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at



Abstract Book

Connecting Society with Science: How can scientists better communicate with the public

ABSTRACTS

Listed in order of Presentation

Ahern*, Lee, Associate Professor of Advertising and Communications, Penn State University *Training Scientists to Communicate in the University Setting* - This presentation will explore various approaches to training scientists to be better communicators. There are various resources and training modules available to scientists, but their effectiveness has not been closely measured or evaluated. There is also discussion about the best practices: should scientists be trained in graduate school, or after? Should training be voluntary or mandated? Where should the training fall on the theory-practice continuum? Observations and experiences will be presented in the hopes of stimulating a broad discussion of the issue.

White Husic*, Diane, Dean of the School of Natural and Health Sciences, Moravian College *Working at the Interface of Science and Policy* - When we hear about the need to better connect society with science, we often think about how scientists can better communicate with the public to enhance understanding of complex challenges such as climate change or help dispel misunderstandings about issues like vaccine safety or genetically modified organisms. Alternatively, we may consider ways to engage various age groups in the excitement of scientific discovery. But another important interface is to connect science and scientists with policymakers. In this session, I will share examples of my work at the United Nations (international), state and local levels and discuss the importance of working in this realm.

McAnulty*, Sarah *Skype with a Scientist Entertain Before you Educate* - In today's fast-paced internet society, it can be challenging to get people to listen to a science lecture. To compete with Netflix and social media feeds it can be effective to focus on entertaining first, and allowing the education to happen naturally. I'll discuss how to hook the public with fun science content to get their attention so you can share science with a wider audience.

Randazzo*, Charles M. Certified GLOBE trainer, Berks Nature Science Educator *Connecting to Science through NASA's GLOBE Program* - In this session I will provide an overview of GLOBE and how it can be implemented in schools, citizen science, and municipalities, and how to become trained for GLOBE. The **G**lobal **L**earning and **O**bservations to **B**enefit the **E**nvironment Program (GLOBE) is a hands-on international science and education program that provides students and the public worldwide with the opportunity to participate in data collection and the scientific process, and contribute meaningfully to our understanding of the Earth system and global environment. GLOBE's vision promotes and supports students, teachers, scientists, and citizens to collaborate on inquiry-based investigations of the environment and the Earth system working in close partnership with NASA, NOAA and NSF in study and research about the dynamics of Earth's environment. GLOBE's mission is to promote the teaching and learning of science, enhance environmental literacy and stewardship, and promote scientific discovery.

Hayden*, Jennifer D., Amy J. Reese, and Audrey J. Ettinger*, Faculty at Cedar Crest College *Science, Ethics, and Society: Using an undergraduate capstone course to develop skills for communicating science to the public* - The rejection of scientific discoveries by some members of the public demonstrates the importance of communicating science effectively to the general public; therefore, developing this skill should be an important component of an undergraduate science curriculum. The *Science, Ethics, and Society* course that we developed provides biological sciences majors with an opportunity to examine the intersection of science and public discourse by focusing on topics including climate change, vaccines, and genetically modified crops as well as ethical issues including the use of human and animal research subjects, and the importance of diversity in scientific voices.

Course assignments include preparing a letter to an elected official or the press regarding a scientific issue, analyzing an example of media treatment of science or scientists, and writing a research description suitable for public consumption. Together, the class readings and written assignments have increased student skills and engagement in communicating science to the public.

Valletta*, Rachel Chief Environmental Scientist for The Franklin Institute, and director of Climate and Urban Systems Partnership *The Climate and Urban Systems Partnership: Reaching city residents with informal climate change education* -The Climate and Urban Systems Partnership (CUSP) is a four-city climate change education initiative based in science centers and museums. CUSP unites climate scientists, learning scientists, and informal education specialists to develop methods for reaching city residents with engaging climate change and environmental science education. The Philly CUSP network comprises nearly 90 partner organizations including academic institutions, city agencies, artists, and community leaders. This session will introduce CUSP's approach to informal climate change education, the CUSP community of practice, and the advantages of partnering with science centers and museums to perform outreach activities.

Miller*, Alyssa Environmental Educator at Schuylkill Center for Environmental Education *Nature in the City* -In Philadelphia, tall concrete buildings, sidewalks, and beige surround students. It is understandable how a group of 7th graders from South Philly could be absolutely terrified of nature. They have been taught that nature is dirty and frightening. There have been many instances in my work as an educator where someone refused to even touch soil because it was dirty. It is extremely important to connect students with their environment. However, the challenge of getting kids to care about something they have had almost zero exposure to is difficult. I have been working to engage students through my work with The National Audubon Society and other nature centers to connect students with their environment and watersheds.

Knecht*, Karen Director of Education, Da Vinci Science Center *The Role of Science Centers and other Informal Science Education Institutions in Connecting the Public with Science* -Science Centers and other similar learning institutions can be a great place for scientists and the public to meet. Learn about resources in the community that can help connect scientists with the public. Gain practical tips about how people learn, effective facilitation techniques for different audiences, and how to develop hands-on activities to engage people in your field of science.

Sawyer*, Brandy M. Director of Science, Technology, Engineering, and Mathematics for Allentown School District *Building Science Fair into the Curriculum and Parent Outreach* -In this presentation, we will discuss the opportunities for schools to incorporate science fairs and engineering practices, both within the curriculum and across the curriculum to improve students' awareness and STEM readiness. In addition, we will discuss different pathways to increase parent involvement in STEM.

General Meeting ABSTRACTS

Listed alphabetically by first author's last name.

Abreu, Leslie*, Miriam Cooperband, Kelly Murman, Stefani Cannon, and Allison Cornell Cedar Crest College, Allentown, PA 18104. *Invasive Spotted Lanternfly (Lycorma delicatula) and its potential hosts.* — The spotted lanternfly is a relatively new invasive pest insect to the United States. This insect threatens the agronomic crops and other agricultural commodities of Pennsylvania such as vineyards, hardwood for the timber trade, and hops. However, it is thought that the Tree of Heaven (*Ailanthus altissima*) is the lanternfly's preferred host. Both are invasive species from the same native area in China. One of the current methods of treatment for the Pennsylvania Department of Agriculture is hiring landscape contractors to eliminate most Tree of Heaven, with some as "trap trees". However, the role of Tree of Heaven in spotted lanternfly survival and diet is not well understood. Spotted lanternflies have been observed feeding on Red Maple (*Acer rubrum*), the most common native tree in Pennsylvania, and Oriental Bittersweet (*Celastrus orbiculatus*) an invasive woody vine from China. The purpose of this study is to determine if a diet exclusively on Red Maple, Oriental Bittersweet, or Tree of Heaven can support the spotted lanternfly from 1st instar—the first of four nymph stages—to adulthood. Lanternflies were isolated in mesh sleeves on each of these plant hosts and raised in similar conditions to determine if Tree of Heaven is truly necessary in their life cycle. Surprisingly our results show no spotted lanternflies survived to adulthood on Red Maple or Tree of Heaven. However, they did survive to adulthood on Oriental Bittersweet. This suggests that feeding on Tree of Heaven may not be required for development to adults, however it does not rule out whether it is required in other aspects of spotted lanternfly biology. (164)

Adamski, Jonathan*, and Matthew Wallace East Stroudsburg University, East Stroudsburg, PA 18301. *A Comparative Study of Hymenopteran Pollinator Diversity.* — This project aimed to compare the diversity of hymenopteran pollinators between two sites found on East Stroudsburg University's main campus. The first site (TRACK) is highly disturbed with numerous anthropogenic habitat features. The second site was a powerline right of way (ROW), located on the north side of campus, and was bordered on both sides by forest. The TRACK site, experiencing higher levels of disturbance, was hypothesized to contain lower diversity than the ROW site (less disturbance). These sites were sampled once per week, weather permitting, using two sampling methods, bowl traps and sweep netting. Specimens were frozen overnight and then identified to the lowest taxonomic level. The diversity of the two sites was quantitatively compared using species richness, the Shannon index, and the Simpson index. We found that the diversity of the disturbed habitat was higher among all indices, contradicting the null hypothesis that disturbance reduces diversity. The high vagility of insects possibly allows them to exploit a disturbed site without being impacted by the disturbances themselves. The three major supergroups ("Symphyta", "Parasitica", and Aculeata) were also measured and compared across the two sites. The ratio of each group found at each site was nearly identical (within 1%). Finally, diversity measures as well as similarity indices (Bray-Curtis dissimilarity) were conducted on the collection methods. Sweep netting yielded much higher counts (n=625) than bowl traps (n=89), though the diversity measures of the two methods were identical. Lastly, the similarity value of the two collection methods was only 8.12%. Diversity measures were about the same, but similarity was low, suggesting that both methods are required to assess the wide range of diversity that can thrive among a given habitat. (167)

Adamski, Jonathan*, and Thomas LaDuke East Stroudsburg University, East Stroudsburg, PA 18301. *Quantifying the Effects of Habitat Disturbance on the Timber Rattlesnake, Crotalus horridus, in Pennsylvania.* — This project examined the relationship between anthropogenic habitat disturbance and population levels in *Crotalus horridus*, the timber rattlesnake. This relied on population and habitat information collected by the Pennsylvania Fish and Boat Commission (PFBC) during a previous study known as the Timber Rattlesnake Assessment Project (TRAP). Geographic information science (GIS) was utilized to measure features such as canopy, trails, and road cover through *C. horridus* habitat. Using the information from TRAP, in conjunction

with GIS technology, quantitative results were produced and analyzed to construct a clear picture of how human interactions affect *C. horridus* populations. Two models were primarily used to explore this relationship: a linear model relating population size as a function of habitat features and a generalized linear model relating presence-absence data as a function of habitat features. An inverse relationship was found between rattlesnake populations and building proximity and density. Additionally, roads, trails, and buildings were farther away from occupied sites when compared to unoccupied sites. These two findings suggest that anthropogenic disturbance impacts *C. horridus* negatively in the commonwealth. The weak relationships between the variables assessed may be, in part, attributable to the use of TRAP reports which were mostly based on one or two site visits and not intended to provide population estimates. Further work will be necessary to refine our models, including improved population estimates and expanding our work to the entire commonwealth. (62)

Ahmed, Sara*, Courtney Amoroso*, and Ann Yezerksi King's College, Wilkes-Barre, PA 18711. *Single Nucleotide Polymorphisms (SNP's) associated with Dyslexia may influence college choice major.* — Dyslexia is a language disorder that affects one's ability to read and write. Various genes have been linked to dyslexia such as ROBO1, FRAXA1, NEDD4L, and KIAA0319. At least 14 loci have been found to be associated to dyslexia. Of these KIAA0319, on the short arm of the sixth chromosome, has been shown to be one of the biggest contributors. This gene encodes for transmembrane proteins that may play a role in the development of the cerebral cortex. In this study the candidate gene KIAA0319 will be analyzed to test the correlation between KIAA0319 genotypes and major within the King's College population. A genotyping method using nested PCR followed by differential restriction enzyme digest was used to collect genotypes of two Single Nucleotide Polymorphisms (SNPs) within this locus. Preliminary data suggests that one of these SNPs does correlate strongly with a major choice in the sciences. Those affected with dyslexia tend to excel in reasoning, critical thinking, and problem solving even while deficient in reading ability. Therefore, college majors such that require hands on and visual experience may be better suited for dyslexics instead of majors that are focused on reading and comprehension. (82)

Albukhari, Faisal*, Stephen Madigosky, and Bruce Grant Widener University, Chester, PA 19013. *A three-year profile (2016-2018) of temperature and humidity in a coffee field located in Sabanilla de Alajuela, Costa Rica.* — To determine the extent of climate variability over a short duration can be useful in assessing how plants such as coffee may react from season to season. Clearly, climate change is one of the most important issues facing humans and especially in regions where agriculture products such as coffee help to support thousands of families. To determine the variability of temperature and humidity in a shade grown coffee field in Sabanilla de Alajuela, Costa Rica (10° 5' 33"N, 84° 12' 13"W) we deployed Onset HOBO data loggers over a three-year duration (Jan 2016-December 2018). Results indicate that there are consistent and distinct seasons over the duration of this study. The warmest temperatures occurred between the months of December through March after which temperatures declined and bottomed in late May to mid June. Correspondingly, the humidity during this period remained higher with less variability. The evaluation of all of the data over this 3-year period indicates that maximum temperatures from May to July are not as high compared to other months. We did not detect any significant temperature changes when comparing data from 2016, 2017, or 2018. We did however see maximum temperatures reaching 33 degrees or slightly higher from mid March to April during 2016 and 2017. Prolonged temperatures at these levels are detrimental to the growth of coffee plants. (154)

Allen, Colin*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Description of Lycobacillus franzii gen. nov. sp. nov. from freshwater creek and transfer of three Bacillus species into the new genus.* — This study focuses on characterizing a bacterial strain designated EAC that was found to be a novel species. The organism was isolated from Lycoming Creek in Pennsylvania. Its genome was sequenced and compared with database sources to find the closest related bacteria for phenotypic comparisons. Based on similarity of 16s rRNA sequences, *Bacillus solisilvae* (99.32%), *B. luciferensis* (98.84%), and *B. acidicer* (98.71%) are the most closely related, as are three unnamed novel species, and all organisms had their genomes sequenced. The average nucleotide identity (ANI) and average amino acid identity (AAI) of these species when compared to type species, *Bacillus subtilis*, reveal these organisms are different enough

to suggest these organisms should not be organized under the *Bacillus* genus. Based on whole genome sequence analysis, we propose that strain EAC, *B. solisilvae*, *B. luciferensis*, *B. acidicer*, and the three unnamed species should be classified into a new genus, *Lycobacillus*, and a new species represented by strain EAC, which will be named *Lycobacillus franzii* gen. nov. sp. nov. (194)

Amelotte, Alexis*, Karina Ortiz-Gomez*, Sarah Smoot*, and Daniel Curlik II York College of Pennsylvania, York, PA 17405. *Acute administration of fluoxetine in adult Rattus norvegicus (Sprague Dawley rats) increased anxiety-like behaviors and decreased locomotor activity.* — Depression and anxiety are being diagnosed worldwide at increasing rates. Historically, selective serotonin reuptake inhibitors (SSRIs) have been used to treat depression, and recently SSRIs have also been tested as treatments for anxiety disorders. Chronic administration of SSRIs is believed to reduce symptoms of anxiety and depression by increasing the amount of serotonin present in the synapse. However, acute administration of SSRIs has been reported to increase anxiety in humans. The reason for these discrepancies is currently unknown. In order to better understand the mechanisms of how chronic administration of SSRIs may decrease anxiety, whereas acute administration may increase anxiety, animal models are often used. Therefore, the current study sought to determine whether acute administration of fluoxetine, a commonly prescribed SSRI, would increase anxiety-like behavior in adult Sprague Dawley rats (*Rattus norvegicus*). Acute injections of 5 mg/kg fluoxetine or vehicle (0.9% saline) were given to rats before testing anxiety-like behavior in the elevated plus maze and motor activity in the open field test. Based on prior research, it was hypothesized that acute administration of fluoxetine would increase anxiety-like behavior while decreasing motor activity. Results of the elevated plus maze confirmed this hypothesis, revealing a significant increase in anxiety-like behaviors following acute administration of fluoxetine. A decrease in motor activity was also observed in the open field test. These results suggest that acute administration of SSRIs induce anxiety-like behavior in laboratory animals, similarly to how they increase anxiety in humans. Moreover, this effect occurs following as little as one injection of the SSRI. By studying the acute effects of SSRIs, potential side effects can be examined to improve the treatment of mental health disorders such as generalized anxiety disorder and depression. (39)

Amick, Jessica*, Morgan Gash*, Suhaa Shafi*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Synthesis of polyamine analogs as possible anti-inflammatory agents for chinese hamster ovary cells.* — This investigation will involve the synthesis of polyamine analogs produced in 100% ethanol as the solvent. These nucleophilic substitution reactions with alkyl halides will produce Bis (3-thiolpropyl), and Bis (4-thiolbutyl) polyamines. The thiol halides used in these syntheses were, 3-chloropropane-1-thiol, and 4-chlorobutane-1-thiol and the polyamine was putrescine. In this study 100% ethanol was used as the greener reaction solvent, which allowed for production of the polyamine analogs to proceed in a less toxic environment. Alcohols are preferred solvents as they are more environmentally friendly, can be reclaimed or recycled, and reactions are run at lower temperatures. It was also found, in this work that the use of 100% ethanol increased the product yield dramatically when compared to the more toxic solvents used in previous studies in our laboratory. As part of this study, the analogs and putrescine were incorporated with Chinese Hamster Ovary cells to observe possible anti-inflammatory effects. (27)

Appadoo, Shania *, Kiyah Bell*, Azad Aghababian*, Alecia McElwee, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Genome based division of the genus Flavobacterium and description of Lycobacterium gen. nov and seven novel species in the genus.* — Calculation of average amino acid identity (AAI) values between different genera within the *Flavobacteriaceae* reveals similarity values between 55% and 75%. Based on this relative evolutionary distance corresponding to different genera, many species within the genus *Flavobacterium* are different enough from the type species of the genus, *Flavobacterium aquatile*, that they should be classified into a different genus, for which we propose the name *Lycobacterium* gen. nov. This division is supported by AAI values and the maximum likelihood alignment of 120 concatenated proteins completed as part of the genome taxonomy database (GTDB). In the Microbiology course at Lycoming College, we have discovered many putatively novel '*Flavobacterium*' species from the Loyalsock Creek based on 16S rRNA gene sequence. Whole genome sequence analysis of eleven strains and closely-related validly-published species confirms their status as seven novel species with average nucleotide identity (ANI) values below 95% vs currently named species. (172)

Arnold, Victor*, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Characterization of meso-tetra (N-methyl-4-pyridyl) porphine tetra tosylate and Inclusion into phosphatidylcholine liposomes.* — Meso-tetra (N-methyl-4-pyridyl) porphine tetra tosylate (TMP-1363) is a water-soluble porphyrin commonly utilized during photodynamic therapy; a technique used to treat acne, and more recently cancer. During photodynamic therapy, molecules classed as photosensitizers are exposed to a specific wavelength of light. When exposed, the molecule produces active oxygen which induces cell death in nearby cells. In order to begin the initial characterization, the UV/VIS spectra of the porphyrin dissolved in water and PBS was collected. There was no discernable difference between the spectra of the two solvents, and the λ_{max} was found to be 421.9 nm. Currently more characterization studies are being carried out, and an attempt is being made to include the porphyrin into Phosphatidylcholine liposomes. Phosphatidylcholine (PC) lipids are a class of phospholipid that contain choline as a head group –and due to its abundance, it can be extracted from naturally occurring resources such as meats, eggs, and nuts. The overall goal is to determine a new model of drug release for this hydrophilic porphyrin and see how it behaves in an in vitro environment, as well as using liposomes as the delivery mechanism for this compound. (19)

Asbrock, Victoria*, Danielle Simons*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Liquid-liquid extraction and analysis of the antioxidant, resveratrol, from various red, rosé and white wines.* — The objective of this study was to extract, isolate and analyze the antioxidant, resveratrol from various red, rosé and white wines. Three different local vineyards were chosen for the study. The three vineyards include Amoré, Black River Farms, and Clover Hill. Chambourcin, Rosé and Chardonnay from each vineyard were selected as the wines for analysis and comparison. The extraction and quantification of resveratrol was conducted in order to compare the amount of this antioxidant found in the different red, rosé and white wines. In order to extract resveratrol liquid-liquid phase techniques were implemented. The concentration of the antioxidant was quantified using ultraviolet spectroscopy at a wavelength of 310 nm. High Performance Liquid Chromatography was also used to isolate and identify the active ingredient from each wine after extraction. The analysis of the data collected from this study will suggest which type of wine contained the most resveratrol. (29)

Ash, Michelle*, and Jeff Stephens Misericordia University, Dallas, PA 18612. *Investigating cell stiffness in wild-type Candida albicans and its morphologies using contact atomic force microscopy.* — Common yeast *Candida albicans* as a wild-type cell presents an ovoid shape; in its pathogenic morphology, *C. albicans* develops a germ tube which develops into a hypha. Development of a hypha is theorized to act as a mechanism for cell survival in less-than optimal environments, such as within the human body. In addition to human serum inducing hyphal growth, *C. albicans*' development of hyphae occurs when the cells are under stress, in basic pH, or exposed to a variety of amino acids. While the environments in which hyphae form are well known, the biomechanical changes associated with this transition are less investigated. Our technique combines the use of an atomic force microscope in contact mode with its force-distance spectroscopy capability to determine the cell stiffness of *C. albicans* in its various morphological states. By measuring cell stiffness in both the cytosol and nucleus for wild-type form and pseudohyphal morphology, and in cytosol and hypha for the hyphal morphology, we are able to determine the degree by which the cell loses its pliability as it assumes pathogenicity. Because of these implications of hyphal growth, we expect the stiffness of *C. albicans* to be significantly higher than that of its pseudohyphal morphology or wild-type form. (8)

Ayer, Danielle*, and Ryan Colyer Cabrini University, Radnor, PA 19087. *The development and characterization of an open body fluorescence microscopy system for fluorescence lifetime imaging.* — This project presents a new system that contains optical components, a prototype photon detector, custom electronics, and custom software for fluorescence lifetime imaging. The system uses a custom nanosecond-timescale modulated diode laser to excite fluorophores within a sample, then through an open body arrangement, collects those photons with a prototype photon detector. The signal from that photon detector is then timed with respect to the laser pulse in a custom circuit which sends information to a custom software package written in Python, which acquires and analyzes the lifetime data. The primary goal of this phase of the project is to characterize the performance of the system under development using

measurements of fluorophores. This will be done by performing a variety of measurements using fluorophores with different fluorescence lifetimes, and then using a type of Fourier analysis called phasor analysis to examine the lifetime values and characterize the quality of the lifetime data obtained. The eventual goal of this project is the construction of a system which combines lifetime measurement with compressive sensing, providing a novel and cost-efficient design for acquiring fluorescence lifetime images under low light conditions, which are favorable for examining biological samples. (35)

Bahr, Lauren*, Ja Seng Tawng Dingrin, Jenna Beachley, and Meg Laakso Eastern University, St. Davids, PA 19087. *Detection of tomato yellow leaf curl virus and determination of viral kinetics in two plant host species.* — *Begomoviruses* are plant viruses that infect food and fiber crops on six continents. They are transmitted by whiteflies, but there is new data to suggest that seed transmission can also occur. This is significant, especially for farmers in developing countries who save their seeds and use them to replant in subsequent years. In order to test for the presence of virus in vegetative and reproductive plant tissues, including seeds, assays were developed to detect viral DNA and viral coat protein in infected plants. Tomato yellow leaf curl virus (TYLCV) was used to infect *Solanum lycopersicum* (tomato) and *Abelmoschus esculentus* (okra) using *Agrobacterium*-mediated transformation. Mock inoculated tomato and okra plants were used as a control. Samples from the leaves at 8, 17, and 22 days post-inoculation (d.p.i.) were collected and processed by freeze drying in liquid nitrogen and grinding in Tris buffer. Using virus-specific antibodies previously developed in the lab, samples were tested for coat protein using Western Blot and ELISA. PCR was used to examine plant samples for the presence of viral DNA using virus-specific primers. Viral DNA could be detected in lower leaves as early as 8 d.p.i., and in upper leaves by 22 d.p.i. This method can be used for testing roots, flowers, and seeds of infected plants for viral DNA and protein, as well as experimenting with other plant species to determine the host range of the virus. (170)

Baranovic, Alison*, and Megan Rothenberger Lafayette College, Easton, PA 18042. *Comparing predator and prey composition among natural, restored, and created vernal pools.* — The fact that several vernal pool restoration and creation attempts in eastern Pennsylvania and New Jersey have been paired with conservation of natural pools in the same area provided a valuable research opportunity to compare amphibian habitat quality, including predator and prey composition and abundance, between project sites and natural, reference pools. We used a total of four natural, four restored, and six created pools distributed over four sites in eastern Pennsylvania and Warren County, NJ. To measure desired outcomes, we used successful reproduction and metamorphosis of two vernal pool indicator species, the wood frog and spotted salamander. Although many previous studies indicate that restored and created pools rarely replace function lost in the destruction of natural pools, success of vernal pool indicator species was not necessarily related to pool type in this study. Results indicate a strong correlation between reproductive success for both species and vernal pool size (i.e., mean depth and volume) and hydroperiod, regardless of pool type. Although none of the pools contain fish, initial observations indicate a relatively high density of green frogs, eastern newts, American bullfrog tadpoles, and various invertebrates in pools with semi-permanent hydroperiods (i.e., containing water for >35 weeks). Wood frogs appear to achieve reproductive success in pools with longer hydroperiods only if predator density is low, whereas spotted salamanders may achieve reproductive success even when predator density is relatively high, suggesting that wood frog eggs may be more vulnerable to predation pressure. Because these methods enabled us to evaluate the effectiveness of different vernal pool creation and restoration strategies in comparison to natural pools that establish a reference range for species and processes, our results provide practitioners with additional information to guide future projects and inform adaptive management of vernal pools. (123)

Barnes, Melissa*, and Katherine Straub Susquehanna University, Selinsgrove, PA 17870. *Applying Best Management Practices to Aid Snyder County in Meeting the Watershed Implementation Plan Phase 3 Reduction Goals in Nitrogen, Phosphorus, and Sediment.* — The Chesapeake Bay is at risk due to excess nutrients that reach the Bay from upstream tributaries. Primarily due to agricultural runoff, the Bay has been exposed to high loads of nitrogen, phosphorus, and sediment that in turn has influenced algal blooms which deplete the Bay's aquatic ecosystems of dissolved oxygen. The Environmental Protection Agency (EPA) has mandated Watershed Implementation Plans (WIPs) that allow states to independently reach reduction goals

by 2025 that will restore the Bay's health to a higher standard. Within Pennsylvania, county targets have been developed. Snyder County specifically has a goal of reducing nitrogen loads by 1.4 million pounds per year, and phosphorus by 72,759 pounds per year. This research focuses on investigating what the most feasible best management practices (BMPs) for Snyder County will be to meet these reduction goals. This study was conducted by using the Chesapeake Assessment Scenario Tool (CAST) for numerical analysis and stakeholder interviews for input about the economic feasibility of implementation practices on sectors of both private/public land. Our results suggest that it is possible to meet the reduction goals by 2025 through the use of farm manure management, stream buffers, streambank fencing, and animal heavy use areas. Recommendations for future study focus on ever-changing nutrient loads and annual updates on BMPs that are being installed in Snyder County. (158)

Barr, Stephanie*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Development of Molecular Tools for Rapid Genotyping of Yeast Strains Used in Beer Production.* — In 2011, Americans drank an estimated 6.3 billion gallons of beer, making it one of the most popular alcoholic beverages in the United States. The brewing process involves making wort, which is a solution of sugars extracted from malted grain that can then be fermented by yeast that convert sugars into carbon dioxide and ethanol. Two of the most common yeasts used are *Saccharomyces cerevisiae*, used to brew ale beers, and *Saccharomyces pastorianus*, used to brew lager beers. The different strains lead to different flavors, colors, and levels of alcohol being produced so it is essential that the proper yeasts are used to brew each type of beer. In large breweries, sometimes the wrong yeast can contaminate the batch of beer. Large breweries reuse the yeast multiple times (re-pitching) so eventually an insignificant amount of yeast contamination can completely ruin an entire batch. Current tests for contamination can take up to a week to obtain results, which wastes time, money, and resources. My research focuses on creating a novel protocol that large beer companies can use to test for contamination in their batches of beer using a quantitative polymerase chain reaction (qPCR) with high resolution melt point analysis (HRM). We are validating PCR primers that target short tandem repeat sequences on the *S. cerevisiae* or the *S. pastorianus* genomes and using HRM to identify diagnostic melting points of the different strains. We are in the process of multiplexing our PCR by targeting multiple loci, and in doing so hope to develop a series of genotyping fingerprints that can be used for the rapid and accurate identification of commonly used beer yeast strains and potential wild contaminants. (13)

Bauer, Anna*, Alyssa Rothman, Sophia Scarpone, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087. *Use of a modified tube dilution method to determine bacterial susceptibility to antimicrobial proteins from Eisenia hortensis.* — The objective of this investigation was to use a broth-based method to determine the concentration of an antimicrobial protein extract purified from the earthworm *Eisenia hortensis* required to inhibit selected bacteria. Protein extracts were prepared using 85% ammonium sulfate precipitation, dialysis, filtration and concentration techniques. Previous results in the lab using a disk diffusion method revealed zones of inhibition for three bacteria, *Micrococcus luteus*, *Micrococcus roseus*, and *Bacillus megaterium*, using disks impregnated with 500 or 2000 mg and placed on agar plates streaked with each of the bacteria. A tube dilution method was developed to address the concentration of extract required to inhibit growth in liquid culture. Overnight tryptic soy broth cultures of bacteria were diluted 1:20 and incubated with three concentrations of extract (0.82, 0.082, and 0.0082 mg/ml) for 16-24 hours. The number of colony forming units (CFUs)/ml for treated and untreated control samples was determined by preparing ten-fold serial dilutions made in phosphate-buffered saline and plating on tryptic soy agar in the absence of extract to permit recovery of bacteria. *M. luteus* was tested in two separate assays with all treatments in duplicate. Statistically significant ($p < 0.05$) decreases in CFUs/ml were observed for *M. luteus* treated with 0.82 and 0.082 mg/ml, but not with 0.0082 mg/ml compared to untreated controls. Preliminary results show that *Bacillus megaterium* is less sensitive to the extract than *M. luteus*, with significant inhibition observed at 0.82 but not 0.082 mg/ml. Experiments are underway to confirm the results observed with *B. megaterium* and to include *Micrococcus roseus* in the scope of this study. In addition, the tube dilution test will be repeated with *M. luteus* using two-fold dilutions of extract within the range of 0.0082 and 0.082 mg/ml to more accurately identify the concentration of extract required for the inhibitory effect. (86)

Bentkowski, Kristine*, Nicole Chinnici, and Joshua Loomis East Stroudsburg University, East Stroudsburg, PA 18301. *Prevalence of Powassan virus and Lyme disease (*Borrelia burgdorferi*) in *Ixodes scapularis* collected from New Jersey and Pennsylvania Black Bears (*Ursus americanus*)*. — Tick borne diseases are on the rise across the United States, with the leading vector of human tick borne diseases caused by *Ixodes scapularis* (blacklegged tick/deer tick). The blacklegged tick is the main vector for Lyme disease in the United States, causing 42,743 cases in 2017, a 9% increase from 2016 (CDC, 2018). The blacklegged tick is also the main vector for Powassan virus Lineage II (Deer Tick virus). Both Powassan virus and Lyme disease are most prevalent in the Great Lakes region and along the northeast coast from Maine to Virginia. The objective of this study was to identify the prevalence of Powassan virus Lineage II and Lyme disease in 742 adult and nymph blacklegged ticks collected in New Jersey from 2015-2018 and 202 adult and nymph blacklegged ticks collected in Pennsylvania from 2017-2018. All ticks were collected from lived trapped or hunter harvested black bears (*Ursus americanus*). Real-time Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) was used to amplify cDNA of the NS5 gene specific to POW Lineage II, and qPCR was used to amplify the 16S rDNA region of *Borrelia burgdorferi* (Lyme disease). This is the first study to evaluate the prevalence of POW virus Lineage II and co-infection prevalence with Lyme disease in the Mid-Atlantic region. (37)

Bergman, Leah*, and James Hunt East Stroudsburg University, East Stroudsburg, PA 18301. *Substrate preference in summer flounder, *Paralichthys dentatus*, in the Barnegat Bay, New Jersey*. — The substrate preference of Summer Flounder, *Paralichthys dentatus*, is observed in the Barnegat Bay, New Jersey. Previous studies about Summer Flounder in the Barnegat Bay claimed that they prefer sand, but only collected data from mud substrate and had little fishing success. In this study fishing occurred from two primary locations, one with sand substrate and one with mud. Data was collected on the chemical and physical conditions of the two sites including dissolved oxygen, temperature, salinity, and clarity. Morphometric data on Summer Flounder and other caught fish species was taken. This study established that there is no substrate preference for this population of Summer Flounder using a Chi-square analysis. There is also a positive correlation between amount of flounder caught and warmer water temperature. Flounder also have a noted preference for whole fish baits such as Atlantic Silverside (*Menidia menidia*) over diced baits such as Atlantic Menhaden (*Brevoortia tyrannus*). Bluefish (*Pomatomus saltatrix*), another species caught in this study, showed a negative correlation between the size of Bluefish caught and higher temperatures. Additionally, smaller bluefish preferred mud substrate over sand substrate, which is established using a Chi-square analysis. (14)

Berkey, Abigail* Wilson College, Chambersburg, PA 17201. *Auditory and visual signals in the Ecuadorian hermit crab, *Coenobita compressus**. — Although they lack the extreme cooperative and colony building behaviors which characterize eusocial species, many non-eusocial invertebrates, such as the land hermit crabs of the genus *Coenobita*, exhibit a complex suite of social behaviors. The ecological significance of these behaviors and the variables which mediate social interactions remain poorly understood. *Coenobita* occupy habitats characterized by change where the distribution of resources, especially food and shells, is in a continual state of flux. Because of the unpredictable and ephemeral nature of these resources, frequent social interactions and intense intraspecific competition are expected to lead to natural selection for signaling systems or communication. While olfaction, sound, and vision are all potential modes of communication in *Coenobita*, the latter two have received relatively little attention. Potential auditory signaling, consisting of “stridulations” or “chirpings,” has been observed in *Coenobita* and antennae movements may provide a mechanism for visual signaling. To explore these possible modes of communication and their roles in the ecology of a non-eusocial invertebrate, I staged a series of experiments focusing on behavior and social interactions in the Ecuadorian hermit crab, *Coenobita compressus*. Trials were conducted to measure the reactions of individual *C. compressus*, in terms of direction and speed of movement, in response to auditory signaling, i.e. recorded stridulations. I also compared the frequency and duration of interactions between individuals following a recorded stridulation vs. an artificial tone. Finally, I examined the potential for visual signaling in this species by observing the movement patterns of the antennae in individuals when exposed to conspecific stimuli. The results suggest that intraspecific signaling

in *C. compressus* may be complex and mediated by multiple variables. Further work is needed to examine the mode and role of communication in this taxon. (187)

Bianchini, Emily*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Exploring protein interactions of Replication Protein A in Saccharomyces cerevisiae using the Yeast 2 Hybrid system.* — Cancer is the second leading cause of death in the U.S. today, with a predicted 1,762,450 new cases and 606,880 deaths in 2019, according to American Cancer Society. Cancer is the formation of malignant neoplasms in the human body as result of mutations in the DNA of cells. Scientists have been studying the correlations between genetic factors and cancer and have identified many proteins that function in the cellular pathways that lead to cancer. One such protein is the highly conserved, singled-stranded DNA binding protein Replication Protein A (RPA) that plays important roles in DNA replication, DNA repair and recombination, cell cycle control, and telomere synthesis. We are studying the underlying causes of cancer using the baker's yeast, *Saccharomyces cerevisiae*, as a model organism. Since yeast RPA and the yeast cellular processes that underlie cancer are highly homologous to human RPA and cellular functions, we specifically wished to identify the proteins that physically interact with RPA. To do so, the Yeast Two Hybrid technique was adopted to create strains of yeast with different versions of RPA attached to a the *GAL4* transcription factor binding domain and used a cDNA library of yeast proteins fused to the *GAL4* transcription factor activating domain. If a physical interaction occurs between RPA and a candidate protein, together, the binding domain and activating domain turn on transcription of the selectable marker *ADE2* that is required for adenine production in yeast cells. Using this system, we have found a number of candidate proteins that physically interact with RPA and we are in the process of identifying those proteins. By gaining a better understanding of the proteins that physically interact with RPA, we will gain a better understanding of its function in important cellular processes involved in the underlying causes of cancer. (109)

