mutans*. For years, sodium fluoride (NaF) has been the primary antimicrobial used to fight *S. mutans* in the oral cavity. However, natural extracts from plants such as cranberry have been shown to have antimicrobial properties and, natural oils found in plants, such as those in thieves oil (TO), have been utilized to inhibit bacterial growth, although little research has been done to examine the antimicrobial properties of TO. The goal of this study was to compare the effects of NaF to the effects of high molecular weight (HMW) cranberry extract and a commercial product of 100% pure TO on the growth of *S. mutans.* The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC), and zone of inhibition (ZOI) in a Kirby Bauer test for each agent were determined for *S. mutans.* Dentition were gathered from a local oral surgeon and mouthwash formulations were made and utilized to test the different reagents on the enamel surface. HMW preparation of cranberry concentrate inhibited growth more effectively at pH 5.5 than at pH 7. The slope of the percent of maximum growth as cranberry extract concentration increased was -0.268 at pH 5.5 vs. -0.123 at pH 7. Also, cranberry extract at pH 5.5 had stronger bactericidal effects than cranberry extract at pH 7. TO was shown to inhibit bacterial growth with an average ZOI of 16.2 mm (s,d.=4.9) though not as effectively as 0.2 % NaF with a ZOI of 18.2 mm (s.d.=1.64). All three reagents showed bacterial inhibition; however, further research is needed to determine the most safe and effective reagent. (**108**)

Luft, Rebecca*, Lewis Gromiller, Edward Levri, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *The influence of fish odor on the dispersal behavior of an invasive snail*. — The New Zealand mud snail (*Potamopyrgus antipodarum*) is a world-wide invasive species with established populations in multiple locations in North America, including Pennsylvania. The snail is known to behaviorally respond to the odor of a fish predator in its native New Zealand in ways that likely decrease the probability of predation. The ability to respond behaviorally to novel predators in their invaded range may increase the invasive ability of the species. New Zealand mud snails have the ability to attach to the surface tension of water and float for long distances. Here we examine this dispersal behavior of the snail and the influence of fish odor on that behavior. We examined dispersal behavior by placing 20 adult snails at a time in a plastic container for 10 minutes and then counted how many snails were found on the floor of the container, the sides, and floating under the surface. Snails were exposed to one of three treatments, no fish odor, odor of blacknose dace, or odor of zebrafish. Six different populations of clones were used in the experiment. Four of the populations are invasive in the US; US1WY, US1PA, US2-1, and US2-29. The two other populations used were clones isolated from New Zealand Lakes; Gunn2 and Map. The proportion of snails found floating was compared between clone and treatment. A preliminary analysis of the data suggests that there are differences between populations in their location preference in the container, but there appears to be no effect of fish odor on the behavior. The significance of these results will be discussed. (**55**)

Lukasak, Becca*, and Lisa Antoniacci Marywood University, Scranton, PA 18509. *Characterization of the SUN Domain Protein Mps3 function in gene expression*. — The yeast nuclear envelope protein Mps3 functions in several aspects of chromosome metabolism such as sister chromatid cohesion, telomere clustering, and DNA damage repair. In addition, Mps3 physically and functionally interacts with the histone variant Htz1. Htz1 was previously identified as a histone variant that prevents DNA from forming silent heterochromatin as a way to regulate transcription. Because of the involvement of both of these genes in chromosome metabolism, it is hypothesized that they may function in regulating gene expression. In order to assess genome expression wild type yeast, *mps3-3*, *mps3-5*, and an *htz1Δ* strain were examined for genome wide expression levels in both asynchronously and synchronized growing cells. The data generated was analyzed for both up-regulation and down-regulation of gene expression in comparison to the wild type strain. Identification of expression differences between the wild type and mutant strains would suggest a function for Mps3 and Htz1 in gene expression. (**8**)

Lundy, Daniel*, Brianna Morris, and Kathleen Bartlow Lycoming College, Williamsport, PA 17701. *Induction of dopaminergic phenotype in SH-SY5Y cells by sequential exposure to retinoic acid and brain-derived neurotrophic factor (BDNF).* — Previous studies (Encinas et al., 2000) have designed a protocol to derive neuron-like cells from the human neuroblastoma cell line SH-SY5Y using sequential exposure to retinoic acid (RA) and brain-derived neurotrophic factor (BDNF). Encinas et al. focused primarily on nonspecific neuronal markers to indicate the presence of fully differentiated neuron-like cells, without addressing the question of neurotransmitter phenotype. The purpose of the current experiment was to determine whether sequential exposure to RA and BDNF is capable of generating dopaminergic neuron-like cells, by specifically examining the expression of dopaminergic markers during differentiation. Using proliferation medium (DMEM/F12 + 10% FBS + 1% Pen-Strep) SH-SY5Y cells were grown and subcultured when confluency reached greater than 90% for up to six total passages. For differentiation experiments, cells were plated at a density of 2×10^4 cells/cm^2 and immediately treated with 10uM retinoic acid for 24 hours. The RA-containing medium was then removed and replaced with serum-free medium containing 50 ng/mL BDNF. Cells were harvested at three timepoints: 0 hours, 24 hours after exposure to RA, and 72 hours after exposure to RA (i.e. 48 hours after BDNF treatment). RNA was isolated from each sample using the Qiagen RNeasy Protocol. Reverse transcription PCR (RT-PCR) was performed using primers directed against human tyrosine hydroxylase (TH), dopamine transporter (DAT), and control genes glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and ribosomal subunit protein RPL-19. Preliminary results show an increase from basal TH expression, and induction of DAT expression, among the differentiated cells. Future directions include the use of quantitative PCR to better determine upregulation of dopaminergic markers. Also, the use of collagen-coated plates will be explored to examine the effects of collagen on cell culture. (**164**)

Lybarger, Vanessa*, M. Dana Harriger, and Christine Proctor Wilson College, Chambersburg, PA 17201. *Evaluation of factors that increase the load of pathogenic E. coli in the Conococheaque, a freshwater creek in Franklin County, Pennsylvania*. — *Escherichia coli*, naturally occurring bacteria in the intestinal tract of humans and animals, are often introduced into the environment and waterways through fecal material. Although most strains of *E.coli* are non-pathogenic, when present, pathogenic strains can inflict severe health effects. Different types of environments affect the ability of *E. coli* to reach and survive in waterways. Once there, they may infect humans through irrigation of food crops and recreation. Monitoring streams for the amount of *E. coli,* while also recoding surrounding land use is important for identifying factors that increase the risk of pathogenic *E. coli* in waterways. This study aims to identify what factors may increase the contamination risk of pathogenic *E. coli* in the Conococheaue creek. Contamination is defined by the EPA as exceeding a threshold of 126 CFU/100 ml. Water samples were collected weekly at five predetermined USDA research sites, each within different land uses. Samples were membrane filtered, filter placed onto *E. coli* selective media, and incubated to determine colony counts. To assess potential risk factors, a variety of environmental indicators were collected. Animal input, streambank integrity, surrounding land use, and weather factors were all examined. Animal input was monitored using trail cameras and track beds, streambanks were monitored using an established USDA habitat assessment rubric. Surrounding and upstream land use for each site was determined using USDA land use maps in a geographic information system. Lastly, weather stations, including rain gauges recorded weather events. A regression analysis was used to determine which factors have a greater influence on increasing the presence of *E. coli*. Results of this study will contribute to the understanding of factors that increase the prevalence of pathogenic *E. coli* is important in prevention of human infections. (**117**)

Markowitz, Lauren*, Olivia Townsend*, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087. *Earthworms as sentinel species for the measurement of macroautophagic biomarkers in response to the heavy metal environmental pollutants cadmium and copper*. — Heavy metal exposure is a relevant concern as ecosystems become progressively filled with pollutants. Improper disposal of electronic devices causes leaching of heavy metals into the soil which affects sentinel species. Toxicity associated with accumulation of cadmium and copper in soil has been shown in both plant and earthworm models. These complications begin as the cell's ability to naturally break down its old organelles and proteins becomes dysregulated. Macroautophagy, a process by which cellular components are degraded through lysosomal machinery, acts as a survival mechanism under stress and serves as an intracellular quality control management system by clearing damaged organelles. Over time, dysregulation of this process can lead to disease and disorders. This study sought to observe the cell's response to differing concentrations of heavy metals in order to document the levels of macroautophagy that occur as a result, and determine the feasibility of using earthworms as bioindicators of soils containing heavy metals. *In vivo* and *in vitro* assays were conducted to measure macroautophagy levels in the earthworm species *Eisenia hortensis* in response to exposure to the heavy metals copper and cadmium. We hypothesized that heavy metal exposure would induce increased levels of macroautophagy which could be detected using fluorescent dyes that bind specifically to the double membrane structures of macroautophagic vesicles using flow cytometry. *In vivo* and *in vitro* assays showed promising observations, with more demonstrable results obtained when using individual earthworms versus batches of earthworms. Inter-assay reproducibility proved problematic throughout this study. For this reason, it was concluded that the method used to measure macroautophagy was not a reliable indication of toxicity in our invertebrate model. The age of the colony could have been a contributing factor to the inconsistent results obtained. Therefore, conducting experiments again with younger colonies may provide more consistent and reproducible results. (**120**)

Marotta, Julianna*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *The role of the Enterobacter cloacae AcrAB-TolC Efflux Pump in Triclosan resistance*. — Multidrug resistant bacterial infections are rising worldwide, shifting from what once was a biological phenomenon to what is quickly becoming a global health crisis. Although bacteria have many mechanisms to target and remove antimicrobial agents from the cell, an overexpression of efflux pumps has been suggested as a general mechanism that increases resistance towards numerous other agents. *Enterobacter cloacae* is a common nosocomial pathogen prevalent in water treatment plants, soil, and sewage runoff, and previous studies have indicated that its AcrAB-ToC efflux pump is associated with the removal of tetracycline and chloramphenicol from the cell, thus increasing organismal resistance to these compounds. For the past several decades, the antimicrobial agent, triclosan has been added to consumer products such as toothpaste and hand sanitizer. A recent FDA ban has blocked its use in most of these products; however, the damage may have already been done as this compound has been found in many environments. In this study, *Enterobacter cloacae* was repeatedly exposed to triclosan, tetracycline, and chloramphenicol, and resistance of the strains was assessed through a Kirby-Bauer disk diffusion test. Triclosan resistant isolates were identified following exposure to all three antibiotic compounds at concentrations that inhibited growth of *E. cloacae* triclosan susceptible cultures. In this study, key genes associated with the AcrAB-TolC efflux pump mechanism (e.g. AcrA, AcrB, and AcrR) as well as the 16S ribosomal RNA gene were sequenced and their expression in both sensitive and resistant strains of *E. cloacae* were studied via RT-qPCR in order to better understand whether triclosan resistance was correlated with a change in efflux pump efficacy. Ultimately, data derived from this study could lead to a potential target of inactivation to revert the multidrug resistance outcome created over the past several decades. (**125**)

Marotta, Julianna*, Logan Exton*, Nicole Raimondi*, Rochelle Koseki*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *triclosan exposure leads to multidrug resistance in diverse bacterial species*. — The long-term, repeated exposure of bacteria to a specific antibiotic has been demonstrated to select for strains that are resistant to not only that antibiotic, but other compounds as well, leading to the development of multidrug resistant strains. Public concern regarding bacteria-caused illness has increased the demand for products that discourage bacterial growth. For the past several decades, the antimicrobial agent triclosan was added to common personal hygiene products such as toothpaste, shampoo, and hand sanitizer. In September 2016, the FDA banned the use of this agent in most products due to insufficient evidence that the compound's efficacy outweighs its negative effects on the environment, human health, and microbial resistance. It may be too late, however, to lessen the ecological impact of this chemical, as triclosan has been detected in soil, sewage, water runoff, and natural bodies of water. Of greater concern is whether triclosan resistance is linked to multidrug resistance. In this collaborative study, *Staphylococcus aureus, Enterobacter cloacae, Enterobacter aerogenes, Bacillus cereus, Micrococcus luteus, and Alcaligenes faecalis* were repeatedly exposed to triclosan and in a short time span (less than one week in many cases), most species developed partial or complete resistance to not only triclosan, but other antibiotic compounds as well. This study illustrates the importance of understanding antibiotic resistance, and further analysis will address mechanisms used across diverse species to block the impact of triclosan with the hope of identifying potential targets for combating multidrug resistance. (**104**)