Blaetz, Margaret*, and Ellen Yerger Indiana University of Pennsylvania, Indiana, PA 15705. *Stop and smell the roses: Native species accumulate less insect herbivory than their invasive congener.* — Many ecosystems are invaded by non-native plants but little is known about how the new plants provide food for animals. Among herbivorous animals, insects are a key link between the trophic level of the plants they eat, and the trophic level of the predators that eat them. To better understand the role of invasive plants in the food web, our project compared the insect herbivory experienced by a population of native rose, *Rosa carolina*, with the herbivory experienced by its close relative, an invasive rose, *Rosa multiflora*. The comparison was conducted in a natural area in Murrysville, PA where both species have been growing abundantly for over a decade and therefore are assumed to have developed a suite of animal associates. Ten undergraduate students visually estimated the percent herbivory on leaves of both species on one day at the end of the growing season. Contrary to expectations, the herbivory experienced by invasive rose was greater than native rose. Explanations for this surprising result may involve greater nutritional food quality of the invasive plant, generalist feeding insects that lack host specificity, or diminished production of deleterious chemicals by the invasive while it undergoes rapid vegetative growth in its new range. (185)

Blodgett, Kassandra*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Investigation of changes to oral bacterial strains over time through genetic analysis of Streptococcus mutans.* — This continuous study of the oral bacterium, *Streptococcus mutans*, investigates changes to the human strains over time in order to better inform the utility of this species in the identification of an individual in forensic cases involving human bites. Oral swabs were collected from individuals and selectively cultured for *S. mutans* colonies using mitis-salivarius agar. Arbitrary primed PCR of genomic DNA from these cultures allowed for a quick genotyping based on similarities and differences between amplicons and allowed for discrimination between individuals. This ongoing study examines the diversity of strains within individuals and changes to the oral biota over time to explore the consistency in sampling methods as an indication for forensic applications. (93)

Bonetti, Irene*, and Anastasia Thévenin Moravian College, Bethlehem, PA 18018. *Mutually exclusive interactions of Connexin 43 Gap Junctions with Src and Zona Occludens-1 (ZO-1) are regulated through*

phosphorylation. — Connexin 43 (Cx43) is a transmembrane protein that constitutes intercellular communication structures, called gap junctions (GJ). These Gap Junctions are responsible for the passage of small molecules and ions, facilitating many critical physiological functions, including cellular growth and development. Connexin 43 C-terminus is phosphorylated at many residues (serines and tyrosines), and phosphorylation is known to regulate GJ function, such as trafficking of Cx43 toward the plasma membrane, GJ assembly, opening and closing, as well as GJ internalization. Cx43 C-terminus interacts with many proteins, including a scaffolding protein, Zona Occludens-1 (ZO-1) and a potent oncogene, Src. Interestingly, Src and ZO-1 binding and interaction with Cx43 GJs are mutually exclusive. Binding of ZO-1 to the last 4 amino acids on Cx43 C-terminus regulates the rate of GJ accrual at the plasma membrane. In addition, GJs remain open and functional when ZO-1 is bound, while ZO-1 detachment coincides with GJ closing. Moreover, it was determined that phosphorylation of S373 (by activated Akt) or through mimicking phosphorylation at that site leads to detachment of ZO-1 from Cx43 C-terminus. Src, on the other hand, phosphorylates Cx43 on two tyrosines (Y247 and Y265), leading to GJ closure and a drop in cell-cell communication. In addition, was recently demonstrated by others that Cx43 GJs, when expressed in glioma cells, recruit Src to a distant region of Cx43 C-terminus (amino acids 266 to 283), causing downregulation of Src oncogenic activity. Our ongoing in vitro and in cells binding studies between Src and phosphomimetic (S373E) and phospho-dead (S373A) mutants of Cx43 show that unlike ZO-1, Src prefers interacting with Cx43 phosphorylated at S373. These results finally provide a molecular explanation as to why Src and ZO-1 have never been observed to interact with Cx43 simultaneously, giving us a better understanding of events leading up to GJ closure and internalization. (74)

Bottega, Caroline*, Megan Rothenberger, Dru Germanoski, and John Wilson Lafayette College, Easton, PA 18042. *A multidisciplinary risk assessment study prior to dam removal in a tributary to the Delaware River*. — The proposed removal of four small dams in Easton, PA along the Bushkill Creek, a tributary of the Delaware River, has provided a valuable opportunity for multidisciplinary risk assessment prior to dam removal. Although dam removal can be an important stream restoration method, improperly planned removals can irreparably harm downstream biota by releasing fine-grained and potentially contaminated sediments. The objectives of this research were to build a long-term (2009-2019) pre-removal monitoring dataset for both water quality and macroinvertebrates, analyze heavy metals and polychlorinated biphenyls (PCBs) in legacy sediment cores, and perform associated toxicity assays to determine the effects of lead, copper, and cadmium on survival and behavior of two common macroinvertebrates in the Bushkill Creek. Monitoring data were collected from sites approximately 35 m upstream and downstream of dams and reference sites located approximately 5 km upstream of all dams. Results indicate that oxygen levels, macroinvertebrate diversity, and proportion of sensitive taxa were significantly lower upstream and downstream of dams in comparison with upstream reference reaches. The strong correlation between water quality and macroinvertebrates in this system implies that removal of the dams would lead to improvements in water quality, biotic integrity, and resilience in lower Bushkill Creek. Legacy sediment analyses suggest that heavy metals may be mobilized upon removal, but that PCB concentrations are far below the probable effect level. Results from toxicity assays indicate that risks to biota associated with mobilized sediments following dam removal will be low. All together, this study suggests that the dams are good candidates for successful stream restoration. (122)

Bowman, Ruric*, Brittany Lenze, and Robert Smith Lycoming College, Williamsport, PA 17701. *Vertical migration of adult Plecoptera (Stoneflies) above forested headwater streams*. — Aquatic insects have a life cycle that includes a larval aquatic stage and an adult terrestrial stage. Stream insects generally stay above the stream channel as adults, but dispersal through upland areas does connect populations in neighboring streams. Vertical migrations up through the forest canopy may be the result of adaptations to avoid predators, complete reproduction, or move above trees for dispersal. Comparing insect abundance between the forested canopy and near the stream can provide information about a species' life history and dispersal behavior and can inform research examining dispersal barriers in human-dominated landscapes. We performed a study that examined the abundance of adult plecopteran that moved into the forest canopy compared to individuals found close to the stream. During the summer 2017 and 2018 and autumn 2018, we

set up malaise and canopy traps at four streams in the Mosquito Creek Watershed (Lycoming County, PA). We deployed traps for 2-week periods in Jun/Jul and Sep/Oct and identified all Plecoptera to family and Ephemeroptera and Trichoptera to order. Preliminary analysis of the data showed that Trichoptera were the most abundant in both the canopy and malaise traps followed by Plecoptera and Ephemeroptera. A significantly higher abundance of adults were captured in malaise than canopy traps for Plecoptera and Trichoptera but not Ephemeroptera. The abundance of plecopteran families captured in both traps ranged from 1,241 individuals (Perlodidae) to 27 (Peltoperlidae), but Leuctridae had the largest number of individuals in the canopy (165 individuals, 20.9% of all individuals caught). The percentage of plecopteran individuals caught in the canopy ranged from 8.1% (Perlodidae) to 25.0% (Perlidae). A significantly greater number of individuals were caught in malaise than canopy traps for four of the six plecopteran families found in our study. (145)

Bradfield, Jacob*, and Meda Higa York College of Pennsylvania, York, PA 17405. *Exploring the importance of Andes Virus glycoprotein glycosylation on host entry and infection.* — Andes virus, in the family *Hantaviridae*, is a rodent-borne virus which is commonly spread through rodent excreta. Andes virus affects pulmonary systems in humans, has a 50 percent mortality rate, and has been shown to be transmitted between humans. There are currently no approved treatments, although supportive care is available for infection. Andes virus has 3 segments, S, M and L. The M segment encodes for the surface glycoproteins Gn and Gc. Gn and Gc are known to play a role in viral attachment and entry into host cells. The Gc protein is identified to be a class II fusion protein. However, Gn is unknown in its role of entry into a host cell. The Gn protein is believed to assist the viral body in entry into a cell. Structural studies further suggest, that the two glycoproteins might interact directly with each other. The purpose of this study is to explore how the Gn protein interacts with attachment and entry of the host cell. To do this, vesicular stomatitis virus (VSV) pseudovirion tool system will be used. These pseudovirions will display mutated Andes virus glycoproteins on the surface and carry a luciferase reporter gene. The purpose of this study is to determine whether mutation of the glycosylation site disrupts viral entry. This could inhibit glycosylation and prevent correct formation and function. This study should help us better understand how Gc and Gn interact and what purpose Gn serves. Better understanding of the function of the protein Gn might allow further research into a potential vaccine or treatment for Andes virus. (92)

Brown, Morgan*, Alec Beck, Katherine Watson, and Steven James Gettysburg College, Gettysburg, PA 17325. *A GYF-domain protein damaged by a reciprocal translocation partially rescues G2/M defects 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. We discovered a previously unreported role in cell cycle regulation for a SR/RRM family protein, called *snxA* (suppressor of nimX-CDK1). *snxA* mutations down-regulate expression of wild-type *snxA* protein and suppress defects at the G2-M transition of the cell cycle. Loss of *snxA* partially rescues heat-sensitive mutations in regulators of the CDK1 mitotic induction pathway, indicating that *snxA* acts normally by antagonizing CDK1-cyclinB to restrain the transition from G2 phase to mitosis (James et al., 2014. GENETICS 198: 617). To determine the genetic basis for down-regulation of expression in *snxA* mutants, we performed whole-genome sequencing followed by de novo genome assembly. This revealed a reciprocal translocation in which part of the *snxA* locus on Chromosome II was joined to a large uncharacterized gene on Chromosome I. This gene encodes a GYF-domain protein, AN6228, which we have named *gyfA*. In other model systems, the GYF domain is known to mediate association with proline-rich motifs in a variety of proteins. Since the “*snxA*” mutant phenotypes result from the simultaneous breakage of *snxA* and *gyfA*, then this raises the question whether the defects in one or both genes is responsible for rescuing G2 phase arrest in CDK1 mutants. Here we demonstrate that a complete deletion of *gyfA*, and a reconstructed *gyfA::snxA* translocation allele, partially suppress CDK1 cell cycle defects. These unexpected observations show that mutations in both *snxA* and *gyfA* suppress G2-M defects independently of one another. Furthermore, the partial suppression afforded by mutations in each gene alone appear to act in combination to produce enhanced suppression in the *snxA/gyfA* translocation mutants. (115)

Buczowski, Stephanie*, and Angela Hess Bloomsburg University, Bloomsburg, PA 17815. *Melanoma Aggressiveness in relation to EphA2 Expression in a Murine Model*. — An aggressive phenotype of melanoma is responsible for the drastic difference between survival rates of patients diagnosed with non-metastatic melanoma versus patients diagnosed with metastatic melanoma. Factors such as proliferation, migration, invasion, and vasculogenic mimicry (VM) are key components in aggressive melanoma development. Many receptor tyrosine kinases are involved in these cellular functions, including EphA2. Previous studies illustrate EphA2 contributes to proliferation, migration, invasion, and VM formation via the MAPK pathway in human melanoma. These data suggest that expression of EphA2 correlates with an aggressive melanoma phenotype making it a potential target in diagnosing and targeting malignant melanoma. However, studies utilizing a murine model have yet to be investigated. This study examines EphA2 across five mouse melanoma cell lines and explores its relation to aggressiveness. These data demonstrate increased EphA2 expression in two K1735 mouse cell lines but not in three B16 mouse cell lines. The MAPK pathway was found to be over activated in these cells and successfully decreased with U0126 treatment. Increased expression of EphA2 correlated with increased proliferation rates in these cells. Moreover, inhibition of the MAPK pathway decreased proliferation and expression of EphA2 in these cells. These results suggest that the MAPK pathway and EphA2 expression are linked in mouse melanoma and represents a potential therapeutic target for this disease. (201)

Burgis, Adam*, Mark Meadowcroft, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The effects of dietary calcium and vitamin D supplementation on bone mineral density in elderly female zebrafish (Danio rerio)*. — The zebrafish (*Danio rerio*) skeletal system is similar to the human skeletal system, supporting the use of zebrafish for studying bone diseases. Furthermore, as demonstrated by a significant decrease of estradiol in aged females, zebrafish undergo ovarian senescence after 13 months of age, making them an ideal candidate for osteoporotic studies. Clinically, a combination of vitamin D and calcium are effective in increasing bone mineral density in postmenopausal women. Thus, we hypothesize that aged zebrafish (>18 months old) will have significantly decreased bone mineral density (BMD) when compared to young zebrafish (≤ 4 months old). Additionally, aged zebrafish with dietary supplementation of calcium and vitamin D will have significantly less decreased BMD when compared to aged zebrafish without a supplemented diet. To test this, three experimental groups; young control (n=9), aged control (n=28), and aged experimental (n=24) were reared for 12 weeks with daily feeding and weekly water exchange. Each experimental group was fed with their respected diets – young and aged control received control diet while the aged experimental were fed experimental diet which was supplemented with 3.85g of CaCO₃/100g diet and 4000IU/1kg diet of vitamin D3. At the end of 12 weeks, fish were euthanized via ice bath hypoxia and randomly assigned to one of two analysis groups – Atomic Absorption Spectrometry (AAS) or Alizarin Red Staining (ARS). For AAS, fish were degraded in 68-70% nitric acid at a concentration of 1ml HNO₃/0.1g zebrafish directly after euthanasia. Fish in the ARS group were fixed overnight in 10% NBF, then transferred to PBS until they were bleached and stained overnight in 0.02% ARS. We expect to see a correlation in AAS peaks and ARS fluorescent intensity, supporting our hypothesis. (102)

Butler, Timera*, Richard Jackson, and Rachel Fogle Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Anatomical effects of sex hormone derivatives on embryonic Danio rerio (zebrafish) development*. — The presence of levonorgestrel (LNG), estriol (E3), and bisphenol-A (BPA) has an impact on the structure, behavior and developmental aspects of *Danio rerio* (zebrafish). Male and female zebrafish from batches K2543, K2533, K2541, and K2528, obtained from the Zebrafish Core at Penn State Hershey, were raised to embryonic day 7 and evaluated twice daily for changes in heart rate and organogenesis. Various concentrations ranging from 25 to 150 ng/mL of each hormone induced a significant response in the transition from the gastrula to pharyngula phase of development. In the pharyngula phase, a substantial decrease in heart rate was measured in the E3 group compared to the control. Additionally, BPA showed a significant increase in heart rate from the beginning of the segmentation period to the end of the pharyngula phase. Levonorgestrel showed an inconsistent change in heart rate observations compared to the control in all trials. Exposure to the sex hormone derivatives resulted in consistent, but distinct, trends in several

variables related to organogenesis, including somite formation, pericardial region thickness, and tail formation. Magnification and imaging with an Olympus 1×51 inverted microscope displayed a positive relationship between exposure to certain minimal concentrations of hormone derivatives (e.g., LNG, E3, or BPA) and growth abnormalities throughout the stages of embryonic development. (54)

Cabassa, Meaghan*, Rachel Rosato*, Dylan Jainchill*, Blyssalyn Bieber, Eric Ho, Manuel Ospina-Giraldo, and Cosima Wiese Misericordia University, Dallas, PA 18612. *Elucidating the molecular and physiological mechanisms underlying reductions of growth and asexual reproduction*

in Lemna minor exposed to elevated concentrations of zinc. — Elevated levels of heavy metals, such as zinc, are found in aquatic ecosystems worldwide. Zinc can be released into surface waters from anthropogenic and natural sources. Aquatic plants are particularly sensitive to the presence of heavy metals as they absorb them through their roots. *Lemna minor* (duckweed), is a small flowering plant commonly found in aquatic environments; as a primary producer, *L. minor* is important for oxygen production and nutrient cycling, and it also provides habitat and shelter for aquatic organisms and terrestrial wildlife. The goal of this research project is to understand the biochemical and molecular mechanisms underlying observed growth reductions in *L. minor* exposed to elevated concentrations of zinc. Cultures of *L. minor* were grown in a modified Hoagland's solution containing 0, 5, 10 and 15 mg/l zinc for 7 days in a growth chamber at 25°C with a 16-hour light period and a light intensity of 400 $\mu\text{mol m}^{-2} \text{s}^{-1}$. In order to determine the transcriptional changes in *L. minor* occurring in response to zinc exposure, a whole transcriptome sequencing analysis was performed using RNAseq. A total of 486,060,942 reads were obtained, which have yielded approximately 146 gigabases of data. Two genes [superoxide dismutase (SOD) and ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO)], which showed an altered expression pattern in the RNAseq experiment, were selected for further study. Gene-specific primers for SOD and RuBisCO were designed, and qPCR data collection and gene expression analysis are in progress. In conjunction with the analysis of gene expression, RuBisCO protein is being quantified from extracts of total soluble protein of *L. minor* using SDS-PAGE. Furthermore, SOD activity is being measured using a spectrophotometric assay. (160)

Campbell, John* Mercyhurst University, Erie, PA 16546. *Analysis of potential biotic triggers of toxin release by the colonial cyanobacterium Microcystis in Lake Erie.* — The underlying mechanisms which trigger the release of toxins from the cyanobacterium *Microcystis* during harmful algae blooms (HABs) are poorly known. Potential biotic triggers include predatory activities of zooplankton grazers, competitive interactions with other algae competitors and interactions between *Microcystis* and its diverse assemblage of endosymbiotic microbes. Population dynamics of *Microcystis* and associated Lake Erie phytoplankton and zooplankton were characterized by biweekly sampling of Presque Isle Bay during the summers of 2016 and 2017. Colonies of *Microcystis* found in samples collected from the bay during various stages of the summer HABs were examined at 1000X magnification using oil-immersion light microscopy. The extracellular polysaccharide sheath of *Microcystis* was found to frequently harbor eubacteria, protozoa, green algae and diatoms. High densities of the nanno-planktonic cyanobacterium *Pseudanabaena mucicola* were associated with *Microcystis* colonies undergoing apparent degradation, suggesting the possibility that this symbiont may have a role in affecting *Microcystis* toxin production. (15)

Carpenter, Carrie*, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Characterization of Psychromonas aquimarina, a new model organism for climate change.* — The current increase of average global temperature puts 25 to 35 percent of plant and animal species at an increased risk of extinction. Changing any environmental factor, such as growth temperature, can significantly impact any organisms' ability to survive. Because of the diversity of organisms on the planet, it is not feasible to study how each individually might adapt, but rather it is more efficient to study select organisms. This research focuses on a psychrophilic bacterium, *Psychromonas aquimarina*, which can survive in colder regions where most bacteria would not. This bacterium was chosen because climate change is affecting the poles of Earth at two times the rate that it is affecting other parts of Earth. *Psychromonas aquimarina* first needed to be characterized, as little was known about the bacterium. *Psychromonas aquimarina* was confirmed gram-negative, rod-shaped, convex colony-forming with an ideal growth temperature of 20°C, but new characteristics were identified in this research. We report

for the first time the doubling time of *P. aquimarina*, 21.05 hrs, and the ability to form a pellicle biofilm between the air-liquid interface. *Psychromonas aquimarina* in growth and protein expression studies at various temperatures exhibited slow but significant tolerance and adaptability. Heat shock protein expression in cold tolerant organisms provide insight to the mechanisms in charge of thermotolerance. *Psychromonas aquimarina* is proposed as a model organism for studies of adaptation to thermal stress imposed by climate change. (127)

Carrero, Joseph*, Hagar Fadel*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Investigation of the release mechanism of naproxen sodium, acetaminophen and ibuprofen from tablet delivery systems.* — Samples of generic formulation tablets containing 220 mg of naproxen sodium, 168 mg of acetaminophen or 200 mg of ibuprofen were exposed to pH = 8.00, phosphate buffer in a dissolution apparatus at 37°C. The rate of drug release from each tablet delivery systems were measured by collecting 5.0 mL samples at 1.0 minute intervals over a period of 90.0 minutes. After collection of the samples was complete the samples were quantitated using a UV spectrophotometer. Naproxen Sodium measured at 330 nm, acetaminophen at 250 nm and ibuprofen at 221 nm. The data was then plotted using a three dimensional kinetic model to identify the release kinetics and obtain the rate constant for each drug. The results observed, based on these dissolution studies, suggest that the rate of drug release from each formulation either increases or decreases depending on the solubility in the buffer system. (28)

Carwell, Shanna*, and Deanne Dulik Garver Marywood University, Scranton, PA 18509. *Synthesis of esterified stevioside as a potential treatment for Lyme's disease.* — Each year, there are approximately 30,000 cases of Lyme's disease reported in the United States. There is currently no cure for this chronic and debilitating disease, and treatments are not effective for eradicating this tick-borne disease. Many scientists and labs have been working to find a compound that will kill the Lyme disease-causing bacteria, *Borrelia burgdorferi*. One compound which has shown some progress in the killing of the bacteria is the alcohol extract of stevioside from stevia leaves. Stevioside has been found to have promising effects on killing the many different forms and shapes of the Lyme disease bacteria. The objective of this research is to successfully extract stevioside from dried stevia leaves and to chemically convert the diol to the diester form with acetic anhydride. The diester form is expected to have better absorption than stevioside itself. The product from the extraction and the chemical synthesis product will be analyzed using high performance liquid chromatography and the structures characterized by tandem liquid chromatography/electrospray mass spectrometry prior to testing for antibacterial effect. (24)

Cervantes, Rebecca*, Dina Ninan*, Anthony Farrugia*, Georgina VanNorden, Francis Mayville, and Joshua Slee DeSales University, Center Valley, PA 18034. *Soursop is truly sour: pro-inflammatory effects of annonacin.* — Annonacin is an acetogenin found in extracts of *Annona muricata* (Soursop). Annonacin is thought to exhibit anti-inflammatory properties which could have implications in the treatment of cardiovascular disease and biomaterial rejection. However, annonacin is believed to have pro-inflammatory effects, which could supersede its beneficial effects. Annonacin was extracted from the North American pawpaw fruit using Soxhlet Extraction, and verified using IR, NMR, and UV spectroscopy. The pro-inflammatory effects of annonacin were determined using Bovine Aortic Endothelial Cells (BAOECs) cultured with varying concentrations of annonacin and the adverse effects on cell growth and morphology were studied. An established model of cellular inflammation uses TNF- α to induce an accumulation of actin stress fibers. Cells were treated with TNF- α , annonacin, or both. These results demonstrate that annonacin alone increases actin stress fiber accumulation in a dose-dependent manner beyond TNF- α and that there is not a synergistic effect of TNF- α and annonacin together. Furthermore, BAOECs treated with annonacin for 72 hr and imaged every 24 hr showed that prolonged exposure to annonacin causes an increase in actin stress fiber production, indicating its pro-inflammatory properties. A wound healing assay was also conducted using BAOECs which revealed annonacin slows wound healing when compared to control cells. Taken together, the data suggest that annonacin is pro-inflammatory in vascular endothelial cells which could lead to its cytotoxic effects. To further understand annonacin's pro-inflammatory effects, a THP-1 cell adhesion assay was conducted using polyurethane films. THP-1 cells are a monocyte-derived macrophage cell line which model the body's response to biomaterials. Cell attachment to the polyurethane films was not

significantly increased when cultured with annonacin. These studies demonstrate that annonacin is pro-inflammatory in the vasculature and slows wound healing but does not significantly increase the immune response to biomaterials. (100)

Christman, Laura*, Sara Wolbert, and Stephanie Justice-Bitner King's College, Wilkes-Barre, PA 18711. *Detection of protein-protein interactions involving the carboxyl terminus of the human cannabinoid 1 receptor.* — The human cannabinoid 1 receptor (CB1R) regulates neurotransmitter release through ion channel regulation and multiple signal transduction pathway activations. CB1R is one of the main components of the endocannabinoid system, which has been studied for its potential for various methods of therapy to treat substance abuse. Substance substitution has been used previously to target the receptor affected by the abused substance, however, these treatments have not been effective in every instance. Chronic use of abused substances causes continued antagonism of the CB1R, which manifests as physiological changes leading to substance abuse, addiction, and other drug seeking behaviors. While certain effects of substance abuse on the CB1R have been previously studied, more information is needed to further understand the function of the cannabinoid 1 receptor and to develop additional treatment methods. Protein-protein interactions are imperative to understanding how signaling complexes like the CB1R are involved in cellular processes and their manipulation can be used as a therapeutic strategy. Protein-protein interactions are modulated by specificity and possibly their regulation of specificity via the carboxyl terminus of CB1R. The yeast two-hybrid system was used as a preliminary method to identify potential protein-protein interactions between the carboxyl terminus of the CB1R and a human brain cDNA library. Determination of protein-protein interactions within the carboxyl terminus of the cannabinoid 1 receptor can provide evidence that may contribute to the identification and characterization of the cellular and molecular mechanisms that lead to drug dependence. (96)

Churylo, Kara*, Richard Portas*, Meghan Freed*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *The telomere position effect of Saccharomyces cerevisiae is not influenced by constitutive telomerase at the telomere.* — Telomeres are sequences of heterochromatin found at the ends of linear chromosomes. Telomeres are necessary for protecting DNA from the end-replication problem, which causes the ends of chromosomes to shorten with each round of replication. When the telomeres become too short, the enzyme telomerase restores lost genetic sequence, thereby lengthening the telomere. Telomerase localizes to the telomeres during late S/G2 phase, but can be modified *in vitro* to be tethered to the telomere throughout the entire cell cycle. Overactive telomerase is implicated in the genesis of most human cancers and studies have additionally shown that tethered telomerase causes an increase in genetic instability. Genes that are close to telomeres can be silenced, known as the telomere position effect (TPE). We tested the effects of tethering telomerase on the telomere position effect in *Saccharomyces cerevisiae*. The strains utilized in this experiment contain the *URA3* gene on the VII-L chromosome. Expression of *URA3* on growth media containing 5-FOA causes cell death; therefore, growth on 5-FOA ascertains that the *URA3* gene is being silenced due to an increase in telomeric heterochromatin. Our data suggest that tethering telomerase has little effect on TPE under normal conditions. (113)

Clarke, Justin*, and Terry Master East Stroudsburg University, East Stroudsburg, PA 18301. *The northern waterthrush: analyzing the distribution and abundance of a secretive songbird in Pennsylvania.* — Northern Waterthrush (*Parkesia noveboracensis*, NOWA) drastically declined in the ~20 years between the first and second Pennsylvania Breeding Bird Atlas (PBBA). This is one of the largest declines of any Pennsylvania breeding species despite higher sampling effort in the second atlas. PBBA data suggested a slight northward range contraction and detectable increase in elevation of occupied blocks, potentially caused by climate change. This study refines the second PBBA distribution and investigates factors that may be responsible for any detected changes in distribution in the core breeding range in northeastern Pennsylvania. In spring of 2017 and 2018, wetland surveys were conducted for singing males. At each of 54 sites, two point counts were conducted to characterize the avian community. Vegetative, physical, and hydrological characteristics, as well as natural history and reproductive behavior, were also recorded. Sites occupied by NOWA were compared to unoccupied but expected-to-be-occupied sites based on the second PBBA or habitat characteristics. We found eighteen occupied sites, three overlapping six confirmed (breeding) atlas survey

blocks, nine overlapping nineteen possible atlas blocks, and three entirely new sites. Plant communities (particularly shrubs and rooted aquatic plants) were found to be different between occupied and unoccupied sites. Climate indices (average precipitation and average, minimum, and maximum temperatures) were compared between atlas years during which the northern margin of the NOWA range moved south about ten km and the southern margin moved north about nine km. (138)

Cobb, Jacquelyn*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Predicting patient response to kidney cancer immunotherapy by stage using the tumor microenvironment.* — Kidney cancer is a leading site of new cancer cases (~64,000) in the US each year, killing ~15,000 people. Renal cell carcinoma (RCC) accounts for ~90% of kidney cancer cases, with the RCC subtypes being: clear cell RCC (ccRCC), papillary RCC (pRCC), and chromophobe RCC (chRCC). Recently, the FDA approved combination checkpoint inhibitor immunotherapy as a first-line treatment for advanced stage ccRCC. Unfortunately, 1 in 4 advanced stage patients do not respond and response varies between stages. This suggests stage-specific differences in tumor biology. Tumor microenvironments (TMEs) directly influence checkpoint inhibitor response in many cancers. Our objective is to profile the TME using immune cell abundance and composition by stage in RCC patients and use it as a predictor of checkpoint inhibitor response based on published clinical outcomes. The mRNA-sequencing and clinical data for ccRCC, pRCC, and chRCC patients in the TCGA discovery cohort and GEO validation cohorts were downloaded. The data were uploaded into CIBERSORT, a tool that quantifies abundances for 22 immune cells based on gene expression. GraphPad Prism and 1-way ANOVAs were used to determine statistical significance between Stages I-IV within and across RCC subtypes. Immune cell abundances and composition varied significantly by stage. Seven stage-specific immune cell abundances were discovered for ccRCC patients. Four linearly increased abundance in advanced stages (Regulatory T cells), while three decreased abundance in later stages (M2 macrophages). Similar to ccRCC patients, pRCC patients had decreased M2 macrophages in later stages. chRCC patients displayed an opposite trend and had significantly increased Stage IV M2 macrophage abundance. Regulatory T cells and M2 macrophages have been reported to mediate clinical response to checkpoint inhibitor immunotherapy. Precision medicine strategies should consider stage-specific TMEs to predict if advanced ccRCC patients will respond to immunotherapy or if another drug would be more appropriate. (204)

Cordova-Ortiz, Esbeiry*, Robert Logan, Kathryn Jacobson, and Sarah Evans Indiana University of Pennsylvania, Indiana, PA 15705. *Specializations of fungal decomposers from the hyper-arid Namib Desert.* — Plant litter decomposition is a major source of CO₂ emissions, and its prediction is crucial for global climate models. Unfortunately, these models consistently underestimate decomposition rates in drylands (which cover 40% of global terrestrial biome) suggesting that some mechanisms have not been fully explored. In arid ecosystems aboveground litter constitutes over half of plant biomass but its decomposition is overlooked in climate models. Since plant litter decomposition is driven by fungi, understanding the strategies that fungi use in decomposition is needed to better model these systems. In the hyper-arid Namib Desert (grassland dominated by *Stipagrostis sabulicola*) another study found that 66% of endophytes, microbes found in living plants, are able to decompose plant litter after the plant died, suggesting endophytes could have an advantage in decomposition by colonizing plants first. However, the energy cost of role switching may make them less competitive at later stages of decomposition compared to other decomposers only found in dead litter. To test this, we incubated early and late stage litter of *S. sabulicola* with saprophytic endophytes and decomposers isolated from dead litter for 28 days to see whether they specialize in decomposing early versus late stage litter. Great strides have been made in studying the structure of microbial communities and although we know who inhabits them, their exact function is still unknown. Exploring the function these microbes play in their environment allowed us to understand what they are doing. This can lead to conclusions about the importance of studying the actual microbes and potentially improve global climate models. (12)

Corey, Thomas*, Colin Herna*, Steven Sweeney*, and Sara Hayik* DeSales University, Center Valley, PA 18034. *Resistivity of conductive silver nanoparticle inks as functions of annealing temperature and mechanical stress.* — Silver nitrate was used to synthesize metallic nanoparticles, which were capped using

different mixtures of polyacrylic acid (5,000 g/mol and 50,000 g/mol, with one sample a 1:1 mix by mass, and the second a 2:1 mix by mass), to produce two ink samples. A viscosifying agent was added to obtain an ink-like rheology for the samples. Once synthesized, the resistivity of each ink sample was measured as a function of annealing time and temperature. The ink was doctor-bladed onto a glass substrate and annealed at various temperatures (20-150°C) over a three hour period. The resistance of each ink sample was measured at multiple time points using a four-point probe connected to a constant-current generator. Additionally, flexible substrates were used in order to measure the resistivity of the ink samples as a function of mechanical stretching. For complete characterization of the inks, they were imaged with a TEM to determine the size of the nanoparticles. (36)

Corpus, Larry* Misericordia University, Dallas, PA 18612. *The nymphal damselflies and dragonflies of upper Meadows Pond.* — The upper Meadows Pond (UMP) is a private, moderately-eutrophic suburban pond approximately 2 hectares in size located in Dallas, PA. The pond accumulates water from snow and rainfall via grass and parking lot runoff, and receives both autochthonous and allochthonous energy input. It is minimally managed, using two aerators from April to October, and annually goes through a cycle of algal bloom due to inputs of fertilizer applied to the extensive surrounding grass areas. In an attempt to determine if biological assessment of the pond's water quality was possible, a 12-month survey of the aquatic macroinvertebrates of the pond was undertaken to develop a species baseline. Nymphs of the various odonate species collected by dip nets made up the bulk of the identified material presented here. The Zygoptera (damselflies) have been tentatively identified to the following families, genera, and species: Calopterygidae, *Calopteryx maculata* and *Haeterina americana*; Lestidae, *Lestes* sp.; Coenagrionidae, *Enallagma eribium*, *Coenagrion* sp., *Argia apicalis*, and *Ischnura verticalis*. The Anisoptera (dragonflies) have been tentatively identified to the following: Aeshnidae, *Boyeria vinosa* and *Aeshna canadensis*; and Gomphidae, *Gomphus exilis*. During the collection of these species from the pond, it was noted that odonate composition in the pond may be affected by the proximity of an adjacent drainage stream that may act as a refuge or species reservoir for those species that can exist equally well in both lentic and lotic habitats. Research is being considered to investigate this potentially unique relationship. (140)

Cortes, Christopher*, Mary Grace Murray*, Nathan Navarro, Elizabeth Walton, Edward Winter, and Aikaterini Skokotas Rosemont College, Rosemont, PA 19010. *Examination of UV sensitivity in haploid yeast cells and spores of Saccharomyces cerevisiae.* — Yeast spores are known to be resistant to many environmental factors including the mutagenic effects of UV light. This study compares the UV sensitivity of haploid cells and spores of *Saccharomyces cerevisiae*. Both cells and spores were exposed to UV radiation at different time intervals and their ability to survive following UV exposure was examined. Our results suggest that dityrosine present in the outer spore wall protects yeast spores from the mutagenic effects of UV light when contained within the ascus. However, treatment with glucuronase to release the spores from the ascus resulted in free spores that were highly sensitive to UV light. Only 1% survival was observed after a 20 sec UV exposure compared to 50% survival for spores that remained in the ascus. This suggests that the ascus provides protection by allowing some spores to hide from UV exposure. Lastly, UV exposure of the haploid strain produced similar survival rates as the spores contained in the ascus. (103)

Costenbader, Sydney*, and Daniel Proud Moravian College, Bethlehem, PA 18018. *All wrapped up: prehensility and the tarsal flexor system in the legs of harvestmen (Arachnida: Opiliones: Eupnoi).* — The order Opiliones, commonly known as “harvestmen” or “daddy long-legs,” is a diverse group of arachnids with more than 6,500 species. Like all arachnids, harvestmen have eight legs; each leg is divided into seven segments, separated by elastic tissues, and terminates in a claw. Harvestmen of the suborder Eupnoi possess a tarsus that is capable of prehensile movements. These abilities are attributed to the tarsal flexor system (TFS), which consists of two tendons that run the length of the tarsus and attach to the internal surface of the claw. We discovered a single intrinsic muscle located dorsally in the first tarsomere, which acts to extend the leg, that had not been previously reported for this group of harvestmen. “Pulleys” aid in keeping the inferior flexor tendon in place against the cuticle because there are no muscles associated with the inferior tendon that are intrinsic to the tarsus. The TFS mechanism harvestmen use to create such prehensile movements is a simplistic system compared to the human hand; however, the comparisons are

relevant and other arthropods utilize similar means of appendage locomotion. We sectioned numerous leg segments in cross and longitudinal sections and confirmed the presences of the tendons and pulleys in this lineage of harvestmen. Kinematics of the distal tarsus was observed by pulling on the inferior flexor tendon with a pair of forceps. While prehensility was not fully observed, the curling motion at the distal tarsus certainly supports the hypothesis that the TFS contributes to prehensility. Our understanding of the TFS may have important implications for the evolution of the arthropod leg, as well as in the development of advanced biomedical technology. (69)

Crowell, Allison*, and Holly Travis Indiana University of Pennsylvania, Indiana, PA 15705. *Fair weather friends: a comparison of invertebrates in vernal and forest pools.* — Natural vernal pools are an area of limited study. Vernal pools offer unique temporary freshwater habitats lacking access to running water. They form after periods of snow melt or rain fall in areas with water retaining substrate. Meanwhile, forest pools are permanent freshwater pools lacking access to running water. These communities could potentially be indicators of ecosystem health, but there is a lack of knowledge on biodiversity patterns between the differing pools. We hypothesize that biodiversity in vernal pools is higher than that of the forest pools. We counted and identified invertebrates found in leaf packs placed in five pools. The leaf packs were collected at different seasonal points to determine seasonal changes in the pool community structure. Two of the pools are forest pools and the other three are natural vernal pools. All five pools are located in forest settings. During collections, we performed a basic water chemistry test to see how the pool environment changed over the season. We found the vernal pools to have a higher species richness compared to forest pools, but not by much. In contrast, the forest pools had the higher overall abundance with a total of 2,037 organisms while the vernal pools had a total of 1,168 organisms. Fluctuations of populations and species richness were observed between collections. Overall, our findings suggest that aquatic life is thriving in both vernal and forest pools, and that seasonal productivity is potentially higher in forest pools. In the future, more leaf packs, water chemistry, and diatoms will be analyzed to assess biodiversity patterns and pool chemical patterns within and across sites. (146)

Cunningham, Moriah*, Schenatsar Dorvillier*, and Eric Ingersoll Penn State University-Abington, Abington, PA 19001. *Effect of 4-thiazolidinones on cancer cell proliferation in vitro.* — 4-thiazolidinones have been reported as potential drug-like molecules due to their possible anticancer and antiproliferative properties in cancer cell lines. The effects of different 1,3-thiazolidin-4-ones compounds on human cervical (HeLa) and gastrointestinal stromal tumor cell lines *in vitro* were observed. The compounds varied in substituent (F, Br, Cl) and placement (ortho, para). The cells were grown in culture and treated with 0-400 μ M concentrations for varying lengths of time. Cell growth was measured by absorbance and some of the compounds resulted in decreased cell proliferation. The most effective compounds showed a substantial inhibitory effect at concentrations as low as 40 μ M. The inhibitory effect occurred rapidly and little to no proliferation was observed after a 24 hr exposure to these compounds. Trypan blue staining indicated that, after 24 hr, the many floating cells in treated cultures were dead, as were many of the cells that were still adherent. Ortho and meta substitutions of bromine and chlorine were the most effective. These results suggest that there are possible implications of 4-thiazolidinones possessing anticancer properties and should be further evaluated for possible mechanisms and uses. (71)

Cusimano, Marissa*, and Anastasia Thévenin Moravian College, Bethlehem, PA 18018. *Do MAP Kinases (MAPKs) regulate tumor suppressive functions of Gap Junctions?.* — Vertebrate gap junctions (GJ), comprised of transmembrane connexin proteins (Cx), are important for mediating direct cell-to-cell communication. Cellular communication via Gap Junctions is key for many cellular processes, such as differentiation, cell growth and electrical activity in organs such as the heart. In addition, Cx43 Gap Junctions are known to interact with the oncogene Src in several types of cancer. Because Cx43 is phosphorylated by many different kinases, including ERK, we aim to understand if Cx43/Src interaction is driven by ERK. The goal of my specific experiments is two-fold: to test if phosphorylation on S279 and S282 by purified active ERK, plays a role in recruiting Src. The second goal is to generate mutants of Cx43 with both sites (S279 and S282) mutated to either alanines or glutamates, to prevent or mimic phosphorylations at these sites, respectively. Preliminary results from the *in vitro* phosphorylation experiments using purified active ERK and

Cx43 C-terminus indicate that active ERK is able to effectively phosphorylate Cx43. By comparing the ability of phosphomimetic Cx43 mutants to recruit Src versus actual, Erk- phosphorylated Cx43, I will be able to pinpoint if phosphorylation events at these sites are truly required to recruit Src. In addition, this research will move our laboratory forward in our design of Cx43-based Src inhibitors. (7)

Dammer, Magdalena*, Amelia Porter Bacon, and John Cigliano Cedar Crest College, Allentown, PA 18104. *Assessing the impact of climate change on the spring phenology of the native trees of Eastern Pennsylvania.* — In the past 4 decades of accelerated anthropogenic climate change, plant phenology has been increasingly used to predict ecological responses to global change, particularly temperature. Observational studies have estimated a 2.8-5.0 day per °C acceleration in plant phenology while experimental studies have predicted less dramatic change. However, plant species do not respond to global change, however, but rather to regional change because it has been found that the primary determinant of temperature sensitivity is at the level of the species and that sensitivity does not vary significantly within a species. We are interested in how climate change is affecting the phenology of seven species of trees native to eastern Pennsylvania present on the Cedar Crest College campus. Observational data on leafing, flowering, and fruiting were collected for the 2017 and 2018 growing seasons. Here we assess the results of these observations. This is the start of a long-term study on native plant phenology. We hope that this data will help to better understand the effects of climate change on North American hardwood forests. (175)

Darbenzio, Gabriella*, and Tammy Tintjer King's College, Wilkes-Barre, PA 18711. *Effects on Artemia salina (Brine Shrimp) When Feeding on Endophyte-Infected versus Non-Infected Grasses.* — The *Epichloë* fungal endophytes are known to produce the alkaloids, including ergot, indole-diterpenes, lolines, and peramine. Though independent of each other, all have been shown to reduce or eliminate herbivory by causing a bitter taste when eaten or causing death. With grasses grown for agricultural purposes this effect is beneficial when pest damage is reduced. It is also important to determine the effects of the alkaloids on livestock feeding on the endophyte-infected grasses. Material from four different grasses (species or cultivars), both endophyte-infected and non-infected, was made into a plant extract. That extract was then added to a multiwell test plates at varying concentrations with 10 brine shrimp per well for a brine shrimp assay. After 24 hours, the brine shrimp were counted for survival. The results showed the endophyte-infected plant extracts caused a greater reduction in brine shrimp survival than the non-infected plant extracts with the exception of one grass. Future work will consider using the assay to test different types of grasses with endophyte-infection and known alkaloid production. This could potentially reveal if the alkaloids have a confirmed effect on the brine shrimp survival as well as how the different combinations of alkaloids work together to reduce brine shrimp survival. The results from this and future studies could help to establish the brine shrimp assay as a first step in assessing the toxic effects on pest species and livestock caused by ingestion of endophyte-infected grasses. (188)

Darok, Matthew*, and John Harms Messiah College, Mechanicsburg, PA 17055. *Elucidating the role of gastrin signaling in the uniquely fibrotic pancreatic tumor microenvironment.* — Pancreatic cancer is currently the third most common cause of cancer-related death in the United States. This lethality is due, in part, to the fact that traditional treatment options are largely unsuccessful. It is hypothesized the highly and uniquely fibrotic nature of the pancreatic tumor microenvironment (TME) constricts blood flow and thereby inhibits chemotherapeutic delivery. The hormone gastrin is produced by pancreatic cancer cells and contributes to their proliferation; previous studies have also suggested it has a role in TME fibrosis. In two independent trials utilizing an orthotopic pancreatic cancer model, we determined that mice treated with a gastrin antagonist (proglumide) demonstrated a statistically significant inhibition of fibrosis in the TME. Studies are underway to determine if this inhibition will increase efficacy of gemcitabine in combination therapy. To further elucidate the cellular mechanism driving the elevated tumor fibrosis, we utilized an *in vitro* model to examine gastrin signaling in both human pancreatic cancer cells (PANC-1) and pancreatic stellate cells (PSC's; cells population potentially responsible for abundant collagen in the TME). Treatment with exogenous gastrin did not result in the elevation of collagen expression in either cell type; and similarly, gastrin antagonists (proglumide; YM 022) failed to suppress collagen expression. However, analysis revealed

PANC-1 cancer cells produce significantly more collagen than the stellate cells, suggesting they may contribute more to the generation of fibrotic tissue in the pancreatic TME than previously believed. (198)

DeLorenzo, LenaRose*, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *Sliding motility and biofilm formation in Mycobacterium smegmatis*. — Tuberculosis is responsible for the deaths of millions worldwide and multi-drug resistance tuberculosis remains a major public health crisis. As a result, it is critical to gain a better understanding of *Mycobacterium tuberculosis*, the bacteria responsible for tuberculosis infection. Therefore, *Mycobacterium smegmatis* is being studied as it is closely related to *M. tuberculosis*. Biofilms, bacterial communities that adhere to one another on liquid or solid surfaces, pose a challenge in treating tuberculosis infections. Biofilms act as a protective coating against disinfectants and medications. Presently, the exact regulatory processes surrounding how mycobacteria form biofilms remains unknown. In order to understand the regulatory processes in biofilm formation, sliding motility is examined because both mechanisms rely on the presence of extracellular glycopeptidolipids. Sliding motility is the sliding of a monolayer of bacteria across a surface. If regulatory processes for sliding motility are better understood, then regulatory processes for biofilm formation will be better understood. Additionally, sliding motility is an unusual phenotype for bacteria and this work will contribute further insights into the regulation of this process. Since previous work has shown that lysine acetylation impacts biofilm formation, we hypothesized that sliding motility may be similarly regulated. (91)

Dix, Tyler*, and Jennifer Elick Susquehanna University, Selinsgrove, PA 17870. *Paleoecological analysis of shell beds from the Trimmers Rock Formation (Upper Devonian-Frasnian) along the Juanita Parkway outside of Newport PA*. — Shell beds from the Trimmers Rock Formation (Upper Devonian) provide evidence of local differences in community diversity. Shell beds from 2 locations, separated by 6km (Newport, PA), were compared to determine the controls acting on deposition of a muddy prograding ramp. These shell beds are comprised of fossils that may have been strongly influenced by high energy storm events, hypopycnal flows, and turbidity currents. The shell beds at these two locations are time equivalent, and may have been deposited by the same regional events, however they are laterally discontinuous and non-correlative. At both locations, the succession consists of reddish-gray sandstone dominated by ball and pillow structures that is underlain by greenish-gray beds of shale and shaly sandstone with intermittent shell beds. These rocks also contain small ripples with a current direction to the northwest. This study focused on 8 thin sections collected along the Juniata Parkway; the number of organisms were counted per unit cm². Some thin sections contained an abundance of loosely packed but abundant brachiopods and crinoids. In other thin sections, bryozoans were more common, with fewer crinoids. A nearby study of similar beds contained a greater abundance of highly packed bryozoans and crinoids with fewer brachiopods. The sedimentology and proximity of the two locations studied suggests that this region in the Upper Devonian, was a shallow, prograding muddy ramp that experienced similar deposition from high energy events. The communities in this environment were dominated by suspension feeders. Some of the communities in this study are similar those described as representing distal ramp from a nearby location. However, the abundance of brachiopods in samples from this study suggests different environmental factors may have influenced this part of the ramp. (162)

Dobrowski, Jennifer M.*, Brianna L. Marrero*, Victoria A. Attinger*, and Audrey J. Ettinger Cedar Crest College, Allentown, PA 18104. *Body coloration and aggressive behavior in young Rocio octofasciata cichlid fish*. — Animal models are often observed in order to study complex behaviors. Cichlid fish provide a useful model system because they can live in a controlled laboratory tank, but they have complex, observable social behaviors, making them simple enough to be studied yet complex enough to give results applicable to other animal systems. One of the hallmarks of cichlid fish species is that their body color changes in response to changes in social status, aggression and fear. *Rocio octofasciata*, the species of cichlids studied here, display three distinct coloration patterns in younger fish including light, medium, or dark background body color and the presence or absence of dark stripes and fluorescent spots. Here, we examined the correlations between coloration and development of aggressive behaviors in *Rocio octofasciata*. This study collected data from two tanks containing separate broods of young fish, located in the same space and maintained at the same temperature and feeding times. The fish have been observed for 20 minute periods

over the course of five months with focal observations of coloration taken every five minutes and non-schooling behaviors recorded continuously. During this period, we have observed both frequent daily changes in body coloration in the fish, and the development of fluorescent spots. Occurrences of aggressive behaviors were noted and compared to the coloration in both age groups. We observed a higher frequency of aggressive behaviors in fish with light colored body color and fluorescent spots, when compared to the darker and medium body color fish. Future experiments will continue to examine the distribution of and changes in coloration patterns within each age group, as well as the impact of a parental presence and induced stress on coloration in *Rocio octofasciata*. Together, these studies will help clarify the relationship between coloration and social status, aggression, and fear. (49)

Dougherty, Ryan*, Megan Rothenberger, and Emily Lynch Lafayette College, Easton, PA 18042.

Terrestrial salamanders as bioindicators of environmental change related to forest fragmentation in Jacobsburg State Park. — Bioindicator species are used by conservation biologists to screen the overall health of an ecosystem, and they can be especially useful when conservation decisions need to be made quickly and with limited resources. Due to their relative abundance in forest habitats, sensitivity to environmental disturbance, and mid-level position in the food web, plethodontid salamanders are considered good indicators of biodiversity and ecosystem integrity in temperate forests. If this can be confirmed on a local scale, plethodontids can be used to inform small scale land use and local park management. Therefore, the objective of this study was to compare abundance and distribution of plethodontid salamanders at two forested sites within Jacobsburg State Park with differing levels of habitat fragmentation and to evaluate the sensitivity of plethodontids to microhabitat changes related to forest fragmentation. Using the artificial cover object (ACO) method, salamander abundance was measured at increasing distances from a road in the fragmented site and a walking path in the isolated site. Salamander abundance was found to be significantly higher in the isolated site, and uniformly distributed under ACOs at all distances from the path. In the fragmented site, however, there were significantly more salamanders found at greater distances from the road, indicating a significant relationship between salamander abundance and road proximity. Salamander abundance was found to be significantly positively related to pH and negatively related to leaf litter depth. Due to their abundance and sensitivities to habitat fragmentation and certain environmental characteristics, the red-backed salamander could be an ideal bioindicator of forest habitat fragmentation in Jacobsburg State Park. (58)

Duckhorn, Julia*, and Troy Shirangi Villanova University, Villanova, PA 19085. *Connecting genes, neurons, and behavior: how the dissatisfaction nuclear receptor regulates Drosophila courtship behavior.* — How genes build the neural circuits that underlie innate animal behaviors is poorly understood. During courtship, *Drosophila* males court females with a series of elaborate innate behaviors, whereas females decide whether or not to mate. Mutations in the Dissatisfaction gene, which encodes a developmental nuclear receptor, cause sex-specific courtship abnormalities in both sexes. To understand how Dsf influences the neural circuits that underlie courtship, we sought to identify the neurons that express Dsf in the fly brain that contribute to courtship. Here, we find that Dsf is expressed in several subsets of neurons in the fly nervous system of both sexes. We identify a small subset (i.e., 3+) of Dsf-expressing neurons in the fly's abdominal nervous system that contribute to most behaviors that are altered in Dsf mutant males and females. Loss of Dsf function causes sex-specific anatomical phenotypes in these neurons, suggesting that Dsf regulates neuronal development and courtship behavior by functioning with the sex determination pathway in flies. This work provides insights into how a developmental gene patterns the circuits for an innate animal behavior. (46)

Dudek, Daniel*, and Josiah Townsend Indiana University of Pennsylvania, Indiana, PA 15705. *Patterns of matrilineal evolution of neotropical leopard frogs (Ranidae: Rana: Pantherana).* — Leopard frogs (Ranidae; subgenus *Pantherana*) are among the most ubiquitous and recognizable amphibians in North and Central America. Shockingly, this group has been a source of taxonomic confusion and controversy for decades. Once thought to represent a single widespread species ranging from Canada to Panama, since the 1970's *Pantherana* have been revised to include no fewer than 28 named species. The historic lack of accurate classification is still apparent in *Pantherana* populations from Central America and extends to even

the most widespread putative species. An outstanding example involves populations from the Pacific Coast, for which the name *Rana forreri* has been incorrectly applied to leopard frogs in Mexico, Guatemala, El Salvador, Honduras, Nicaragua, and Costa Rica. To resolve the genetic relationships and taxonomic status of these populations, we analyzed 50 samples of lowland and insular leopard frogs, including 14 samples from Pacific Coast populations in Guatemala, Honduras, Nicaragua, and Costa Rica, using the mtDNA loci 12S, 16S, and cytB. Maximum likelihood and Bayesian phylogenetic results strongly support the relationship between all coastal populations from Guatemala south through Costa Rica represent a single unnamed species. Surprisingly, four samples thought to represent *R. miadis*, a species considered endemic to the Little Corn Island off the Caribbean coast of Nicaragua, appear to be conspecific with Pacific Coast populations, despite the presence of another species, *R. taylori*, in the Atlantic lowlands of Nicaragua, suggesting a potentially valid taxon that could be applied to Pacific Coast populations. Time divergence estimation, patterns of diversification, and historical biogeography are discussed. (81)

Eytcheson, Morgan*, and Holly Travis Indiana University of Pennsylvania, Indiana, PA 15705. *Ephemeral Life: A Comparison of Invertebrates Found in Several Types of Pools*. — Vernal pools are temporary freshwater habitats that form after rainfall. Due to their ephemeral nature, they may harbor unique animals that do not otherwise thrive in permanent bodies of water. These biological communities have the potential to inform about ecosystem health, yet little is known about biodiversity patterns across pool types. We test the hypothesis that vernal pools have higher biodiversity than more permanent forest pools, and that both have more biodiversity than abandoned mine pools. We counted and identified invertebrates found in leaf packs placed in six pools: three vernal pools, two forest pools, and a small, slow-moving flow of abandoned mine drainage (n=3 leaf packs per pool, per collection date). Bags from each pool were collected once every 2-4 months at different seasonal points to determine temporal changes in community structure. All pools were in forest settings and without fish. We found that ephemeral pools had the highest species richness with 15 species, compared to 15 in forest pools and only 4 species in the AMD pool. Forest pools had the highest overall abundance with 2,037 total organisms found, compared to 1,168 in the vernal pools and 6 in the AMD pool. Some populations fluctuated dramatically between seasons; for example, Chironomidae midges in one of the forest pools increased from 74 to 1,093 individuals between the first and second collection dates. Species richness also differed between collection dates, with 14 families found in the first collection of all pools but only 9 in the second. Our findings suggest that both vernal and forest pools are well used by aquatic life, and that forest pools may be more productive seasonally. Additional leaf packs will be analyzed to assess biodiversity patterns within and across sites over the next few years. (147)

Fairfield, Meagan*, and Christine Proctor Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Assessing eastern oyster, Crassostrea virginica, restoration success in the Chesapeake Bay using spectral classifications*. — *Crassostrea virginica*, the eastern oyster, is an important aquatic filter feeder. A two-inch oyster can filter approximately 50 gallons of water a day while an acre of oyster beds can filter out 543 pounds of nitrogen per year. Over-harvesting of the eastern oyster combined with increased pollution, in 2017 the Chesapeake Bay received a C grade for overall health with little to no improvements from previous years. Oyster bed restoration is one method to combat estuarine pollution. Once completed, restoration projects require continually monitoring of health and growth. This process typically involves an immense amount of man power, time and money to execute and monitor the restoration site. I hypothesized that using remotely obtained imagery to measure oyster bed growth would be a more economical and efficient approach. Using Landsat 8 imagery, a spectral signature was created for the following landcover types: oyster beds, shallow water, deep water, developed land, undeveloped land, and wetlands. Scatter plots of the spectral signatures revealed that the appropriate bands to use for classification of oyster beds were within the blue, green, and near-infrared spectrums. Using those bands, I completed a supervised classification to identify all oyster beds within the Choptank River. However, it was determined that the resolution of the satellite imagery was too coarse to pick up the smaller beds. In conclusion, this technique has potential to efficiently measure oyster bed growth if completed with higher resolution near-infrared imagery. (163)

Fairfield, Meagan*, and Christine Proctor Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The use of road kill surveys to predicting road mortality hotspots in northeastern North Carolina.* — There is perhaps no other human impact as transportation infrastructure whose far-reaching, cumulative effects on wildlife are so destructive and demanding of attention, yet so commonly underestimated. Vehicular collisions have now surpassed hunting as the leading direct human cause of vertebrate mortality on land. While the number of common species killed along roads is staggering, the population effects can be devastating for small and declining populations. In response, many local, state, and federal agencies are incorporating mitigating structures into highway design to reduce the occurrence of wildlife-vehicle collision. Past studies have found that road kill locations along roadways act as reliable indicators of wildlife crossing areas. We conducted road kill surveys along a 19 km stretch of HWY 64 running through the northern portion of Alligator River National Wildlife Refuge in Dare County, North Carolina. Road killed animals were collected and identified by walking along both sides of the highway every 7 – 10 days during summer months (April – August) and every 14 days in all other months (September – March) from March 2009 to March 2011. Every vertebrate animal mortality was identified to as precise a taxonomic level as possible. We also recorded UTM coordinates, date, sex, age, and location on roadway (e.g. road or shoulder). All road kills were either removed from the search area or marked with paint to avoid double counts in subsequent surveys. Additionally, we opportunistically collected data on medium and large-sized mammal road kills, as they did not persist between surveys. Road kill events for each species were tallied per 0.16 km segment along the highway. Habitat variables and proximity to canal crossings were extracted for each 0.16 km highway segment using land cover data. Negative binomial generalized additive models were used to determine which variables best explained where road kills occurred along the highway. The most parsimonious model included taxonomic group, month, and sex as predictor variables. When broken down by taxonomic group, month and sex best explained the location of reptile road kills, month and habitat best explained the location of both amphibian and avian road kills, while habitat and distance to a canal crossing best explained the location of mammal road kills. These results can be used to guide the placement of mitigating structures and identify landscape features that will increase the success of such structures. In addition, the results from this study can inform future mitigation projects. (125)

Farrell, Keegan*, Monique Barrese*, and Lisa Antoniaci Marywood University, Scranton, PA 18509. *Identification of a Physical Interaction between Yeast Proteins Htz1, Cdc5, and Rad24.* — Yeast proteins Htz1, Cdc5, and Rad24 all interact with the nuclear envelope protein Mps3. Mps3 is a nuclear envelope protein that is involved in DNA damage repair, sister chromatid cohesion, and telomere clustering. Mps3 functions in several chromatin related processes and interacts with many chromatin associated proteins. The objective of this study was to determine if these proteins (Htz1, Cdc5, and Rad24) that interact with Mps3 are also physically interacting with each other. Htz1 is a histone protein that is involved in transcriptional regulation of RNA polymerase II by preventing the spread of silent heterochromatin to block gene expression. Cdc5 is a polo-like kinase that has several functions including adaptation to DNA damage during meiosis as well as mitotic regulation of the nucleus and nuclear envelope. RAD24 is part of the Replication Factor C complexes and is important for DNA damage checkpoints. protein. Using Co-Immunoprecipitation and Western Blotting techniques physical interactions between these proteins is being investigated. (104)

Fehn, Michaela*, Amber Grohowski, Cassidy Heid, Kellie Kalada*, Kabita Kandel, Michael Kovalick, and Kenneth Klemow* Wilkes University, Wilkes-Barre, PA 18766. *Assessing success of a Forest Reclamation Approach in a northeastern Pennsylvania anthracite mine site – A baseline assessment.* — Recent approaches to mine reclamation involve hand-planting native trees to quickly produce a forest, in comparison to older approaches that produce meadows of grasses and legumes. Such Forest Reclamation Approaches (FRA) have been successful in the central and southern Appalachians, but have not been widely attempted in the northern Appalachians – particularly Pennsylvania. An FRA was initiated at the Avondale site of northern Luzerne County in northeastern Pennsylvania in April 2017. Several thousand tree seedlings of white pine (*Pinus strobus*), trembling aspen (*Populus tremula*), white oak (*Quercus alba*), red oak (*Q. rubra*), chestnut oak (*Q. prinus*), and hybrid chestnut (*Castanea x dentata*) were planted within a 15 acre area.

Subsequent survival and growth of those seedlings were assessed in forty eight 10 x 10 m plots in May-June 2018. White pine was the most abundant species, followed by poplar. Red oak and white oak were less abundant. Survival rates of all of the planted species exceeded 90%, and did not differ based on microtopographic position. Sources of mortality included deer browse and failure to establish in the site. Early successional woody species such as staghorn sumac (*Rhus typhina*) were noted in approximately 30% of the plots. This study serves as a baseline, and will be continued into future years, and will include assessment of stem height growth and root crown expansion. (178)

Fetchen, Miranda*, Miriam Cooperband, and Allison Cornell Cedar Crest College, Allentown, PA 18104. *Dietary habits of the spotted lanternfly Lycorma delicatula*. — The spotted lanternfly (*Lycorma delicatula*) is a recently invasive pest in the United States that poses great risks to the ecosystem and crops. The spotted lanternfly goes through distinct developmental stages, molting between each stage: Instar 1, Instar 2, Instar 3, Instar 4, Adult. Little is known about how this insect behaves in its new environment. Previous studies have shown that the spotted lanternfly feeds on over 70 species of trees in its new habitat, including species native to North America and invasive species from the same range of China. Its preferences for native trees compared to Asian trees is unknown. The objectives of this study were to A.) document preference, if any, for a native tree (black walnut) or an invasive tree (tree of heaven), B.) observe how the dietary habits of the spotted lanternfly change across its five developmental stages. We set up five greenhouses on Cedar Crest College campus containing one tree of heaven, one black walnut, and 15 spotted lanternflies each. We observed which trees the spotted lanternflies were feeding from twice a week from the first instar to adulthood. We found significant shifts in their preference for feeding on invasive compared to native trees later stages in their development. (64)

Fox, Cassandra*, Daniel Ressler, and Jonathan Niles Susquehanna University, Selinsgrove, PA 17870. *Data resolution and scale of land use data alter the ability to predict the benefits of riparian buffers on fish populations*. — Forested riparian buffers are a best management practice used in stream restoration projects because after some time, they will provide shade to the stream water, bind soil under tree roots, and trap sediment and nutrients moving in from nearby landscapes. Land use datasets are being used to prioritize stream segments for stream restoration based on the existing abundance of forest cover around a stream bank. The U.S. Geological Survey Land Use data is a 30-m resolution dataset that covers the nation, but higher resolution data are becoming available like the Chesapeake Conservancy's 1-m data for the Chesapeake Bay Watershed. The objective of this study is to use these data sources to predict fish populations in small streams by building regression relationships from sites that have had fish population surveys which are undergoing or have undergone stream restoration. Streams across a wide range of land uses and water quality impairments have been selected at 27 sites within Northumberland, Montour, Center, Snyder and Union Counties (PA). Each site has been characterized by electro-fishing 100-m reaches as well as sampling sediments from the stream bottom in each reach. Stream corridors are constructed by creating an 11-m, 100-m, and 500-m buffer from the stream center-line that extends 1000-m upstream from the electrofishing origin point. Multivariate statistical analyses were conducted in R. From the correlations found, the width of the corridor and the resolution strongly influences the ability to predict fish populations. The Chesapeake Conservancy 500 meter corridors showed the best correlations between the 4 different fish variables (all fish, trout per 100m², fish per 100m² and lithophillic per 100m²). All of these variables showed the best relationships with either forested or suburban surrounding landscapes, so it can be concluded that using a wide range of surrounding land use to predict fish populations is conceivable. (157)

Froess, Joshua*, and Amy Danowitz Mercyhurst University, Erie, PA 16546. *Synthesis of isoxazolines to inhibit the quorum sensing pathway in Vibrio fischeri*. — Antibacterial resistance is becoming a large, global, public health issue. With this, new strategies are being researched into fighting this problem that is encumbering the world today. The inhibition of quorum sensing is one of these strategies. Quorum sensing is the ability for bacteria to express certain behaviors based on their population density. The bacteria undergo this process by using small molecules called acyl homoserine lactones (AHL) to communicate with each other. This research is attempting to inhibit quorum sensing through the synthesis of different molecules called isoxazolines. These molecules are being used to inhibit this process because they have a

similar structure to AHL. The isoxazoles that are being used are synthesized with different R groups on the 4-prime position of the benzene ring. They are also being modified by increasing the number of hydroxyl groups on the molecule to increase their solubility in aqueous media. This group of molecules is being focused on due to previous research which indicated that this type of functionality leads to isoxazoles that are more successful at inhibiting quorum sensing. These molecules are designed to specifically inhibit the quorum sensing process in *Vibrio fischeri*. *V. fischeri* are used because they are non-pathogenic, and their bioluminescence is under the control of their quorum sensing pathway. This provides a clear read-out for monitoring quorum sensing inhibition. Additionally, the LuxIR system in *V. fischeri* is a common pathway in many bacteria, including bacteria that are harmful to human health. (22)

Fuanta, René* East Stroudsburg University, East Stroudsburg, PA 18301. *A potential application of intrinsic fluorescence towards the evaluation of inhibitors.* — *Mycobacterium tuberculosis* (*M.tb*) is an acid fast bacillus, causative agent of tuberculosis which is the world's leading cause of death in people coinfecting with HIV. *Mycobacterium tuberculosis* shikimate kinase (*MtSK*) is a bisubstrate enzyme, catalyzing the conversion of shikimic acid and ATP to shikimate-3-phosphate and ADP respectively. On the basis of selective toxicity, *MtSK* stands as a potential target for new antimycobacterial chemotherapeutic agents that would interfere with the shikimate binding domain, but with little or no effect on the ATP binding domain. Across an array of various sources of SK, *MtSK* is peculiar as one with no tryptophan residues. Thus, the insertion of tryptophan moiety via site-directed mutagenesis would elucidate substrate and inhibitor kinetics with spectrofluorimetric techniques. Tryptophan was introduced at target sites on the enzyme-LID domain (V116W), extended substrate binding domain (E54W) and nucleotide binding domain (N151W). The molecular masses of all proteins were confirmed using ESI-MS and their secondary structure evaluated by circular dichroism (which was quite similar for all proteins). These variants have activity (ATP and Shikimate-dependent) comparable to the wild-type and their tryptophan emission spectra confirms that they are tryptophan bearing. Upon evaluation of dissociation constants (K_d) using fluorescence quenching, they seem to be a reflection of their K_m , but N151W had no K_d with respect to shikimate. We have also evaluated the use of tryptophan as a reporter for inhibitor binding with the use of an inhibitor (compound 1) to ATP and Shikimic acid and found no quantifiable change in fluorescence emission, supporting the fact that the compound is a non-competitive inhibitor. Further kinetic characterization of these inhibitors is ongoing. (197)

Gallo, Michael*, Janessa Gerhart, Anthony Varshavskiy, Damien Thévenin, and Anastasia

Thévenin Moravian College, Bethlehem, PA 18018. *Antiproliferative effects of gap junction protein delivery to glioma cells utilizing a cancer targeting peptide.* — Connexin43 (Cx43) is a transmembrane protein that assembles to form gap junction (GJ) channels which are critical to intercellular communication processes. The carboxy terminus of Cx43 (Cx43CT) is known to interact with c-Src, a non-receptor tyrosine kinase, that plays a role in the regulation of cell proliferation. Src has a high degree of activity in gliomas and is known to be oncogenic in these tumors. Interestingly, glioma cells have a characteristic reduction in expression of Cx43 and previous research by others demonstrated that reintroduction of Cx43 carries antiproliferative effects; Cx43 proteins reintroduced into these cells lead to Src recruitment to Cx43CT, accompanied by the inhibition of Src's oncogenic activity. There are a number of phosphorylation sites along the Cx43CT within or near the Src-binding region, leading us to hypothesize that they likely play a role in controlling the process of Src recruitment. In our design of Cx43-based cancer therapeutics, we aim to identify the phosphorylation state of Cx43 that best recruits and inhibits Src. Two phosphorylation sites in particular (S279 & S282), lie directly in the Src-binding region. Phosphomimetic constructs were created to mimic dual-phosphorylated, and dual-unphosphorylated states of Cx43CT to explore the impact of 279/282 phosphorylation/dephosphorylation on Src binding. We are working on the design of tumor-targeting peptide-Cx43 conjugates that will selectively deliver the Cx43CT to glioma cells. pHLP (pH-Low Insertion Peptide) is a cell-penetrating peptide with a high degree of specificity for the acidic tumor microenvironment, that will insert into the cell membrane at a lower pH. By linking the Cx43CT to pHLP, we have selectively reintroduced Cx43 to the cytoplasm of cancerous cells, localizing it near the cell membrane. Preliminary results demonstrate that pHLP-Cx43 peptide causes cytotoxicity in rat glioma cells in a phosphorylation-dependent manner. (6)

Gasparovic, Nathaniel*, Ronald Brown, and Amy Danowitz Mercyhurst University, Erie, PA 16546. *A combined quantum mechanics/molecular mechanics approach to calculating protein-ligand interactions.* — This research is an investigation into potential ligands as effective inhibitors for the quorum sensing mechanism of bacteria. The overarching goal is the development of an alternative to antibiotics by disabling the virulence capabilities of bacteria through inhibiting their quorum sensing properties. This has the potential to lead to a way to combat bacteria without breeding resistance within the bacteria in the way a traditional antibiotic would. In order to test the effectiveness of the ligands, they are being investigated using a combined quantum mechanical/molecular mechanical (QM/MM) computational approach with the Gaussian09 software program. The binding energies of a series of ligands to the LasR structure will be found as a function of ligand structure and the level of computational treatment of the surrounding binding site. The B3LYP/6-31G (d,p) quantum mechanical (QM) level was used to treat the ligand and the most significant amino acids in the protein-ligand interactions, while the UFF molecular mechanics level was used for the bulk of the protein. (128)

Gerasimidis, Kyriaki*, Rya Scull, Jessica Azzarano, Jessica Baranoski, Lavinia Harrison, Megan Wojick, Sonia Spadafora, Olivia Mancini, Epoh Fonge, and Melinda Harrison Cabrini University, Radnor, PA 19087. *Discovery and Annotation of Cluster AN Arthrobacter Phages.* — Bacteriophages are viruses that infect a bacteria host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. We have discovered novel phages from the bacterial host *Arthrobacter* sp. ATCC 21022. The phages were collected from soil and water samples by students from various places around South Eastern PA and Southern NJ. and their genomic DNA isolated. After isolating the genomic DNA, they were photographed through the use of an electron microscope and then the DNA was sequenced. The Phages genomes were then annotated using various bioinformatics tools, such as DNA Master; Phamerator; HHpred and GeneMark to determine gene location and function. Using comparative genomics, unique characteristics of the phage's genome were also explored. This study presents a comparison of several bacteriophage genomes that were isolated from this research: Stull; MLou; Lady Griffin; Pontos; Scuttle; Teensy; Dearnley; MMW; Juliage. The genomes of these phages were annotated as a collaborative effort by many students and faculty. (89)