McIntyre, Kelcy*, Audrey J. Ettinger, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Ginkgo biloba as a potential prophylactic treatment for stroke.* — Stroke is the leading cause of long-term disability and the third leading cause of death in the United States, and treatment options are limited. In ischemic stroke, the initial event causes neuronal death and subsequent activation of cellular apoptosis pathways, expanding the area of damage. Both prophylactic treatments to limit the initial amount of cell death and therapeutic intervention to reduce secondary damage are needed. Antioxidants provide a useful strategy for both goals, blocking apoptosis in affected cells and preventing the spread of apoptosis to neighboring cells. *Ginkgo biloba* leaf extract, long used as an herbal remedy in traditional medicine, has been shown to contain several components with antioxidant properties. Previous work has demonstrated that the purified *G. biloba* extract EGB761 blocks apoptosis in cultured cells, potentially indicating its usefulness as a neuroprotectant. The aim of this study was to extend those previous experiments to an over-the-counter, easily purchased version of this herbal supplement to determine its effectiveness as an anti-stroke prophylactic. Primary brain and body cell isolates from *Gallus gallus* embryos were pre-treated with the herbal supplement (or PBS) 24 hours before apoptosis induction by hydrogen peroxide treatment. Cell viability was assessed by trypan blue exclusion at 0-24 hours post-treatment, and indicated that the treated cells had improved acute survival when compared to the PBS negative controls. Apoptotic gene expression differences were investigated using an apoptotic array, and two independent assays showed down-regulation of apoptotic genes, such as caspases, and up-regulation of anti-apoptotic genes. These results support the use of an easily-accessible, commercially-available crude herbal supplement to provide protection from apoptotic cell death. Future work will utilize Western blots to confirm caspase activity reduction, qRT-PCR to confirm changes in gene expression, and a biochemical assay to assess the free radical scavenging activity of the *G. biloba* supplement. (**16**)

Mendez, Marta*, Michael Bilger, and Jack Holt Susquehanna University, Selinsgrove, PA 17870. *Response of benthic macroinvertebrate communities to variations in discharge during the summer months of 2015 and 2016 in the upper main stem of the Susquehanna River*. — This is the eighth year in a long-term study of benthic macroinvertebrate communities (BMI) in the upper main stem of the Susquehanna River from mid-summer collections. BMI communities are useful for stream assessments because their occurrences reflect both water quality (assessment) and habitat variation (temporal and spatial). The two sample sites are located near the Sunbury Generation LP and below the Adam T. Bower inflatable dam at Sunbury, PA. Furthermore, they are seven miles below the confluence of the West Branch and North Branch, which remain chemically and physically distinct due to poor lateral mixing. The sites are in the channel west of Byer's Island. Site 1 is in the West Branch plume (WBP), and site 2 in the North Branch plume (NBP). Following EPA guidelines for passive sampling in non-wadeable streams, we used rock baskets and Hester-Dendy

Multiplate samplers, both of which emphasize drifting and colonizing BMI. In particular, we are reporting results taken during 2015 and 2016, which were subject to very different flow regimes. For example, the average discharge measured at the Sunbury USGS gage during July was 36,500 gps in 2015 but 3,832 gps in 2016. BMI community composition at the two sites had a 91% Bray-Curtis similarity during summer 2015, but it fell to 50% during the same period in 2016. The low flow of 2016 had the greatest negative impact on the occurrence of individuals in the families Hydropsychidae and Isonychiidae, but numbers of Heptageniidae increased in response to low flow. The Hilsenhoff Biotic Index (HBI) score rose at sites 1 and 2 from 3.51 and 3.62 in 2015 to 5.36 and 5.16 in 2016. Shannon Diversity Index (SDI) similarly declined from 2015 (1.50 and 1.61) to 2016 (1.15 and 1.39). Results such as these underscore the importance of multiyear sampling in assessments of environments as variable as large rivers. We will report on samples taken during the fall of 2015 and 2016. (**85**)

Merz, Phillip*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Exploring the heterogeneity of a shallow unconfined aquifer using multiple geophysical methods*. — An understanding of subsurface geology in general and more specifically the aquifer geology has been a critical factor in groundwater management. This is also extremely valuable in remediation of waste water and the protection of drinking water sources. In order to achieve this goal, hydrogeologists have utilized a variety of geophysical methods to analyze the makeup of the subsurface with minimal physical intrusion. The idea behind the integration of methods is to complement their strength. Recent examples of this method in this field was used successfully by Doetsch et al. (2011) who mapped a gravel aquifer using Ground Penetrating Radar (GPR) and Electric Refraction Tomography (ERT). cooperatively to locate groundwater while being able to denote surrounding geology simultaneously. In this study, we used multiple geophysical methods to create a more accurate map of the geology of an aquifer. Three geophysical methods were selected to be utilized cooperatively to analyze an unconfined shallow aquifer in CEER, a research facility in Susquehanna University. These methods include GPR, Seismic Refraction and ERT. An additional well drillings was also performed in this site to ground truth our findings. In this study 21 ERT profile were used individually and combined in a model have provided areas of low resistivity which consisted of saturated areas of the aquifer. While the ERT has failed to identify the different geological formation of this aquifer, the seismic refraction was more accurate on the geology yet failed to determine with certainty areas of high water content. The GPR was extremely useful in the identification of the water table and did help further support the seismic refraction in the identification of additional details of the geological structure of the aquifer. (**95**)

Mink, Jennifer*, Jonathan Matejcek*, Kelsey Elliott, Linda Lowe-Krentz, and Joshua Slee DeSales University, Center Valley, PA 18034. *Localization of BMP6 in vascular endothelial cells treated with heparin*. — Bone morphogenetic protein 6 (BMP6) has been found to bind heparin and influence the activity of bone morphogenetic proteins, which are members of the transforming growth factor-β (TGF-β) superfamily of proteins that regulate proliferation, differentiation, pattern formation, and apoptosis. It can be predicted that BMP6 upregulation plays a role in the anticoagulant functions of heparin, but not much is known about the heparin anti-inflammatory mechanisms. There is a known link between BMP6 and smooth muscle cell physiology, but it is unclear how BMP6 upregulation affects physiology. A microarray completed during previous research indicated a 1.899-fold increase in BMP6 for vascular smooth muscle cells treated with heparin in comparison to untreated cells. Current research looks to validate these findings by observing localization and expression changes of BMP6 in response to heparin treatment. (**170**)

Motsko, Jeremy*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Impact of Walker and Faylor Lakes on Middle Creek (Snyder County, PA) using physical, geochemical & benthic metrics*. — In recent years, dams have received extensive scrutiny for their effects on stream and river systems throughout the U.S. Direct land use has also been observed to have an effect on the water quality of streams and rivers (Robins et al. 1987). The main focus of these studies is often on large scale dams and reservoirs. One less studied field is the effects of small impoundments on streams and the cumulative effects they have on higher order water systems. The presence of two water impoundments; Walker and Faylor Lakes located respectively on the South and North branches of Middle Creek in Snyder County, Pennsylvania are believed to have a significant effect on the geochemistry and the benthic communities of these two headwater streams. This study focused on measuring physical properties onsite and water grab samples for geochemistry in laboratory, in addition to kick sampling for the benthic study from all 7 sites. The sampling sites were selected to cover both upstream and downstream. An additional site on the main merging stem of Middle Creek was also selected to confirm if the chemical analysis. All sites were checked for T°, pH, Ke, DO, TDS, ORP, COD, BOD5 TSS, F, Cl, NO_2^-, Br, SO_4^{2-}, NO_3^-, P, K, NH_4, K, Mg^{2+} and Ca^{2+}. Preliminary results showed that the T, pH, DO, BOD5, K were high in the lakes than both upstream and downstream sites. ORP, Ke, TDS, NO_3^2– were found lower with respect to the upstream and downstream branches. While Na, K and Cl seemed to decrease gradually from upstream to downstream sites, Ke and TDS increases in Faylor but not in Walker lake. Because the upstream of the two lakes is similar the minor difference of their impact on the downstream sites is strongly believed to occur because of the geometry. (**94**)

Murman, Kelly*, and Thomas C. LaDuke East Stroudsburg University, East Stroudsburg, PA 18301. *A comparative dietary analysis of five species in the streamside salamander guild (Plethodontidae) in eastern Pennsylvania.* — The diets of five species of streamside salamander (*Desmognathus fuscus, Desmognathus ochrophaeus, Eurycea bislineata, Gyrinophilus porphyriticus, and Pseudotriton ruber*) will be analyzed using a non-lethal stomach flushing technique. The gut contents will be compared to invertebrate samples collected from the environment to assess similarity and attempt to determine where these species forage for food and whether there is evidence of prey selectivity. This project will also examine if the composition of the species assemblage affects the diet of the member species by sampling at multiple localities with different assemblages. Sampling will occur in spring, mid-summer, and fall in order to determine if there are any seasonal shifts in the diets of these species. (**31**)

Musheno, Sarah* Lycoming College, Williamsport, PA 17701. *Habitat preferences, and population structure and stability, in two Eastern Hellbender meta-populations in a Tributary of the West Branch of the Susquehanna River*. — Two meta-populations of the Eastern Hellbender salamander (*Cryptobranchus a. alleganiensis*), in a single tributary of the West Branch of the Susquehanna River, were surveyed for population parameters (density, sex ratios), habitat preferences (rock size, location within the stream channel), and local distribution in August 2016. Our overall objective was to determine if the two populations were stable or if they were in decline. Analyses of population data show that density, habitat preferences, and distribution did not change since a similar survey of the two meta-populations three years earlier. Analyses of habitat use show that hellbenders take up residency in or near the thalweg, where the majority of cover rocks are located. Peripheral cover rocks are only rarely used by hellbenders. We found a positive relationship between the size (total body length) of hellbenders and the size (length) of the cover rocks. Population size/age structure and sex ratios were similar between sample years. Sex ratios tend to favor males over females. Migrations between the meta-populations were documented in 2016 and during prior surveys. Most migrants were young males and all movements were in an upstream direction. The results of this study indicates ongoing stability in this tributary despite significant declines and local extinctions in eastern hellbender populations throughout the Susquehanna River watershed. Concurrent with population monitoring, we supported applied conservation initiatives that include installation of artificial instream habitat structures and the collection of fertile eggs for head-starting juvenile hellbenders for future reintroduction into the watershed. (**33**)

Mylin, Lawrence* Messiah College, Mechanicsburg, PA 17055. *Detection of simulated pathogenic Escherichia coli O157:H7 using an end point polymerase chain reaction assay developed for a mid-level Microbiology for Health Professions course laboratory*. — *Escherichia coli* O157:H7 is one of several pathogenic *E. coli* strains that cause illness in humans. Infections often result from the consumption of contaminated, uncooked or under-cooked meats, vegetables or milk. Cattle are a common reservoir for *E. coli* O157:H7 which can colonize their intestinal tract without causing disease. Infection (of humans) by *E. coli* O157:H7 may be asymptomatic or may result in mild gastric discomfort with abdominal cramps, bloody diarrhea and/or life-threatening hemolytic uremic syndrome. The enhanced pathogenicity of *E. coli* O157:H7 results from acid resistance, the presence of the *Stx1* and *Stx2* genes which encode Shiga (*Shigella*-like) protein toxins, and other factors that enhance formation of intestinal lesions. The Shiga toxin proteins act by inhibiting protein synthesis in host cells by specifically inactivating host ribosomes. An end point PCR exercise was developed in which simulated “pathogenic” *E. coli* isolates are distinguished from “non-pathogenic” isolates by the number and size(s) of products. Two pairs of primers were designed to simultaneously amplify a ~200 bp region of the *Stx1* gene or a ~500 bp region of the ampicillin resistance gene, both harbored on plasmids. The *Stx1*-encoding plasmid harbored by simulated “pathogenic” isolates contains both targets; the pUC19 plasmid harbored by simulated “non-pathogenic” isolates contains only the ampicillin resistance gene target. Each student prepares a crude extract from a small cell sample taken from an assigned, pre-grown “candidate” patch and uses a small portion to prepare one reaction. The reactions from the class are subjected to thermocycling (<1 hr), and then the products loaded onto a single (or two) 2% agarose gel and separated by electrophoresis (~45’). All students are provided with a digital photograph of the gel(s) and are required to analyze the results for all candidates. The complete learning experience will be described. (**126**)