Gilbert, Katelynn*, Deborah Austin, Rachael Picard, and M.Dana Harriger Wilson College, Chambersburg, PA 17201. *Short-term characterization of a biofilm in a free-flowing freshwater creek in south-central Pennsylvania.* — Previous research has been conducted on the relationship between bacteria and algae within lakes, and demonstrated a positive correlation between bacterial growth and algae mats as a type of biofilm. Biofilms are heterogeneous mixtures of microorganisms such as bacteria and algae that are held together by Extracellular Polymeric Substance (EPS). A free flowing, freshwater system is a unique environment in comparison to a stagnant system. Many environmental factors can impact the aquatic system as it proceeds downstream from the headwaters. This then affects biofilm growth within the system to varying degrees. The purpose of this study was to characterize populations of microorganisms within a biofilm collected from a creek, and determine how the growth of those organisms was affected over time and with temperature changes. Five sample sites were used along the Conococheague creek in south-central Pennsylvania, beginning 11.9km from the headwaters and ending 29.6km downstream from the headwaters. The factors examined in this experiment included ambient air and water temperature, Gram positive and negative bacteria, and photosynthetic autotrophs within the biofilm. Sampling was performed at each site on three days over a two week period in November 2018. Three sub-samples of biofilm were collected at each site, one from each edge of the creek and from the middle. Data indicates that a common genus of algae between the five sites was *Closterium*, while points further downstream had genera of cyanobacteria that were not as prevalent in the headwaters, such as *Lyngbya*. Initial analysis indicates that over the course of the study, photosynthetic organism populations were more greatly affected by temperature than bacterial populations. Statistical analysis is ongoing to determine whether there is significance between or trends evident among experimental parameters. (142)

Godfrey, Elizabeth*, Emily Esquea*, Ashna Goyal*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Factors which influence chromosome loss in Saccharomyces cerevisiae.* — Genomic

instability is linked to the development of cancers in humans. This instability can result from a variety of factors, including aneuploidy caused by nondisjunction events. *Saccharomyces cerevisiae* is an effective model organism for the study of cancer in due to its homology to the genetic structure of human chromosomes. Our laboratory studies factors which influence the loss of a single chromosome in *S. cerevisiae*. We employ an *ADE3/8* color assay in a haploid disomic *S. cerevisiae* strain which contains an additional copy of Chromosome VII. We have previously shown that caloric restriction and constitutive telomerase activity affect the incidence of chromosome loss in this strain. Ascorbic acid, commonly referred to as vitamin C, is correlated with a decrease in cancer incidence in both animal and human models of cancer. Our preliminary data from this study suggest that ascorbic acid does not impose a significant effect on chromosomal loss in *S. cerevisiae*. (110)

Grams, Nicholas*, and Manuel Ospina-Giraldo Lafayette College, Easton, PA 18042. *Structural characterization of Phytophthora sojae carbohydrate esterase family 10 genes and comparative analysis of their expression during infection of Glycine max*. — *Phytophthora sojae* is an oomycete pathogen that causes the disease known as root, stem, and leaf rot in soybean plants, frequently leading to massive economic losses. Despite its importance as a plant pathogen, the mechanism by which *P. sojae* penetrates the host is not yet fully understood. Evidence indicates that *Phytophthora* is not capable of penetrating the plant cell wall solely through mechanical force, suggesting that alternative factors facilitate breakdown of the host cell wall, in addition to degrading the host cell membrane. Members of the carbohydrate esterase (CE) enzyme superfamily, which include carboxylesterases and lipid-degrading sterol as well as acetylcholine esterases (collectively known as CE Family 10), have been suggested to be important for this penetration process. This study aims to explore the role of *P. sojae* CE Family 10 genes in soybean cell wall and cell membrane degradation by looking at their relative transcriptional activity during soybean infection. The newly revised version of the *P. sojae* genome was searched for the presence of putative CE Family 10 genes and conducted an extensive sequence analysis of all gene models found. In addition, we have quantified the relative expression of each gene during infection of susceptible (Williams) and resistant (Williams 82) soybean cultivars over a 48-hour time period. Total RNA from inoculated tissue was extracted at several time points after inoculation and subjected to quantitative PCR analysis for CE Family 10 gene expression. Results suggest that CE Family 10 genes are important for both the biotrophic and necrotrophic stages of the *P. sojae* infection process and provide molecular evidence for stage distinction during infection progression. Furthermore, bioinformatic analyses have identified several conserved gene and protein sequence features that appear to have a significant impact on observed levels of expression during infection. These results also agree with previous reports implicating other carbohydrate-active enzymes in *P. sojae* infection. (9)

Greco, Graziella*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *Tethered telomerase inhibits trinucleotide repeat expansions in Saccharomyces cerevisiae*. — Telomerase is a specialized reverse transcriptase that lengthens telomeres in the eukaryotic model organism *Saccharomyces cerevisiae*. In wild-type cells, the catalytic component of telomerase associates with the telomeres in a cell-cycle regulated manner; critically short telomeres are preferentially lengthened during late S-phase. Tethering telomerase to the telomere has been shown to increase genome instability and marker gene mutation rates. We have examined the impact of tethering telomerase on the number of trinucleotide repeat (TNR) expansions in *Saccharomyces cerevisiae*. Our results indicate that tethering telomerase to the telomeres by transforming TNR tract-containing yeast with a plasmid bearing a CDC13-EST2 fusion has the unexpected effect of decreasing the number of TNR expansions. These results may indicate a novel relationship between the maintenance of telomeres and the replication of trinucleotide repeat tracts. (112)

Greco, Graziella*, Brad Evert*, Francis Mayville, and Joshua Slee DeSales University, Center Valley, PA 18034. *Wine your way to good health: anti-inflammatory effects of resveratrol*. — Resveratrol, an antioxidant found in red wine and grapes, is thought to possess anti-inflammatory properties in relation to cardiovascular disease, and may have beneficial effects on incisional wound healing and the body's response to implantable devices. Liquid-liquid extraction of resveratrol from red wine was performed, and used to study its anti-inflammatory effects *in vitro*. After culturing Bovine Aortic Endothelial cells (BAOECs) in

resveratrol to ensure there was no adverse effect on normal cell growth and morphology, it was concluded that there was no effect due to resveratrol addition. An established way to model inflammation in BAOECs is by using Tumor Necrosis Factor- α (TNF- α), which induces a large accumulation of actin stress fibers. Our data suggest that resveratrol pretreatment reduces the amount of actin stress fiber accumulation, caused by TNF- α , thus exhibiting anti-inflammatory properties. A large amount of inflammation in the cardiovascular system is caused by a wound to the endothelial layer. A wound healing assay was conducted to determine the wound healing properties of resveratrol. Resveratrol was shown to dramatically aid in the wound healing process, compared to an untreated control. Furthermore, the immune response of the body to implantable devices was investigated using a THP-1 cell adhesion assay to polyurethane, a common biomaterial used in medicine. When a foreign material is introduced into the body, an immune response is stimulated, and monocyte-derived macrophages stick to the biomaterial, hindering its function. THP-1 cells are a good *in vitro* model of the monocyte-derived macrophages found in the immune system. THP-1 cell attachment to the polyurethane was significantly reduced in the presence of resveratrol. These data indicate that resveratrol possesses promising anti-inflammatory qualities that may prove to be useful in the prevention of cardiovascular disease, improving wound healing, and decreasing biomaterial rejection. (130)

Greco, Graziella*, William Stollsteimer*, and Lara Goudsouzian DeSales University, Center Valley, PA 18034. *The effects of the antioxidants resveratrol and glutathione on growth of a mitochondrial mutant strain of Saccharomyces cerevisiae.* — As mitochondrial genes have been well conserved from *Saccharomyces cerevisiae* humans, yeast is an appropriate model for human mitochondrial diseases. Mitochondrial diseases are often associated with deficiencies in ATP synthase. ATP synthase is an enzyme that catalyzes the final steps of mitochondrial ATP synthesis. Point mutations at the *ATP6* gene which cause a decrease in the formation of ATP synthase complexes are responsible for most human mitochondrial diseases, such as Leigh syndrome. Our strain contains a deletion mutation of the nuclear *FMC1* gene, which causes yeast grown at high temperature to possess far fewer ATP synthase complexes in the mitochondria than are found in a corresponding wild-type strain. Thus the *fmc1 Δ* mutant mimics the mechanism of human mitochondrial disease. Reactive oxygen species are a significant cause of mitochondrial and nuclear DNA damage. Antioxidants stabilize free oxygen radicals and for this reason they of interest in the analysis of mitochondrial mutant yeast strains. We examined if there was any change in the growth patterns shown at high temperatures in the mitochondrial mutant due to the presence of two different antioxidants, resveratrol and glutathione. (111)

Groce, Zachary*, and Ahmed Lachhab Susquehanna University, Selinsgrove, PA 17870. *Using ground penetrating radar to search agriculture fields for unmarked graves in Beaver Springs, Pennsylvania.* — Ground penetrating radar is a common instrument when searching for methods of non-invasive exploration of the sub-surface. In the case of searching for unmarked graves, taking the appropriate steps can lead to satisfying results. Uncertainty may occur when analyzing the ground for historic graves or burial sites exceeding 50 years. These studies require proper methodological planning, a thorough examination of the soil characteristics, and historic research. Using 50cm transects, a wheat field was analyzed that may have unmarked graves dating back to the 1810's in Beaver Springs, Pennsylvania. While no obvious graves were discovered, areas of interest were discovered and handed over to the Snyder County Historical Society for further examination. These areas of interest are compared to another site from Selinsgrove, Pennsylvania with marked graves from the mid-1900's and early 2000's. A study of this sort benefits local communities by providing details about the burial locations of ancestors. As an expanding technological field, ground penetrating radar is an important tool moving forward in engineering, archaeology, and scientific research. Using this instrument and expanding on previous research can help new ground penetrating radar discovery methods develop and assist in reducing errors and complications. (168)

Guest, Rachel*, Kathryn Yomes, Anthony Hoffman, and Christopher Taylor Mercyhurst University, Erie, PA 16546. *Recent developments towards generating imine nucleophiles.* — Substituted amines and imines are key functional groups used in a variety of applications, such as drug discovery and 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 act as strong

nucleophiles. These reactions would be useful since they form complex amines that could be used as tools in 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. (34)

Hacker, Charlotte*, Dr. Shafqat Hussain, Ghulam Muhammad, and Dr. Jan Janecka Duquesne University, Pittsburgh, PA 15282. *Panthera uncia* (snow leopard) dependence on livestock in northern Pakistan and its implications with human-wildlife conflict mitigation. — Snow leopards (*Panthera uncia*) are threatened predators in central Asia where pastoralism is the primary income source. Livestock depredation causes financial burdens on herders that encourage retaliatory killing to not only eliminate the animal, but also to recover from financial loss by selling the carcass into the illegal wildlife trade. Snow leopard related crimes are higher in Pakistan relative to other range countries. Such crimes may be initially motivated by livestock loss. Dietary analysis from noninvasively collected snow leopard scat via DNA metabarcoding by sequencing the genetic markers 12S and COX1 using Next-Generation Sequencing (NGS) allows for reliable inference of dietary composition. This study sought to use DNA metabarcoding to acquire knowledge of domestic animal prevalence in the diet of snow leopards in Baltistan, Pakistan. Desired outcomes were to determine persecution risk and to explore whether the reported trade of snow leopard parts may be related to higher livestock depredation. A total of 76 scats were sequenced, assessed for quality, and mapped to a comprehensive reference database. The majority of dietary items were large bodied ungulates (65.1%). Of these, over one-third (35.2%) were found to be domestic goats, sheep, and cows. Smaller-bodied prey items such as rodents and birds accounted for 34.9% of diet composition, indicating they may play a larger role in shaping snow leopard diet than previously thought. Based on substantial livestock dependency, snow leopards in Pakistan are likely at increased risk for retaliation and poaching. Domestic animals may be targeted as a food source due to a decrease in wild prey populations. Continued dietary monitoring, studies to assess native biomass, and programs such as livestock insurance and incentive initiatives should be applied to meet the conservation goals and initiatives. (65)

Hance, Gabrielle*, Zan Usmani*, and Stephen Madigosky Widener University, Chester, PA 19013. *The effect of rainfall events on the thermal stratification of a primary forest at the Amazon Conservatory of Tropical Studies (ACTS) Iquitos, Peru.* — Due to its equatorial juxtaposition, the Amazon rainforest is one of the most climatically stable environments on Earth. The towering and complex physical structure of the forest helps to define the variability in microclimates noted throughout the canopy from ground level to the upper most reaches of the forest. In this study, we traveled to the Amazon Conservatory of Tropical Studies (ACTS) in northeast Peru to examine the microclimatic profiles in an undisturbed area of the forest. Additionally, we examined how these thermal profiles were affected by rainfall events. To accomplish this, three sample lines containing temperature probes spaced several meters apart were hung from three different trees that varied in height. Rain gauges were also deployed in order to quantify rainfall. Rain and temperature data were collected for a week during July 2018. Our data suggests that rainfall events cause significant changes in the temperature profiles within the forest. During a heavy rainfall event, all of the temperature profiles depressed to levels lower than those observed on days with little to no rainfall. The profiles then seemed to change in a manner where the microclimates that were higher in the canopy were cooler than those at the bottom of the canopy, which is the reverse of what is normally observed. Documenting these effects can provide insight on how organisms within these microclimates adapt to rainfall events. Furthermore, this study in conjunction with previous studies is now beginning to reveal precisely how even minor rainfall events change the thermal profiles of the forest. This has profound consequences for all animals and especially those that play an important role in pollinating rainforest trees, shrubs, and vines. (155)

Hannah, Wallace*, and Michael Foulk Mercyhurst University, Erie, PA 16546. *Puff FISHing: Mapping *Sciara coprophila* salivary gland polytene chromosome amplicons using fluorescence in situ hybridization (FISH).* — The unique biology of the fungus fly *Sciara coprophila* makes it a useful model organism for the analysis of DNA amplification. During late larval development, the DNA in the salivary

glands replicates repeatedly, up to thirteen times, without any intervening cell divisions. These DNA copies remain synapsed together in tight register, forming giant polytene chromosomes. Subsequently, at up to 18 loci, individual origins of replication fire several more times resulting in localized DNA amplification above the polytene level. Transcription of the genes at these loci create distensions in the polytene chromosomes forming DNA puffs. The locations of these puffs have been mapped cytologically. One of these DNA puffs, at the II/9A locus has been extensively studied. The other amplicons have been less well characterized and is known about their sequences. Recently, the *Sciara* genome has been sequenced and assembled and as part of this project the sequences of 13 regions amplified in the polytene chromosomes were identified. The goal of this project is to map these amplicons using a fluorescence *in situ* hybridization (FISH) protocol to identify the DNA puff the corresponds to each amplicon. Currently, we are optimizing the FISH protocol using the well characterized II/9A locus. Experiments testing PCR design, including the length of the probe, optimization of the labeling procedure and *in situ* hybridization conditions will be presented. The optimized procedure will be used to map the newly identified amplicons to their corresponding DNA puff in the polytene chromosomes. (79)

Harris, Sebastian*, and Amy Savage Rutgers University-Camden, Camden, NJ 08102. *Exploring the relationship between Allegheny mound ant colonies and neighboring reptile and amphibian species richness.*

— Ants are one of the most abundant and ecologically important animal groups throughout the planet's terrestrial ecosystems (Wilson 1990, Holldobler and Wilson 1990). One common attribute of ants is their ability to dominate resources and space in an environment (Andersen 1991). However, the ecological influences of ants are not limited to their use of local resources. They are also widely recognized as ecosystem engineers (Folgarait 1998). For instance, ant mounds and subterranean ant nests have been found to provide overwintering habitat for several reptiles and amphibians (Criddle 1937, Carpenter 1953, Pisani 2009). While published observations provide insight into very specific snake-ant relationships, there has not been, to our knowledge, any hypothesis-driven studies on the relationship between ant colonies and neighboring reptile and amphibian communities. As ant nests have been found to provide refuge for several overwintering reptiles and amphibians, they may be associated with greater reptile and amphibian species richness than surrounding unmodified habitats. Furthermore, their influence on local habitat properties (vegetation cover, soil moisture, soil temperature, etc.) may facilitate habitat selection of neighboring herpetofauna. However, ants are also likely to behave aggressively towards reptiles and amphibians in defense of their nests and territories. Hence, our study focuses on one of the most prominent mound building ant species, *Formica exsectoides*, and aims to address the following questions: 1) Are habitats occupied by *Formica exsectoides* colonies associated with higher or lower reptile and amphibian species richness and abundance than surrounding habitats where *F. exsectoides* is absent? 2) Can particular habitat properties engineered by *F. exsectoides* explain any patterns we observe? Specifically, does the clearing of vegetation provide basking microhabitats for snakes, but negatively affect soil conditions (temperature, moisture, and pH) for salamanders? This study will begin in early May 2019 and conclude in late September 2019. (165)

Herman, Sean*, and John Campbell Mercyhurst University, Erie, PA 16546. *Effect of recreational trail development on salamander communities of riparian forest habitats near Lake Erie in Pennsylvania.* — Woodland salamanders are known to be abundant in North American forests, and consume a considerable number of insects and other invertebrates in the leaf litter of the forest floor. They serve as indicators of the health of a forest ecosystem and are sensitive to human disturbance. In order to evaluate the impact of recreational trail development and use on forest amphibians near Erie, PA, I surveyed woodland salamander communities in two similar riparian forest habitats with different histories of human activity — Wintergreen Gorge and Asbury Woods. Using historical data from 1998 that was collected before the Asbury Woods trail system was developed, I conducted field observations to see if trail use has affected the salamander populations. Over 15-man hours of sampling effort (visual encounter surveys) in Fall 2018 produced 43 specimens and a total of 3 species, with 29 of the specimens coming from Asbury Woods. A total of 24 red-back salamanders (*Plethodon cinerea*) were observed. Other species found at the Erie County sites in the fall were Four-toed and Northern dusky salamanders (*Hemidactylium scutatum* and *Desmognathus fuscus*).

Twenty cover boards were placed in salamander sampling areas at both forest sites to determine whether supplemental cover is utilized by the woodland salamanders. Dominant species of salamanders currently found at Asbury Woods are the same species found in 1998. (59)

Herzog, Hannah*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104.

Commensal Streptococcus intermedius reduces infection of pathogenic Porphyromonas gingivalis in oral epithelial cells. — The oral cavity harbors hundreds of bacterial species, including commensal as well as pathogenic groups. For example, *Streptococcus intermedius* is one of several species of oral commensal bacteria. On the other hand, *Porphyromonas gingivalis* is the main culprit of periodontal disease. The pathogen invades oral epithelial cells to escape immunosurveillance and antibiotics. Our aim is to test whether *S. intermedius* can reduce intracellular invasion of *P. gingivalis* into oral epithelial cells. *S. intermedius* 0809 and OKF6 oral epithelial cells were grown at 37°C and 5% CO₂. *P. gingivalis* 33277 was grown at 37°C in anaerobic conditions. *S. intermedius* was added to and allowed to bind to OKF6 cells for 1 hour at 37°C and 5% CO₂. Excess bacteria was washed away and then *P. gingivalis* was added for 1 hour and allowed to invade OKF6 cells and OKF6 cell pre-exposed to *S. intermedius*. Our results show that pre-exposure to commensal *S. intermedius* significantly reduces *P. gingivalis* by over 50%. We are currently testing the possible mechanism of interaction between OKF6 cells and *S. intermedius* that reduces *P. gingivalis* invasion. In conclusion, oral commensal *S. intermedius* is helpful in the prevention of *P. gingivalis* invasion and reduces the chances of the pathogen escaping immunosurveillance and antibiotics. The potential agent(s) produced by *S. intermedius* may be used as putative additional therapeutics in the treatment for periodontal disease. (84)

Hill, Brianna*, Jennifer Moss*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *The effect of Replication Protein A phosphorylation on the cellular response to DNA Damage.* — In 2019, there will be about 1.7 million new cancer diagnoses and 606,880 people are expected to die from cancer-related causes and therefore it is crucial that we further our understanding of this disease. 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. Previous research has shown that 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 of this research is to understand how RPA phosphorylation is involved in the cellular response to DNA damaging agents by identifying genes involved in checkpoint pathways and DNA repair mechanisms that genetically interact with RPA. Specifically, we are examining the genetic interactions between RPA and the DNA repair genes *KU70* and *RAD52* in response to the DNA damaging agents phleomycin, hydroxyurea, and camptothecin. A better understanding of RPA's role in DNA repair and cell cycle pathways will allow researchers to better understand the underlying causes of cancer. Current chemotherapy treatments are not specific and target any actively replicating cell, this causes unnecessary and unwanted damage to the patient's otherwise healthy cells. Overall, a better understanding of the underlying causes of cancer will allow for more selective chemotherapeutic drugs, which is in the best interest of the patient. (108)

Houman, Brianna*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Examining the role of Replication Protein A in telomere synthesis in the budding yeast Saccharomyces cerevisiae.* — There are many different methods to kill cancer cells, but most of them harm healthy cells and thus cause harmful side effects when treating patients with cancer. One property found in actively dividing cells such as cancerous cells is the activation on telomere synthesis. Telomeres are non-coding DNA regions found at the end of chromosomes and they are synthesized by the enzyme telomerase. Every time linear chromosomes replicate, small amounts of DNA at the ends of chromosomes are due to the end replication problem. Telomeres protect the genes located near the ends of linear chromosome from being lost during DNA replication by serving as a buffer of non-coding DNA. In most cells, telomerase is turned off because they do not need to divide frequently, but cancerous cells that arise from these non-dividing cells find ways to reactive telomere synthesis. One protein that is involved in telomere synthesis is Replication Protein A (RPA). Our research focuses on trying to better understand the role of RPA in telomere synthesis by using Telomere Fragment

Length Southern blot analysis and PCR based techniques to exam the length of telomeres in yeast strains containing mutations in RPA and known telomere genes. We are specifically interested in understanding the role of RPA phosphorylation in regulating telomere synthesis by using yeast strains that contain mutations that affect the phosphorylation state of RPA. Our results indicate that RPA phosphorylation may regulate telomere synthesis. We hope that a better understanding of the regulation of telomere synthesis will provide insights into novel targets for cancer cell treatment. (107)

Hudak, Andrew*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Identifying a clinical classifier based on differential expression of PD-L1 and a cancer immunotherapy resistance and response protein across kidney cancer subtypes.* — Cancer immunotherapy has recently emerged as a promising treatment for nearly all types of cancer. Specifically, checkpoint inhibitors (CIs) have been approved as first-line therapy by the Food and Drug Administration (FDA) for treatment of Renal Cell Carcinoma (RCC), the most common type of kidney cancer. CIs attempt to re-establish the ability of the immune system to implement a cytolytic attack against tumor cells. Within RCC, proteins targeted by CIs are PD-1 and CTLA-4, with current FDA trials underway for development of CIs targeting PD-L1. However, not all patients are responsive to CIs, while other patients experience treatment-associated adverse clinical events. Predicting the optimal treatment as to avoid such an event is difficult, with few established biomarkers for prediction of patient response to CI therapy. Here we demonstrate that PD-L1 and INPP4B, a cancer immunotherapy resistance and response (CIRR) protein, expressions vary according to RCC subtype. Overall, PD-L1 and INPP4B expression was highest in chromophobe RCC (chRCC), implying biological relevance. Low PD-L1/High INPP4B expressors conferred better chRCC-specific survival when compared with Low PD-L1/Low INPP4B patients, suggesting a clinical relationship between PD-L1 and INPP4B expression. Previously, CIRR proteins have not been considered for clinical classifier status, independently or as a combinational classifier with immunotherapy target proteins. Therefore, we present a potential clinical classifier, or predictive biomarker, for treatment of chRCC. This novel, combinational clinical classifier could be utilized to predict chRCC patient response to CI therapy, to provide targeted treatment based on immunotherapy target protein and CIRR protein expression levels. (4)

Huff, Jillian*, Tara Halterman, and Sarah Ruffell University of Pittsburgh at Bradford, Bradford, PA 16701. *Increased percentage of pathogenic bacteria with human activity on university campus.* — The main goal of this experiment was to determine if there was a correlation between student movement on a university campus and the percentage of pathogenic bacterial strains present on fomites. In total, sixteen door handles were tested in the physical education building over an eight hour period. Bacterial swabs were used to create streak plates to determine the population composition, while sequencing was used to identify the bacterial species. Five bacterial strains were identified: *Janibacter hoylei*, *Kocuria rhizophila*, *Micrococcus luteus*, *Paenibacillus glucanolyticus*, *Paracoccus yeei*, and Methicillin-resistant *Staphylococcus aureus* (MRSA). This study identified a strong positive correlation between human activity and the percentage of pathogenic bacteria, notably MRSA, on door handles. (193)

Hunter, Tracy*, Alexis Nagengast, and Stephen Madigosky Widener University, Chester, PA 19013. *Detection of sex determination gene (doublesex) by degenerate PCR in Stiphra species.* — Sex determination (SD) is a series of genetic pathways initiated by a chromosomal difference that result in differences between males and females. These pathways vary by species and their similarities can be used to examine evolutionary relationships. Exaggerated differences between the two sexes, known as sexual dimorphism, are commonly observed in insects. Examination of the SD pathway in the fruit fly *Drosophila* has identified several gene products that appear to be exclusive to SD such as the doublesex (dsx) gene in the final step. DSX has been identified in insects further up the evolutionary tree, like beetles (*Cyclommatus metallifer finae*), which supports the idea that SD pathways in insects evolved from the end of the pathway (here, dsx) to the beginning. Because *Stiphra* species are further up the phylogenetic tree than both honeybees and beetles, there should be sex-specific expression of dsx that results in the sexual dimorphism of the species. To examine this, samples of female *Stiphra* DNA were processed by PCR using degenerate primers for the dsx gene from female stag beetles. The PCR products were separated by gel electrophoresis and the largest products were gel purified and amplified in a second nested PCR. Three products of the nested PCR were

isolated and sequenced. With these DNA sequences, comparisons were made using NCBI BLAST, an online genetic comparison tool. The largest product (approximately 500 bp) was also the highest quality sequence returned, and mapped to a binding domain in a beetle species. The gene product amplified during nested PCR matches an RNA-directed DNA polymerase with a binding domain similar to dsx. Future investigations will include using a primer designed by aligning the dsx sequences of the closest relatives of the *Stiphra* species to attempt to amplify the 500 bp product examined in this experiment. (98)

Hurt, Hayley*, Anne Vardo-Zalik*, Sarah Stetzer, and Philip Kaufman Penn State University-York, York, PA 17403. *The curious case of sand fly identification: a story of morphology, molecules, and confusion.* — New world sand flies (genus *Lutzomyia*) are found throughout North America, with 14 recognized species reported. Sand flies are important vectors for human parasites such as *Leishmania spp.*, and for a variety of wildlife diseases, including lizard malaria (*Plasmodium spp.*) and other blood-borne pathogens in reptiles and mammals. *Lutzomyia vexator* is the primary vector for saurian malaria in northern California, and a population of presumed *L. vexator* from Florida was recently examined to better understand the genetic diversity of this important fly species across its geographic range. Upon examination of staple morphological features for sand fly identification (antennal ascoids and female spermathecal structures), the sand flies were not found to be *L. vexator*, but rather *L. shannoni* and *L. cruciata*. Molecular analysis of the specimens (cyt b and COI) confirms these identifications, and genetic comparisons between the *L. cruciata* population in Florida was compared to that of a very structured *L. cruciata* metapopulation in Mexico. Our results highlight the importance of utilizing a combination of identification markers for insect species level designations, and our genetic analysis supports the impression that these sand flies have restricted dispersal capabilities. (166)

Jacobson, Emily*, Sapanna Chantarawong*, Linda Lowe-Krentz, and Joshua Slee DeSales University, Center Valley, PA 18034. *Heparin-induced BMP6 expression and localization changes in vascular smooth muscle cells.* — Heparin, a drug with anti-coagulant properties, has been shown to influence the activity of bone morphogenetic protein 6 (BMP6), which is a member of the transforming growth factor-B (TGF-B) superfamily of proteins that regulate proliferation, differentiation, pattern formation, and apoptosis. It can be predicted that BMP6 upregulation might play a role in the anticoagulant functions of heparin; however, the anti-inflammatory mechanisms of heparin are not well characterized, and the role of BMP6 is under investigation. There is an established link between BMP6 and smooth muscle cell physiology, but it is unclear how BMP6 affects this physiology. Microarray data collected from serum-deprived vascular smooth muscle cells treated with heparin for 24 hours indicated a 1.899-fold increase in BMP6 mRNA compared to untreated control cells. Fluorescent microscopy, using antibodies specific for BMP6, shows that short-term heparin treatment less than 40 minutes does not significantly alter the expression of BMP6. Current research investigating the expression of BMP6 in response to 24-hour treatment in serum-deprived vascular smooth muscle cells showed an increase in BMP6 protein expression, however, media assayed for the presence of secreted BMP6 did not show significant changes relative to untreated control cells. Taken together, our results demonstrate that heparin treatment for 24 hours upregulates both BMP6 gene and protein expression, but BMP6 is not excreted as this time point. (99)

James, Michelle*, and Giancarlo Cuadra Muhlenberg College, Allentown, PA 18104. *Examining the antagonistic interaction between Streptococcus intermedius and Porphyromonas gingivalis.* — The oral cavity is home to numerous bacteria: commensals such as *Streptococcus intermedius* and even pathogens such as *Porphyromonas gingivalis* which is an anaerobic, Gram-negative species, responsible for periodontal disease. The pathogen invades oral epithelial cells in order to avoid immune cells and antibiotics. Unpublished data from our lab show that *S. intermedius* successfully hinders *P. gingivalis* intracellular invasion of oral epithelial cells. We are investigating the possibility of an antagonistic interaction between commensal *S. intermedius* and pathogenic *P. gingivalis*. *S. intermedius* was grown overnight in BHI broth at 37°C, 5% CO₂ atmosphere. *S. intermedius* overnight culture was serially diluted 1:10 in TSBY broth. Then, 10 µl from each dilution were plated in triplicates in blood agar. In addition, fresh TSBY broth was also plated on blood agar and used as control. Inoculated and control blood agar plates were incubated overnight under the same conditions or anaerobically at 37°C. *P. gingivalis* was grown anaerobically at 37°C in TSBY broth overnight. The next day, 10 µl of *P. gingivalis* culture were plated right next to the 24-hour spots where *S.*

intermedius had grown colonies. Blood agar plates were placed into anaerobic incubation for another three days. We find that pre-grown colonies of *S. intermedius* significantly reduce the growth of *P. gingivalis*, developing a zone of inhibition in the spot of the pathogen. Further experimentation will be conducted in an effort to determine the putative *S. intermedius* substances that inhibit *P. gingivalis* growth. The active ingredient(s) could be used as therapeutic agent(s) to help treat or prevent periodontal disease in dental patients. (85)

Januszkiewicz, Eric*, Nicole Chinnici, and Thomas LaDuke East Stroudsburg University, East Stroudsburg, PA 18301. *Detection of Snake Fungal Disease caused by Ophidiomyces ophiodiicola among Timber Rattlesnakes (Crotalus horridus) in Pennsylvania.* — Snake Fungal Disease (SFD) is a recently emerging disease caused by infection from *Ophidiomyces ophiodiicola*. Free-ranging snake populations are being affected by this fungal pathogen throughout many Eastern and Midwestern U.S. states. Characteristically, infected individuals display swelling, lesions, crusts, and nodules of the skin that are generally found on the head but can also be found throughout the body. The fungus is difficult to identify based solely on symptoms and was not definitively identified in the state of Pennsylvania prior to this analysis. Ninety-four total timber rattlesnakes (*Crotalus horridus*) from sites within eight different counties in the northeastern and northcentral regions of Pennsylvania were captured and swabbed to test for the presence of SFD. Real-time PCR was used to detect the pathogen DNA. Of the 94 snakes, 15 (16%) were positive with three individuals being infected on both the head and body, six individuals infected on just the head, and six individuals infected on just the body. There were no relationships found between infection rates and color phase, sex, length, or county captured. The cause of emergence and spread of this pathogen is largely unknown. Timber rattlesnakes have been listed as a candidate species in Pennsylvania in the past and are currently considered a species of special concern. The presence of SFD in these populations raises concerns. Long term monitoring studies may be helpful to examine the effects this fungal pathogen may have on individuals and populations. (61)

Jensen, Gregory*, and Steve Perry Cairn University, Langhorne, PA 19047. *The role of serotonin in regulating the hypoxic hyperventilatory response of larval Danio rerio (zebrafish).* — Serotonin (5-HT) containing neuroepithelial cells (NECs) are oxygen sensitive chemoreceptors found throughout the skin of larval *Danio rerio* (zebrafish). Zebrafish larvae are sensitive to changes in ambient PO₂ as early as 2 days post fertilization (dpf) and hyperventilate in response to hypoxia beginning at 3 dpf. Tryptophan hydroxylase (tph) is the rate-limiting enzyme in 5-HT synthesis; three tph paralogs are present in zebrafish (tph1a, tph1b and tph2). Although 5-HT has been implicated as a key neurotransmitter mediating hypoxic hyperventilation, it has not been possible to discern the role of 5-HT specifically contained within the NECs in promoting hypoxic hyperventilation. The purpose of this study was to determine the role of NEC 5-HT in regulating the hypoxic ventilatory response in larval zebrafish. It was hypothesized that 5-HT is a key neurotransmitter released from NECs which contributes to hypoxic hyperventilation. Immunohistochemistry was used to determine the distribution of tph paralogs and their role in 5-HT production in NECs. Tph1a was present in NECs and nerves innervating NECs. Exposure to the non-selective tph inhibitor, para-chlorophenylalanine (pCPA), or translational gene knockdown of tph1a, diminished 5-HT expression within NECs. Exposure to acute hypoxia (PO₂ = 30 mmHg) revealed a blunted hypoxic ventilatory response (reduced breathing frequency) in zebrafish exhibiting depleted 5-HT in NECs. The hypoxic hyperventilatory response was rescued with application of 5-HT. The results of these experiments demonstrate that tph1a is responsible for 5-HT production in NECs of larval zebrafish, and that 5-HT released from NECs is involved in establishing their hypoxic hyperventilatory response. (132)

Jones, Morgan*, and Sean Georgi York College of Pennsylvania, York, PA 17405. *Effects of the neurotoxin 6-OHDA on planaria, Dugesia dorotocephala.* — Planaria are invertebrate flatworms and considered one of the most primitive species to contain a central nervous system (CNS). The planarian CNS shows numerous similarities to the vertebrate CNS, including the usage of the neurotransmitter dopamine to control movement. As such, it has been proposed that planaria could serve as a potential model system for Parkinson's disease, a neurodegenerative disorder in which dopaminergic neurons are lost. Previous research has shown that dopaminergic neuron degeneration can be induced in numerous vertebrate and

invertebrate species using the neurotoxin 6-hydroxydopamine (6-OHDA), however this has not yet been shown in the brown planarian species *Dugesia dorocephala*. The purpose of this study was to determine the effects of 6-OHDA on *Dugesia dorocephala* through behavioral analysis and Quantitative Polymerase Chain Reaction (qPCR) for Tyrosine Hydroxylase, a marker of dopaminergic neurons. Both the behavioral assay and qPCR showed significant differences between control planaria and those treated with 6-OHDA after 7 days of treatment. These results suggest that the 6-OHDA treatment induced dopaminergic neuron degeneration in *Dugesia dorocephala*. However, when comparing these data to previous work, our experiments suggest that 6-OHDA was less effective at inducing dopaminergic neuron degeneration in *Dugesia dorocephala* than in other planarian species. (53)