Namous, Fadia*, Brianna Hill*, and André Walther Cedar Crest College, Allentown, PA 18104. *Replication Protein A phosphorylation modulates cellular responses to chemotherapeutic DNA damaging agents in the budding yeast, Saccharomyces cerevisiae*. — In 2017 there will be approximately 1.6 million new cancer diagnoses and ~600,000 Americans are expected to die of cancer. The budding yeast *Saccharomyces cerevisiae* has been widely used as a model organism to understand the underlying causes of cancer because of the significant level of homology in cell cycle and DNA maintenance pathways. This research is focused on the highly conserved, single-stranded DNA binding protein Replication Protein A (RPA). RPA plays central roles in DNA replication, DNA repair, cell cycle control, and telomere synthesis, which are pathways often dysfunctional in human cancerous cells. RPA is phosphorylated in a cell cycle dependent manner and in response to DNA damaging agents suggesting a possible role in regulating the cellular response to DNA damage. The goal is to understand how RPA phosphorylation is involved in cellular response to DNA damaging agents by identifying genes involved in checkpoint pathways and DNA repair mechanisms that genetically interact with RPA. The goal is to elucidate the role of RPA phosphorylation in regulating genetic pathways responsible for responding to different DNA damaging chemotherapeutic drugs including: camptothecin, phleomycin, and hydroxyurea. We will present results showing that cells containing RPA mutations that cause RPA to behave like it is always phosphorylated, are less sensitive to Phleomycin than the wild type, which can be phosphorylated and dephosphorylated in a cell cycle dependent manner. Special attention to this observation has led us to want to explore different strains of *Saccharomyces cerevisiae* with a special focus on the Asp and Ala adjustments. A better understanding of RPA’s role in each of the DNA repair and cell cycle pathways and how it interacts with other genes will allow researchers to understand some of the underlying causes of cancer and assign better agents to selectively target cancer cells. (**138**)

Namous, Nadia*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *The role of RPA phosphorylation in cell cycle regulation and telomere synthesis*. — Cancer is the second leading cause of death in the USA, and is caused by uncontrolled cell division of cells within the body. Of the many hallmarks of cancer outlined by Hanahan and Weinberg, this project focuses on replicative immortality, cell cycle regulation, and resisting cell death. Our research is focused on Replication Protein A (RPA), which is a highly conserved heterotrimeric single-stranded DNA binding protein involved in DNA replication, recombination, repair, and regulation of cell cycle progression and telomere synthesis. The focus will be on the effects of phosphorylation of the second subunit of RPA in yeast *Saccharomyces cerevisiae* because yeast RPA, also known as RFA, is highly homologous to human RPA in structure and function. Furthermore, genetic manipulation of yeast is simple making it easy to generate strains containing mutations that affect RPA phosphorylation. We have examined RPA function in the cell cycle checkpoint process of adaptation that happens when cells accumulate unrepaired DNA damage and in regulating the length of telomeres located at the end of chromosomes. In the presence of unrepaired DNA damage, cells will stop at the G2/M checkpoint, but will eventually release from the checkpoint arrest and resume the cell cycle in a process known as adaptation. Adaptation was observed by microscope in strains containing RPA mutations and mutations in known adaptation genes. To examine telomeres, several genes involved in the telomere regulation model such as EST1, PIF1, RIF1, TEL1, KU70 have been knocked out in the presence mutant forms of RPA and we have been examining telomeres by Telomere fragment length Southern Blot analysis and Telomeric PCR. An understanding of the function of RPA in cell cycle control and telomere synthesis will provide significant insights into important cancer causing pathways. (**136**)

Nguyen, Hang*, and Linda Kennedy Mansfield University, Mansfield, PA 16933. *Organic decompostion rates in forest and non-forest soils: A pilot study*. — This poster describes a pilot study conducted in Northern Tioga County, Pennsylvania at the Mill Cove Environmental Area. The goals of the study were to 1) determine if soil organic decomposition rates differed between forest and non-forest soils, and 2) determine if soil organic decomposition rates differed seasonally. The study involved burying nylon t-bags for a period of 90 days, and quantifying the change in mass over that period. This investigation is part of a global study presently being conducted by a team of professors in the Netherlands in an attempt to produce a global map of soil organic decomposition rates. The group of professors developed a field and laboratory protocol, known as the Tea Bag Protocol, which allows researchers around the world to participate in this study. Two types of tea bag are buried in the same location and for the same amount of time. The difference in original organic composition of the two teas results in different rates of decomposition, and comparison of the two allows the researcher to determine a soil organic rate of decomposition for the burial site (Keuskamp et al. 2013). Tbags were buried in an upland forested area and a lowland non-forested area adjacent to Mill Creek. The bags were buried in June, then September and retrieved after 90 days. The retrieved tea bags were oven dried and weighed. The results indicate that decomposition rates are higher during the summer months and that decomposition rates are higher in the forested soils. The higher summer decomposition is expected as microbes are more active and more numerous during the warmer months. The higher rate in the forested soil suggest that the microbe community is more active and numerous in a forest soil than an active floodplain soil. (**59**)

Novella, Dominic*, and Mel Zimmerman Lycoming College, Williamsport, PA 17701. *Evaluation of three stream restoration projects in Loyalsock Creek watershed*. — During the past 10 years, fish habitat structures consisting of root wads, log vanes, mudsills and other constructed materials have been placed along streams and creeks in North Central PA (Lycoming and Sullivan Counties). Three of the projects in the Loyalsock Creek Watershed have involved monitoring by Lycoming College's Clean Water Institute. Pre and post monitoring of fish populations and water quality (based on chemistry and macroinvertebrates) were completed along Mill Creek and Wallis Run (Lycoming County) and Elk Creek (Sullivan County), where structures have been added over the past several years. All sites have shown significant increases in trout populations since the installation of the fish habitats, which were designed and permitted by the PA Fish and Boat Commission. Funding for the construction on these projects included Chief Oil and Gas (Elk Creek project), Growing Greener grants to the Rose Valley/Mill Creek Watershed Association (Mill Creek Project) and Anadarko Oil and Gas /North Central Pennsylvania Conservancy (Wallis Run project). Other project partners included Lycoming and Sullivan County Conservation Districts, Loyalsock Creek Watershed Association, PA Fish and Boat Commission. The Mill Creek project occurred in two phases starting in Wallis Run was also phased in starting in 2010. The latest project on Elk Creek (two phases in 2015 and 2016) restored habitats that had been destroyed by flooding in the years leading up to and including 2011, when Tropical Storm Lee caused hundreds of millions of dollars in flood damage to residential areas in Pennsylvania alone. In 2015, Phase I on Elk Creek began with 12 multi-log veins. In 2016 Phase II occurred with a 220′ mud sill was put in to reduce bank erosion and to also help bring back trout populations. (**98**)

Oberer, Megan*, and David Singleton York College of Pennsylvania, York, PA 17405. *A comparative toxicological and carcinogenic assay of electronic cigarette vapor*. — Over the past five years, electronic cigarettes (e-cigarettes) have become a popular alternative to cigarettes in the smoking community; however, they are known to have a plethora of organic compounds that are hazardous to human health including but not limited to formaldehyde, FeNO, heavy metals, and carbonyls. Currently, little is known about the specific health related risks due to e-cigarette vapors. This study utilizes three variations of the Ames test, which correlates the frequency of reversion of histidine auxotrophy of the bacteria S. typhimurium when exposed to various mutagens. The number of revertants is then related to the mutagenic and carcinogenic properties of on the compounds being tested. The three variations of the Ames test include a disk diffusion assay, a plate incorporation assay, and a 96-well plate fluctuation assay. Additionally, several strains of S. typhimurium are being validated. A comparison of the three assays in determining the mutagenic potential of e-cigarette liquids is currently being performed. (**158**)

Orgitano, Ryan*, and Mel Zimmerman Lycoming College, Williamsport, PA 17701. *Detection of Eastern Hellbender (Cryptobranchus aleganiensis alleganiensis) environmental DNA in Northcentral Pennsylvania strerams using qPCR*. — Environmental DNA (eDNA) amplification through methods of Quantitative PCR (qPCR) is a rapidly developing technique in the field of conservation genetics. The procedure allows biologists to better understand the distribution of cryptic species, such as the hellbender (*Cryptobranchus alleganiensis alleganiensis*), in a timelier manner than that of traditional rock flipping surveys. It requires only a 1 liter water sample, taken downstream from the site in question. Over the late summer and early fall of 2016 I sampled 11 different sites on 5 separate watersheds; Little Pine Creek in Lycoming County, Oswayo Creek in Potter County, the Allegheny River in Potter County, the First Fork of the Sinnemahoning Creek in Clinton County, and the Driftwood Branch of the Sinnemahoning Creek also in Clinton County. Each of these watersheds were identified as high probability areas for hellbender presence when taking into account anecdotal reports, habitat structure, and relative crayfish densities. Of the 11 sites, hellbender eDNA was amplified at 4. The Line Pine Creek site in which hellbender eDNA was amplified was a site of known hellbender inhabitation, helping validate the technique in field use. Hellbender eDNA was also identified at one site in each the Oswayo, Allegheny, and First Fork of the Sinnemahoning watersheds; these sites were not previously identified as locations in which hellbender populations currently exist. The hellbender survey team traveled to the Oswayo site to conduct a full survey of the site where DNA was amplified. They caught and tagged 12 individual hellbenders at this site. Ideally, the team will travel to the other two sites during the next survey season in order to survey those sites as well. Amplifying eDNA at a location has not proven to be a reliable indicator as to the density of hellbenders in a given location; however, it does validate the presence of hellbenders in the near upstream vicinity. Likewise, this technique cannot disprove the presence of hellbenders in a given location even if no eDNA is amplified in any given sample. We hope to continue to explore more watersheds of high hellbender probability in the near future and be able to identify locations of populations which have not yet been studied. (**34**)

Overpeck, Jordan, Bethany Grace*, Yesha Patel*, and William J. Biggers Wilkes University, Wilkes-Barre, PA 18766. *Effects of hydrogen peroxide on survival, metamorphosis, and catalase levels in the marine polychaete annelid Capitella teleta*. — Benthic organisms living in marine sediments often have to adjust to increased levels of environmentally produced hydrogen sulfide originating from the bacterial breakdown of organics in sediments, as well as increased levels of the reactive oxygen species hydrogen peroxide originating from superoxide anions produced from abiotic and biotic sources and also singlet oxygen from photosensitizing reactions. We have investigated the effects of hydrogen peroxide on the survival, metamorphosis, and catalase levels of the marine polychaete annelid *Capitella teleta,* which is an opportunistic species that has a high tolerance to hydrogen sulfide and is one of the dominant species in areas receiving high organic loading. Micromolar levels of hydrogen peroxide were found to induce the settlement and metamorphosis of larvae of *C. teleta* in a concentration dependent manner and also cause the induction of increased catalase levels in the larvae as a protective antioxidative response to hydrogen peroxide. Larvae however were found to be much more susceptible to the toxic effects of hydrogen peroxide compared with adult *C. teleta* indicating that adults of this species have more antioxidant potential than the larvae. These results indicate that environmentally produced hydrogen peroxide levels may affect the settlement, metamorphosis, and recruitment of *C. teleta* larvae into organically polluted areas. (**88**)

Patel, Goral*, Stephanie Justice-Bitner, Robert Levenson, and Jessica Petko Penn State University - York, York, Pa 17403. *Genetic determination of the Wntless protein interactome.* — The Wnt signaling pathway is a highly conserved pathway involved in embryonic development, adult neural connectivity, and cancer. Wntless (Wls) is a protein that is required for the secretion of these Wnt signals. Previous studies have shown that morphine can block Wnt secretion through an interaction between the mu opioid receptor and Wls. To determine whether other proteins in the nervous system can similarly interact with and regulate Wls function, we performed both traditional and membrane yeast-2 hybrid (Y2H) screens with human fetal brain cDNA libraries. In these screens, we identified 14 potential interactors of the C-terminal tail of Wls and 19 potential interactors of full length Wls. Some of these interactions were confirmed using directed Y2Hs, GST pulldowns, and co-immunoprecipitation assays. The known functions of the newly identified Wntless interacting proteins include protein trafficking, cell structure/adhesion, protein modification, and addiction (dopamine transporter, the cellular target of cocaine), while many are of unknown function. Additionally, we tested several neural G-protein coupled receptors as candidate interactors of Wls. In these studies, we show the adenosine receptor (A2A – target of caffeine), and cannabinoid receptors (CB1 and CB2 – target of THC) also physically interact with Wls. These results implicate that Wls may be involved in multiple signaling pathways related to reward and addiction. Future studies will investigate the functional relevance of these novel interactions. (**154**)

Perez, Alexis*, and Barbara Fenner King's College, Wilkes-Barre, PA 18711. *The effects of glutamate on trkB.t1-mediated calcium release in SH-SY5Y cells*. — Glutamate is the major excitatory neurotransmitter in central nervous system. The main functions of glutamate are brain metabolism, cognition, memory, and learning. Tropomyosin receptor kinase B (trkB) is a tyrosine kinase receptor. TrkB is the high-affinity receptor for brain-derived neurotrophic factor, meaning that it induces survival and differentiation. Two trkB receptors are expressed in the brain, full-length and truncated trkB (trkB.t1). This study is going to be focusing on the truncated trkB receptor.

TrkB.t1 receptors bind to and internalize brain-derived neurotrophic factor, regulating memory and cognition, potentially through calcium signaling in neurons and astrocytes. The purpose of this study is to determine if trkB.t1 facilitates the effects of glutamate on calcium release. To observe these interactions, we modeled physiological conditions by using 10µM of glutamate in SH-SY5Y cells (a neuroblastoma cell line). The present study aims to investigate the mechanism(s) of glutamate-induces changes in trkB.t1 signaling. Therefore, we hypothesized that physiological concentration of glutamate would affect trkB.t1 calcium signaling. To observe these changes, we used calcium assays and multi-label fluorescence microscopy. Current studies are treating cells with the fluo-4 direct calcium assay and labeled with antibodies specific for trkB.t1. Metamorph and ImageJ will be used to quantify changes in calcium and trkB.t1 expression in SH-SY5Y cells. (**166**)

Persons, Matthew Susquehanna University, Selinsgrove, PA 17870. *The effect of single and multiple courting males on female mating decision rules in the wolf spider Tigrosa helluo*. — Female mating decisions can influence the intensity of sexual selection on males, but there are few studies that document the extent to which mating decision rules change based on the temporal or spatial availability of potential mates. For females that encounter males sequentially, they may use a simple courtship duration threshold to assess male quality. Males that exceed this threshold are allowed to mate while males that don't, are rejected. Among social animals where females can directly assess the courtship of multiple males simultaneously, females may use a relative intensity rule whereby they choose the male that either begins courting first or shows the highest level of courtship within a particular time period. We tested the type and flexibility of mating decision rules of the wolf spider *Tigrosa helluo* under three conditions: 1) single male courting, 2) multiple males courting females simultaneously, or 3) single male allowed to court for six minutes or until a female showed receptivity before introducing a second male. Under single male conditions, females showed a strong threshold rule based on courtship intensity and duration with 54% of randomly paired males mating. Females generally required six minutes of sustained male courtship before showing receptivity. Under conditions of multiple matings, females showed receptivity using the same threshold rule and did not discriminate based on the source of the courtship display. Preliminary results suggest that males can exploit this receptivity rule by waiting until females show receptivity toward a competitor and then driving him off. This alternative mating strategy allows males to reduce the costs of courtship and sexual cannibalism risk. Inflexible mating rules that are adaptive under conditions of sequential male encounters may allow males to sexually parasitize the courtship displays of attractive males thereby relaxing sexual selection under conditions of high spider density. (**49**)

Petokas, Peter* Lycoming College, Williamsport, PA 17701. *Eleven Years of Research on the Eastern Hellbender Salamander in Pennsylvania and New York: Status and health of populations in the Susquehanna River Watershed*. — Research on eastern hellbender (*Cryptobranchus a. alleganiensis*) population ecology in north-central Pennsylvania was conducted over eleven summer field seasons from 2006-2016. Over one thousand eastern hellbenders were micro-chipped. Data collected included individual health, population stability, habitat preferences of adults and juveniles, chrytrid fungus prevalence, food habits, and nest site selection. Applied conservation projects included the installation of in-stream habitat structures and a head-starting program in cooperation with the Upper Susquehanna Coalition and the Bronx Zoo. Collected evidence indicates wide-spread decline and local extinctions throughout the Susquehanna River watershed in New York and Pennsylvania. Very few local populations remain that are self-sustaining with regular annual recruitment. Most local populations underwent rapid decline due to a high mortality rate caused by unknown agents, possibly chemicals or a contagious disease. Unless the underlying cause of the declines is identified and treated, the fate of the eastern hellbender in the Susquehanna River basin will be total extinction. The success of early reintroduction programs in other river basins is not yet determined, but efforts to restore or enhance populations may give us needed time to identify the cause of declines and to improve the chances for survival when captive-reared hellbenders are released back into the watershed. (**63**)

Phillips, Emily*, and Stephen Mech Albright College, Reading, PA 19604. *Comparison of survivorship and Botfly infection in White-Footed Mice in logged and unlogged forest areas*. — Logging affects small mammal populations in many ways. In particular, parasite load and overall survivorship are important population parameters that may be affected by logging. In order to determine the effects logging has on survivorship in small mammal species, we used logged and unlogged sites within Nolde Forest, near Reading, PA to estimate survivorship and botfly infestation of white-footed mice (*Peromyscus leucopus*). Here we focus on the survivorship and botfly infection rates during the fall trapping season. Based on our data, we concluded that survivorship of *Peromyscus leucopus* was minimally affected by the logging, however, survivorship was higher in the selectively logged site during the fall season. Although botfly infection was not related to habitat management, botflies showed a higher probability of infecting individuals with a higher body mass. (**2**)

Pintsch, Tanya*, Shealyn Marino, Matthew Suchocki, and Michael Steele Wilkes University, Wilkes-Barre, PA 18766. *Long-term patterns of weevil infestation in the fruits (acorns) of two oak species: Is there a predator satiation effect?* — Pre-dispersal, insect seed predation can significantly influence the reproductive success of many plant species. In oaks, for example, larvae of weevils (*Curculio* spp.) feed extensively on the cotyledon of acorns following immediate maturation of these fruits. Previous studies suggest weevil damage can in some cases result in nearly complete predation of an individual tree's acorn crop. However, most investigations on insect infestation are based on short-term studies. Here, we assessed weevil and insect prevalence and acorn damage in acorns of individual trees of two oak species (norther red oaks [*Q. rubra*] and white oaks [*Q. alba*]) over a >25-years in northeastern Pennsylvania. In contrast to other studies we found that prevalence levels consistently ranged < 30% per individual trees of both species, only rarely exceeding this level in some individual trees. We also found that infestation was significantly higher in the basal end of acorns often inflicting only partial damage to acorns. Based on these results and related studies from our laboratory, we suggest that these oaks may exhibit specific adaptations for tolerance and resistance to insect damage that allow oaks to successfully manage weevil and other insect infestation. (**50**)

Plumer, Mariah*, Nicholas Yurek, Jason Spevak, and Anne Szklarski King's College, Wilkes-Barre, PA 18711. *Evaluation of alkene bromination methods according to Green Chemistry Principles*. — The bromination of alkenes is a common reaction performed in undergraduate organic chemistry laboratory courses. Bromine (Br_2), the standard reagent used for this transformation, is a highly toxic and corrosive substance. To make the reaction safer, new reagents have been introduced as alternatives to liquid bromine. In this project, five different reagents were used to brominate three commonly used alkene substrates in order to determine which method is the most efficient and cost effective. The ideal reaction conditions should result in a high yield of product, be easy to use and safe to handle, and minimize the production of waste. Each reaction performed was evaluated according to the Principles of Green Chemistry and the EcoScale, which is an evaluation tool that incorporates atom economy, the E-factor, process mass intensity and safety. Each reaction was given a score in accordance with these methods and compared. The results of this analysis will be discussed. (**145**)

Polekoff, Sarah, Adam DiCaprio, Matthew Dougherty, Madelyn Franklin*, and Kathryn Goddard Ursinus College, Collegeville, PA 19426. *Effect of dam removal on the macroinvertebrate community in the Darby Creek, Delaware County, PA.* — The macroinvertebrate community above and below the breached boulder dam built in 1919 at Kent Park in Upper Darby Pennsylvania was studied prior to the removal of the dam in October 2012. We sampled using a 500 µm d-frame net in two riffle and two run sites above the dam and two riffle and two run sites below the dam using the PA DEP protocol (2007). While the indices of biotic integrity both above and below the dam are low in comparison to streams in other parts of Pennsylvania, the macroinvertebrate community below the dam, where the water riffles over rocks, was healthier (~35-50/100) than above the dam (~20-30/100). The stream above the dam had a fine silt bottom prior to the removal of the dam. The above dam site was dominated by taxa tolerant of stream impairment such as worms (Oligochaetes) and nonbiting midges Chironomidae while the below dam site included riffle beetles (Elmidae), stoneflies (Plecoptera), mayflies (Ephemeroptera), and caddisflies (Trichoptera). We have continued to study the macroinvertebrate community above and below the dam site after the removal of the dam. The above and below dam site communities have grown more similar over time; although the index of biotic integrity below the dam has not changed significantly, the scores for the samples above the former dam site have continued to rise to become more similar to the below dam community. (**114**)

Quain, Melanie*, Terry Master, and Thomas LaDuke East Stroudsburg University, East Stroudsburg, PA 18301. *Territorial aggression between captive Panthera leo and Panthera tigris amovensis*. — During the months of March through August 2016, observations were conducted to examine the level of territorial aggression among Lion (*Panthera leo)* and Amur Tiger (*Panthera tigris amovensis*) individuals in several zoo environments. The project was sponsored by the Philadelphia Zoo to satisfy an internship requirement. Individuals were observed over the course of 12 weeks while inside their assigned enclosures. Interaction intensity was measured on a scale from 1-4, each characterized by specific behaviors. Interactions between pairs of individuals of each species were observed when both individuals were on the ground and when one interactant was in the overhead walkway and one was on the ground. The number of interactions between pairs of individuals and intensity was logged on a spreadsheet matrix of aggressor vs. recipient for each observation period. The number of interactions at each aggression level were combined and averaged across all interactions between the same two individuals. The results of the observations showed that most aggressive interactions were level one encounters for both species. Lions displayed higher levels of territorial aggression when compared to Amur Tigers. Level one encounters were higher for ground to ground interactions compared to ground to overhead walkway encounters and they were also more common for juveniles compared to adults. In the upcoming month, more observations will be conducted to increase sample sizes and better solidify the initial results reported here. (**72**)

Reeder, Joshua*, Justin Hoffman, and Karen Campbell Albright College, Reading, PA 19604. *The effects of agricultural landscapes on bat foraging activity.* — This study is a comparison of bat activity at different agricultural sites assessed by echolocation recordings in partnership with the Rodale institute. Rodale institute is a non-profit organization that does organic agricultural research. Since Rodale has many organic plots we decided to compare bat foraging activity over organic fields compared to that of conventional fields. We also are comparing activity within the organic plots which are; grain fields, orchards, and vegetables. When comparing the plots, we are looking at the effects of tree line with the grains and orchards, and also insectary strips with the vegetables. Preliminary data shows that statistically tree lines does have an effect on bat foraging and that the insectary strips have no significant effect. In the future we would like to continue the acoustic monitoring alongside insect counts and classification to see if it has any significant effect as well. (**35**)

Rehrig, Atasha*, Michael Blazaskie, and Angela Asirvatham Misericordia University, Dallas, PA 18612. *Are A-Kinase Anchoring Proteins involved in myelination?* — Cyclic AMP, the universal second messenger, coordinates the balance between Schwann cell differentiation and its proliferation. Proliferation occurs by enhancing heregulin, a growth factor secreted by neurons. To promote differentiation, Schwann cells upregulate Krox-20, which promotes myelination. While the cAMP-Protein Kinase A pathway is known to stimulate promyelinating signals, not much is known about the downstream effectors. In the cell, protein Kinase A is anchored by A-Kinase anchoring proteins (AKAPs) that scaffold signaling complexes to regulate cAMP levels. Based on previous studies, it was hypothesized that AKAP95, a nuclear AKAP involved with mitosis and cell cycle progression, may play a role in balancing proliferating or myelinating signals in Schwann cells. Experiments were conducted to determine the expression of Krox-20, AKAP95 and cyclin D3, a temporal coordinator of cell cycle. Immunoblot analysis of Schwann cells treated with both heregulin and forskolin, revealed a marked decrease in the expression of AKAP95, Krox-20 and cyclin D3 compared to heregulin or forskolin treatments. In contrast, the levels of cAMP were significantly higher in Schwann cells treated with forskolin, and heregulin+forskolin in comparison to heregulin only or control. Correlating with the levels of cAMP, forskolin-treated Schwann cells exhibited the highest rate of proliferation in comparison to other treatments. These results suggest that in the proliferating phenotype, a synergistic activation of Schwann cells by cAMP stimulating pathways and heregulin does not promote myelinating signals or expression of AKAP95. The location of Krox-20 and AKAP95 in mitogen-treated Schwann cells were examined by immunofluorescence. While both Krox-20 and AKAP95 were located in the nucleus, forskolin treatment of Schwann cells resulted in overlapping staining patterns in comparison to heregulin and forskolin-stimulated cells. (**13**)