Jones, Rebekah*, and John Harms Messiah College, Mechanicsburg, PA 17055. *Prevalence of a variant gastrin receptor RNA and correlating genomic polymorphism in human pancreatic cancer*. — The five-year survival rate of pancreatic adenocarcinoma (PDAC) is an abysmal 5%. The gastrointestinal hormone, gastrin, has been implicated as a driver of cell proliferation and pancreatic tumor growth via its receptor (CCK2R). Our lab has focused on the etiology of CCK2_{i4sv}R, a hyperactive splice variant of the gastrin receptor which has been associated with increased pancreatic tumor aggressiveness. While previous studies have correlated a single nucleotide polymorphism (SNP; C>A) in the receptor with decreased survival and potential expression of the variant receptor, we have previously reported the A-allele, alone, is not causative of missplicing. To determine if the SNP is part of a multifactor phenomenon resulting in CCK2_{i4sv}R, we undertook an analysis of normal and cancerous human pancreatic specimens. Tissue samples were genotyped, and CCK2R and CCK2_{i4sv}R mRNA were quantified by Real Time RT-PCR. An elevated incidence of the A-allele in PDAC samples (48%) compared to the normal population (14%) may support a correlation between the SNP and pancreatic cancer. Surprisingly, the splice variant receptor was detected with higher frequency in normal pancreatic tissue than cancerous, though it should be acknowledged that normal specimens derived from pancreatic resections may not be truly normal. Efforts to bolster sample size and test truly normal samples are ongoing. (5)

Judd, Ashley N.*, Amy E. Faivre, and John A. Cigliano Cedar Crest College, Allentown, PA 18104. *Pollen collection from local bee species to measure potential pollinator effectiveness at Wildlands Conservancy, Emmaus, PA*. — Conservation biologists and farmers alike are concerned with the rapid decline of bee species. This decline has been connected to pesticides, parasites, habitat loss and climate change, to name a few. Bees provide essential mutualistic interactions with plants. These pollinator interactions lead to the production of fruits and seeds often harvested for medicinal or agricultural purposes, as well as providing important food for a number of animals. This research conducted at Wildlands Conservancy in Emmaus, Pennsylvania documented the diversity of plants visited by local bee species and quantified the amount of pollen bees carried to determine which species might be the best pollinators. Bee species observed included *Apis mellifera* (honey bee), *Bombus spp.* (bumble bees), and *Xylocopa spp.* (carpenter bees). Samples were taken from the underside of each bee's thorax using a fuschin gel cube. The cube was melted onto a microscope slide and pollen grains collected from the bees were identified to the plant family level, and to species level where possible and the number of pollen grains of each species collected was counted. From this information it can be surmised which bee species may be the best pollinators. It also provided insight on plants in the local area that provide the most pollen sources for the bees. These plant species could be managed for the benefit of the local bee populations. (177)

Kalimon, Olivia*, and Daniel Widzowski Indiana University of Pennsylvania, Indiana, PA 15705. *Effects of acute or chronic mirtazapine on methamphetamine-induced locomotor sensitization*. — Mirtazapine is an atypical antidepressant that blocks various neuroreceptors and has also been shown to reduce methamphetamine (MA) dependence; however, there are also negative side effects due to the drug's lack of binding specificity. We want to discover a drug similar to mirtazapine that will block serotonin 5-HT₂ receptors, specifically in receptor 5-HT_{2A}, that will maintain the positive effects and lose the undesirable ones. We demonstrated that selective 5-HT_{2A} antagonist volinanserin, and inverse agonist pimavanserin both dose-dependently reduce 5-HTP-induced head twitch in mice. We then validated the methamphetamine sensitization assay and were able to show that both acute and chronic dosing of mirtazapine decreased

locomotor activity in MA conditioned mice, indicating reduced sensitization. Ongoing studies are testing mirtazapine and related compounds in additional head-twitch response and sensitization assays. Determining dose-response curves for mirtazapine and other compounds used in humans will provide a basis for mechanistic studies and translating doses from mice to humans. (48)

Kenwood, Matthew*, Hannah Merges*, Ian Johnson, Brianna Quarles, Mary Fuchs, Matthew Fontanese, and Kathryn Goddard Ursinus College, Collegeville, PA 19426. *Pollution resistance may be evolving in the mummichog Fundulus heteroclitus in the lower Darby Creek in southeastern Pennsylvania.* — Some populations of the small fish called *F. heteroclitus* suffer from toxic and teratogenic effects due to polychlorinated biphenyls (PCBs) and other pollutants. *F. heteroclitus* from some polluted populations in Massachusetts have evolved pollution resistance, avoiding these detrimental effects. A portion of “AHR1”, one of the proteins that brings pollution into the fish’s cells, has been found to contain mutations that appear to confer resistance. Darby Creek in southeastern Pennsylvania flows past two EPA Superfund sites that leach PCBs and other contaminants into the creek. Through analysis of a specific DNA sequence (the mitochondrial DNA control region) we are determining whether the *F. heteroclitus* population downstream of the Superfund sites, a nearby control population, and a coastal population consist of the northern or southern subspecies or a mixture of both because pollution responses may differ between the subspecies. We are examining the sequence the AHR1 gene in the population exposed to the Superfund site leachate to determine if mutations have occurred that could be involved in pollution resistance in comparison to the control populations. Preliminary analysis has revealed some sequence difference between the three groups in AHR1. Thus, we are investigating how pollution may be driving evolution. PCBs and the other pollutants involved have been used by humans for a little over two centuries. *F. heteroclitus* can reproduce at two years of age. Thus, it appears that *F. heteroclitus* pollution resistance may evolve rapidly. (141)

Khan, Maria*, and Anna Blice-Baum Cabrini University, Radnor, PA 19087. *The role of ubiquitin-proteasome system (UPS)-associated genes in the preservation of cardiac and muscle function in Drosophila melanogaster.* — One of the leading causes of death in the elderly is cardiovascular disease (CVD). Complications resulting from CVD kills an estimated 70% of people over 70 years old. Understanding key factors associated with age associated heart function decline remains a critical step in identifying targets for therapeutic interventions. Previous studies have implicated a decline in proteostasis in explaining declining cardiac function with age. Up until recently, researchers have focused heavily on autophagy as a major contributor to cardiac aging, but relatively little has been discerned about the role of the ubiquitin proteasome system (UPS) in aging heart cells. To gain greater understanding of this phenomenon the E2 ubiquitin ligase CG14739 was individually knocked down in cardiac and skeletal muscle. The expected outcome was a reduction in function due to loss of proteostasis. Reduced CG14739 in cardiac muscle resulted in an intensified age-associated decline in heart function, as indicated by decreased heart rate, diastolic function, and fractional shortening. In skeletal muscle, the reduction of CG14739 resulted in declining flight performance. Ideally, overexpressing UPS candidates will ameliorate age-associated cardiac function decline. Future work will test this hypothesis. (94)

Ki, Kwanho*, and Michael Butler Lafayette College, Easton, PA 18042. *Determination of biliverdin’s antioxidant capabilities.* — Reactive oxygen species (ROS) are highly reactive substances that chemically damage macromolecules such as proteins and lipids. This damage, known as oxidative damage (OD), accrues and can be detected in cells, tissues, and blood. Oxidative damage is unavoidable as all metabolic processes will produce ROS, and substances called antioxidants can neutralize ROS. When organisms have low levels of antioxidants relative to ROS, there is a greater accumulation of OD which can expedite the aging process, disrupt cell signaling, and impair immune function. Thus, antioxidants are critical to the health and functioning of organisms. One putative antioxidant is biliverdin, which is produced during the breakdown of red blood cells. Several studies have suggested biliverdin’s potential antioxidant properties. However, these studies were performed only in test tubes or in cultures of mammalian cells, which produce enzymes that rapidly convert biliverdin into another molecule called bilirubin. This study investigated the antioxidant properties of biliverdin using European starlings (*Sturnus vulgaris*), which do not have the enzyme that converts biliverdin to bilirubin. Starlings were fed mealworms, injected with either highly oxidized oils to

induce OD in the bird, or mealworms without oil (hence no increase in oxidative damage). After 30 minutes, groups were injected with either biliverdin or saline. Sixty minutes after injections, when exogenous biliverdin had maximally entered circulation, we collected a blood sample. This allowed us to observe whether groups given oxidized oils had lower levels of OD in lipids and proteins when treated with biliverdin, as compared to groups given oxidized oils but treated with saline. Preliminary data has shown that OD in lipids seems to be lower when birds are treated with biliverdin as opposed to saline. Further tests and analyses will be run to confirm the statistical significance of our data. (101)

King, Carli*, and Mary Morrison Lycoming College, Williamsport, PA 17701. *Sholl analysis of Purkinje neuron morphology using MetaMorph software.* — Cerebellar Purkinje neurons are commonly characterized by their highly branched dendrites that receive information from granule neuronal inputs, making them an efficient model for studying dendritic development. Purkinje neurons were used in this study to review the effects of pharmacologic inhibitor treatments on dendrite growth. Currently in the laboratory, the effects of manipulating specific signaling pathways are assessed by quantitatively evaluating cell body size, dendrite branching, and dendrite length using manual tracing with MetaVue software. This study evaluates the feasibility of using Sholl analysis with the full MetaMorph software to collect quantitative measurements on Purkinje neurons with highly branched processes. To validate the semi-automated Sholl analysis algorithm, computer-generated data were compared to data collected from manually tracing each neuron. Purkinje neurons treated with a pharmacologic inhibitor LY294002 to inhibit the PI-3 Kinase signaling pathway had significantly more intersections at the 10 mm Sholl ring than Purkinje neurons that received no treatment ($p < 0.05$). Purkinje neurons that received no treatment had significantly more intersections at the 60 mm Sholl ring than Purkinje neurons treated with inhibitor LY294002 ($p < 0.05$). Preliminary data suggest the new semi-automated Sholl analysis algorithm can be used to analyze the morphology of Purkinje neurons accurately. This work will contribute to our understanding of which specific signaling pathways regulate the morphology of cerebellar Purkinje neurons. (43)

Knopsnider, Kaitlin*, Michael Tyree, Ellen Yerger, Timothy Tomon, and Carolyn Copenheaver Indiana University of Pennsylvania, Indiana, PA 15705. *Estimating the timing of hemlock woolly adelgid infestation of lightly to moderately declining eastern hemlocks using tree ring analysis.* — Pennsylvania's historic state tree, the eastern hemlock (*Tsuga canadensis*), is being devastated by an exotic insect from Asia, hemlock woolly adelgid (HWA). Eastern hemlock shows almost no resistance and its loss as a late-successional forest species could have far-reaching ecological effects. This work seeks to determine if tree-ring analysis, as a measure of plant vigor, is a sensitive enough method to estimate the timing of HWA. Hemlock cores were extracted from two sites that were reported to be infested by HWA in western Pennsylvania. These trees ranged from lightly to moderately declining hemlocks based on qualitative assessment of the tree canopy. A minimum of 15 hemlocks ranging from light to moderate impact at each site were selected for sampling. Only hemlocks with a canopy position of dominant or codominant were chosen. The cores were mounted and sanded to 400 grit prior to visual cross-dating. Additionally, all cores were cross-dated using COFECHA. HWA infestation produces a visible signal in the variance of the master chronology of lightly and moderately declining hemlocks around 2010. Thus, the estimated timing of infestation is estimated to be 2010. Average annual ring widths were calculated for each individual tree of each vigor class for the 5 years prior and 5 years after 2010. There was a 19% ($P = 0.05$) decline in average tree-ring width after infestation in lightly declining hemlocks. In moderately declining hemlocks, there was a 37% ($P=0.01$) decline in average ring widths after infestation. Therefore, the signal and timing of hemlock woolly adelgid infestation can be estimated using tree-ring analysis. The signal and timing of hemlock woolly adelgid infestation allow a rapid determination of tree health. Tree rings provide a more detailed story than the appearance of the needles in the very trees that have a detailed history in Pennsylvania themselves. (183)

Konopka, Emily*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Investigation of a novel 'Bacillus' species suggests that it should be classified in a new genus..* — A bacterial strain designated SJS was isolated from the Lycoming Creek and identified as a novel species. Its genome was sequenced and compared to those in databases to determine the closest relatives for phenotypic comparisons. The validly published type strains with the most similar 16S rRNA sequences were *Bacillus mangrovi* (98.3%), *B.*

indicus (97.5%), *B. lacus* (96.9%), and *B. idriensis* (96.5%). Of this group, only *B. indicus* has had its genome sequenced. Trees constructed with BLAST best hits using the 16S rRNA sequence, the *rpoB* gene or with the Genome Taxonomy Database (120 concatenated proteins) revealed several other unnamed strains that are also closely related to our SJS strain. Comparison of average nucleotide identity (ANI) and average amino acid identity (AAI) values with various *Bacillus* species showed that these organisms are different enough from the type species, *Bacillus subtilis*, that they should not be members of the same genus. Based on whole genome sequence analysis, we propose that strains SJS and FJAT-42376 are separate species of a new genus that we will call *Noelibacillus* and *B. indicus* should be reclassified into a new genus, *Chappellibacillus*, along with a new species represented by the genome of strain HMSC76G11. (195)

Kramer, Emilie*, and Mary Morrison Lycoming College, Williamsport, PA 17701. *Control of Purkinje neuron dendrite development by the MAP kinase and PI3 kinase signaling pathways.* — The cerebellum is an important part of our nervous system because it is responsible for coordinating gross and fine motor movements, balance, and eye movements. The effective functioning of the cerebellar circuit is completely dependent on the proper functioning of Purkinje neurons, which provide the sole output of motor error information from the cerebellum. Research has shown that neurotrophins, such as brain-derived neurotrophic factor (BDNF), are responsible for regulating Purkinje cell growth, differentiation and function. This research focused on the inhibition of the mitogen-activated (MAP) kinase pathway, which is a signaling pathway downstream of TrkB, the main BDNF receptor. I used the MetaVue software program to measure the longest dendrite, cell body area, and total cell area of Purkinje neurons in mixed cerebellar cultures treated with varying concentrations of the MAP kinase inhibitor PD98059 and immunostained with anti-Calbindin-D_{28k}. I hypothesize that the inhibition of this cellular pathway will result in a decrease in total cell area, cell body area, and total dendritic area, but longest dendrite length will not display a significant decrease in length, in keeping with preliminary results from a previous student. Inhibition of the MAP kinase pathway significantly decreased the longest dendrite, the total cell area, and the total dendritic area. Inhibition only significantly decreased cell body area for the 100uM PD98059 treatment group. The data from this research might be able to help ataxia patients in the future. By understanding the development of Purkinje neurons and what helps them grow, we might be able to create drugs that can reverse or slow down the degeneration of these neurons. (44)

Kufner, Michaella*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Exploring the relationship between menthol cigarette smoking, microRNA regulation, and racial disparities in lung cancer.* — African Americans (AA) have a higher incidence of non-small cell lung cancer (NSCLC) than European Americans (EA), despite smoking less. AA that do smoke are more likely to smoke traditional cigarettes with menthol. A recent public health epidemic highlights increased electronic cigarette use with flavorings, such as menthol, amongst youth. The *CYP* gene family metabolizes tobacco and the *UGT* gene family metabolizes menthol. MicroRNAs (miRNAs) regulate *CYP* and *UGT* mRNAs, and miRNA expression varies by race in NSCLC. We hypothesize AA and EA have population-specific miRNA expression differences that drive *CYP* and *UGT* gene expression, and serve as a potential determinant of the lung cancer health disparity. Clinical, miRNA, and mRNA sequencing data for LUAD patients ($n = 82$ AA, $n = 734$ EA) were downloaded from The Cancer Genome Atlas (TCGA). Patients with both miRNA and mRNA data were analyzed ($n = 50$ AA, $n = 342$ EA). Differential expression (DE) analyses using Partek Genomics Suite 7.0 (1-way ANOVA) were done to identify DE miRNAs and DE mRNAs. *CYP* and *UGT* targets were identified and analyzed using t-tests. PCA for all available LUAD patients showed race to be a strong source of variation (miRNA $F = 20.55$, mRNA $F = 14.86$). Thirteen significant DE miRNAs and 908 significant DE mRNAs were identified ($P + FDR < 0.05$). EA showed more significant downregulation for both miRNAs and mRNAs, and AA showed more significant upregulation for both. Six DE miRNAs drive significant expression of two *CYP* genes (miR-374b + *CYP1A2*; miR-1304, miR-548j, miR-3667, miR-374b, miR-1252 + *CYP2U1*). This significant trend was not observed for *UGT* genes. There are population specific miRNA and mRNA expression differences between AA and EA. The DE miRNAs that regulate *CYP* genes could be a determinant of the lung cancer health disparity. Future analyses will include smoking status, stage, genetic ancestry, and other NSCLC subtypes. (2)

Kunkel, David*, and Grace Chen Misericordia University, Dallas, PA 18612. *Experimental Study of Garlic Mustard (*Alliaria petiolata*, *Brassicaceae*) in Luzerne County, PA.* — Invasive species are a serious threat to their introduced area as they often disrupt the native community structure. Garlic mustard, *Alliaria petiolata*, is a notorious invasive plant species that has spread across North America since its introduction to New York in 1868. This species threatens forest understory communities as it alters soil nutrient composition and plant-microbe interactions. Two ecological hypotheses, the Resource Availability Hypothesis (RAH) and the Biotic Resistance Hypothesis (BRH), were tested here in the context of the invasion of *A. petiolata*. RAH explores the resource allocation trade-off between plant growth and defense, but it is not commonly tested in invasive species. BRH, on the other hand, is commonly used to explain the unlikelihood for a species to invade a habitat with high biodiversity. Here we tested RAH and BRH with *A. petiolata* by correlating plant fitness and coverage with light, herbivory, biodiversity, and human disturbance in five sites in Luzerne County, PA. Each site contained five randomly selected plots, each of which contained three 1×1 m quadrats. Our results suggest that RAH is not supported in relation to the invasion of *A. petiolata* as herbivory damage and light intensity were not related to plant performance. BRH was also not supported in this system as the biodiversity of the plot did not correlate with *A. petiolata* fitness and coverage. However, as the distance between the plot and the nearest road decreased, *A. petiolata* fitness and coverage increased, indicating that the invasion is facilitated by human disturbance. Overall, our results suggest that altering light, herbivory, or biodiversity in the invading areas may not be sufficient for the management of this invasive species. More extensive human intervention by minimizing road constructions and disturbance is required for controlling the invasion of garlic mustard in the U.S. (174)

Lauricella, Amanda*, Matthew DeBenedetto*, and Robert Kurt Lafayette College, Easton, PA 18042. *Functional Analysis of Macrophages and Neutrophils in Early Innate Immune Response to Murine Mammary Carcinomas.* — The aim of this project was to characterize the leukocytes recruited in the innate immune response to different mouse breast cancer cell lines. We used two different murine mammary carcinomas, both syngeneic in BALB/c mice, to study the early tumor immune response. The innate immune response is the first line of defense where pathogens are identified and removed. Macrophages and neutrophils are the two main types of white blood cells necessary for this first line defense. Because macrophages and neutrophils are part of this initial response, they are nonspecific and contain a variety of receptors in order to maximize the types of pathogens they are able to identify. In this study, *E. coli* was used to measure the positive phagocytic capacities of the leukocyte populations which was analyzed using flow cytometry. Data showed that over three time points (24 hour, 48 hour, 72 hour) the injection of 168 tumor cell line resulted in a larger number of macrophages than neutrophils, specifically at the 72 hour time point. EMT6 did not show a significant consistent pattern across all time points. (72)

Le, Vinh*, and John Harms Messiah College, Mechanicsburg, PA 17055. *Cloning a fluorescent fusion protein for detection and localization of the gastrin receptor.* — Pancreatic ductal adenocarcinoma (PDAC) is the fourth leading cause of cancer-related death worldwide. It is promoted by multiple cellular signaling events. Gastrin, a hormone that regulates several aspects of gastrointestinal physiology and maintenance of the gastrointestinal mucosa, is abnormally expressed in pancreatic cancer cells and promotes PDAC growth. Its effects are chiefly mediated through the seven membrane-spanning G protein-coupled receptor, CCK2R. Upregulation of CCK2R and the cancer-associated splice variant, CCK2_{i4sv}R, have been shown to contribute to tumorigenicity, with the latter promoting increased tumor aggressiveness. Our lab has previously reported the development of monoclonal antibodies specific to CCK2R and CCK2_{i4sv}R. However, immunofluorescence and Western blotting detection were achieved in cells transiently-transfected with these receptors, and detection at physiological levels and in stable transfections has proven difficult. As such, sensitivity of these monoclonal antibodies has not been determined. To fully characterize these antibodies and develop accurate receptor quantification, we report development of a plasmid encoding a fusion of enhanced green fluorescent protein (EGFP) to the C-terminus of CCK2R/CCK2_{i4sv}R under the constitutive control of a beta-actin promoter with CMV-enhancers (pCAGEN.neo). This positive-control fusion protein will enable determination of antibody sensitivity and selectivity and additionally permit *in vitro* tracking of receptor subcellular localization. (70)

Levri, Edward*, Colin Berkheimer, and Kellie Wilson Penn State University-Altoona, Altoona, PA 16601. *Predator avoidance behaviors come at the cost of growth in an invasive aquatic snail.* — Many species demonstrate variation in behavior that is context dependent that theoretically maximizes fitness. The New Zealand mud snail, *Potamopyrgus antipodarum*, exhibits multiple avoidance behaviors when chemically detecting fish predators. Since these behaviors only seem occur when predators are detected, it is predicted that they must come at some fitness cost. We hypothesized that when these behaviors are exhibited they reduce the feeding efficiency of the snail and would thus come at a cost of growth. To test this, we exposed juvenile snails of four different populations to either plain water or water containing the odor of a predatory fish, the blacknose dace for six weeks. Snails exposed to the fish odor grew significantly slower than snails not exposed to fish odor. We also found variation between populations in growth rate. The results explain why these snails do not exhibit these behaviors in the absence of predators. (17)

LoVine, Brianne*, Samantha Mullin*, and Francis Mayville DeSales University, Center Valley, PA 18034. *Liquid-liquid extraction and analysis of the antioxidant, resveratrol, from various red, rosé and white wines.* — The objective of this study was to extract, isolate and analyze the antioxidant, resveratrol from various red, rosé and white wines. Three different growing locations were selected for this study. The three vineyards include US west coast (Oregon), US east coast (New York) and France. Merlot, Rosé and Chardonnay from each vineyard location were selected as the wines for analysis and comparison. The extraction and quantification of resveratrol was conducted in order to compare the amount of this antioxidant found in the different red, rosé and white wines. In order to extract resveratrol liquid-liquid phase techniques were implemented. The concentration of the antioxidant was quantified using ultraviolet spectroscopy at a wavelength of 310 nm. High Performance Liquid Chromatography was also used to isolate and identify the active ingredient from each wine after extraction. The analysis of the data collected from this study will suggest which type of wine contained the most resveratrol. (26)

Lutz, Gregory*, and Anne Vardo-Zalik Penn State University-York, York, PA 17403. *Exploring the physiological changes that Hymenolepis diminuta inflicts upon Tribolium confusum.* — Two theories on the causation of behavioral modification of hosts during a parasitic infection are sickness syndrome and chemical modulation. When infected with the tapeworm *Hymenolepis diminuta*, the beetle *Tribolium confusum* has been shown to display increased surface seeking behavior. To test how *Hymenolepis diminuta* affects *Tribolium confusum*, we attempted to modify beetle surface seeking behavior through a variety of methods including infection by a known parasite (*Hymenolepis diminuta*), infection by known pathogen (*Serratia marcescens*), and the use of agonistic and antagonistic chemicals (Dopamine, Tyrosine, Mianserin HCl). Two weeks post tapeworm infection, beetles were exposed to standard flour, or flour mixed with an agonist, antagonist, or bacteria. After one week of exposure, beetles were monitored for surface seeking behavior three times over a 24-hour period. Through the use of PCR analysis, we determined an overall tapeworm infection rate of 48% in experimentally infected groups. All data were analyzed using nested ANOVA and no significant change in behavior between experimental groups infected by parasites and those infected by pathogens ($P > 0.05$) was observed. The data also indicated no significant correlation between surface seeking behavior and infection or chemical exposure ($P > 0.05$). Currently, semiquantitative PCR is being performed to identify differences in gene expression of dopamine, octopamine, and tyrosine receptors between tapeworm infected and control beetles, as well as across the different beetle experimental groups. While surface seeking behavior was not observed to vary significantly in our study, the expression pattern of these genes that affect exploratory nature may still provide insight as to whether or not these pathways are affected by the presence of the tapeworm. (66)

Mader, Emma*, and John Campbell Mercyhurst University, Erie, PA 16546. *Analysis of possible causes of winter fish kills in Lake Erie waters adjacent to a coke manufacturing operation.* — Over three years (2017-2019), winter die-offs of Gizzard shad (*Dorosoma cepedianum*) were observed at Erie's East Avenue Boat Launch, where a coke manufacturing operation discharges heated water into Lake Erie. We investigated potential causes of the fish mortality, including thermal shock, disease/parasites, oxygen depletion beneath ice, and chemical contaminants. The methodology included testing the nearby water quality and temperature, as well as dissection of dead shad collected at the site on January 19, 2017 and February 6,

2018 and February 14, 2019. Necropsies on the Gizzard shad produced no evidence of disease-causing parasites that are known to kill Gizzard shad in Lake Erie. The lack of ice cover in the areas where the die-offs occurred and behavior of *D. cepedianum* were not consistent with winterkill due to oxygen depletion. We suspect that the fish were attracted to the site by the warm water discharge from Erie Coke, and that thermal shock and/or chemical contaminants discharged to Lake Erie by Erie Coke are responsible for the die-offs. The likelihood of releases from Erie Coke into groundwater of toxins such as benzene, naphthalene, polycyclic aromatic hydrocarbons (PAHs) and arsenic lead to the hypothesis that a combination of thermal and chemical pollution from Erie Coke is responsible for the gizzard shad mortality. On February 14, 2019, water temperatures measured at the die-off site showed steep horizontal and vertical temperature gradients (> 10°C) in the area where fish were congregating at the mouth of the stream on Lake Erie. (16)

Mahadevan Padmanabhan, Tejas*, and Cuong Diep Indiana University of Pennsylvania, Indiana, PA 15705. *Testing the r1 peptide on kidney development in zebrafish.* — Almost 10% of American adults suffer from some sort of chronic kidney disease and current therapies for end-stage kidney disease are not ideal. Unlike humans, zebrafish can regenerate new kidney tissues after injury using stem cells that express the *lhx1a* transcriptional activator. *lhx1a* is also expressed in stem cells during kidney development in zebrafish and other organisms, including humans. Mutations in *lhx1a* results in kidney agenesis, indicating that its function is essential for kidney formation. To understand the molecular function of *lhx1a*, we carried out a genetic selection for interacting proteins. We found that *lhx1a* interacted with itself, suggesting homodimerization of *lhx1a*. Deleting the LIM domain of *lhx1a* enhanced dimerization. Others have shown that deleting the LIM domain of *lhx1a* also activated the protein, converting into an active transcriptional activator. Therefore, we hypothesize that the LIM domain negatively regulates homodimerization and activation of *lhx1a*, and thus activation of *lhx1a* requires dimerization. To determine whether *lhx1a* dimerization is physiologically relevant *in vivo*, we performed a different genetic selection to identify small random peptides that bind to *lhx1a*. We rationalized that such peptides binding to *lhx1a* would affect its dimerization and function (negatively or positively). Our pilot selection resulted in one peptide (called R1) that bound to *lhx1a*. We injected 1-cell embryos with this mRNA and observed pericardial edema in almost 100% of 1-day old embryos (compared to a negative control peptide). Since the kidney does not function until embryos are 2 days old, the edema is likely caused by a heart defect instead of a kidney phenotype. Although *lhx1a* function is not directly connected to the heart, it is expressed in nerve cells that regulate heart contraction. Thus, we are currently determining whether the R1 peptide affects heart function. (129)

Mancini, Olivia*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Do Yaf9 and histone H3 acetylation stimulate NuA4 binding to chromatin?* — NuA4 is the only essential lysine acetyltransferase (KAT) complex in the yeast strain, *Saccharomyces cerevisiae*. It is involved in stimulating transcription initiation and elongation along with DNA repair and the cell cycle. NuA4 participates in these processes as a KAT complex by transferring an acetyl group from acetyl-CoA to lysine side chains. NuA4 is comprised of thirteen subunits, but contains only one enzyme, the catalytic subunit Esa1. Thus the other subunits must help Esa1 recognize NuA4's ~100 substrates. During transcription, NuA4 acetylates histones H4 and H2A. The goal of this project is to help understand the role of NuA4 subunit Yaf9 and histone H3 acetylation in stimulating NuA4 interaction with chromatin. Isolated Yaf9 has been shown to preferentially bind acetylated histone H3 lysine 27 (H3K27ac). In vitro data from our lab suggests that Yaf9 may not bind the same target as part of NuA4. I will examine NuA4-chromatin interactions in vivo by coimmunoprecipitation and in vitro by nucleosome pull-down in yeast strains lacking Yaf9 in combination with mutations that reduce H3 acetylation. We expect *yaf9Δ* cells to have reduced NuA4 interaction with chromatin, although the role of H3 acetylation is unclear. This work will help us understand how NuA4, a key regulator of transcription binds and interacts with chromatin, which may be a mechanism that can apply to other coactivator complexes as well. (119)

Marold, Joseph*, Laura Gearhart*, and Avijita Jain Indiana University of Pennsylvania, Indiana, PA 15705. *Photoactive Ruthenium(II) Polypyridyl Complexes: Synthesis, Redox, Photochemical, and DNA Interaction Studies.* — Ruthenium (II) complexes with polypyridyl ligands have been of interest due to their interesting

photochemical, photophysical, and electrochemical properties. Typically, complexes with general formula of $[\text{Ru}(\text{NN})_2(\text{NN}')]\text{PF}_6$ are extensively studied due to their ease in synthesis (where NN and NN' represent dipyrrolyl ligands). Herein, we report synthesis, characterization, redox, photochemical, and DNA interaction studies of two new Ru(II) complexes, $[\text{Ru}(2,9\text{-dmp})(\text{bpy})(\text{CH}_3\text{CN})_2](\text{PF}_6)_2$, and $[\text{Ru}(2,9\text{-dmp})_2(\text{bpy})](\text{PF}_6)_2$, where 2,9-dmp = 2,9-dimethyl-1,10-phenanthroline and bpy = 2,2'-bipyridyl. The interaction between the Ru(II) complex and DNA under dark and photolysis conditions was explored by gel electrophoresis using a pUC18 DNA. (25)

Marotta, Julianna*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. *Genetic characterization of molecular mechanisms underlying triclosan resistance in novel Enterobacter cloacae strains.* — Multidrug resistant (MDR) bacterial infections are rising worldwide, shifting from a biological phenomenon to a rapidly growing global health crisis. The creation of multidrug resistant strains has been exacerbated by the overuse of antimicrobial compounds such as triclosan, which for decades has been added to consumer products. Consequently, it has accumulated in the environment, providing a selective pressure that may lead to the creation of novel MDR bacterial strains and contribute to this global crisis. We have previously described the establishment of triclosan resistant *Enterobacter cloacae* strains (EncJM9aD, EncJM9aTE, EncJM9aCH, and EncJM1aA) following repeated exposure to triclosan, chloramphenicol, or tetracycline. This study furthers the characterization of these novel strains via qPCR-CNV analysis, which demonstrated that extra *fabI* gene copies were acquired during triclosan exposure. To further address the involvement of *fabI* overexpression in triclosan resistance, EncJM1a (sensitive) and EncJM9aD (resistant) *fabI* copies were cloned into IPTG-inducible vectors in *Escherichia coli* T7 cells. Triclosan tolerance of the transformants indicated that induced expression of wildtype *fabI* allowed for bacterial growth at 10-fold higher concentrations of triclosan, compared to native expression of the gene. Different thresholds of triclosan resistance were noted for EncJM9aD *fabI* gene copies, with the highest yielding growth at 100-fold higher concentrations of triclosan. A novel PCR-RFLP assay also demonstrated that two of three EncJM9aD *fabI* copies have the G93V/S mutation, previously described to be correlated with triclosan resistance in *E. coli* strains. Future work involves DNA sequencing the *fabI* gene copies, as well as promoter regions of the genes associated with the AcrAB-TolC efflux pump and OmpF porin. Data derived from this study could lead to a better understanding of the mechanisms underlying multidrug resistance, providing a tool for assessing the impact of triclosan on the creation of novel MDR strains. (190)

Matson, Jaime*, Jean-Francois Therrien, and Allison Cornell Cedar Crest College, Allentown, PA 18104. *Variation in paternal care and its possible consequences on offspring development in a farmland raptor.* — The American kestrel (*Falco sparverius*) exhibits a biparental care system, in which both the male and female parent contribute to the care of their offspring. We examined paternal care and how it affects offspring growth and development. We took video recordings and conducted behavioral surveys in the field on parental care at 9 wild kestrel nests around Hawk Mountain Sanctuary in Kempton, Pennsylvania during the summer of 2018. Kestrels are sexually dimorphic, making it easy to tell the male and female apart in the field. Parental care behavior was observed for a total of 6 hours at each nest throughout the nestling period. In order to document offspring development, we measured tarsus length (leg bone), body mass, wing length, and hematocrit (percent of red blood cells by volume) of chicks once a week for three weeks (7, 14, and 21 days after hatching). Preliminary results show that only 3/9 males provided parental care early in the nestling period, however by the third week of observations 6/9 males showed parental care. Nestlings with paternal care activity during week three surveys showed on average 11% higher body mass than nestlings with no paternal care, however this difference was largely due to sex related size dimorphism, with nests showing more paternal care marginally more likely to have more female chicks ($F = 4.2$, $P = 0.08$, $df = 1, 7$, linear model). This talk will explore this variation in paternal care and its possible consequences on the offspring development. (137)

McDonald, Deanna*, and Jennifer Elick Susquehanna University, Selinsgrove, PA 17870. *Paleoecology and Taphonomy of shell hash beds on Route 11-15.* — Shell beds from the Trimmers Rock Formation (Upper Devonian) along Rt 11/15 were compared to beds 10 km away, and represent similar environments. These beds were compared to determine the controls acting on deposition of a prograding ramp. These shell beds are comprised of fossils that may have been strongly influenced by periodic high energy storm events,

hypopycnal flows, and turbidity currents. The shell beds at these two locations may have been deposited by the same regional events, however they are laterally discontinuous and non-correlative. Along Rt 11/15, the rock is greenish gray, shale with laterally discontinuous thin beds of shaley sandstone that contain ripples, laminae, and shell beds. This succession is overlain by reddish-gray sandstone dominated by ball and pillow structures. This study focused on samples collected north of Liverpool, PA; the number of organisms were counted per unit cm². Thin sections contain bryozoans, brachiopods, and crinoids with less abundant tentaculites, carbonized plant material, and fish bone. Preliminary results indicate that bryozoans (fragmented) dominated the environments where the sediment was deposited. Some crinoid columnals were very small; larger crinoid columnals were more articulated. Brachiopods are not very abundant in these samples. Additionally, invertebrate burrows were found in these rocks. Along PA Rt 322, at Watts Twp. Exit 1, the Trimmers Rock Formation appears very similar to the exposure along Rt 11/15. When plotted on a ternary diagram, the fossils at both locations tend to plot in similar areas, which suggests that they were influenced by similar environments. The communities in this Upper Devonian prograding muddy ramp environment were dominated by suspension feeders. The shell beds in the Trimmers Rock Formation represent an environment influenced by a current, that may be part of the distal ramp where the energy is low, and where occasional events concentrate skeletal fragments. (161)