Rei, Esther*, and Debra Wohl Elizabethtown College, Elizabethtown, PA 17022. *Comparing the oral microbiome of the Amish and non-Amish communities.* — The oral cavity consists of several habitats suitable for bacterial colonization comprised of the hard and soft palates, along with the supragingiva, tongue and teeth. The sum of interactions between microorganisms and their environment constitute a microbiome. The oral microbiome offers niches specific for innocuous bacteria to reside in while resisting the invasion of bacteria that causes dental carries or periodontal disease. The aim of this study is to elucidate the similarities and dissimilarities of the oral microbiome between the Old Order Amish and the non-Amish population of the central Mid-Atlantic States. We hypothesized that the oral microbiomes of the two communities would be distinct due to varying dental and dietary practices. Supragingival plaque samples were obtained from volunteers along with oral health questionnaires; community DNA was extracted, the V4 region of the 16s rRNA gene was amplified using Polymerase Chain Reaction (PCR) and further analyzed using Illumina and QIIME. The study enrolled 46 participants. Selection criteria limited the study to individuals between the age of 20 and 70 with no indication of periodontal disease, which reduced the sample size to 30 participants: 13 non-Amish and 17 Amish. Based on our oral health questionnaire, the non-Amish are more likely to prioritize oral hygiene (i.e., brushing, flossing, and visiting a hygienist regularly) in comparison to their Amish counterparts. Further analyses will identify any variances between the oral microbiome of the two communities. We anticipate the Amish and non-Amish supragingival plaque samples will reflect differences in the community composition, such as, *Streptococcus mutans* associated with dental carries. Oral microbiome data along with health questionnaires may help elucidate how the composition of the oral microbiome resists the colonization of the bacteria that cause oral health problems. (**112**)

Stettler, Joshua*, Daniel Ressler, and Jonathan Niles Susquehanna University, Selinsgrove, PA 17870. *Habitat requirements of Brook Trout and Brown Trout in Pennsylvania streams*. — Environmental factors play a large role in determining what species are capable of living and reproducing successfully in an ecosystem. For aquatic ecosystems – temperature, altitude, land use, and mine drainage are some of the most restrictive factors that aquatic organisms need to adjust to. By calculating these factors when catching fish such as the Brook trout and Brown trout, we are able to estimate population sizes and environmental preferences in local streams. Data was obtained from Susquehanna University's "Freshwater Research Initiative" laboratory, as well as the Pennsylvania Fish and Boat Commission. Based on early results, Brook trout prefer colder, higher altitude, forest covered streams. Brown trout favored slightly warmer, lower altitude streams. (**86**)

Rivers-Hamilton, Janeyah*, and Rebecca Urban Lebanon Valley Collge, Annville, PA 17003. *The suppression of Garlic Mustard by Common Chickweed.* — Invasive species negatively impact the environment and cause economic harm. Two common invasive plants in eastern deciduous forests are *Stellaria media* L. (common chickweed) and *Alliaria petiolata* L. (garlic mustard). A field study was conducted that investigated soil pH and population traits of *A. petiolata* in the presence and absence of *S. media*. *Alliaria petiolata* grown near *S. media* had smaller leaves (T= -6.5; P<0.001) and biomass (T= -7.4; P<0.01). The data suggest that *S. media* may inhibit *A. petiolata*, this is likely due to the allelopathic chemicals released into the soil by *S. media* may restrict its distribution and impact on eastern deciduous forest. (**27**)

Rosado, Rousanna*, Brian Gray, and Bradley Rehnberg York College of Pennsylvania, York, PA 17405. *The physiological and anatomical effects of dietary high fructose corn syrup-65 compared to sucrose in CD-1 mice (Mus musculus)*. — Obesity promotes many health problems including type 2 diabetes. A diet high in sweeteners has been linked to both obesity and type 2 diabetes. Due to its inexpensive production, high fructose corn syrup (HFCS) currently accounts for 40% of all caloric sweeteners. Research on dietary sweeteners has involved sucrose and HFCS, but most studies have been short term. Furthermore, HFCS studies have only looked at HFCS-55 (55% fructose to 45% glucose). However, recent studies have shown that most popular sodas and fountain drinks contain a higher concentration of HFCS (HFCS 65%). In the current study the effects of HFCS-65 were compared to sucrose over a 7-month period. Metabolic markers, weight gain, eating habits, activity levels, and gut microflora were measured to determine the effects of these 2 sweeteners. Thirty mice were randomly assigned to 3 different groups. The control group received water, a second group received a 10% sucrose solution, and a third group received a 10% HFCS-65 solution. Mice weight, activity levels, and fecal matter were collected weekly. Food and liquid consumptions were recorded every 2 days. Blood glucose data were collected once every 2 weeks. A1C, adipose tissue, and liver fat were measured at the conclusion of the experiment. It was found that HFCS-65 and sucrose caused similar effects in metabolic markers, activity levels, adipose tissue, and liver fat. Eating habits were significantly affected by the type of diet the mice were consuming. However, mice were able to adjust the caloric intake thus resulting in little difference between groups. (**162**)

Saccone, Nicholas*, Ann Yezerski, Elizabeth Hoover, Tyler Grogan, and Matthew Evers King's College, Wilkes-Barre, PA 18711. *Dyslexia-related single nucleotide polymorphisms have an influence on college major choice.* — Developmental dyslexia is a reading disability characterized by the inability to combine phonetic units to form words. People affected by this disorder have trouble learning to read despite an otherwise normal level of intelligence. Although therapy can improve reading ability in affected persons, dyslexia carries long-term effects which may influence future educational or occupational choices. It has been shown that dyslexia is controlled by at least a dozen genetic loci. There are currently several genes; notably KIAA0319, EKN1, DCDC2, and ROBO1, which have been indicated to have association with developmental dyslexia and reading disability. Our study examined seven single nucleotide polymorphisms (SNPs) on three of these genes, KIAA0319, EKN1, and ROBO1. 248 subjects donated cheek cells for the study, and DNA was extracted for analysis. Samples were genotyped by either DNA sequencing or PCR followed by restriction enzyme digest. Genotypes were then compared for possible associations with choice of college major controlling for gender and geographic location of their birth. Preliminary results suggest that at least two of these SNP's, one in KIAA0319 and one in EKN1 are correlated with a choice of a major in the sciences versus other fields, especially when considering the Physician Assistant major in particular. (**163**)

Sarara, Donna*, Sarah Jane Groves*, and André Walther Cedar Crest College, Allentown, PA 18104. *Identification of phosphorylation dependent protein-protein interactions with Replication Protein A using the Yeast Two Hybrid assay.* — The second leading cause of death in the United States is cancer. Cancer is a disease caused by uncontrollable cell division at an abnormal rate. As cells divide during the cell cycle, DNA damage may accumulate leading to genetic mutations. A protein involved in the DNA replication and repair pathways is Replication Protein A (RPA). It is a single-stranded DNA binding protein that can be phosphorylated at the second subunit and it is known to interact with other proteins. When RPA is phosphorylated, protein-to-protein interactions with RPA may become altered. The focus of our study was to identify proteins that interact with RPA in a phosphorylation dependent manner. We used the Yeast Two Hybrid assay, a screening system that identifies protein interactions by measuring the activation of transcription occurring within physically interacting proteins, to identify protein interaction in *Saccharomyces cerevisiae*. This yeast two hybrid assay was used to screen 6000 yeast proteins to identify the proteins that interact with phosphorylated RPA. Three hundred potential interacting protein candidates have been identified and we have been characterizing these candidates to identify proteins that interact differently with phosphorylated and unphosphorylated proteins. We have been isolating and sequencing plasmids of selected RPA interacting candidates showing a phosphorylation dependent interaction and identifying them by Basic Local Alignment Search Tool (BLAST) analysis. A better understanding of how RPA phosphorylation regulates interactions with other cellular proteins will provide insights into RPA's role in cellular processes that are often dysfunctional in cancerous cells. (**137**)

Scales, Laura*, and Carlos Iudica Susquehanna University, Selinsgrove, PA 17870. *First record of Physaloptera sp. in Eastern Coyotes (Canis latrans) from Pennsylvania, USA*. — Eastern Coyotes (*Canis latrans*) have rapidly expanded through the North-Eastern United States and are frequently seen not only in rural or uninhabited spaces, but also in urban areas. Consequently, interactions between Eastern Coyotes, humans, and domesticated animals are now common. This may pose a real threat to human health as numerous endoparasites that infect canids may also be hosted by humans. The stomachs of one hundred and fifty-eight Eastern Coyotes, representing nine counties, were collected from hunts between 2009 and 2012 in Pennsylvania, U.S.A. and examined for parasites. Twenty-four endoparasites were found in two counties, Erie (northwest-corner of Pennsylvania) with two individuals and Clearfield (central Pennsylvania) with twenty-two. Specimens were relaxed and cleared using standard protocols and compared to a pictorial atlas for identification (University of Pennsylvania, Diagnosis of Veterinary Endoparasitic Infections Index). Preliminary identification confirms the presence of *Physaloptera* sp, and two additional taxa. This is the first record of *Physaloptera* sp. in Eastern Coyotes in Pennsylvania and may represent the first documentation in which a species of *Physaloptera* is found to share the stomach of Eastern Coyotes with other taxa. (**53**)

Schafer, Kaitlin*, Jarret Colvin, Amy Bradley, and Michael Steele Wilkes University, Wilkes-Barre, PA 18766. *Tolerance vs. resistance in an animal-dispersed seed; long-term patterns of weevil infestation in oak acorns across a latitudinal gradient.* — Plants that depend on animal-mediated dispersal produce seeds that both attract dispersal agents and allow resistance and/or tolerance to seed predators. The oaks, for example, produce acorns that have little physical defense, are high in lipids, but are also high in defense compounds (tannins). Previous work from our lab shows that chemical gradients in acorns (e.g., higher nutrient and fat, and lower tannin levels) direct insect, bird and mammal damage away from the embryo, allowing partially consumed seeds to germinate and establish. In this 6-year study, we investigated variation in insect predation in the acorns of *Quercus* *rubra* and *Q. alba* across a latitudinal gradient extending from NY to NC. Contrary to our predictions, we find that insect infestation is higher in northern latitudes. We also find that insect damage (from *Curculio* larvae) is significantly higher in the basal half of acorns across this latitudinal gradient and that the chemical gradients within acorns generally correlate with this pattern of seed predation. We conclude that due to specific characteristics (seed size, seed chemistry), acorns have evolved a combined strategy of tolerance and a resistance, that allow them to successfully germinate, even after attacked by seed predators. (**51**)

Schell, Joseph*, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. *Building surveys for bats in the Delaware Water Gap National Recreation Area*. — The Delaware Water Gap National Recreation Area includes 70,000 acres along the middle section of the Delaware River in Pennsylvania and New Jersey. When the recreation area was established it included existing farms and villages, and as a result numerous historic homes, barns, and other buildings are present within the park. Big brown (*Eptesicus fuscus*) and little brown (*Myotis lucifugus*) bats commonly reside in buildings during the summer and may use buildings as maternity roosts. As a result, the many buildings in the park present a challenge for park staff responsible for both maintenance and conservation of wildlife. This is especially a concern because the disease white-nose syndrome (WNS) has devastated populations of hibernating bats. During the summer of 2016, we surveyed 26 park buildings for use by bats. We conducted both exterior & interior surveys, making direct observations of bats and looking for signs of recent bat use. Signs of use included piles of guano, staining of siding, and possible entry points. We observed bats roosting at 9 park buildings, 6 apparent maternity roosts and 3 probable day roosts. We used acoustic monitoring to identify the species present at 4 of the 6 maternity roosts and made emergence counts at 3 roosts. We documented both big brown and little brown bats roosting in the Westbrook Bell Barn. In addition, we counted 175 big brown bats emerging from the Robbins House, 67 big brown bats from Black's Barn, and 82 little brown bats from bat houses at Walpack Church. Based on these surveys, we offer management recommendations for bats in park buildings and suggest the installation of bat houses near current roosts. We also offer guidelines for future bat exclusion efforts at park buildings. (**71**)

Schmidt, Robert*, David Dunbar, and Melinda Harrison Cabrini University, Radnor, PA 19087. *Investigating promoters in bacteriophage catdawg*. — Mycobacteriophages are viruses that infect a mycobacteria host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. The development of these therapies depends on an improved understanding of mycobacteriophage biology, including the identities and functions of the phage proteins and their interactions with the host. The studies conducted used innovative techniques for the functional characterization of these proteins and elements that allow the proteins to be expressed upon infection of bacterial hosts. Within this research project 5 unique putative promoter regions were selected from *mycobacteriophage* genome (CatDawg) based on RNA sequencing data; oliognucleotides were selected from each promoter sequence and the promoters were inserted into a Golden Gate Expression expression system in which either a red fluorescent protein or a blue florescent protein indicated the promoter was expressing. Out of the 5 selected; 3 were tested for expression in the Golden Gate Assembly and 2 out of the 3 thus far have been expressed in *E.coli* and indicate strong promoters. (**128**)

Selinsky, Constance*, Alexandra Morgan*, Shannon McGee, Megan Morrison, Hadley Wellen, Lindsey Welch, and André Walther Cedar Crest College, Allentown, PA 18104. *Optimization of carbon sources for biodiesel fatty acid production in the oleaginous yeast Cryptococcus neoformans*. — Fossil fuels like crude oil, coal, and natural gas are used as the primary source of energy on planet Earth. As the global need for fuels is sure to remain, clean burning, renewable alternatives to dwindling fossil fuel will be needed. Biodiesels generated from oils and fats provide a potential alternative fuel source that can produce less harmful pollution, while also being efficient and cost effective. Oleaginous yeasts capable of generating greater than 20% fatty acid content/biomass are a promising renewable source for biodiesel precursors, but they are limited because they have few if any molecular tools that could be used to increase fatty acid production beyond wild-type levels. The focus of our research has been to develop the oleaginous *Cryptococcus* yeast as a novel system for the effective generation of lipids needed for biodiesel production. Our lab has previously shown that mutated strains of the oleaginous yeast *Cryptococcus neoformans* that are nonpathogenic can be used to generate fatty acids for biofuels, and for the first time this provides an oleaginous yeast system with molecular tools to allow for the direct genetic manipulation of fatty acid production. *Cryptococcus neoformans* is known grows on and near trees and can use plant lignin in wood as a source of carbon, thus allowing it to grow in the absence of processed sugars. Our research has focused on identifying liquid medias and carbohydrate sources that yield optimal growth conditions to produce high lipid yields. (**110**)

Shifflet, Kathleen*, and Karl Kleiner York College of Pennsylvania, York, PA 17405. *Influence of Tree of Heaven (Ailanthus altissima) on Black Locust (Robinia pseudocacia) growth and root nodulation by Rhizobia*. — Allelopathy has historically been thought to be a direct interaction between a source plant's root exudates and a target plant of another species, but the mechanism has not been clearly elucidated. Soil microbial communities can play a large role in structuring plant communities, and past studies have demonstrated how allelochemicals affect these microbial communities and plant community structure. Some invasive plant species have the ability to invade native plant communities by disrupting the microbial community in the soil. Tree-of-heaven (*Ailanthus altissima*) has displayed allelopathic tendencies, and it is unclear whether it can interfere with the soil community surrounding its roots. We hypothesized *Ailanthus* would reduce the growth of black locust (*Robinia pseudoacacia*), a native leguminous tree species by the alteration of its soil microbial community. The allelopathic agent of *Ailanthus*, ailanthone, may inhibit the inoculation of *R. pseudoacacia* roots with *Rhizobia*, a mutualistic soil bacteria. *Ailanthus* and *R. pseudoacacia* were grown in coupled pots, one set facilitated the intermingling of the roots of both species, while the other pair did not. The hypothesis that *Ailanthus* would negatively impact *R. pseudoacacia* was not supported. The growth of *R. pseudoacacia* was not reduced by the presence of *Ailanthus*. Unexpectedly, *Ailanthus*' growth was significantly less when it was grown with *R. pseudoacacia*. *Ailanthus* had no impact on the nodulation of *R. pseudoacacia.* Our results indicate that stands of *R. pseudoacacia* may be resistant to invasion by *Ailanthus* because *Rhizobia* is unaffected by the presence of this known allelopath. (**18**)

Smith, Jasmine*, and André Walther Cedar Crest College, Allentown, PA 18104. *Identification of phosphorylation dependent protein-protein interactions with Replication Protein A in Saccharomyces cerevisiae*. — Cancer is a deadly disease that affects a large population of people and can be caused by the failure to properly repair DNA damage, which often leads to mutations. Replication Protein A (RPA) is a single stranded DNA binding protein composed of three subunits that plays important roles in DNA replication and repair pathways. For RPA to work efficiently in these pathways, it needs to physically interact with other proteins in the cell. The dysfunction of RPA can lead to incorrect repair of DNA and can therefor lead to cancer. Replication Protein A can be phosphorylated on the second subunit in a cell cycle manner and in response to DNA damaging agents suggesting a role in regulating RPA function. This phosphorylation may effect which proteins are capable of interacting with RPA. Therefore, this project focused on identifying proteins that physically interact with RPA in a phosphorylation-dependent manner using a yeast two hybrid analysis in the model organism *Saccharomyces cerevisiae.* This yeast two hybrid assay was used to screen 6000 yeast proteins to identify the proteins that interact with phosphorylated RPA. Three hundred potential interacting protein candidates have been identified and we have characterized 80 of these candidates to identify 12 proteins that interact with phosphorylated RPA, but not unphosphorylated RPA. An improved understanding of the regulation of RPA interactions with cellular proteins will provide a greater understanding about cellular processes such as DNA repair and replication and will provide insights into the underlying causes of cancer. (**6**)

Smithbauer, Michelle*, Angela Spagnoli, Maureen Levri, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *The effect of inflorescence height on reproductive success in Mountain Laurel (Kalmia latifolia)*. — Mountain laurel (*Kalmia latifolia*) produces different numbers of inflorescences and flowers per inflorescence on each plant every year. Previous work has shown that there may be a reproductive advantage to having inflorescences higher on the plant. If this is true, then we hypothesized that plants should disproportionately provision inflorescences depending on height. We examined the effect of inflorescence height on different measures of reproductive success including the number of flowers per inflorescence, fruit set, total fruits produced, total fruit weight, and average fruit weight. We used a total six inflorescences on each of 11 plants measuring the height of each inflorescence off the ground. A preliminary analysis of the data suggests that mountain laurel increases the size of the inflorescence with increasing height of the inflorescence and therefore also results in more fruits higher up the plant. There was little evidence of increased fruit weight with increasing height of the fruit. (**21**)

Spagnoli, Angela*, Maureen Levri, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Seasonal weather patterns and the reproductive effort of a long-lived perennial, Mountain Laurel (Kalmia latifolia)*. — The cost of reproduction may be an important constraint on the energy available for growth in plants. Severe winters may cause plants to change their resource allocation as a result of stress. Mountain laurel (*Kalmia latifolia*) produces variable numbers of inflorescences and flowers per inflorescence per plant each year. This study examined the influence of various weather related factors (temperature, precipitation, and snowfall) on the reproductive effort of mountain laurel. One hundred twenty-five plants were assessed in the Seminar Forest on the Penn State Altoona campus. The number of inflorescences and individual flowers were counted for each plant over the course of five consecutive years (2011-2016). Weather data was then correlated with inflorescence production. We hypothesized that severe winters would reduce allocation to floral display due to the energetic cost of winter stress. Results suggest temperature has little effect on reproductive effort. However, increased winter precipitation appears to positively correlate with the average number of inflorescences a plant produces each season. (**20**)

Spence, Laura*, Samantha Loh, Laura Scales, and Carlos Iudica Susquehanna University, Selinsgrove, PA 17870. *Age determination of voles (Microtus spp, Schrank, 1798) based on wear of the occlusal surfaces on individual molars consumed by barn owls (Tyto alba, Scopoli, 1769)*. — Meadow voles (*Microtus pennsylvanicus*, Ord, 1815) are an integral part of the food web as they often bridge the gap between producers and carnivores. Due to their large biomass and the fact that they “feed” everybody else in the ecosystem, we want to understand the age distribution of the meadow vole population. We examined the wear on the occlusal surface on individual molars found in barn owl (*Tyto alba*) pellets that were collected from nests in a 0.16 km^2 range in central PA. The molars were identified to species by using an *ad hoc* pictorial atlas made from the Natural History Collection at Susquehanna University. Our preliminary results have revealed that all 584 of the individual molars collected are from *Microtus pennsylvanicus.* Based on the occlusal wear of all 584 molars, we defined three age classes (i.e. juvenile, adult, and senior) and we sorted samples accordingly. As most of the sampled molars seemed to have medium wear, the most represented age class corresponded to adult individuals. This may prove useful in future studies where age determination of the prey population will indicate the ages of voles that are available in the surrounding area, or may represent which age classes the owls selected for consumption, providing an indirect way to establish a relative age structure of the voles available for consumption or directly eaten by owls. (**40**)

Sprague, Trinity*, Amelia Poplawski, Jun Ling, and Frank DiPino* Misericordia University, Dallas, PA 18612. *Site-directed mutagenesis of human PAK2 autophosphorylation sites*. — P21 Activated Kinase 2 (PAK2) has been linked to a variety of cancers, such as breast cancer. PAK2 undergoes autophosphorylation and phosphorylates a number of proteins in key signal transduction pathways. Through bioinformatics analysis based on the consensus sequence of PAK2, we identified several PAK2 substrates throughout the cytoplasm, nucleus, and membrane of the cell. These potential targets of PAK2 are involved in basic cellular processes such as growth, motility and survival. The extensive network of PAK2 substrates makes these links to cancers and other pathologies possible. Elucidation of PAK2 regulation is vital for determining its role in cancer, as this understanding will provide avenues for developing chemotherapeutic treatments that target PAK2. While there has been extensive research on the role of the threonine autophosphorylation residue within the activation loop of PAK2, there is little data regarding the various serine autophosphorylation residues within the PAK2 regulatory domain. The work described here is part of developing a site-directed mutagenesis approach to deactivate the individual serine autophosphorylation sites, so that we can gain insights into the role of the autophosphorylation sites in the regulation of PAK2 activity and their effects on physiological functions. We have now cloned, purified, and sequenced the human PAK2 gene, and primers have been designed and synthesized for use in the site-directed mutagenesis of the serine autophosphorylation sites. In the future, the PAK2 genes altered in this manner will be transfected into breast cancer cells to examine the effects of mutating these autophosphorylation sites. This will provide a more comprehensive understanding of the functional roles of PAK2 in breast cancer. (**153**)

Stonecipher, Jacob*, Marquise Henry*, and Anya Goldina Elizabethtown College, Elizabethtown, PA 17022. *Using a controlled water-flow enclosure system to assess ability of Orconectes rusticus to discriminate between different chemical cues*. — Crayfish detect and communicate using chemical signals that convey information about social status, territoriality, food, and mating opportunities. The crayfish *O. rusticus* is an invasive species that has taken over most watersheds in the country. Traditional eradication methods have not been successful. It might be possible to take advantage of the chemical signaling used by crustaceans to selectively attract and trap *O. rusticus*. The aim of this experiment was to assess the effectiveness of a water flow enclosure system we built to examine *O. rusticus*' ability to discriminate between different chemical signals. The enclosure contains a trough separated by plexiglass into 3 compartments forming a Y-shape. Each arm is connected to an independent water supply, allowing different chemical signals to be pumped into the halves of the trough. There are outflow holes on the opposite side of each arm of the trough. Using this system, we examined if the crayfish can distinguish between water sources with and without food. Food signal was prepared by dissolving ground algae pellets in water. Ten crayfish were isolated and not fed for one week. After the isolation period crayfish were placed in the center compartment of the enclosure for 5 minutes. At the end of the acclimation period, water from each arm was pumped into the enclosure. The arm containing the food signal was randomized to control for side bias. Each crayfish was also tested with just water, and its behavior was used as baseline. During all trials, crayfish were videotaped and their moving patterns were analyzed. Preference or avoidance was determined by selective movement towards or away from the side containing the food signal, respectively. This enclosure will be used for future studies to examine how chemical signals can be used to enhance trapping efficiency of the invasive *O. rusticus*. (**81**)

Sullivan, Kaelan*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Anesthetic effect on gene expression of MT2 and BCL2 and apoptosis in Gallus gallus embryos across retinal* *development*. — Millions of infants undergo a surgery or procedure involving anesthesia each year worldwide. Although using anesthesia is common, its effects on neuronal development are relatively unknown. To gain further understanding of the impact of anethesia on neuronal development, retinas of developing chicken embryos were cultured with the anesthetics propofol and lidocaine. After treatment, gene expression and apoptosis were assayed using quantitative PCR and a caspase-3 apoptosis assay respectively. After testing, it was determined that the anesthetics chosen had little to no effect on regulating expression of the selected genes or inducing apoptosis in our model. (**157**)

Swartz, Sophia*, and Darl Swartz Delaware Valley University, Doylestown, PA 18901. *Molecular-based selection for anthocyanin in L. sativa*. — The overall goal is to identify a minimally destructive, real-time PCR-based method allowing for rapid genotypic selection in lettuce seedlings. The obligate self-pollination aspect in *Lactuca sativa* (lettuce) plants impedes the propagation of traits of commercial interest. A novel nested microplate method was developed for high-throughput application to facilitate the sampling of root tissue as a source of DNA for genotyping. Initial trials at the individual sample (microfuge tube) level suggested that minimal DNA isolation methods (heat treatment and freeze/thaw cycles) yielded amplifiable DNA for plastid and anthocyanin biosynthesis pathway genes. To develop a genotyping assay, we used online data tools discover the mutations within the “Salinas” genome. These mutations code for a nonfunctional anthocyanidin synthase (ANS) gene which is responsible, in part, for the green phenotype in this cultivar. Genomic DNA was isolated from green- and red-leaf cultivars and a region spanning the point mutation was amplified, sequenced, and the two sequences aligned. A single point mutation (G>T) was found in the green-leaf cultivar, giving a premature stop codon in exon 2. Using real-time PCR followed by high-resolution melt analysis (HRM), we can distinguish between homozygotes and an artificial heterozygote via differences in Tm (G = 78.340.037, T = 77.740.096, G/T = 77.990.071°C; *n* = 6). To further facilitate detection of the SNP in genomic DNA, we have designed a FRET-based hybridization probe and a label-free probe for asymmetric PCR/HRM. These assays increase the Tm difference, facilitating more robust assays that can be used in our high-throughput assay design. The nested microplate model is being refined by testing different methods of DNA extraction to establish a near-direct PCR protocol that minimizes potential for errorThese studies will show if the genotypic selection process can be considerably accelerated on a potentially high-throughput scale. (**26**)