McHugh, Jessica*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Yaf9 stimulates NuA4 interaction with histone H3 tails.* — Regulation of gene expression is critical for normal cellular function. One of the major mechanisms by which gene expression is regulated is chromatin, the protein-DNA complex that makes up chromosomes. Chromatin blocks access to the DNA and thus must be disassembled before a gene can be expressed. The NuA4 protein complex from yeast plays a crucial role during chromatin disassembly. This work investigated whether NuA4 subunit Yaf9 helped NuA4 bind to histone H3 acetylated on lysine 27. We utilized *in vitro* binding assays to look at whether NuA4 purified with or without Yaf9 could bind to unacetylated histone tail peptides [H3(1-21) or H3(21-44)] or peptides acetylated on lysine 27 (H3K27Ac) or lysines 14, 18, 23, and 27 (H3-4Ac). We found that NuA4 lacking Yaf9 bound more weakly to all of the peptides than NuA4 containing Yaf9, suggesting that Yaf9 does stimulate NuA4 binding to nucleosomes, but not specifically to H3K27Ac. Surprisingly, WT NuA4 binding to histone tail peptides was not stimulated by acetylation. Further work is needed to understand just how important histone acetylation is in stimulating NuA4 binding. (117)

McLaughlin, Sean, Olivia Lawler*, and David Andrew Lycoming College, Williamsport, PA 17701. *Genetic influence of spontaneous walking behavior in Drosophila melanogaster.* — The *Drosophila* Genetic Reference Panel (DGRP) was developed to aid in identifying the genetic influences of quantitative traits, those phenotypes that result from the cumulative effect of multiple genes and the environment. In order to employ the DGRP for genome wide association studies (GWAS), phenotypic characteristics of hundreds of animals must be collected. This inherently limits the ability to analyze difficult to quantify phenotypes, such as certain spontaneous behaviors. We sought to increase the throughput of analyses by employing the automated analysis software Ethovision XT®. We proposed that Ethovision XT® would be able to extract walking behaviors in a manner comparable to manually-acquired data, but in a fraction of the time, thereby enabling a GWAS of spontaneous walking. We first performed a sensitivity analysis of Ethovision XT® on a subset of previously-analyzed videos of spontaneously-behaving flies and identified software settings that provided results comparable to manually-scored results. We then applied these same settings to the entirety of our previously-recorded data set and found that the DGRP stocks exhibit a continuous variation in spontaneous walking behavior between lines characteristic of quantitative traits. We submitted our phenotypic results to the DGRP GWAS analysis web tool and identified genetic polymorphisms of interest for walking. Candidate genes were previously implicated in central nervous system synaptic function and regulation of the neuromuscular junction. We sought to further verify the influence of these genes on walking behavior by performing RNA interference (RNAi) experiments to reduce expression of these genes in neural tissue. The results from this experiment indicate that the reduction of expressions in several genes does indeed influence spontaneous walking. We plan on adapting our use of Ethovision XT® to analyze other behaviors in

flies, including grooming, in order to elucidate genes of interest in other ecologically and evolutionarily relevant behaviors. (38)

McMaster, Zachary*, M. Dana Harriger, Tonia Hess-Kling, and Derek Kling Wilson College, Chambersburg, PA 17201. *Analysis on the effects of pre-operative physical therapy on range of motion in individuals undergoing total knee replacements.* — There are approximately 800,000 total knee replacement (TKR) procedures performed annually in the United States. This number is projected to increase to 3.48 million per year by 2030. This study investigated knee range of motion of patients at various timepoints after TKR surgery, as well as the total number of visits required to regain full range of motion at the knee. One group of patients underwent pre-operative physical therapy, while the other group only had post-operative physical therapy. By strengthening the quadricep muscle before surgery, less atrophy may occur. The atrophy can occur due to a condition known as muscle inhibition. Having a stronger quadricep going into surgery may result in fewer post-operative physical therapy visits. Under the guidelines of Health Insurance Portability and Accountability Act (HIPAA) and Institutional Review Board (IRB) regulations, data regarding age, body mass index, knee range of motion, and clinical visits at Waynesboro Physical Therapy and Sport's Medicine and its affiliates for patients who underwent a TKR in the previous 5 years was collected. When analyzing the data, an ANOVA and t-test will be most useful in determining the significance of differences between the groups. Analysis will also include the difference in knee range of motion at one-week post-op. A comparison of interest includes examination of BMI as it relates to the number of visits needed for pre-operative physical therapy and post-operative physical therapy vs. solely post-operative physical therapy. Preliminary data indicates that patients that undergo physical therapy prior to surgery typically have better outcomes after TKR surgery. (134)

Mekheal, Marina*, and Jessica Petko Penn State University, University park, PA 16802. *Expression of doublesex sex determination genes in the common house spider, Parasteatoda tepidariorum.* — Sex-determination pathways in vertebrates and invertebrates have been shown to utilize conserved genetic switches to induce sex-specific gene expression. Most animals, with the exception of mammals, utilize DM containing transcription factor (ex. doublesex in *Drosophila*, mab in *C. elegans*, and doublesex and mab related transcription factors DMRTs in other organisms). However, regulation mechanisms of these sex determination switches are rapidly evolving and can vary even between closely related species. The common house spider, *Parasteatoda tepidariorum*, is an emerging model for evo/devo research. Historically, basally branching arthropods, such as the arachnids, have been underrepresented in molecular developmental biology research. In addition, spiders have undergone an ancient genome duplication along with additional local gene duplications. The impact of these additional gene paralogs is of great interest in the evolution of genomes and novel traits. The purpose of this study was to determine the phylogeny and expression of doublesex gene paralogs in *P. tepidariorum*. Through a BLAST search of the transcriptome, five orthologs of doublesex were found, two of which were determined to have sex-specific expression by RT-PCR. Regulation of doublesex in many insect species often involves sex-specific splicing of doublesex. One of the six doublesex paralogs showed differential splicing between sexes. In situ hybridization indicates that these paralogs have distinct embryonic expression patterns throughout development. Paralogs with sex differences in splicing or expression are transcribed in gonads and primordial germ cells. Future studies aim to determine whether knockdown of doublesex orthologs would affect sexual development of offspring. (67)

Melo, Mercy*, Allison Cornell, and Jean-Francois Therrien Cedar Crest College, Allentown, PA 18104. *Relationships among morphological and physiological parameters in developing American kestrel chicks.* — Currently, little is known about how wild altricial birds allocate resources during development towards physiological and morphological maturation. Morphological changes, such as mass, tarsus length, and wing length, are commonly measured in birds, but only provide a somatic measure of chick development. Combined with morphological measurements, measuring physiological parameters, such as hematocrit (percent of red blood cells in the blood by volume) and metabolite concentration (glucose, triglyceride), can provide crucial insights on life history traits and population dynamics. Nestbox-breeding kestrels are an ideal study system for measuring development in nestlings because the setup allows for easy capture and

repeated measures. In addition, kestrels are known to have a varied diet which might influence individual variation. Our study aims to describe a more comprehensive view of chick development by observing morphological and physiological parameters, including hematocrit, which is linked to oxygen carrying capacity; glucose, a variable indicator of food consumption; and triglyceride concentration, an important energy storage molecule. To observe these traits, American kestrel chicks were sampled from nestboxes in Berks county, Pennsylvania, on days 7, 14, and 21 of the nestling period (hatch day= day 0), and were grouped according to nest, nestling sex, and age in order to assess development of morphological and physiological traits. Comparing data between the two sexes of nestlings reveals a significant difference in hematocrit in chicks on day 7 of development, with females having the higher mean hematocrit ($p=0.03$, $t=-2.3707$). Later in the nestling period, differences in hematocrit become less significant, but significant differences in mass appear, again with females having higher the higher mean ($p=0.05$, $t=-0.075973$). As both physiology and morphology contribute to chick quality, it is imperative to understand how these traits relate during development as the production of high-quality chicks is essential for a declining species, such as the American kestrel. (152)

Metheny, Jacob*, Samantha Lucas, Zan Usmani*, Theresa Tran, and Itzick Vatnick Widener University, Chester, PA 19013. *Effects of environmental acidification on oxidative stress in Red Swamp crayfish (*Procambarus clarkii*)*. — The average pH levels of freshwater and marine aquatic environments throughout the world are decreasing and affecting the aquatic organisms that inhabit them. This study was designed to examine the effects of environmental acidification on oxidative stress of a freshwater crustacean, the Red Swamp crayfish (*Procambarus clarkii*). We assessed oxidative stress by measuring Thiobarbituric Acid Reactive Substances (TBARS), and Glutathione Peroxidase activity (GSH) in the hepatopancreas. TBARS are a byproduct of lipid peroxidation and, GSH is one of the main antioxidant enzymes that protect cellular components from peroxides and other reactive oxygen species formed during oxidative stress. (148)

Metkus, Mary*, and Troy Shirangi Villanova University, Villanova, PA 19085. *Hormonal and neuronal control of behavioral maturation in *Drosophila melanogaster**. — Most animals undergo a period of maturation before being able to mate and reproduce. While the physiological basis of maturation has been investigated, the molecular and neuronal mechanisms underlying behavioral maturation are poorly understood. Here, we investigate behavioral maturation in the fruit fly *Drosophila*. For the first two days after they emerge as adults, *Drosophila* females are markedly unwilling to mate with males until they sexually mature. The onset of sexual maturation in *Drosophila* females is regulated in part by Juvenile Hormone (JH) and its receptor, *Methoprene Tolerant* (*Met*). The neurons that JH acts upon to regulate behavioral maturation, and how JH regulates maturation at a cellular level are unclear, however. In the present work, we identify a specific subpopulation of neurons in the female nervous system that express *Met*, and appear to regulate female behavioral maturation in response to JH signaling. These findings set the stage to understand how JH regulates maturation at cellular and molecular levels and provide general insights into behavioral maturation. (47)

Miller, Jason*, and Jessica Schedlbauer West Chester University, West Chester, PA 19383. *The influence of edge effects on soil respiration and soil carbon storage in temperate deciduous forests of southeastern Pennsylvania*. — Forest fragmentation leads to the development of edge effects, which can influence ecosystem processes such as soil carbon cycling and storage through the alteration of microclimate. However, few studies have quantified how these processes change at temperate deciduous forest edges, despite the prevalence of fragmented forests. The aim of this study was to investigate the impact of edge effects on soil carbon cycling and storage in Eastern deciduous forests of southeastern Pennsylvania during the 2018 growing season. At each of three study sites, three 100 m transects were established with plots at 5, 15, 30, 60 and 100 m from the forest edge. Monthly measurements of soil respiration, soil temperature, and gravimetric soil moisture content were made in each plot. Litter biomass, as well as composite and bulk density soil samples were collected once in each plot. Decomposition rates were also assessed in each plot via a litterbag study. Soil respiration rate and soil temperature were significantly higher at the forest edge relative to the forest interior ($p < 0.001$) and were highest in the middle of the growing season ($p < 0.0001$). Throughout the growing season, gravimetric soil moisture significantly decreased and was significantly

higher in the forest interior, relative to the forest edge ($p < 0.0001$). Litter biomass, soil carbon content, and decomposition rate did not differ significantly along the edge to interior gradient ($p > 0.05$). It is evident that edge effects alter both soil moisture and soil temperature conditions in fragmented forest ecosystems, leading to greater soil respiration rates at the edge. Anthropogenic land use change has led to widespread forest fragmentation, creating substantial edge area. As a result, a greater release of carbon dioxide is likely in fragmented forest ecosystems relative to contiguous forest, creating a positive feedback to climate change. (180)

Miller, Jessica*, and Jeanne Berk Cedar Crest College, Allentown, PA 18104. *Synthesis and characterization of N-[(1H-indol-3-yl)(phenyl)methyl]aniline via the Mannich reaction.* — Mannich bases are an important class of compounds due to their antibacterial properties. The synthesis of N-[(1H-indol-3-yl)(phenyl)methyl]aniline was accomplished via the Mannich multi component reaction, involving indole, benzaldehyde, and aniline. In the reaction, aniline and benzaldehyde react first to form a Schiff base, then it reacts with indole to form the Mannich base. The reaction was studied using different solvents with or without catalysts, or ionic liquids based on butylmethylimidazolium [BMIM] to determine the best reaction conditions and yield. The results showed that water gave the fastest reaction time, 45 minutes, while the ionic liquid [BMIM]Tfa (trifluoroacetic acid) gave the easiest workup and greatest yield at 74%. The use of trifluoroacetic acid as a catalyst with water as the solvent increased the average yield from 22% to 49%, while the other catalysts showed no increase. The reaction was followed using TLC and showed that all of the reactions formed the same product. Products were purified and characterized using infrared spectroscopy (FT-IR) and proton nuclear magnetic resonance spectroscopy (^1H NMR) showing that all of the reactions yielded the same product. (21)

Moreira, Victoria*, and Elizabeth Skendzic Delaware Valley University, Doylestown, PA 18901. *Change in photosynthetic activity in deciduous trees as photoperiod decreases.* — The research project conducted in fall of 2018 tested the hypothesis that the photosynthetic activity in deciduous trees would gradually decline as the season progressed. This decline could be measured through various parameters with a handheld instrument, the MultispeQ designed by PhotosynQ. Approximately four times a week over the course of nine weeks, the MultispeQ was used on five selected deciduous trees (two *Cornus florida*, one *Quercus coccinea*, and two *Magnolia virginiana*) to measure several parameters. One relationship found was between the amount of relative chlorophyll and the quantum yield of Photosystem II. Amount of relative chlorophyll maintained a steady rate within each of the trees until a steep drop when the molecule was quickly deconstructed. Photosystem II, which uses chlorophyll to harvest energy from light, showed a gradual decrease in quantum yield even as chlorophyll levels were constant. The results of this study give potential directions for future work with MultispeQ at Delaware Valley University, given the extensive presence of agriculture on the campus. (182)

Morgan, Alexandra*, and Andre Walther Cedar Crest College, Allentown, PA 18104. *Optimization of growth conditions for biodiesel fatty acid production in the oleaginous yeast Cryptococcus neoformans.* — Fossil fuels such as coal, natural gas, and crude oils supply roughly 81% of the energy that is consumed each year in the United States, but these fuels are in finite supply and their combustion is harmful to the environment. This has led to increased efforts to find alternative fuels sources that are cost efficient, as well as clean burning. The major goal of this project is the production of biodiesels that are made from lipids such as fatty acids isolated from biomass. Our focus is on oleaginous microorganisms that produce large amounts of lipids giving them oily characteristics. One often used organism is the oleaginous yeast *Rhodoturula glutinus* that produces a fair amount of lipids and is easy to grow, however it requires expensive sugars to grow and few molecular tools available for genetic enhancement. We have chosen to examine the well-studied, oleaginous yeast *Cryptococcus neoformans* a source of biomass for biodiesel production. Due to *C. neoformans* clinical significance in causing infections in immuno-compromised individuals, there is extensive knowledge concerning its genome, and a number of tools that have been developed for genetic manipulation. We have shown that avirulent mutant strains of *C. neoformans* produce not only comparable, but better lipid yields than what has been seen with *R. glutinus*, indicating that *C. neoformans* may be a better organism for use in the production of biodiesel fuel. We are in the process of

examining growth with mutant strains of *C. neoformans* and altering liquid medias, as well as carbon sources, to optimize lipid yield. The ability to use *C. neoformans* as source of biomass for lipid production provides an exciting novel renewable source of biodiesel. (11)

Muller, Rebecca*, and Akeisha Belgrave Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Relating bacterial cell wall synthesis to bacterial antibiotic susceptibility*. — Antibiotic resistance is a growing concern to both the medical/pharmacological community and the general public. As efforts to decrease the prevalence of such resistance are underway, an important consideration is the morphology and mechanisms of the targeted bacteria. Gram negative, rod-shaped bacteria have a cell wall containing approximately 1-3 layers of peptidoglycan (PG) meshwork. The protein-mediated synthesis of this meshwork allows for an increase in length of the bacteria without significant change in width and occurs in a three-fold process: 1) severing peptide crosslinks, 2) inserting new glycan-based material, and 3) re-crosslinking of peptide bonds. The current study evaluates the independence of the rates at which these steps occur and their relationship to cell susceptibility. *Escherichia coli* NR698—a strain with imp4213 deletion and a resulting permeability of the outer membrane—was grown to varying cross-link densities and treated with a fluorescent conjugate of vancomycin, as well as Wheat Germ Agglutinin 488, which binds to the cell wall. After fluorescent observation of cells, cross-link density seems to have a negative relationship with cell susceptibility. (83)

Mullin, Samantha*, Claire Gogel*, and Joseph Leese DeSales University, Center Valley, PA 18034. *House Hunters: Cichlid Edition – Females in a monogamous pair determine nest site location*. — For territorial animals, one of the most important decisions faced during their lifetime is determining where to establish a territory. This is especially true when a territory includes a breeding substrate or nest site. For many taxa, decisions about territory sites are made individually, but for monogamous species, a pair-bond may form prior to a territory and nest site being selected. Here, we explored which sex might be more likely to choose a nest site using a monogamous fish, the convict cichlid, *Amatitlania siquia*. In nature, little is known regarding how and when convict cichlids choose nest sites, but studies suggest a combination of strategies in which either the male selects the nest site before courting females or the pair selects a site together. Based on this, we hypothesized that males are more likely to determine a nest site, even after a pair-bond has formed. We tested this hypothesis by observing pair-bond formation; then after a pair-bond formed, we placed males and females in separate compartments of a divided aquarium with their own nest site. After 24 hours, the divider was removed, and the location of both individuals in the aquarium was observed for several days. Overall, females seemed to stay with the nest site they were acclimated to, and the males showed less preference, in many cases moving to the female side. These results suggest that the female, rather than the male, may be more likely to choose both territory and nest site after pair-bond formation in this system. While unexpected, this result could indicate that females have been selected to be more discerning of nest sites as they require smooth surfaces to deposit their eggs. To support and clarify our results of which sex determines the nest site, we increased the male nest site quality by adding artificial plants for cover. (50)

Nekich, Payton*, and Christine Proctor Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The mental health benefits of exposure to nature*. — Many people believe that living near green space is beneficial to our health and state of wellbeing. Researching the validity of this statement is increasingly important as diagnosed cases of depression increased by 18.4% between 2005 and 2015 and greater than 50% of the world's population lived in urban environments by 2015. Indeed, there is growing evidence that better mental health is linked to green space like community gardens or parks found throughout urbanized areas. Previous research points towards the amount of vigorous physical exercise performed in an outdoor setting, elements of natural environments, and family history of mental illness as contributing factors. Therefore, I hypothesized that Harrisburg, PA residents who spend more time in green space will identify as having better overall mental health. To assess this, I distributed a survey to adult city residents via community Facebook pages. The survey included closed-ended questions based on a scale rating from 0 to 4 and covered the following 4 categories: background, mental health, primary workspace, and the environment. No identifying information was collected. Over a 7-week period, a 144 complete responses

were received. Survey results were analyzed using a one-way ANOVA with significance set at a p-value of 0.05. Mental health tracked the number of outdoor walks per week except for the 50 and above age group, who experienced better mental health as compared to all other age groups. This suggests that other factors not included in this study contributed to improved mental health for adults 50 and older. The study did not find any statistically significant relationships however, a trend was found supporting my hypothesis that exposure to natural air and sunlight improved overall mental health. These results highlight the importance of urban green space for urban resident wellbeing. (186)

Nolt, Makenzie*, and Jessica Petko Penn State University-York, York, PA 17403. *Addiction behaviors in female Parasteatoda tepidariorum*. — Addiction is a dysfunction of the natural reward system. The natural reward system is what drives organisms to eat, drink, and reproduce. Over the years, humans have found a way to stimulate the natural reward system with other substances such as drugs and alcohol. The molecular basis of the artificial stimulation of the reward system is not completely understood; however, a common component in the mechanism of all drugs of abuse is the neurotransmitter dopamine. Addictive substances cause overstimulation of dopamine receptors leading to a rewarding feeling which encourages the organism to repeat the behavior. This role for dopamine is evolutionarily conserved in many invertebrate (nematode worms and insects) and vertebrate (rodents, fish, primates) models which all have demonstrated an affinity for drugs of abuse. Arachnids are an interesting model for the study of evolutionary neurobiology because of an ancient genome duplication. This duplication has led to multiple copies of genes for most neurotransmitter receptors and neurotransmitter synthesizing enzymes. In the 1950's, famous studies by Peter Witt demonstrated that spider web patterns of orb weaving spiders are altered by addictive substances. However, it remains unknown whether spiders find these drugs rewarding. In this study, I designed a conditioned place preference apparatus to study the behaviors of the common house spider, *Parasteatoda tepidariorum* (*P. tep*). Mature female *P. tep* were offered 10% ethanol or distilled water through q-tips and their behavior was recorded for several weeks. The results show that female *P. tep* spiders made more contacts with alcohol-soaked q-tips, spent more time drinking at alcohol-soaked q-tips, and built more of their webs on alcohol-soaked q-tips as compared to those that chose water-soaked q-tips. These results suggest that female spiders do find alcohol rewarding. Future studies will aim to test the role of dopamine and duplicated dopamine receptor genes in these behaviors. (45)

O'Neill, Justin*, and Josiah Townsend Indiana University of Pennsylvania, Indiana, PA 15705. *Exploring species boundaries in mesoamerican coastal leopard frogs through the application of ecological niche models in a phylogenetic context*. — True frogs (Family: Ranidae), represent a cosmopolitan group of amphibians with a confused and contentious taxonomic history. Despite the family's ubiquity and widespread usage as a model organism, Ranidae suffers a lack of attention from systematic biologists, especially those species in Mesoamerica. South of Mexico there are potentially dozens of unrecognized or unnamed lineages, many incorrectly assigned or invalid species, and a lack of knowledge on the distributional limits of existing species. Recent phylogenetic analysis of Mesoamerican leopard frogs has revealed two geographically distinct clades: a Pacific coastal clade and a Caribbean clade. Two sister species represent the Caribbean clade: *Rana brownorum*, currently believed to be inhabiting low to mid elevations in the south-eastern Mexico, Guatemala, and Honduras, and *Rana taylori*, considered to occupy low and mid elevations in Nicaragua and Costa Rica. The distributional limits of these two species remain uncharacterized. To offer some taxonomic stability to these species, the current study sought to delimit potentially suitable distributional areas via ecological niche modeling (ENM). We constructed models with the ENM software packages MAXENT and WALLACE. Our modeling efforts produced two Caribbean coastal distributions that corroborate the existence of a previously hypothesized contact zone in eastern Honduras/Northeastern Nicaragua. These results provide impetus for further sampling efforts to investigate the predicted contact zone and the factors that help these two species remain distinct. (63)

Olaoye, Ibukunoluwa*, and Michael Foulk Mercyhurst University, Erie, PA 16546. *Using fluorescent in situ hybridization (FISH) to map amplicons in the larval salivary gland polytene chromosomes of the fungus fly, Sciara coprophila*. — As a normal part of larval development in the fungus fly, *Sciara coprophila*, the salivary gland DNA replicates multiple times without intervening mitoses. The copies remaining synapsed

together in strict register, resulting in the creation giant polytene chromosomes. After polyenization individual origins of replication at up to 18 loci fire several more times leading to localized DNA amplification. Subsequent transcription of the genes at these loci results in the formation of DNA puffs. One of these puffs, at locus II/9A, has been extensively studied but little is known about the others. Recently, the *Sciara* genome was sequenced and assembled and as a part of this project 13 regions that are in the polytene chromosomes were identified. The purpose of this research is to map the locations of these newly identified amplicons to the DNA puffs in the larval salivary gland polytene chromosomes of *Sciara coprophila* using fluorescent *in situ* hybridization (FISH). Initially, the well-characterized II/9A DNA puff will be used to test and optimize the FISH protocol for its use on other amplicons. An amplicon specific probe will be generated using polymerase chain reaction (PCR) then labeled with a fluorescent tag. This probe will then be hybridized to the polytene chromosomes and will be observed by fluorescence microscopy. The location of fluorescence will indicate the location of the amplicon on the polytene chromosomes. Once the protocol is optimized with the II/9 locus, it will be used to map the newly identified amplicons, whose locations with the *Sciara* genome are currently unknown. (78)

Orner, Amber*, Justin Sweitzer, John Harms, and Lawrence Mylin Messiah College, Mechanicsburg, PA 17055. *Immunotherapy targeting an insertion sequence in an altered tumor-associated growth receptor associated with aggressive pancreatic cancers.* — With a five-year survival rate of 7%, pancreatic cancer is one of the most lethal forms of cancer. Recent studies have found that a misspliced variant of the cholecystokinin (CCK) receptor that retains a 69 amino acid intron-encoded segment is associated with aggressive pancreatic cancers. While normal CCK receptors bind gastrin and signal for increased production of digestive enzymes, the lengthened CCK2_{i4sv}R receptor variant also appears to promote increased cell proliferation through autocrine stimulation and may enhance the outgrowth of aggressive pancreatic tumors. The intron-encoded segment represents a potential target for T cell-mediated immunotherapy because it is located in a cytoplasmic loop of the receptor. We have found that immunization of C57Bl/6 mice with a synthetic peptide corresponding to 20 amino acids of the variant receptor intron-encoded sequence stimulates the induction of T cells. In the present study, we sought to determine whether intron-peptide-specific T cells could control the formation of tumors by PANC02 murine pancreatic tumor cells engineered to co-express the CCK2_{i4sv}R variant human receptor. Groups of mice were immunized three times at weekly intervals with emulsions containing the intron peptide or a control peptide mixture. Peptide-specific T cell responses were confirmed in a subset of each group by ELISPOT, and pre-determined numbers of cultured PANC02-CCK2_{i4sv}R cells were transplanted into both flanks of each of the remaining immune mice. Tumor progression was monitored over four weeks after which tumors were excised and preserved for histological analysis, and splenic frequencies of peptide-specific T cell frequencies were measured by ELISPOT. Both intron-peptide-specific and control-peptide-specific T cells were detected in varying frequencies in tumor-bearing individuals from each group. While immunization with the intron-peptide did not prevent progression of the transplanted tumors, the presence of the intron-peptide-specific T cells appeared to correlate with a reduced rate of tumor growth. (199)

Owens, Allyson*, Rachel Stubler, and Quyen Aoh Gannon University, Erie, PA 16541. *The role of trans-golgi network and endosomal adaptors in nitrogen-regulated growth of Saccharomyces cerevisiae.* — Cell membrane trafficking is the transportation of vital cellular materials, such as nutrients, waste products, and proteins between the plasma membrane and organelles. Membrane trafficking is facilitated by a host of proteins that concentrate cargo and mediate vesicle formation. The ability to correctly regulate membrane trafficking under different environment conditions is essential for cell growth. In this proposal, the role of trafficking in regulating cell growth under different nitrogen conditions is examined using the yeast *Saccharomyces cerevisiae*. Specifically, we worked to determine how clathrin adaptors that function at the *trans*-Golgi Network (TGN) and endosomes regulate cell growth in preferred and non-preferred nitrogen sources. We used spectrophotometry to measure the growth of mutant yeast with various deletions of clathrin adapters. The results of this study will add to a growing body of knowledge of how clathrin adaptors affect the overall fitness of the cell and may reveal how membrane traffic is differentially regulated depending on environmental conditions. (106)

Paul, Maggie*, and Ronald Kaltreider York College of Pennsylvania, York, PA 17405. *Over-expression of JAG1; how it alters Notch3, NF- κ B, NOS, and how these pathways affect Duchenne Muscular Dystrophy.* — Duchenne Muscular Dystrophy (DMD) is recessive progressive degenerative muscular disorder, caused by a mutation occurring in the dystrophin gene. The progression of the disorder leads to muscle loss in patients starting with the legs and continues until it affects the heart and lungs leading to death. Multiple pathways such as NOCTH3, NF- κ B and NOS are linked in the progression of this disorder, and the protein JAG1 has recently been linked as well. JAG1 is a signal protein that helps adjacent cells communicate through NOTCH receptors by a series of signaling reactions. To clarify whether this protein is involved with DMD, we used human skeletal muscle cells (SJCRH30) from the bone marrow of cancer patient, with JAG1 overexpression plasmid. Cells were transfected with plasmid alone or in combination with TNF-alpha. RNA was isolated from the untreated and treated cells, and gene expression was determined for JAG1, NOTCH3, NF- κ B, NOS, and Dystrophin using RT-qPCR. Our results demonstrated that JAG1 had no effect on gene expression levels for NOTCH3 and NF- κ B alone or in combination with TNF-alpha. Cells treated with TNF-alpha alone showed a decrease in the expression of Dystrophin. These results demonstrate that JAG1 does not influence on the NOCTH3, NF- κ B, and NOS gene expression, suggested that it does not play a major role in these signaling pathways. However the relation between JAG1 and dystrophin remains unclear. As JAG1 has been indicated in DMD, further studies are required to establish the role it plays in this disease. (97)

Perez, Christina*, Michael Shin, and Richard Schaeffer Messiah College, Mechanicsburg, PA 17055. *Heavy Metal Ion Toxicity and its Effect on Arabidopsis thaliana mutants rack1b, rack1c, and mtp1.* — *Arabidopsis thaliana* was used as model system to study how plants respond to and process heavy metal ions. This experiment studied three genes that were potentially involved in plant responses to heavy metal ion stress: *rack1b* and *rack1c*, which encode for scaffolding proteins involved in stress responses to abiotic stressors, and *mtp1* which encodes for a vacuole cation transporter. These mutants were studied using a tolerance assay to view their response in various concentrations of Cd²⁺, Ni²⁺ and Zn²⁺. An accumulation assay using Ni²⁺ was also run for the *rack1c* and *rack1b* mutants. The *rack1c* mutants were more tolerant of Cd²⁺ at 60 μ M. They behaved like the wild type on the other metals however, they absorbed less nickel than the wild type in the accumulation assay. The *rack1b* mutant showed no growth or tolerance differences from the wild type. It could not be determined whether the *mtp1* had differences in tolerance compared to the wild type at all concentrations on Cd²⁺ and Ni²⁺. On Zn²⁺ the *mtp1* mutants had overall shorter root lengths compared to the wild type, however these mutants also demonstrated a greater number of secondary roots. Previous research on *mtp1* mutants under abiotic stress discussed how this could represent a protective mechanism adopted by the plants¹, although for the purposes of this experiment this cannot be determined until an accumulation assay is run. It also had decreased symptoms of chlorosis as compared to the wild type. ¹Desbrosses-Fonrouge A-G, Voigt K, Schröder A, Arrivault S, Thomine S, Krämer U. *Arabidopsis thaliana* MTP1 is a Zn transporter in the vacuolar membrane which mediates Zn detoxification and drives leaf Zn accumulation. FEBS Letters. 2005;579(19):4165-4174. doi:10.1016/j.febslet.2005.06.046. (120)

Perrin, Alexia*, and Mel Zimmerman Lycoming College, Williamsport, PA 17701. *A limnological assessment of Rose Valley Lake.* — Rose Valley Lake is 369-acre man-made reservoir located in Lycoming County and managed by the PA Fish and Boat Commission for recreational fishing and boating. Since 2000, the Lycoming College Clean Water Institute (CWI) has been a partner with the Loyalsock Creek Watershed Association to complete the chemical and biological assessment of the lake. Carlson's Trophic State Index (TSI) for lakes was created so that scientists can measure and record on a scale of 0 to 100. Each major division (10, 20, 30, etc.) represents a doubling in algal biomass. The index score/ calculation uses data on Secchi disk transparency, chlorophyll, and total phosphorus. These quantities and other biologically helpful nutrients are the primary factors of a body of water's TSI. Nutrients such as nitrogen and phosphorus have a tendency to be limiting resources in standing water bodies, so amplified concentrations tend to result in increased plant growth, a body of water's trophic index is used to make a rough estimate of a lakes biological condition. Over the last decade the lake has been changing from mesotrophic to eutrophic. This year the lake appears to be trending from Eutrophic to Hypereutrophic (TSI of 60-100). This trend indicates

the lake is in transition from the highest amount of biological activity to possible reduction in water quality. In addition, zooplankton samples were taken and show a dominance of rotifers especially *Keratella*. (150)

Pham, Lauren*, and Ann Yezerski King's College, Wilkes-Barre, PA 18711. *Physiological Effects of Environmental Atorvastatin on Northern Leopard Frogs (*Rana pipiens*)*. — As global usage of pharmaceuticals increases annually, so does the buildup of residual and metabolites of pharmaceuticals and personal care products (PPCPs) in the resulting effluent wastewaters and their interacting waters. Studies have shown various effects of these PPCPs on fish species both physiologically and behaviorally; however, studies on other aquatic vertebrates is lacking. Frog species are considered indicator organisms in that they are often the first to respond to environmental changes. This study aimed to test the physiological effects of the anti-cholesterol medication, Atorvastatin, on Northern Leopard frogs (*Rana pipiens*). Atorvastatin has been reported as the most frequently used lipid regulating drug available and therefore appears frequently in wastewater analysis. One of the most notable, negative aspects to using Atorvastatin is that in many instances patients have reported chronic or extreme muscle pain, weakness, and in severe cases myopathy. Therefore, the presence of this pharmaceutical in environments interacting with wastewater may have an effect on the aquatic and semi-aquatic animals, including amphibians that are dependent on the waters. A group of 45 frogs were split between Control, Low, and High experimental groups and were treated while living in aquaria that contain varying levels of Atorvastatin (0.02 µg/L and 0.24 µg/L based on values for treated wastewater and ten-fold those values averaged from the literature). Human dosage is typically 40 mg/day, which is about 200 times the highest concentrations in the experimental groups. Physiological testing was done using the sciatic nerve to stimulate the frogs' lateral gastrocnemius muscle. The muscles were stimulated at various voltages and frequencies to test the muscle sensitivity, strength, and reaction time. Measurements included: minimum and maximum thresholds of contraction, maximum twitch, latency of contraction, and tetanus. (149)

Plumer, Mariah, Nilang Suthar*, and Jill McCue King's College, Wilkes-Barre, PA 18711. *The Synthesis of water-soluble porphyrins/metalloporphyrins and the interrogation of their interaction with quadruplex DNA*. — Water-soluble porphyrins constitute a versatile class of compounds that have received attention for their affinity for DNA and their potential use as therapeutic and diagnostic agent in cancer treatments. Previous studies on porphyrin-DNA interactions focused on charged water-soluble porphyrins. In the case of cationic porphyrins, the binding modes (intercalation, outside groove binding (major and minor) with or without self-stacking on the surface of the DNA) are driven by electrostatic attractions between the negatively charged phosphate groups on the DNA backbone and the positively charged porphyrins. However, cationic porphyrins have shown minimum or no selectivity for quadruplex DNA against duplex DNA, which is of specific interest. Neutral porphyrins have attracted much less attention due to the limited number of neutral water-soluble porphyrins. This study aims to focus on the synthesis of neutral pyrrole-modified, water-soluble porphyrins and their metal-complexes, which have yet to be studied. Specifically investigating the non-electrostatic interactions with human telomeric AG₃(T₂AG₃)₃ G-quadruplex DNA (Tel22) using UV-Vis spectroscopy and Surface Enhanced Raman Scattering (SERS). (30)

Polanco, Laura*, Robert Kurt, and Chun Wai Liew Lafayette College, Easton, PA 18042. *Analysis of multiple signaling pathways in human monocytes using an experimental and computational approach*. — Mechanisms within a host work on a molecular level to carry out communication to ensure the survival and proper functioning of the organism. The toll-like receptor (TLR) signaling pathway plays an important role in communication between the immune system and possible threats to an organism. Previously we used an agent-based model to study the TLR signaling cascade in tumor cells and white blood cells. The model and experimental data revealed that the distinct responses elicited by tumor cells and white blood cells were related to different levels of specific signaling components including positive (NFκB, TAB3) and negative (IRAKM) regulators of TLR signaling. Here we focused on the TLR signaling pathways in a monocyte cell line (THP-1) to model the behavior of human monocytes. We used increasing concentrations of lipopolysaccharide and flagellin added to THP-1 cells to study the TLR4 and TLR5 signaling cascades respectively. Data from the TLR5 single signaling cascade showed a steady increase in NFκB activation, while data from the TLR4 signaling cascade showed an increase at an earlier dose of agonist followed by a

decline in NFkB activation. These data may indicate that TLR4 has greater sensitivity to its agonist than TLR5. Data from the computational models look similar to the experimental data supporting the utility of the models. Because cells in an organism rarely receive a single signal at any given time we are completing analysis of simultaneously treating the THP-1 cells with both LPS and flagellin to determine the impact of dual signaling in the monocytes. Our work is continuing this research to model the relationship between multiple signaling pathways in order to gain a greater understanding of cellular communication. (77)

Polohovich, Sarah*, and Jessica Schedlbauer West Chester University, West Chester, PA 19383. *Changes in carbon distribution, structure, and composition in an isolated forest fragment: implications for future management.* — Pressures from white-tailed deer browsing, non-native species, forest fragmentation, and changing climate threaten the carbon storage capacity and community composition of many Eastern deciduous forests. As forests age they can shift from carbon sink to source as older trees die, creating a positive feedback to climate change by releasing CO₂ to the atmosphere. Further, pressures on Eastern deciduous forests are known to lead to low recruitment and a more homogenous forest that is less resilient to disturbance. The potential for these negative consequences was explored in the Gordon Natural Area, an Eastern deciduous forest in southeastern Pennsylvania. Study objectives were to quantify changes in three major carbon pools, aboveground biomass (AGBM), belowground biomass (BGBM), and coarse woody debris (CWD), as well as determine structural (stem density, AGBM) and compositional changes over a five-year period. Nine 0.2 ha plots were censused in 2013 and 2018 to determine species and quantify the parameters above. The quantity of carbon in living and dead biomass has grown significantly ($p < 0.05$), as total AGBM and CWD increased significantly over the five-year period (325 ± 22 to 361 ± 22 Mg ha⁻¹ and 13 ± 3 to 24 ± 6 Mg ha⁻¹, respectively). When broken into stem diameter size classes, stem density and AGBM increased significantly in large diameter trees (60+ cm, $p < 0.01$). Small diameter trees were mainly comprised of Norway maple (*Acer platanoides*) and American beech (*Fagus grandifolia*), while the canopy was dominated by tulip poplar (*Liriodendron tulipifera*) and oak species (*Quercus* sp.). As more large trees die, an increased release of CO₂ to the atmosphere is likely, thereby amplifying the effects of climate change. Additionally, the understory tree species that replace aging canopy trees will result in a future forest that is more homogenous, with abundant non-natives, thereby jeopardizing important forest ecosystem services. (181)

Quain, Melanie*, Jan Janecka, and Lisa Ludvico Duquesne University, Pittsburgh, PA 15282. *Genetic Variability of White-Tailed Deer (*Odocoileus virginianus*) in Southwestern Pennsylvania and Applications for Forensics.* — White-tailed deer, *Odocoileus virginianus*, became scarce during the 20th century, prompting conservation efforts by hunters and wildlife managers focused on recovering species. Various strategies were implemented, including: reintroductions from areas that still had large deer populations; developing bag limits; and seasonal restrictions. This effort was very successful leading to the recovery of white-tailed deer across the U.S. Currently, white-tailed deer are one of the most abundant and widely-distributed large-bodied mammals in North America. In addition, they are one of the most important game species. However, there are several important management concerns. In numerous states, including Pennsylvania, Chronic Wasting Disease (CWD) negatively impacts deer populations and has become a major health concern. In addition, there are areas where poaching of deer negatively affects management and reduces legal hunting opportunities. Population genetics provides important information on demography history and the structure of populations, which can be applied to forensics to combat poaching. We genotyped 14 microsatellites for 96 white-tailed deer from southwestern Pennsylvania to examine levels of genetic diversity in this area of the state. The number of observed alleles range from 11-16 alleles with the observed heterozygosity ranging from 0.526-0.974 and the expected heterozygosity ranging from 0.790-0.910. Landscape connectivity is important to understand because dispersal across the landscape affects the spread of CWD in Pennsylvania. In addition, we have developed a molecular panel to assist the Pennsylvania Game Commission in prosecuting poachers by identifying individual deer in forensic samples. Exploring genetic variation of white-tailed deer provides important insights into the population dynamics of this important species and aids in development of tools for wildlife management and law enforcement. (80)

Rabin-Court, Joelle*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *DNA methylation and X-linked microRNAs associated with lung cancer sex-disparities.* — Lung cancer is the leading cause of cancer-related deaths and has the third-highest incidence of all cancers in the United States. Males have a higher lung cancer incidence than females. The average age of diagnosis for lung cancer is 70. For reasons unknown, recent studies and epidemiological data have observed young females ages 30-49 have a higher lung cancer incidence than young males. Females have consistently lower smoking prevalence than males, even as smoking rates have declined amongst all adults in recent decades. MicroRNA (miRNA) genes encode short, noncoding RNAs which inhibit translation of protein-coding genes. DNA methylation is an important epigenetic regulator of miRNA gene expression. Strong evidence exists of sex-specific differences in DNA methylation and miRNA expression. This suggests a biological basis for the disparity. To our knowledge, no study to date has explored X-inactivation status and if it varies by age and sex. We identified 28/118 X-linked miRNAs proven to be associated with lung cancer. Using the Partek Genomics Suite 7.0 Methylation Workflow, a total of 9/28 X-linked miRNAs were differentially methylated by sex: *MIR384*, *MIR509-1*, *MIR542*, *MIR502*, *MIR98*, *MIR374A*, *MIR503*, *MIR106A*, and *MIR450B* (1-way ANOVA, $P + FDR = <0.05$). GraphPad Prism 7.03 analyses revealed none of these corresponded with differential miRNA expression (two-tailed t-test, $P + FDR = <0.05$). Interestingly, 1/9 differentially methylated X-linked miRNAs (*MIR503*) demonstrated variable X-inactivation (0-36%). When stratified by both age and sex, we observed a statistically significant difference in DNA methylation between young females (40-49 years) and young males (42-49 years). However, this trend did not hold when comparing young females (40-49 years) and older females (50-87 years). Our findings prompt further investigation into the biological pathways regulated by these 9 X-linked miRNAs associated with lung cancer, and potentially their co-occurrence with sex hormone status. (1)

Rachii, Diana*, and Maria Winters Delaware Valley University, Doylestown, PA 18901. *Synthesis and acid/base properties of o-benzylhydroxylamine inhibitors of indoleamine 2,3-dioxygenase.* — Recent studies on Indoleamine 2,3-Dioxygenase (IDO1) catalytic mechanism in kynurenine pathway linked its contribution to immune escape by tumors. IDO1 inhibition has a potential to treat cancer and restore a normal antitumor immune response. IDO1's catalytic mechanism through a heme iron bound alkylperoxy intermediate state has been considered in the proposed design of inhibitors. The two inhibitors, 2,4-dichlorobenzyl hydroxylamine and 3-iodobenzyl hydroxylamine, were synthesized to mimic the alkylperoxy species of IDO1's catalytic mechanism. The drugs were purified and isolated as their hydrochloride salts. pK_a values were determined to study acid/base properties of the compounds. (33)

Raffensberger, Nathan*, Marielle Roberts-McDonald, and Barbara Fenner King's College, Wilkes-Barre, PA 18711. *The effects of BV2 microglial cells on glutamate-stressed SH-SY5Y cell death.* — Inflammation is a common factor in neurodegenerative diseases such as Alzheimer's and Parkinson's. Microglial cells are brain immune cell that are important in removing cellular debris, phagocytosing injured or apoptotic neurons, and neurite pruning during development and learning. In Parkinson's disease, the LRRK2 protein is associated with increased microglial activity leading to pathological destruction of healthy or reversibly distressed neurons. We are interested in understanding the local chemical signaling and cell-cell interactions driven by BV2 microglial cells that result in neuronal death. The present study investigated the effects of BV2 microglial supernatants on healthy and reversibly-distressed SH-SY5Y cells (neuroblastoma cells line). Specifically, differentiated SH-SY5Y cells were reversibly stressed with 100mM glutamate or reduced serum media (control) for 24 hours. The presto blue survival assay and bright field microscopy were used to determine the effects of the BV2 microglial cell supernatants on cell death. We hypothesize that microglial-induced neuronal death requires neurons to be pre-stressed. Our preliminary data suggest, based on Unpaired T-Test there is significant difference ($p = 0.0309$), between SH-SY5Y cells that were exposed to 100mM of glutamate and those that were not. This data needs to be further investigated when determining if BV2 has neuroprotective properties. (76)

Reeves, Christa*, Kristen Roth*, and Paul Wilson East Stroudsburg University, East Stroudsburg, PA 18301. *From golf course to wildlife refuge; quantifying restoration efforts with low-cost sensor technology using stream discharge and turbidity.* — With natural landscapes becoming increasingly scarce, the issue of

restoration is of the utmost importance. Abandoned agricultural land has been the traditional target of restoration efforts. However, due to shifting pastimes and economics, the popularity of golfing has declined resulting in golf course closures opening large tracts of land for restoration. Cherry Valley is a 193-acre parcel in the Pocono Plateau that is home to a large number of Federal Trust species, including 5 federally listed threatened or endangered species. Cherry Creek, which runs through Cherry Valley, drains into the Delaware River, providing drinking water for 15 million people. The quality of water that reaches the Delaware depends on healthy riparian corridors along its tributaries. As a golf course the Cherry Valley site was stripped of natural vegetation and planted with ornamental/invasive species. This former golf course is now being restored as part of the Cherry Valley National Wildlife Refuge. Native vegetation is being replanted and riparian corridors restored. A control site with a well-protected woody wetland and an above average riparian zone at Aquashicola Creek was studied for comparison to quantify change at Cherry Valley. Low cost Mayfly data loggers have been employed along with periodic supplemental grab samples on both systems. Real-time monitoring, starting in May of 2017 for Cherry Creek and July at Aquashicola Creek, has allowed the parameters of discharge, temperature, conductivity and turbidity to be assessed both prior to, during and following storm events. Using rainfall data provided by Hobo self-tipping rain buckets, we have been able to construct highly accurate hydrographs to depict discharge lag times on both the Aquashicola and Cherry creeks. Ecological change and restoration efforts are slow and difficult to assess, but as the restoration at Cherry Valley progresses the long-term change can be quantified by using these two parameters. (126)

Replogle, Kirsten*, and Lindsey Welch Cedar Crest College, Allentown, PA 18104. *Solvent effect on the hydrogenation of α -methyl-trans-cinnamaldehyde with the use of metal chloride additives.* — The compound α -methyl-trans-cinnamaldehyde is often used in fragrances and flavorings. It also serves as a model compound for selective hydrogenation. Results of the investigation of the hydrogenation of this compound using Pd/C in various solvents and hydrated metal chlorides will be presented. The solvents used were isopropyl alcohol (IPA), toluene, cyclohexane, and acetonitrile. The hydrated metal chlorides used were $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$, $\text{SnCl}_2 \cdot 2\text{H}_2\text{O}$, $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$, and $\text{NiCl}_2 \cdot 2\text{H}_2\text{O}$. Reactions were carried out at atmospheric pressure using a hydrogen balloon. Progress was monitored with a GC/MS. Both nonpolar aprotic solvents, cyclohexane and toluene, were more selective than the polar protic solvent, IPA. Between the two nonpolar aprotic solvents, toluene produced a higher percent conversion under all conditions tested. The reduced selectivity of cyclohexane compared to toluene follows a trend previously stated in literature. In all solvents tested, $\text{SnCl}_2 \cdot \text{H}_2\text{O}$ had the lowest percent conversion. $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ was the least selective metal chloride tested in all solvents. Toluene, cyclohexane, and IPA were all non-selective towards the unsaturated alcohol product. The unsaturated alcohol, β -methylbenzenepropanol, was observed in acetonitrile, but the reaction was not selective towards its formation. Comparison of these results to those of cinnamaldehyde may explain the mechanism of hydrogenation for these aromatic aldehydes. (32)

Robbins, Taylor*, Allison Cornell, and Jean-Francois Therrien Cedar Crest College, Allentown, PA 18104. *Differences in biparental behavior in Falco sparverius depending on sex.* — Biparental relationships involve a male and female both taking care of their offspring. We studied the parenting behavior of *Falco sparverius* (American kestrels) which are known to be biparental, in order to assess if time spent performing parental care such as incubation and feeding trips was equal among the sexes. During the Summer of 2018, 9 nest boxes located around Hawk Mountain Sanctuary in Kempton, PA were recorded from a distance with a video camera for one hour on 6 days, equaling 6 hours of video for each nest box. The video recordings were reviewed and the sex of the parent, number of visits for each parent, length of each parent visit, incubation time, and type of prey brought back were recorded. In total, females visited their nest boxes twice as much as males (42 vs 20 visits total). Females incubated their young eleven times longer than males (248 vs 22 minutes total), and females brought back 1.5 times more prey than males (14 vs 9 prey total) over the 54 hour observation period. These findings suggest that even though both sexes provide for their young, females spend more time than males. This could be due to the males' uncertain paternity of the offspring or the males could be contributing more during pre-hatching care or post-fledging

care. The males' behavior could also be unnoticed as they could be delivering prey to the female off camera. (136)

Ross, Ashley C.*, Adriana E. Sorrentino*, and Audrey J. Ettinger Cedar Crest College, Allentown, PA 18104. *In ovo assays investigating potential roles of Hypericum perforatum and Δ^9 -tetrahydrocannabinol in biological development.* — Herbal remedies, such as *Hypericum perforatum* and Δ^9 -tetrahydrocannabinol extracted from *Cannabis sativa*, are currently studied as antioxidants that provide neuroprotective effects. However, substances that provide neural protection in adults may also act as teratogens in developing embryos, causing disruptions that result in birth defects. Since many herbal remedies are available as over-the-counter products, pregnant women may consider them safe for ingestion, posing a potential risk to fetal development. The current study investigated the effects of two herbal remedies on embryonic development using *Gallus gallus* as a model system. Chicken eggs were injected on day five post-fertilization with solutions of over-the-counter *Hypericum perforatum* or chemical-grade Δ^9 -tetrahydrocannabinol, at either a concentration comparable to the expected human blood concentration or five times that concentration, and incubated for seven days. On day 12 post-fertilization, embryos were sacrificed, dissected, and assessed in comparison to control embryos. In initial experiments, embryos treated with *Hypericum perforatum* showed no visible external abnormalities, but internal organs appeared to have less clearly defined borders compared to control embryos observed at this stage in development. Embryos treated with Δ^9 -tetrahydrocannabinol showed no visible external or internal abnormalities that indicate a disruption in development. During dissection, tissues were isolated and stored for molecular analysis. Future analysis of gene expression using RT-PCR of individual specific developmentally significant genes and via pathway focused PCR arrays will examine potential effects of herbal treatments on development at a molecular level. (52)

Ross, Ayla*, Daniel Dudek, and Josiah Townsend Indiana University of Pennsylvania, Indiana, PA 15705. *Revising taxonomic relationships of highland frogs (Anura: Ranidae: Rana maculata) from Nuclear Central America.* — Understanding the phylogenetic relationships of Ranid frogs in Central America is important to assessing threats impacting individual populations. The group with the most potential for investigation is the *Rana maculata* complex, currently thought to be a single species living along montane creeks from Mexico to Nicaragua. We analyzed the phylogenetic relationships and phylogeography of Mesoamerican true frogs (Anura: Ranidae: *Rana maculata*) using three mitochondrial (12S, 16S, CO1) and one nuclear (Lig4) loci. A subsample ($n = 32$) of the 75 samples were used for multi-locus concatenated trees. We used Maximum Likelihood (RAxML) and Bayesian Inference (MrBAYES) to determine relationships between the taxonomical groups. Population models showed two distinct lineages consisting of a widespread group in Honduras, Nicaragua, and Guatemala and a localized group found in Honduras and Nicaragua. The combination of phylogenetic and phylogeographical analysis lend support to two lineages under the name of *Rana maculata*. (60)

Rotell, Sarah*, Shannon Real*, and Lisa Antoniaci Marywood University, Scranton, PA 18509. *Characterization of Genetic and Physical Interactors of the Yeast Protein Cdc5.* — Cdc5 is a polo like kinase that functions as an important regulator of multiple mitotic events including sister chromatid cohesion dissolvment. In several genome wide screens Cdc5 has been linked to the kinase Cdc28. Cdc28 is the catalytic subunit of the main cell cyclin dependent kinase found in yeast and therefore regulates many cell cycle events such as timing within mitosis, DNA replication, chromosome separation and the configuration of spindle fibers. Using Co-IP and Western blotting techniques we want to confirm the genome wide screen data generated between Cdc5 and Cdc28. In addition, our lab is interested in pursuing genetic interactions with Cdc5 and several other proteins involved in specific cell cycle events. Double mutants of *cdc5-77* with either *mps3-5*, *rad24delta*, or *elg1delta* were generated and tested for genetic interactions. All of these proteins function in sister chromatid cohesion and DNA damage repair pathways and therefore are hypothesized to either interact together as a complex or regulate each other's function in yeast. (105)

Rothman, Alyssa*, and Sheryl Fuller-Espie Cabrini University, Radnor, PA 19087. *Characterization of the molecular basis of antimicrobial activity found in protein extracts of the earthworm Eisenia hortensis.* —

Invertebrates possess a robust innate immune system that defends against a wide variety of pathogens. Antimicrobial proteins provide such protection and have been identified in the coelomic fluid of the earthworm *Eisenia fetida*. This research characterized the molecular basis of antimicrobial activity found in an earthworm protein extract from *Eisenia hortensis* against a panel of 14 gram-positive or gram-negative bacterial species. Using a Kirby-Bauer disk diffusion susceptibility test, the sensitivity of the panel to antimicrobial compounds in the extract was tested. The extract was prepared using 85% ammonium sulfate precipitation, dialysis, filtration, and concentration techniques. Two bacteria, *Micrococcus luteus* and *Bacillus megaterium*, exhibited sensitivity to the extract when grown on Mueller-Hinton agar containing filter paper disks impregnated with 500 or 2000 mg of extract. The inhibitory activity of the extract was notably reduced after treating the extract with lipid removal agent (calcium silicate). Lipids purified from the extract using chloroform:methanol failed to exhibit antimicrobial activity. The inhibitory effect of the extract on *M. luteus* was further analyzed using flow cytometry. Cell membrane integrity in the presence of different concentrations of extract at different time points was measured using the viability dye propidium iodide. Significant results ($p < 0.05$) were observed 30 minutes after treatment with 0.59 and 0.059 mg/ml in a dose-dependent manner compared to untreated samples. Large cellular aggregates formed in the presence of the extract as determined by forward scatter in the flow cytometer and verified by phase contrast microscopy. This effect may be due to membrane destabilization causing the release of DNA from the bacterium leading to an increase in viscosity and stickiness of the cells. DNA from extract-treated *M. luteus* was shown to be intact and therefore not subject to the induction of apoptosis and DNA fragmentation by the antimicrobial compound. (189)

Rugelis, Nicholas*, Ronald Brown, and Christopher Taylor Mercyhurst University, Erie, PA 16546. *Using Quantum Mechanics and Molecular Mechanics (QM/MM) to model the effects of kinase domain mutations on the binding of HER2 kinase inhibitors.* — HER2 is a receptor tyrosine kinase that is a part of the epidermal growth factor receptor HER family and is known to be overexpressed in some human breast cancers. An understanding of the mutated and/or conformationally changed versions of the structures involved in the protein ligand binding will aid in the development of further treatments and therapies of HER2-mediated breast cancer. Our research uses QM/MM methods to model the protein ligand binding, by computing binding energies. These will be compared for a series of ligands and for conformationally changed and/or mutated versions of these structures. The QM method will utilize density functional theory for the ligand and most significant amino acids. The initial ligand that we will start examining in the binding process is Tak-285 with the EGFR protein (pdb file 3POZ). (23)

Rumbaugh, Tristen*, Andrea Nagy, and Catherine Santai Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Spectroscopic analysis of adulterated petroleum products using low-field nuclear magnetic resonance spectroscopy.* — Time-domain nuclear magnetic resonance spectroscopy (TD-NMR) and low-field nuclear magnetic resonance spectroscopy (LF-NMR) are different techniques that vary in their range of magnetic field strengths that they possess, which is a determining factor for the type of analysis that can be done. In this study, LF-NMR was used to perform a time-domain analysis of petroleum products, diesel and kerosene. This is a type of analysis is typically performed using TD-NMR. Diesel and kerosene are two petroleum products that have different characteristics such as viscosity, boiling point, and hydrocarbon length. Diluting, or adulterating, diesel fuels with kerosene is a common practice which allows gasoline companies to cut costs of production. This procedure, however, alters the chemistry of the fuel which can subsequently, at high enough concentrations of kerosene, make the consumption of this fuel mixture damaging to the mechanical engine within which the fuel is combusting. LF-NMR, although not conventionally used to conduct this type of analysis, was used to successfully measure the transverse relaxation time of three different diesel samples adulterated with kerosene. The average transverse relaxation time for unadulterated diesel was measured to be 0.71 s, while the average transverse relaxation time for kerosene was measured to be 1.29 s. These values agree with those measured using traditional TD-NMR^[1]. The transverse relaxation time correlated linearly with the percent of kerosene in the mixtures, as seen in previous TD-NMR studies^[1]. The measured differences in the relaxation times are inversely related to the viscosity of the diesel and kerosene (3.39 cSt and 1.20 cSt, respectively). This research supports the use of

the LF-NMR spectroscopic method for analysis of adulterated petroleum products. Cunha, D. A., Montes, L. F., Castro, E. V., & Barbosa, L. L. (2016). NMR in the time domain: a new methodology to detect adulteration of diesel oil with kerosene. *Fuel*, 166, 79-85. (10)

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Characterization of stress-related signaling molecules in Parasteatoda tepidariorum. — Across numerous species, an enduring impact on behavior is seen when an organism is exposed to stress throughout crucial developmental periods. A recent study conducted on *Caenorhabditis elegans* demonstrated a correlation between octopamine and serotonin modulation and developmental stress. Developmental starvation increases octopamine production which blocks serotonin function, a crucial regulator of male-specific behavioral development. Studying the influence of developmental starvation on behavior of spiders, specifically *Parasteatoda tepidariorum*, may aid in defining how more advanced invertebrates are affected when exposed to stress during important periods of development. To proceed with this study, the octopamine and serotonin signaling system of *P. tepidariorum* must be understood. We conducted various RTPCR analysis of octopamine receptor genes and rate limiting enzymes of neurotransmitter synthesis across developmental stages. *In situ* staining tests were conducted to determine specific locations of expression of octopamine receptors, however, no expression was detected at any of the embryonic stages analyzed. Moreover, two pilot studies were conducted to determine the maximum starvation times for two different ages for *P. tepidariorum*. Our future studies will determine whether periods of starvation alter levels of expression of octopamine receptors and synthesis enzymes, as well as mating behaviors. (55)

Scheidel, Brandon*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *Histone H2A N-terminus may stimulate NuA4-mediated H4 acetylation.* — NuA4 is the only essential lysine acetyltransferase (KAT) complex in yeast. It is involved in transcription, DNA repair, and cell cycle regulation. While NuA4 has been shown to preferentially acetylate histones H4 and H2A while they are part of a nucleosome, how NuA4 interacts with nucleosomes is not well understood. There is evidence that NuA4 subunits Eaf3, Esa1, Epl1, Arp4, Yaf9, and Yng2 participate in nucleosome binding. Eaf3 stimulates binding to methylated histone H3 lysine 36 (H3K36me). Esa1 may bind to unmodified H3 N-terminal tails. Yaf9 may bind acetylated H3K27 (H3K27ac). Yng2 stimulates binding to H3K4me. Cryo-EM structures suggest that NuA4 may bind to the face of the nucleosome, but the actual points of contact for the complex are not known. To better understand what amino acid residues in the histones are important for NuA4 binding, I started screening a histone mutant library for defects in H4 tetra-acetylation (H4ac). Defects in H4ac are likely to be due to effects on NuA4, since NuA4 is the only complex in yeast that can tetra-acetylate H4. I measured H4ac by Western blot in whole cell extracts of a histone mutant library starting with H2A mutants. My preliminary results suggest that multiple amino acids in the N-terminus of H2A reduce H4ac. This suggests that they may be involved in NuA4-nucleosome interactions or NuA4 activity on nucleosomes. I will follow these up by measuring NuA4-chromatin interactions in these mutants. My results suggest that NuA4 may bind and acetylate H2A first before acetylating H4. (116)

Schell, Joseph*, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301.

Distribution and occupancy measures for eastern small-footed bats (Myotis leibii) in the Delaware Water Gap National Recreation Area. — Eastern small-footed bats (*Myotis leibii*) have traditionally been considered rare throughout their range in eastern and central North America. However, recent research suggests that this apparent rarity may be due in part to habitat specificity and also survey techniques that are ineffective for this species. We surveyed for eastern small-footed bats at 14 talus and boulder sites in northeastern Pennsylvania and northwestern New Jersey using visual searches, mist netting, active acoustic monitoring, and passive acoustic monitoring. Our acoustic monitoring used Binary Acoustic Technology AR125 and Pettersson D500X detectors with SonoBat 4 classification software. We detected eastern small-footed bats at 6 of the 14 sites. We then used occupancy modeling to compare the efficacy of the 4 different survey techniques at documenting this species. Active acoustic monitoring had the highest detection probability (0.40 ± 0.20), followed by passive acoustic monitoring (0.30 ± 0.075). Both visual roost surveys and talus slope mist-netting were unsuccessful at detecting the species (0.00). We also measured 3 environmental covariates to assess the importance of these environmental characteristics on occupancy. The

environmental covariate that yielded the most parsimonious model was one where occupancy varied with talus slope area ($w = 0.1907$). We provide management recommendations for the species in the Delaware Water Gap National Recreation Area including continued monitoring of identified sites, identification of additional roosting sites, and use of public education to advocate for the protection of the species. (139)

Schmoyer, Joseph*, and David Singleton York College of Pennsylvania, York, PA 17405. *Bacillus Bacterial Strain Isolated from York College as a Source for the Production of Polyhydroxyalkanoates (PHAs)*. — Microorganisms are able to generate a wide range of other kinds of polyhydroxyalkanoates by combining different hydroxyl fatty acids with different chain lengths. PHAs are created by microbes from renewable resources and are a biodegradable polyester. The microorganisms that degrade PHAs secrete an enzyme such as PHA depolymerase, that cause a hydrolysis to the PHA polymers then these products can be used as an energy source for growth. The goal of this study was to isolate bacteria from the soil collected at York College of Pennsylvania and to determine if they can produce PHAs to make a biodegradable plastic when using a regular carbon source as well as volatile fatty acids. Bacteria were isolated from the soil of a Kentucky Coffee and White Oak tree and characterized by using the lipophilic stain Nile Red, using fluorescent microscopy, flowcytometry, and a plate reader assay, as well as by DNA sequencing of 16S ribosomal DNA genes. The data collected determined that *B. drentensis* can produce PHAs at high levels in comparison to the other bacteria. Also, fluorescent microscopy and UV light determined that the Nile Red dye did bind to the PHA granules of the bacteria by fluorescing bright orange. Overall, *Bacillus drentensis* is a promising species to use when making a potentially biodegradable plastic and through more research, this species may be an answer to society's environmental crisis of the over usage of regular plastic materials. (173)

Schwarz, Kyrstin*, Jennifer Shelly, and Gary Fortier Delaware Valley University, Doylestown, PA 18901. *Study of indicators of stress in working therapy dogs: a question of welfare*. — Current data supports that Animal Assisted Interactions are beneficial for people; physically, mentally, and psychologically improving their well being. However, the biggest argument against AAI currently is the question of welfare: Are the animals involved put under unnecessary stress? Handlers often report that these activities are therapeutic for the people they interact with as well as their dogs, but is that accurate? The goal of this study is to determine whether animal welfare is being compromised through data collection in three different areas: salivary swabs to measure levels of cortisol and oxytocin; videos to measure stress behaviors using an ethogram with pre-defined stress behaviors; and an owner questionnaire to quantify the owner's ability to perceive their dog's stress. All data is collected twice for each dog: once prior to the session beginning to provide a baseline to compare to, and once during the session to see how the dog's stress changes while partaking in an Animal Assisted Activity. The behavioral analysis shows a mix of decreasing stress behaviors and increasing stress behaviors, while the average of all the dogs shows an overall decrease in stress behaviors. However, there was never presence of extreme stress behaviors, such as drooling, trembling, or whale eye. The data from the owner questionnaire shows a relationship between the owner's stress levels and the owner's perception. While the results on the salivary swabs have not yet been quantified, we expect to see elevated oxytocin, whereas cortisol levels may be variable. Furthermore, the data from the behavioral analysis and owner questionnaires suggests that some dogs are nervous or stressed regardless of the environment. We plan to continue this Spring to compare how the dogs' stress changes over time working with one specific class to determine whether a bond is formed between the dog and the children. (133)

Shafer, Mark*, and John Campbell Mercyhurst University, Erie, PA 16546. *Investigating contamination effects from a coke manufacturing operation using seed germination tests and Gammarus (Amphipoda) toxicity bioassays*. — Soil contamination in an area immediately adjacent to a coke manufacturing operation in Erie, PA was investigated in February 2019. Soil samples were collected from sites near the plant's perimeter and from control sites in an urban wetland near Mercyhurst University and a rural park remote from the city. Two bioassays were used to evaluate toxicity/pollution of the soils. The first assay included seed germination experiments using *Lactuca sativa* (lettuce), *Brassica juncea* (mustard), and *Brassica oleracea var. capitata* (cabbage) to determine whether the factory-contaminated soil inhibited seed germination and early

growth. These three species are known to have different resistance to soil toxicity (listed above in order from most vulnerable to most resistant). *Gammarus fasciatus* (amphipods) collected from the coke operation's NPDES-permitted warm water discharge stream at the edge of Lake Erie were also used to evaluate the toxicity of the contaminated soil to aquatic life. The amphipods were placed in jars with each of the soils as bottom substrate and their mortality in 72-hour tests were compared. (153)

Shields, Daniel*, and Sarah Ruffell University of Pittsburgh at Bradford, Bradford, PA 16701. *Determining the antibacterial effectiveness of different vinegar/oil concentrations on bacteria obtained from grocery store produce*. — This study investigates the antibacterial characteristics of different vinegar/oil concentrations on bacteria collected from grocery store produce. Four bacterial species were identified on the produce: *Bacillus siamensis*, *Pseudomonas aeruginosa*, *Bacillus altitudinis*, and *Bacillus subtilis*. The three strains of *Bacillus* bacteria identified on the open produce are not pathogenic to humans. However, *P. aeruginosa* is a multidrug resistant, pathogenic bacterium that is very prominent in hospitals worldwide. Extra virgin olive oil and red wine vinegar ratios were studied due to their extensive presence in food flavoring. Significant growth inhibition was observed in all bacterial isolates under a vinegar to oil ratio of 1:0 with a gradual decrease in inhibition as the olive oil concentration increased. Through this study, it is clear that the percentage of vinegar in the vinegar/oil mixture significantly influences the growth of bacterial species on produce, most notably *P. aeruginosa*. (192)

Smith, Tiffany*, and Christine Proctor Harrisburg University of Science and Technology, Harrisburg, PA 17101. *The effect of hydrous ferric oxide deposits on benthic macroinvertebrate community structure*. — By 2016, over 15 billion tons of coal had been mined from Pennsylvania with approximately 250,000 acres of mine lands left abandoned. Once abandoned, water flows into mines and interacts with rock forms previously unexposed. The exposure of pyrite- and carbonate-containing rocks to water and oxygen leads to the production of acid, decreasing the pH of water flowing out of mines. This form of pollution is referred to as Acid Mine Drainage (AMD). However, efforts to remediate AMD lead to the precipitation of hydrous ferric oxides (HFO) which deposit as solids along stream beds and banks. It is hypothesized that these HFO deposits create physical blockages of food and habitat resources for macroinvertebrates, a key part of aquatic ecosystems. The goal of this study was to determine the impact of HFO deposits on macroinvertebrate communities within the Swatara Watershed. To accomplish this, we collected benthic macroinvertebrates from 6 sites separated into 3 treatment groups: unaffected by AMD, affected by AMD, and remediated with HFO deposits present. All collected macroinvertebrates were identified to family. Overall community health was determined via the calculation of an Index of Biotic Integrity (IBI), which quantifies pollution tolerance and species diversity by averaging 6 separate indexes. The IBI ranges in value from 0 to 100 with 0 indicating no species present and 100 a healthy and diverse community. The 3 treatment groups were compared using an ANOVA with a significance threshold of $p=0.05$. No statistical difference in IBI was found between streams unaffected by AMD and those with HFO solids present. Streams affected by AMD had a significantly lower IBI. However, remediated streams with HFO deposits had lower overall community diversity. These results suggest that the HFO deposits post AMD remediation do not preclude the reestablishment of pollution intolerant macroinvertebrates but lowers overall community diversity. (124)

Smithbauer, Michelle*, Casey Weber, Maureen Levri, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Floral height influences pollinator visitation 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 in mountain laurel, inflorescence size increases with height off the ground, and there may be a reproductive advantage to having inflorescences higher on the plant. To test the hypothesis that higher flowers lead to greater reproductive success we examined the pollinator visitation rate on flowers at different heights on plants in the field. Mountain laurel flowers use an unusual pollen delivery system. Anthers are held in pockets of the corolla under pressure and, when disturbed, will catapult pollen onto the pollinator. Thus flower visitation can be determined by noting the number of anthers that been dislodged from the pockets. For quantifying pollinator visitation rate in nature, we used about 5 flowers high on a plant and 5 flowers low on the same plant, controlling for inflorescence

size, and determined how many anthers were manipulated by pollinators at one day and two days after the flowers opened. A preliminary analysis of the data from both experiments suggests that, in mountain laurel, flowers higher on the plant are visited more by pollinators. This suggests that the greater reproductive investment observed in higher inflorescences may result in greater reproductive success and that the provisioning of more resources to inflorescences higher on the plant may be part of a strategy to increase fitness. (68)