Swayser, Brandon*, and Terry Master East Stroudsburg University, East Stroudsburg, PA 18301. *Monitoring habitat use of Hooded Warblers (Setophaga citrina) in three understory types in the Delaware Water Gap National Recreation Area*. — Previous avian point count studies conducted by East Stroudsburg University showed that Hooded Warblers (*Setophaga citrina*) in the Delaware Water Gap National Recreation Area occurred more frequently in understory habitat containing invasive Japanese Barberry (*Berberis thunbergii*) compared to native-dominated understory. The current study advances this previous research by determining if habitat affinity and fitness are influenced by understory type. Three plot types, including native-dominated, barberry-dominated, and mixed understory types, were surveyed in each of ten 2×2 sq. km blocks chosen in a stratified random manner in the southern third of the Delaware Water Gap National Recreation Area. All male Hooded Warblers in the 30 plots were observed, captured, aged and banded during the first field season. Preliminary results indicate that the majority of Hooded Warbler territories located were in barberry-containing habitat (either barberry-dominated or mixed plot types). The majority of males in plots with barberry present were older birds, (aged based on molt limits) suggesting that this is a preferred nesting habitat. Nest monitoring during summer 2017 will allow for comparison of reproductive success among the three plot types. Vegetation composition and structure is being investigated using the BBird Protocol, and compared between nest sites and random, available sites among the three plot types during summer 2017 to determine vegetative characteristics important to nesting Hooded Warblers. (**69**)

Szerszen, Krystal*, and Barbara Fenner King's College, Wilkes-Barre, PA 18711. *The effects of mechanical stress on neurite outgrowth, oxidative stress, and TrkB.t1 Expression in SH-SY5Y Cells.* — Traumatic brain injury (TBI) is caused by a blow, bump or penetration of the skull resulting in disruption of the brain (Vos et al. 2012). Chronic traumatic encephalopathy (CTE) is a progressive neurodegenerative disease caused by repetitive mild traumatic brain injury (mTBI) (Lucke-Wold et al. 2014). Brain derived neurotrophic factor (BDNF) has been shown to be linked to neuronal injury and repair and aids in neuronal survival by stimulating neuronal growth and differentiation (Teppola et al. 2016). BDNF is a ligand for tropomyosin-related kinase B (TrkB) receptor which can switch neuronal pathways on and off. TrkB.t1 and trkB.tk+ contribute to neuronal signaling through different signaling cascades. Altered trkB.t1 expression is associated with neurodegenerative diseases (Fenner 2012). SH-SY5Y cells are a suitable model because the cells can be differentiated and trkB.t1 is best expressed after differentiation (Kovalevich and Langford 2013). The purpose of this project was to induce mechanical damage in SH-SY5Y cells, as a model for CTE, and determine its effects on trkB.t1 expression. I predicted the mechanically damaged cells expression of trkB.t1 would increase because of the link between neuronal injury and increased trkB.t1 expression. To determine the effects of mechanical damage on trkB.t1 expression, SH-SY5Y cells were mechanically damaged by scraping the cells, thus simulating mTBI. After the mechanical damage was induced in the cells, the cells were prepared and immunofluorescent imaging was performed to analyze the cells' accumulation of trkB.t1. Bright field imaging (BFI) analysis indicated a higher concentration of S-type cells in the scraped condition, longer neurite outgrowth in the differentiated cells, a higher density of SH-SY5Y cells in the scraped undifferentiated condition and it may be the case that trkB.t1 expression is decreased in scraped cells. This project will be expanded and neurite outgrowth and oxidative stress in relationship to mechanical stress will be analyzed. (**167**)

Taylor, Stephanie*, Alexandra Lisi*, and Leocadia Paliulis Bucknell University, Lewisburg, PA 17837. *The annotation and analysis of Contig43 on Chromosome 4 of Drosophila eugracilis*. — The fourth chromosome of many *Drosophila* species, commonly known as the dot chromosome, has a large heterochromatic region that has interesting genes with similar levels of expression to those in euchromatic regions. The Genomics Education Partnership (GEP) compiles annotations of various species of *Drosophila* for use in comparative genomic analysis, with the goal of understanding how gene expression is regulated on the dot chromosome. As a part of this effort, we studied 70,000 base pairs on the dot chromosome of *Drosophila eugracilis,* using *Drosophila melanogaster* as a reference. Using the GEP UCSC Genome Browser Mirror and the NCBI Basic Local Alignment Search Tool (BLAST), we hypothesized that there are two genes within this contig, with the orthologs dati and lgs in *D. melanogaster*. The *D. eugracilis* dati gene appears to have 11 exons, with 4 alternatively spliced isoforms (dati-PA, dati-PB, dati-PC, and dati-PD). The *D. eugracilis* lgs gene has six exons and only one isoform (lgs-PA). We will also study transcription start sites for these genes on *D. eugracilis*. (**150**)

Thomas, Nicolas*, Zoe Waizenegger*, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Toward the characterization of egg lipids in the presence of small molecules with differential scanning calorimetry*. — Differential scanning calorimetry (DSC) is a technique that can analyze the thermotropic phase behavior of many biological compounds. DSC has been widely used in the study of lipids and has been proven to be a very helpful technique in the analysis of lipids' thermotropic behavior. Past experiments have shown that lipids tend to undergo three different transitions when being analyzed by DSC. The three transition types that have been shown to be consistent between lipids include the subtransition, pretransition, and the main transition. Both the subtransition and pretransition are considered to be the minor transitions of the lipids, where molecular reorientation and packing is associated with minor endotherms. The main transition is considered to be the one major “melting” transition where the lipids transition between the gel-to-liquid-crystalline phases. Previous research with the addition of small molecules shows a shift in this melting transition. Our current research involves using DSC to characterize phosphatidylcholine lipid phase transitions, using egg lecithin extracted from store-bought eggs. Studies involving the addition of small hydrophobic molecules to these egg lipids and how the presence of these molecules affect the thermotropic phase behavior of the lipids is ongoing. (**141**)

Van Woert, Andrew*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Integration of multiple aqueous geochemical analyses to assess five headwater streams in Bald Eagle State Forest, PA*. — Headwater streams are an important part of the river continuum and make up for more than 90 percent of the streams within a major rivers watershed (Leopold et al. 1964). Little is known about headwater streams and their impact on larger stream systems. The headwaters of Penn’s Creek provide clean water to a large river system and increase Penns creek’s volume as it makes its way to the Susquehanna River. To understand the impact of these headwaters, a study was conducted along the same elevation of four headwater streams and longitudinally along Green Gap: one of the 4 streams. All four streams are located on the northern versant ranging from beginning to end over the same elevations. In addition, the 4 streams flow over the same geological outcrop formations. Grab samples and physical data were performed onsite and long term data was completed by sondes, pressure transducers and temperature loggers. Chemistry of the streams was analyzed using Piper Diagrams, and Stiff Diagrams. Water quality was assessed using Water Quality Index (WQI). The Piper Diagrams indicated that the streams were a bicarbonate type water while the stiff diagrams analyzed the change in the water chemistry down the slope. Transversal (data from the 4 streams along the same elevation) analysis showed similar analysis which prove that the base flow were originated from similar formations. Longitudinally the pH (5.2) of the stream at the spring indicated that the CaCO3 was in a lower concentration and the water was not gaining CaCO3 from the sandstone formations. However as the water flow downstream, the geology changed to a shale formation releasing CaCO3 and neutralizing the high bicarbonate water to a pH of 6. Diagrams showed that the streams were high in calcium and Magnesium, which characterize water in this type of geological formations. (**93**)

Vera, Andrew*, Stephanie Justice-Bitner, and Jessica Petko King’s College, Wilkes-Barre, PA 18711. *Using the yeast two-hybrid method to identify novel protein interactors of the cannabinoid type 1 receptor.* — The endocannabinoid system is a group of endogenous lipids and their receptors that target specialized receptors located in the central and peripheral nervous system and play important roles in pain, appetite, mood, memory, and addiction. One such receptor, the cannabinoid type 1 (CB1) receptor, is the primary endocannabinoid receptor in the brain. The CB1 receptor is known for its neurological influence in maintaining homeostasis in the human central nervous system and as a neuronal target for Δ9-tetrahydrocannabinol (THC) in marijuana. As a G protein-coupled receptor (GPCR), CB1 functions in cellular signaling by creating large complexes of signaling molecules. However, the proteins that constitute of these signaling complexes are largely unknown. To discover novel protein interactors of the CB1 receptor, a yeast two-hybrid screen was performed using the second intracellular loop of the receptor as bait. This loop was chosen because it had not been studied in previous yeast two-hybrid screens reported in the literature. This screen yielded 29 potential interactors out of a total of 9 million human brain cDNAs screened. The identities of these interactors include proteins known to function in neurotransmitter release and in neurodegeneration. These proteins are of particular interest as it is known that chronic marijuana use can induce changes in neurotransmitter release and in the morphology of the brain. (**168**)

Vera, Karolina*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Comparison of created versus natural vernal pools with implications for wetland restoration and amphibian conservation*. — The primary threat to amphibians, which are more vulnerable to extinction than any other group of vertebrate animals, is habitat destruction. Vernal pools are seasonal bodies of standing water that provide vital breeding habitat for 45% of amphibian species in northeastern North America. The ecological importance of vernal pools has led to a number of vernal pool restoration and construction efforts, yet follow-up studies show that constructed pools rarely replace functions lost in the destruction of natural pools. Therefore, the objectives of this study were to investigate an important gap in amphibian conservation ecology by comparing various environmental parameters among four natural, six created, and five enhanced vernal pools in eastern Pennsylvania and New Jersey. The specific parameters included in this study were hydrology, water physiochemistry, surrounding vegetation, canopy cover, land use, and soil type. We then examined linkages between these environmental parameters and wood frog abundance and reproductive effort – parameters that have been identified as estimates of vernal pool "success." Preliminary results indicate that average depth, volume, and maximum wood frog egg mass number of natural pools is significantly greater than that of created pools. Some of the created pools, one of which is lined, have longer hydroperiods than the natural and enhanced pools. Physiochemistry, soil organic matter content, plant species diversity, and canopy cover appear to be similar among the different types of pools. Continued monitoring and analysis this breeding season will provide more information to enable better management of existing vernal pools and creation of more functional breeding habitat. (**65**)

Walton, Elizabeth*, Nathan Navarro*, Christopher Cortes, Archana Ganta, James Hughes, Edward Winter, and Aikaterini Skokotas Rosemont College, Rosemont, PA 19010.*The role of dityrosine in the protection of Saccharomyces cerevisiae spores from ultraviolet light*. — Yeast spores are known to be resistant to many environmental factors including the mutagenic effects of UV light. Yet, yeast spores are nearly colorless and lack a protective pigment such as melanin. Instead, the outermost spore wall of yeast contains dityrosine, a chromophore that absorbs UV light at 300-320 nm corresponding to the mutagenic range of UV light. To further study the role of dityrosine, a mutant strain, dit1 that is deficient in dityrosine production was created and the spores were exposed to UV light for 3 minutes. Our preliminary results indicate that 60% of the spores survived in the wild-type strain compared to 20% survival in the dit1 mutant strain suggesting that dityrosine protects yeast spores from the mutagenic effects of UV light. (**135**)

Wan, Xinlei*, and Carsten Sanders* Kutztown University, Kutztown, PA 19530. *Plant mitochondrial and chloroplastic Cytochrome c polypeptides as substrates of an evolutionarily distinct eukaryotic cytochrome c biogenesis system*. — Cytochrome *c* is an ubiquitous electron carrier protein that contains at least one heme cofactor covalently attached to the cysteine sulfhydryl groups of a conserved CXXCH motif within the polypeptide substrate. Multiple evolutionarily distinct cytochrome *c* maturation (Ccm) systems catalyzing this heme ligation process have been defined. Ccm system I (containing nine or more components) is present in α- and γ-proteobacteria, in archaea, and in mitochondria of plants and red algae. Ccm system II (comprising four components) is used by β-, δ- and ε-proteobacteria, Gram-positive bacteria, as well as chloroplasts of plants and algae. Ccm system III (consisting of two or more components) is confined to mitochondria of fungi, metazoans and some protozoa. It includes one cytochrome *c* heme lyase (CCHL), which is characterized by a restricted polypeptide substrate specificity. It is able to attach heme cofactors to Ccm system III-type eukaryotic but not Ccm system I- or II-type prokaryotic polypeptide substrates. It has been proposed that CCHL-compatible polypeptide substrates require the amino-terminal consensus sequence $A/K_5G_6XXI/L_9F_{10}XXXC_{14}XXC_{17}H_{18}$. We discovered that in contrast to cytochrome *c* polypeptides from prokaryotic organisms, those from plant mitochondria and chloroplasts harbor this consensus sequence although those cytochrome *c* polypeptides are like prokaryotic ones naturally matured by Ccm systems I and II, respectively. Here, we show for the first time that Ccm system I mitochondrial and Ccm system II chloroplastic cytochrome *c* polypeptide substrates from *Zea mays* and *Arabidopsis thaliana* can indeed be covalently attached with heme when coexpressed with a *Saccharomyces cerevisiae* Ccm system III CCHL protein model in an *Escherichia coli* heterologous host. (**23**)

Womesdorf, Alivia*, and Larry Corpus Misericordia University, Dallas, PA 18612. *Distribution of Blackfly Larvae (Diptera: Simuliidae) from Trout Brook, Luzerne County, Pennsylvania*. — Trout Brook (TB) is a 2nd-order stream near Dallas, Luzerne Co., PA, and one of the main watershed drainages for the Back Mountain hill and valley region. Larval blackflies were collected from TB commencing in March 2016 and ending in December 2016. Larval and pupal collections were made monthly from one site at TB, which consisted of two riffles and one run over a substrate of large rocks and cobble. Larvae and pupae were collected from three separate rocks pulled from the near, middle, and far side of the stream. Physiochemical data was collected during each site visit, including stream width and depth, flow speed, DO, pH, water temperature, and conductivity using a PASCO GLX data logger with probes. Three water samples were taken during each site visit for laboratory analysis of alkalinity, nitrates, ammonia, chlorine, and phosphate. At this point, a total of 1,986 aquatic macroinvertebrates have been collected, including 208 larvae that have been identified as being in the genus *Prosimulium* (Diptera: Simuliidae). March, April and May 2016 had the highest numbers of blackfly larvae collected, probably due to the high water flow bringing the greatest amount of FPOM from upstream sources as well as cooler, more oxygenated water. The greatest number of simuliid larvae, 153, were collected during the April 2016 visit. It is suggested that the decrease in larval simuliids during July and August may be due to a number of factors, including decreased water flow, warmer water and decreased dissolved oxygen levels. In addition, several rain spates in July may have scoured rock surfaces, thereby removing larval simuliids and all other attached macroinvertebrates. (**44**)

Yoon, Sung Bo, Matthew Miller, Katlyn Tyrpak, Keane McCullum, Shannon Sell, Evan Shirey, Glenn Jones, and John Harms* Messiah College, Mechanicsburg, PA 17055. *A cancer-associated intronic polymorphism does not promote alternative splicing of the CCK2 receptor in pancreatic cancer cells*. — Pancreatic adenocarcinoma is an aggressive cancer with low life expectancy and poor five-year survival. The gastrointestinal hormone, gastrin, and its primary receptor, CCK2R, have been implicated in colon and pancreatic tumor growth. Additionally, a receptor splice variant, $CCK2_{i4sv}R$, results from the abnormal retention of the fourth intron and exhibits increased intracellular signaling and greater tumor growth relative to fully-spliced CCK2R. Two recent studies have associated a single nucleotide polymorphism (SNP; c.811+32C>A, rs1800843) in CCK2R with increased risk of pancreatic cancer, lower survival, and expression of $CCK2_{i4sv}R$. By contrast, a third study showed no such association and observed no impact on splicing in transfected cells. To further test the hypothesis that the SNP impacts splicing efficacy and thus $CCK2_{i4sv}R$ expression, we developed novel mini-gene constructs to more accurately model $CCK2_{i4sv}R$ splicing—requiring splicing of the third intron while testing retention of the fourth intron in the context of each SNP allele. Human pancreatic cancer cells, BxPC-3, and murine pancreatic cancer cells, PANC02, were each stably transfected with the mini-genes. To accurately quantify the relative abundance of each splice variant, a novel SYBR Green-based Real-Time RT-PCR assay was developed that precludes amplification of unspliced RNA or gDNA while independently quantifying each splice variant. In BxPC-3 transfectants exhibiting receptor RNA, $CCK2_{i4sv}R$ RNA was detected in both A-allele (6/8) and C-allele clones (5/7). Fully-spliced CCK2R was the predominant variant in both, accounting for 99.3% of receptor RNA. $CCK2_{i4sv}R$ RNA represented only 0.51% of total receptor RNA in A-allele clones and 0.78% in C-allele clones. Similarly, in PANC02 cells, fully-spliced CCK2R was predominant in both alleles (97.1%, A; 98.2%, C) and no correlation between the SNP and intron 4 retention was observed. Together, these data do not support a causative association between the C>A polymorphism alone and intron 4 retention in $CCK2_{i4sv}R$ in pancreatic cancer. (**11**)

Youkoski, Jenna*, Cassidy Heid*, Casey Gregory, Angelena Campisi, and Kenneth Klemow Wilkes University, Wilkes-Barre, PA 18766. *Analysis of vegetation communities within natural gas pipeline corridors of northeastern Pennsylvania.* — Unconventional natural gas development has been rapidly proceeding in Pennsylvania for the past decade. Transporting gas to market requires the build-out of a projected 30,000 miles of natural gas pipelines over the next 20 years, fragmenting forests throughout the state. Conservationists are concerned that pipeline corridors represent likely avenues for the spread of alien and invasive plant species into areas currently dominated by native forests. A several month project coinciding with the construction of the Transco Pipeline in portions of Luzerne County, PA called for an assessment of vegetation at the construction site and in three other sites unaffected by construction. The plants at each site were identified and percent covers assessed within 1m x 1m plots along transects set up within seven separate pipeline corridors arrayed in the four sites. The transects and plots were set up to include environmental diversity in the form of differing soil textures, slopes, and degree of waterlogging of the soils. Analysis of the data showed an unexpectedly high level of species diversity (144 species), with two dominating species (rough goldenrod and swamp dewberry), and a small percentage (<5%) of alien species. Statistical analysis through multi-dimensional scaling revealed several community types, including mixed meadow, heath, and wetland. Future research will examine the degree to which soils and other physical features (slope, rock outcrops) impact plant community composition. This research will inform future attempts to revegetate pipeline corridors to enhance their ecological features. (**19**)

Zawacki, Victoria W.*, and Elise M. Heiss King's College, Wilkes-Barre, PA 18711. *Nitrification in the Lake Lacawac water column*. — Nitrification is a two-step, biogeochemical process which connects reduced and oxidized forms of nitrogen in the environment. The first step of nitrification, ammonium oxidation, converts reduced ammonium (NH_4^+) to oxidized nitrite (NO_2^-). The second step, nitrite oxidation, further oxidizes NO_2^- to nitrate (NO_3^-). Although together they are called "nitrification," these two processes are carried out by distinct groups of microorganisms. Thus, rates and responses to environmental conditions may differ. Nitrification rates were measured during the summer of 2016 in the water column of Lake Lacawac, a 52 acre, 12m deep, nearly-pristine protected lake in the Pocono Mountains of Northeast Pennsylvania. Ammonium and nitrite oxidation rates were calculated separately using stable isotope (^{15}N) tracer methods. Samples were collected over three months (June, July, August) at 3 depth ranges: near-surface (1-2m), mid-column (5-6m) and near-bottom (10m). During all three sampling months, ammonium oxidation rates were lower than nitrite oxidation rates. Rates of both ammonium and nitrite oxidation were consistently low in the near-surface (1-2m) and mid-column (5-6m) depths, and increased at the depth of 10m (near-bottom). Environmental parameters which may be driving these observed trends were investigated, including: temperature, dissolved oxygen, pH, conductivity, and substrate concentration. The differences in rates and responses to environmental parameters between ammonium and nitrite oxidation further show the need to study "nitrification" as two separate biogeochemical processes. (**91**)

Zimmerman, Eric*, and Jodi Yorty Elizabethtown College, Elizabethtown, PA 17022. *Investigating the effects of anti-CD40 treatment on Fas ligand-induced apoptosis in dendritic cells*. — Dendritic cells (DCs) are a unique cell type of the immune system, capable of presenting antigens to Tcells to elicit a primary immune response. DCs can be classified into several different subtypes, depending on which specific membrane proteins they express. There is an increasing amount of controversy in the literature regarding apoptosis in DCs, as several pathways are implicated in DC apoptosis. One pathway relies upon caspase activation following extrinsic signaling through Fas. Previously, the lab investigated the treatment of cultured dendritic cells, the DC2.4 cell line, with both lipopolysaccharide (LPS) and anti-CD40. Past work suggested that LPS activates pro-apoptotic pathways in DCs, whereas anti-CD40 has been purported to enhance DC activity and inhibit apoptotic pathways. In fact, anti-CD40 is being used in immunotherapy studies to combat specific cancers by eliciting a stronger immune response. Flow cytometry experiments have shown that LPS upregulates characteristic activation proteins expressed on DC2.4 cells, including MHC proteins, CD40, and CD80. In initial experiments, this same upregulation of proteins was not seen in cells that were treated with only anti-CD40. The goal of this study is to elucidate whether or not anti-CD40 treatment modulates caspase activation and Fas ligand-induced apoptosis in DC2.4 cells. Caspase activation will be monitored using Western blotting, and apoptosis will be detected via immunofluorescence and/or flow cytometry. Potential modulation of the Fas-ligand induced apoptotic pathway via anti-CD40 may increase therapeutic efficacy of DCs. (**160**)

Zimmerman, Mel*, and Ashley Bresee Lycoming College, Williamsport, PA 17701. *Cataloging and monitoring MS4 storm water outfalls within an urbanized area of Lycoming County*. — During 2015-2016, monitoring, cataloging, and verifying of storm water outfalls, following PA-DEP protocols, within Lycoming County MS4 region was contracted between Lycoming County and the Lycoming College Clean Water Institute (CWI). The urbanized area of Lycoming County consists of 8 municipalities and boroughs. This project was started in 2010, by Lycoming County, to locate and monitor storm water entry points to the West Branch Susquehanna River, and its tributaries, as part of Pennsylvania's commitment to the Chesapeake Bay initiative. Initially, 260 outfalls were located and put into the Lycoming County GPS database. In 2016, Clean Water Institute interns were tasked with locating and verifying outfalls, from previous studies, within the urbanized area of Lycoming County. Using the DEP protocol, each outfall was cataloged based on GPS location, pipe diameter, pipe material, and pipe shape. Outfalls were split between flow or no flow present categories. Flowing outfalls were further analyzed based on odors, floatables, turbidity, and color. Samples were collected at flowing outfalls and analyzed for pH, alkalinity, conductivity and TDS could be measured. All outfalls were assessed for exterior damage, deposits, stains, abnormal vegetation, poor pool quality, and pipe benthic growth. Based on these parameters, each outfall was rated for the potential impact to the West Branch Susquehanna River. Overall, 205 outfalls were located and verified for the summer of 2016. (**119**)

Zimmerman, Mel*, and Ryan Orgitano Lycoming College, Williamsport, PA 17701. *Contribution of Lycoming College CWI to PFBC unassessed waters project (2010-2016)*. — This is the 7th year that Lycoming College CWI has participated with PA fish and Boat Commission in the Unassessed Waters Project. To date, the CWI team has completed a total of 501 streams in the Loyalsock, Lycoming, and Pine Creek Watersheds (about 20% of the total amount of streams sampled for this project). In the past 3 years, streams in the Genesee, Alleghany, White Deer Hole Creek, Black Hole Creek, Quenshukeny, Pine Run, and Antes Creek watersheds, as well as unnamed tributaries in Tioga County have been completed. Data for this project has been logged into the PFBC Unassessed Waters Data set for consideration of trout stream protection. The number of class A, B, C, D, and E streams from each watershed will be presented. On average, 50% of the streams sampled support wild trout and nearly 20% are considered class A or B trout streams. A breakdown of the benefit and limitations of this program will be presented. In addition, a comparison of the Alleghany Plato Region and the Ridge-Valley Plato Region will be done, in terms of supporting trout populations. In 2016, Lycoming College sampled 46 streams in the Lycoming, Pine, and Larry's Creek watersheds. Additional Creeks in the Tioga River Watershed were also sampled. (**99**)