Spadafora, Sonia*, Isabella Romani*, Rya Scull, Jessica Azzarano, Jessica Baranoski, Caroline Germain, Kyriaki Gerasimidis, Matt Mastropaolo, and Melinda Harrison Cabrini University, Radnor, PA 19087. *A Proteomic Study of Lysin Genes in Novel Bacteriophages: Arby and Scuttle*. — Bacteriophages are viruses that infect a bacterial host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. We have discovered novel phages from the bacterial host *Arthrobacter sp.* ATCC 21022. The phages were collected from soil and water samples by students from various places around Southeastern PA and Southern NJ, and their genomic DNA was isolated. Following isolation, they were photographed through the use of an electron microscope, and then the DNA was sequenced. The phages' genomes were then annotated using various bioinformatics tools such as DNA Master, Phamerator, HHpred, and GeneMark to determine gene location and function. Using comparative genomics, unique characteristics of the phage's genome were also explored. This study also focused on the lysin genes of phages Arby and Scuttle. Lysins are being used as antibacterial agents due to their high effectiveness and specificity in comparison with antibiotics, which are susceptible to bacterial resistance. The lysin gene sequences were examined, and homology models were generated. (196)

Sponsel, Kayla*, and Daniel Ginsburg Immaculata University, Immaculata, PA 19345. *H3 acetylation does not stimulate NuA4 interaction with chromatin*. — NuA4 is the only essential lysine acetyltransferase (KAT) complex in the yeast *Saccharomyces cerevisiae*. It plays important roles in transcription activation, DNA repair, and cell cycle regulation. It participates in these processes by acetylating histones H4 and H2A along with ~95 other targets. We are interested in elucidating NuA4 function during transcription activation. It has been shown during transcription that H4 acetylation by NuA4 stimulates H3 acetylation by the SAGA complex, recruitment of chromatin modifying complexes SWI/SNF and RSC and chromatin disassembly. All of this promotes both transcription initiation and elongation. It is still not completely clear how NuA4 interacts with chromatin. NuA4 subunit Yaf9 has been shown on its own to bind histone H3 acetylated on lysine 27 (H3K27ac), but it is not clear whether it behaves similarly as part of NuA4. The goal of my project is to understand whether histone acetylation stimulates NuA4 interaction with chromatin. To address this question, I am measuring histone H4 tetra-acetylation (H4ac) by Western blot in whole cell extracts of yeast strains that have lysine to arginine mutations in the acetylation sites of histones H3, H2A, and H2B. Because NuA4 is the only complex in yeast that can tetra-acetylate histone H4, I expect defects in H4ac to be due to changes in NuA4 binding to chromatin or activity. My preliminary results suggest that H3 acetylation does not stimulate H4ac. This is consistent with other results from our lab that lead us to conclude that Yaf9 does not bind H3K27ac in the context of NuA4. (118)

Srour, Meghan*, and Christopher Brey Marywood University, Scranton, PA 18509. *In vivo promoter analysis of klf-1 gene in Caenorhabditis elegans*. — Type 2 diabetes (T2D) is a pressing health issue today that affects millions worldwide. Genetic research on T2D is difficult to perform on humans, therefore the use of a model organism is more practical. *Caenorhabditis elegans* are used in the laboratory to study gene interactions because their genome has already been fully sequenced and they have quick reproductive potential. Krüppel-like transcription factor (*klf*) genes are a homologous transcription factor family shared between humans and *C. elegans*. In *C. elegans*, the *klf* genes contribute to adipose fat accumulation in the intestine of the worm. The primary aim of this study is to see what section of the promoter region in the *klf1* gene codes for the expression of the green fluorescent molecule (GFP) in their intestine. The *klf* gene expresses in the worm as fatty deposits in this region. By using GFP as a marker for the gene, it will help us gain insight into where the protein expresses and what the consequences are when we delete this sequence from the promoter region. It was found that various regions of the promoter are essential for expression of

the GFP protein. We discovered that at 380 bp upstream of the start codon, no GFP expression was observed in the intestine. We are now in the process of analyzing this sequence to determine what transcription factor binding sites are crucial for GFP expression in the intestine. (131)

Steckbeck, Rachel*, Kristen Hasse, Caleb Smith, Madison Wright, H. Scott Kieffer, and Michael Shin Messiah College, Mechanicsburg, PA 17055. *The effect of caffeine ingestion and the CYP1A2 polymorphism on long anaerobic exercise performance.* — Caffeine is a stimulant commonly used in athletics. Recent research suggests that variants of the CYP1A2 genotype, AA (responder) and AC/CC (non-responder), may influence the ergogenic effects of caffeine on exercise performance. We hypothesized that AA subjects would experience a greater power increase upon caffeine ingestion compared to AC/CC subjects. To test this, 33 subjects completed two 90 second Wingate Anaerobic Tests on a cycle ergometer. Relative peak power (PP) and relative mean power (MP) were computed. An oral bolus of caffeine (CAF), 6mg·kg⁻¹, or placebo (PLA), maltodextrin, was given in a randomized and counterbalanced design 60 minutes prior to testing. Buccal epithelial cells were collected via mouth rinse. Genomic DNA was extracted using QiAmp Mini spin columns and a 920 bp fragment of the CYP1A2 gene was amplified using PCR. Genotypes were identified by digestion with restriction enzyme *Apal* and gel electrophoresis. A 2 (condition) x 2 (genotype) x 3 (time) repeated measures ANOVA with Fisher LSD post-hoc ($p < 0.05$) was used to compare PP and TW. Our results showed that the condition (PLC vs CAF) showed no difference in PP. Genotype showed a non-significant increase in PP for AA (516.6 ± 117.3 W) compared to AC/CC, (495.4 ± 130.4 W). Time showed a significant decrease in PP in each 30-second segment; however, there were no interaction effects of time for condition ($p=0.60$) or genotype ($p=0.40$). There was no difference in TW over the 90 seconds and no significant difference in total power for genotype. TW significantly decreased over each 30-second phase; however, there were no interaction effects for condition ($p=0.63$) or genotype ($p=0.87$). Overall, the results indicate that CAF did not impact PP or TW during long-anaerobic testing. In addition, neither the AA nor the AC/CC genotype influenced PP or TW following the ingestion of CAF. (95)

Sweitzer, Justin*, and Lawrence Mylin Messiah College, Mechanicsburg, PA 17055. *In search of improved strategies to induce T cell immunity targeting a receptor expressed by aggressive pancreatic cancer cells.* — Pancreatic cancer is difficult to detect, at diagnosis is often in advanced stages, and has usually metastasized making surgical resection or chemotherapy ineffective. We propose immunotherapy as a strategy to treat pancreatic cancer. We seek to determine if appropriate immunization can stimulate production of T cells that can destroy pancreatic cancer cells based on recognition of portions of a unique protein sequence inserted into the cytoplasmic face of a form of the cholecystokinin receptor (CCK2_{i4sv}R) associated with aggressive tumors. Previous studies by our group have demonstrated that a synthetic peptide corresponding to a portion of the insertion sequence can stimulate the production of T cells in C57Bl/6 mice. Syngeneic pancreatic cancer cells (PANC02) engineered to express the human CCK2_{i4sv}R provide a model system with which the efficacy of T cell-based immunity targeting the altered receptor can be tested. The goal of this study was to determine whether immunization strategies designed to enhance the activation of professional antigen presenting cells would lead to induction of higher frequencies of CCK2_{i4sv}R insert-sequence-specific T cells. Two “improved” immunization strategies were compared to vaccination with simple peptide emulsions: a) vaccination using peptide-pulsed, *in vitro*-activated dendritic cells, and b) TriVax immunization in which a mixture of anti-CD40 monoclonal antibody and polyIC were injected intravenously with the synthetic peptide. Neither of the alternate strategies generated robust T cell responses to the pancreatic cancer peptide or to another MHC class II-restricted control peptide, but did induce immunity to a control MHC class I-restricted epitope peptide. These results imply that an epitope within the pancreatic cancer-associated insert-sequence peptide is recognized by CD4+ T cells. (200)

Tate, Jesse*, and Valbona Hoxha York College of Pennsylvania, York, PA 17405. *The role of ABC transporters, MDR65 and MRP4 in acute alcohol sensitivity.* — Alcohol is one of the most abused substances worldwide. Alcohol sensitivity is sexually dimorphic in humans and *Drosophila*, with females being more sensitive to alcohol than males. However the molecular mechanisms to alcohol sensitivity are largely unknown. We used a simple way to expose flies to ethanol and measure sex differences to acute ethanol sensitivity. Using this assay, we found that at lower and high dosage of ethanol concentration there is no

sexual dimorphism, hence both males and females sedate at similar rate. However, levels of 70% ethanol show a sexual dimorphism in sedation time. Next, we investigated the role of ABC transporters (ATP-binding Cassette) MDR 65 and MRP4 in ethanol sensitivity. Using the Gal4-UAS binary system in the fruit fly, *Drosophila melanogaster*, we expressed MDR65 – RNAi and MRP4– RNAi in glial cells. Our study found that expression of RNAi for both MDR65 and MRP4 transporters does not affect ethanol sensitivity, in males or females. Our study suggests that MDR65 and MRP4 do not play a significant role in ethanol sensitivity. (40)

Tews, Veronika*, and Austen Barnett DeSales University, Center Valley, PA 18034. *Interrogating the Ancestral Role of EGF Ligands in Insect Oocyte Development.* — The EGF pathway is a deeply conserved signaling cascade used in a variety of contexts during animal development. In the highly studied insect *Drosophila melanogaster*, three TGF- α ligands (Spitz, Keren and Gurken) and one neuregulin (Vein) activate the pathway by binding to the EGF receptor (EGFR), while the protein Argos antagonizes EGFR activation. Spitz, Keren and Gurken share a high degree of sequence similarity, and it has been hypothesized that these genes are the result of ancient, insect-specific gene duplication event. To test this hypothesis, we performed an insect-centered phylogenetic analysis of putative Spitz, Keren and Gurken orthologs. This revealed that Gurken split from the ancestral TGF- α ligand early in dipteran evolution, and that Spitz and Keren were the result of a separate gene duplication event in the dipteran clade Tephritidae. To better understand the evolution of these ligands in insects, we looked at one developmental event in which all three TGF- α ligands are used in *Drosophila*, the establishment of oocyte dorsal-ventral polarity. In the *Drosophila* oocyte, Gurken activates EGFR in the overlying follicle cells via paracrine signaling. This, in turn, leads to the autocrine activation of Spitz and Vein, which is later attenuated by the inhibitor Argos (Wasserman & Freeman, 1998). To understand the selective pressures leading to the fixation of EGF ligand duplicates in insects, we explored the conservation of this pathway in the hemipteran insect *Oncopeltus fasciatus*, which utilizes only one TGF- α ligand. *Of-Egfr* is expressed in the overlying somatic follicle cells in the ovarioles, as has been described for other insect species (Lynch *et al.*, 2010). However, unlike the ubiquitous expression of TGF- α mRNA described in other insects (Lynch *et al.*, 2010), *Of-TGF- α* mRNA was detected in the oocyte nucleus. *Of-vein* and *Of-argos* mRNAs were also detected late in oogenesis, with *Of-vein* being expressed in the follicular epithelium overlying the oocyte nucleus. *Of-aos* mRNAs were detected early in the oocyte, and then in the follicle cells overlying the oocyte nucleus of late-stage oocytes. *Of-TGF- α* mRNAi resulted in the abolition of oocyte polarity, and inhibits the activation of *Of-vein* and *Of-argos*. These data indicate that the ancestral insect TGF- α ligand acted to activate Vein and Argos in the context of oocyte dorso-ventral polarity. (51)

Thillepan, Mathura*, Swetal Rathod*, and Jessica Petko Penn State University-York, York, PA 17403. *Sex determination in Parasteatoda tepidariorum: analysis of virilizer and transformer splice variants.* — Sex determination is a process by which organisms use environmental or genetic cues to dictate the development of male- and female-specific traits. Both mammals and fruit flies (*Drosophila*) use the XX/XY genetic determination system. The presence of the Y chromosome determines sex in mammals, while dosage of the X chromosome dictates sex in *Drosophila*. The X chromosome of flies encodes splice factors, such as virilizer (Vir), which leads to female-specific splicing of proteins in high doses. Another splice factor, sex lethal (Sxl) is a target of Vir in the *Drosophila* sex determination pathway. Female-specific splicing of Sxl leads to alternative splicing of transformer (tra) and doublesex (dsx). The sex determination pathway in *Drosophila* is well documented, but little is known about it in other arthropods. We are interested in studying sex determination mechanisms in arachnids. Because of an ancient genome duplication, spiders exhibit an X₁X₂O system in which spiders with one copy of each X are male and those with two of each are female. This helps us better understand the evolution of gene regulation. Our laboratory analyzed the expression of five Dsx orthologs in the common house spider, *Parasteatoda tepidariorum*. Dsx proteins are the most conserved across arthropod sex determination pathways. For this project, we aimed to identify the orthologs of other sex determination pathway regulators that lie upstream of Dsx. No orthologs for Sxl were found in the *P. tep* transcriptome, so we conducted phylogenetic analysis for spider orthologs of Tra and Vir. We then examined alternative splicing and sex-specific expression of these genes using semi-qRT-PCR. Our

results showed that Vir had a female sex-specific splice variant, while the splice variants of Tra did not show sex-specificity. Future studies will focus on the expression patterns and functions of these two genes in the gonads of *P. tep.* (57)

Thomas, Nicolas*, Joseph Cirilo, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Toward using ouzo-like colloids to deliver retinoic acid to SH-SY5Y neuroblastoma cells.* — Nanoparticles have important applications throughout various academic fields and most notably in the field of medicine as drug delivery mechanisms. It is essential to characterize nanoparticles, colloids in this current research, and determine whether or not they are stable enough to be used as drug carriers. Previous research has shown that n-phenyl-1-naphthylamine (NPN), dimethyl sulfoxide (DMSO), and water can be used to make colloids. The current research presents the characterization of these colloids, with retinoic acid (RA) encapsulated in them, with the use of fluorescence, absorbance, light scattering, and particle sizing techniques. Preliminary data indicates that the colloids are 170nm in radius. Absorbance and fluorescence data shows that the RA and NPN pellet together when centrifuged. Additional research is ongoing to fully characterize these colloids, including quantitation of the retinoic acid in these nanoparticles, and testing the ability of the colloids to deliver RA to cells, specifically SH-SY5Y neuroblastoma cells to induce differentiation. (18)

Triolo, Chloe*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Profiling DNA methylation of cancer immunotherapy resistance and response genes in African Americans and European Americans with non-small cell lung cancer.* — Lung cancer is the leading cause of cancer-related death in the US, with the most common type being non-small cell lung cancer (NSCLC). LUAD and LUSC are the most frequent NSCLC subtypes. African Americans (AA) have higher rates of new cases and deaths in comparison with European Americans (EA), even though they smoke less. Novel biological determinants, like DNA methylation (which turns off gene activity), may be involved. Cancer immunotherapy is a revolutionary treatment approach across cancers that involves or uses components of the immune system. There are 554 mRNA and microRNA (small regulatory RNAs that prevent mRNA translation) genes essential for cancer immunotherapy resistance and response (CIRR). AA lung cancer patients may not benefit from these therapeutic advances as much as their EA counterparts if their underlying lung tumor biology differs. If CIRR genes are silenced by DNA methylation they will not be expressed, and cannot aid cancer immunotherapeutic strategies. We hypothesized CIRR genes are differentially methylated and expressed in NSCLC from AA compared with EA. DNA methylation, mRNA-sequencing, and microRNA-sequencing data for AA ($n=73$) and EA ($n=623$) in The Cancer Genome Atlas were downloaded. Differential methylation and gene expression analyses were carried out using Partek Genomics Suite 7.0 and GraphPad Prism 8.0. Statistically significant racial differences in DNA methylation were observed in 30 LUAD genes and 56 LUSC genes ($FC = +/- 2$, $P \text{ value} + FDR = \leq 0.05$). In both NSCLC subtypes, the CIRR gene *UCKL1* (an oncoprotein that promotes cancer immunotherapy resistance) was also differentially expressed by race. Increased *UCKL1* expression in AA compared with EA suggests cancer immunotherapy may be less effective in this population. A combination of DNA methylation inhibitors and *UCKL1*-targeted therapy, followed by cancer immunotherapy, should be explored as a treatment option for AA to help reduce the health disparity. (3)

Valkanas, Michelle*, and Nancy Trun Duquesne University, Pittsburgh, PA 15282. *Identifying the effects bacteria have on the efficiency of passive remediation systems designed to treat abandoned mine drainage.* — Passive remediation systems are increasingly becoming a cost-effective choice for treatment of abandoned mine drainage. Their ability to remediate both acidic and circum-neutral discharge has proven to be successful overtime. Currently, these systems are designed based on geochemical processes, with minimal regard to the naturally forming microbial communities. We aim to identify the roles microbial communities, specifically bacteria, play in passive remediation systems. We designed an in vitro system to determine the influence bacteria have on soluble iron, manganese, and sulfate levels in two passive remediation systems in Pennsylvania that treat acidic mine drainage (Boyce and Middle Branch). Slurries were taken from settling ponds throughout the remediation systems, sterilized and reinoculated with bacteria from different points in the systems. We have found biologically-driven iron-oxidation that resulted in iron precipitation (e.g. a decrease in dissolved iron levels) occurring in both systems, while Middle Branch also

had manganese-reduction that led to resolubilization (e.g. an increase in manganese levels). Our findings suggest that the microbial communities in remediation systems can have both positive and negative effects on system efficiency (e.g. removal of metals). Further understanding of the microbial communities present in passive remediation systems could help to improve system performance and longevity. (121)

Valles, Kristen*, and Brian Gray York College of Pennsylvania, York, PA 17405. *Identifying mechanisms of growth inhibition of zinc oxide nanoparticles on Bacillus cereus*. — Foodborne pathogens can easily infect consumer goods during handling and storage. Nanoparticles, specifically zinc oxide, are noted for their antimicrobial effects while remaining food-safe. *Bacillus cereus* is a common toxigenic contaminant of dairy products. Previous studies demonstrated zinc oxide nanoparticle (ZnO-NP) inhibited *Bacillus cereus* growth in media and milk cultures. Proposed mechanisms included membrane disorganization, production of reactive oxygen species, and chromosomal damage. In this study we examined the mechanism of ZnO nanoparticles on *Bacillus cereus* grown in milk media. Using a metabolic marker of cell growth, we determined the EC50 for ZnO-NP in tryptic soy broth supplemented with milk. Polymerase-chain reaction and agarose gel electrophoresis methods were used to check chromosomal integrity of the bacteria after exposure to ZnO-NP. No evidence of DNA damage was observed. Taken together, these findings suggest the most likely mechanism of antimicrobial action for ZnO-NP is membrane disorganization. Future studies will determine the EC50 for zinc oxide nanoparticles in pasteurized and unpasteurized milk in order to better proscribe their usage in products for human consumption. This research further underlines the great potential in using zinc oxide nanoparticles for effective and safe usage in food storage methods due to their antimicrobial capabilities and food-safe properties. (88)

Vargas, Jasmin*, and Khadijah Mitchell Lafayette College, Easton, PA 18042. *Tumor Immune Cell Abundances, Efficacy, and Survival Rate*. — African Americans (AA) have a higher risk of lung cancer compared with European Americans (EA) and an overall lower survival rate. Whether the health disparity is due to social determinants, biological differences, or a combination of both is unknown. Unfortunately, AA patients are dramatically underrepresented in lung cancer clinical trials (6.0% AA vs 83.4% EA). Bioinformatic prediction tools, such as CIBERSORT, can determine treatment-related immune cell abundances and help to bridge the knowledge gap about lung tumor biology in the most common subtypes (LUAD and LUSC) and differential chemotherapy drug response. AA and EA have different immune cell abundances, which can predict chemotherapy drug response. Gene expression (mRNA-sequencing) and patient demographic data were extracted for AA and EA with LUAD ($n = 50$ AA, 349 EA) and LUSC ($n = 24$ AA, 274 EA) in the TCGA database. The data was uploaded into CIBERSORT to profile immune cells ($n = 22$). GraphPad Prism 7.3 was used to compare statistically significant differences in immune cell abundances by 1-way ANOVAs. Clinical inferences were drawn from the literature. Three immune cell abundances were population-specific between AA and EA with LUAD (increased M1 macrophages, decreased plasma cells and eosinophils in AA) and LUSC (decreased plasma cells, M1 macrophages, and mast activated cells in AA). All statistically significant immune cells have been associated with chemotherapy drug responses. Immune cell abundances are different in AA and EA lung cancer patients, but vary by high and low expression across lung cancer subtypes. Immune cell signatures and subtype may be relevant to the efficacy of lung cancer treatments for AA patients. Future lung cancer clinical trials should include more AA and consider population-specific immune cell abundances in subtypes when evaluating chemotherapy drug efficacy. (203)

Waizenegger, Zoe*, Justin Lansberry*, and Julie Belanger King's College, Wilkes-Barre, PA 18711. *Characterization of thermal transitions of DPPC lipids in the presence of small molecules with DSC*. — Differential scanning calorimetry (DSC) is a technique that has been used to analyze the thermotropic phase behavior of many biological compounds, such as lipids. Phosphatidylcholine lipids, when dispersed in an aqueous milieu, form bilayer membrane structures that undergo phase transitions when being analyzed by DSC. Previous research with the addition of small molecules to hydrated lipid membranes shows a shift in this melting transition. The resulting shifts in melting transition have been characterized at lower onset temperatures, as well as lower enthalpies of reaction. The DSC was used to characterize the main transition in liposomes in the presence of N-Phenyl-1-naphthylamine and cholesterol. The trends observed through

this project have been lower onset melting temperatures, lower enthalpies of reaction, and lower peak melting temperatures in the presence of cholesterol and NPN. The presence of these molecules has lowered the temperatures and enthalpies of reaction compared to the DPPC liposomes and DMSO stock solution control sample. These findings are important in understanding the thermotropic phase behavior when small hydrophobic drugs are incorporated into the hydrophobic region of the bilayer of liposomes for potential applications in drug delivery. (20)

Wasik, Jeremy*, Jenna Mickel*, and Lara LaDage Penn State University-Altoona, Altoona, PA 16601.

Spatial-dependent neural growth in enriched, complex environments in the eastern fence lizard (Sceloporus undulatus). — A major determinant of increased spatial cognition is due to environmental variants and behavioral adaptations, both of which directly influence growth of the hippocampus. The hippocampus is the portion of the brain that functions in spatial processing, specifically spatial memory. As the demand for spatial cognitive behaviors increase, the hippocampus experiences growth in size, neuron number, and other neural attributes. Previous research has found that factors such as physical activity, integration amongst other animals, and an enhanced complex environment increases the requirement for spatial memory function, reflected by increases in hippocampal attributes. The purpose of the current study was to observe how increasing environmental complexity and enrichment, such as a complex spatial setting, increased living area, and integration amongst other lizards, expanded cortical (hippocampal homologue) growth compared to lizards housed in isolation. The current study used two treatment groups, eastern fence lizards (*Sceloporus undulatus*) housed in an enriched complex environment and lizards housed in standard laboratory cages. We predict that lizards housed in enriched and complex environments will display larger cortical volumes compared to the lizards housed in standard laboratory conditions. (41)

Wasserman, Adam*, and Thomas McGuire Penn State University-Abington, Abington, PA 19001.

Antiproliferative Effects with "Targeting" Cytotoxicity: Exposing Gastrointestinal Stromal Tumor Cells to Ascorbate. — Ascorbate (ascorbic acid or vitamin C) shows clinical relevance as an adjuvant with a variety of chemotherapeutic agents that can either halt the proliferation of cancer cells or initiate cell death. In this study, gastrointestinal stromal tumor (GIST) cells were exposed to varying concentrations of ascorbate to study its effects *in vitro*. The findings illustrate dose-dependence with the highest concentrations resulting in a significant drop in GIST proliferation. In another experiment, GIST cells were exposed to ascorbate for 2 hours a day to simulate *in vivo* pharmacokinetics and similar results are apparent. Ascorbate operates extracellularly and intracellularly through pro-oxidant mechanisms. The creation of reactive oxidative species (ROS) damages cellular structures such as the cell membrane, DNA, RNA, and proteins. The accumulation of ROS alters structural integrity, metabolic pathways, and biological molecules, all of which lead to diminished proliferation. An additional experiment with catalase (an anti-oxidant) reversed the effects of ascorbate resulting in normal GIST cell growth, strongly suggesting that ascorbate utilizes ROS. Normal cells have a sufficient amount of catalase, whereas cancer cells lack anti-oxidative enzymes to accrue more beneficial mutations. Therefore, ascorbate would only damage GIST cells and have no effect on normal cells *in vivo*. While further testing *in vivo* is necessary and additional cell lines should be tested, we predict that physicians and oncologists could treat their patients using ascorbate in combination with other therapeutic drugs in efforts to eliminate GISTs. (73)

Weber, Casey*, Michelle Smithbauer, Maureen Levri, and Edward Levri Penn State University-Altoona,

Altoona, PA 16601. *Floral height influences pollinator visitation in Mountain Laurel (Kalmia latifolia) when inflorescence density is controlled.* — Mountain Laurel produces variable numbers of flowers at different heights on the plant. Previous work has shown that inflorescences higher on the plant have on average more flowers than inflorescences lower on the plant. To determine if pollinators prefer flowers higher while controlling for inflorescence density, we conducted an experiment where inflorescences of the same size were placed high and low on netting away from other mountain laurel. We used 40 inflorescences with 3 flowers each and placed 20 inflorescences 10 cm apart horizontally and 80 cm apart vertically. Visitation by pollinators can be determined by examining flowers for disturbance of their anthers. Each flower was checked one, two and three days after the beginning of the experiment to determine pollinator visitation occurred which was measured by the number of anthers (out of 10) that were manipulated. A preliminary

analysis of the data indicates that flowers higher on the screen were more visited at a greater rate than lower flowers. This suggests that there may be an advantage for a plant to disproportionately provision inflorescences based on height. (179)

Wilkins, Ashley*, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. *The impact of lysine acetylation on cell aggregation in Mycobacterium smegmatis*. — Recent studies using *Mycobacterium smegmatis* have shown that lysine acetylation, a protein regulatory system, affects biofilm formation. Biofilm formation is the production of extracellular polymeric substances that make bacteria less susceptible to antibiotics and other environmental stressors. It is not fully understood as to why lysine acetylation affects biofilm formation, so in this study, colony morphology and aggregation index are used to gain more insights regarding the variations of biofilm formation in lysine acetylation mutants. Skewing the lysine acetylation regulatory circuit in multiple ways led to changes in both colony phenotype and cell aggregation. This work provides a broader understanding of mycobacterial physiology and will lead to an identification of the lysine acetylated proteins involved in biofilm formation. (90)

Williamson, Thalia*, and Karen Campbell Albright College, Reading, PA 19604. *Impact of sound pollution on bird behavior*. — One reported effect of urbanization is a drastic increase in sound pollution, but very little field research exists to determine the impact of noise on wild organisms. Sound pollution likely has a major impact on organisms, such as birds, that rely heavily on vocalizations. We investigated how sound pollution affects bird behaviors such as feeding, preening, perching, and aggression. To observe how sound pollution affects behavior, we established two feeders at different edges of the same wooded area. One feeder was by the highway (high disturbance), where sound pressure levels exceeded 80 decibels; while the other feeder was on the neighborhood side (low disturbance), where the average noise level was 57 decibels. We monitored each feeder for approximately two hours every morning for 10 weeks and observed a total of 247 bird visits, with 230 visits occurring at the low disturbance (LD) feeder and 17 visits at the high disturbance (HD) feeder. Only 4 species visited the HD feeder, but 12 species visited the LD feeder. Analysis of the behavior data showed a significant relationship between level of disturbance and behavior. While behaviors did differ between species, behaviors such as avoidance, calling, and perching also differed between sites. Future analysis will further characterize the impact of sound pollution on specific bird behaviors. (135)

Winkowski, Madison*, and Jessica Petko Penn State University-York, York, PA 17403. *Pharmacological characterization of dopamine receptors in the common house spider, Parasteatoda tepidariorum*. — Dopamine is a neurotransmitter involved in everything from sense of smell, locomotion, decision-making and reward. The receptor for dopamine is a G-protein coupled receptor or GPCR, it snakes through the cell membrane seven times. GPCR receptors are divided into sub families based on structure and pharmacological properties. Insects have three subfamilies while humans only have two, DOP1, DOP2 and DOP3. Invertebrate DOP1 and DOP2 are supposed to increase cAMP while DOP3 is supposed to decrease cAMP. Aberrant cAMP signaling can be caused by alterations in gene expression and neural connectivity associated with addiction. The common house spider, *Parasteatoda tepidariorum*, have six dopamine receptors where humans have five. The extra receptor is thought to have risen from a complete genomic duplication at the base of the spider's evolution tree. By determining how the spider's dopamine receptors behave, on a pharmacological level, there will be a better understanding of the evolutionary reward-based system that gets hijacked with addiction. (56)

Witt, Allyssa A.*, and Amy E. Faivre Cedar Crest College, Allentown, PA 18104. *Using pollen tubes to estimate floral visitor activity for azalea (Rhododendron sp.) on the Cedar Crest College campus*. — Species of azalea are popular plants for horticulture. In order to understand how frequently plants in a garden setting are visited by potential pollinators, the amount of out-cross pollen deposited on stigma surfaces was observed. Open flowers of unknown age were collected in the spring of 2018 to gauge the level of potential pollinator activity on these garden plants. In the fall of 2018, flowers were tagged and monitored to ensure only flowers open for a single day were collected. All flowers in the study were collected in vials containing FAA (formalin:acetic acid:70% ethanol). The samples were then switched to 70% ethanol. These were rinsed with water, softened with NaOH and stained with aniline blue. Aniline blue binds to callose in pollen tubes

allowing them to be observed using fluorescence microscopy. The number of pollen grains on the stigma surface and the percentage of those that germinated pollen tubes reaching the top of the ovary were recorded. These observations will provide more information on how effective flower visitors in this garden setting are at bringing out-cross pollen to azaleas. Observations thus far do indicate differences in the number of floral visitors to each individual azalea bush, with some having extensive out-cross pollen deposited. Scientists are increasingly interested in the role garden plants play in supplementing pollinator diets, as more native habitats and plants are lost as a source of food. (176)

Woods, Tessa*, Colin Berkheimer, Krista Silvis, Rachel Mills, Kellie Wilson, Jingyi Xu, Kevin Yoder, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Reproductive characteristics and habitat type in the invasive New Zealand mud snail in Polecat Creek, Wyoming.* — The New Zealand mud snail (*Potamopyrgus antipodarum*) is a world-wide invasive species and is very abundant in the Greater Yellowstone Ecosystem. In Polecat Creek, Wyoming, densities of the invader have been recorded up to 700,000/m². In its native New Zealand, the snail varies in density and life-history characteristics by habitat within the same water body. The purpose of this study is to determine if there are differences between New Zealand mud snails inhabiting different habitats within Polecat Creek. Here we compare the ratios of *P. antipodarum* to native gastropods within three different habitats (stream bank, reeds, and macrophytes). A preliminary analysis of the data suggests that there are significant differences in the proportion of New Zealand mud snails in the three habitats compared to native gastropods, and that these differences may result in different life history measures between habitats. (144)

Woodward, Claire*, Julia Palmucci, and Steven James Gettysburg College, Gettysburg, PA 17325. *Mutation of a novel fungal protein disrupts microtubule stability and cell division in Aspergillus nidulans.* — WD40 proteins constitute one of the largest eukaryotic protein families. They participate in a wide variety of cellular processes, including cytoskeletal and microtubule dynamics, regulation of cell division, and signal transduction. WD40 domains exhibit great sequence diversity, complicating their characterization. WD40 domains are approximately 40 amino acids in length, ending with tryptophan and aspartic acid (WD). WD40 proteins harboring 6-7 WD40 repeats adopt a conserved β -propeller structure — a flat, circular plate ideal for facilitating protein-protein interactions. We identified a conserved fungal protein, WD1, in *Aspergillus nidulans* containing seven WD40-repeat domains. A null mutation in WD1 (Δ WD1) confers cold-sensitive lethality and mitotic catastrophe at 20°, characterized by greatly reduced or absent cytoplasmic and spindle microtubules and fragmentation of chromosomes. In addition, the Δ WD1 null mutant is sensitive to the microtubule-destabilizing drugs benomyl and nocodazole at semi-permissive temperatures. These observations reveal a critical role for WD1 in promoting microtubule stability and cytoskeletal dynamics. In order to strengthen evidence of the role for WD1 in microtubule-related processes, we are examining genetic interactions between Δ WD1 and other mutants affecting microtubule function. For example, Δ WD1 appears to confer synthetic lethality in combination with *benA33*, a heat-sensitive and benomyl-sensitive beta-tubulin mutation that blocks chromosome segregation by hyperstabilizing microtubules. We are also testing the possibility that microtubule-stabilizing drugs such as taxol will rescue Δ WD1 defects. We are working to understand the precise functions of WD1, as this intriguing fungal protein is unstudied in any other model system. (114)

Wyche, Deanna*, Klaudia Walewska*, and Joyce Belcher Cabrini University, Radnor, PA 19087. *Quercetin hydrate in the acceleration of osteoblast differentiation and function in vitro.* — In the human body, formation of bone by osteoblast cells and osteoclastic bone resorption are coupled in order to maintain a healthy skeleton. Bone mass naturally declines with age due to enhanced osteoclast activity. Osteoblast differentiation progresses through stages of cell proliferation, matrix deposition, and matrix mineralization. The objective of this study is to identify potential agents, which could regulate skeletal homeostasis on the cellular level. One such candidate agent is quercetin hydrate (QH), a non-citrus flavonoid that has been previously studied in its role as an antioxidant. We aimed to evaluate the direct effects of QH on osteoblast cell proliferation and differentiation *in vitro*. QH was added to the pre-osteoblastic cell lines MC3T3-E1 and MG-63 at two concentrations. Cell proliferation and toxicity were assessed at 3 and 7 days of QH treatment via biochemical assays. Cell cultures were differentiated *in vitro* to 14 and 21 days with osteogenic media

and stained to visualize matrix deposition and calcium/phosphate mineral maturation. Alkaline phosphatase was assessed at days 14 and 21 to assess osteoblast enzyme activity and function. Cultures treated with QH showed significant increase in cell proliferation and viability at both treatment doses. In response to QH treatment, there were no toxic effects observed. We observed more mineral matrix staining in QH-treated cultures compared to untreated control. Von Kossa and Alizarin Red staining demonstrated enhanced osteoblast matrix deposition and mineralization associated with QH treatment. We observed an increase in Alkaline Phosphatase enzyme activity with QH treatment. Collectively, these findings suggest QH plays a role in the promotion of osteoblast cell differentiation, matrix organization and maturation *in vitro* and could potentially promote skeletal health by acting as a bone anabolic agent. (75)

Xu, Jingyi*, Kevin Yoder*, Colin Berkheimer, Kellie Wilson, Tessa Woods, and Edward Levri Penn State University-Altoona, Altoona, PA 16601. *Size influences desiccation tolerance in an aquatic invasive snail.* — One of the reasons that the New Zealand mud snail (*Potamopyrgus antipodarum*) is such a successful aquatic invader is its ability to resist desiccation while it is transported from one water body to another. The snail is small in size ranging from 0.5 mm to 6 mm in length. Smaller individuals are less likely to be detected attached to clothing and gear. The purpose of this experiment was to determine if there is variation due to size in desiccation tolerance. Snails of three different size classes (2.2-2.4 mm, 3.2-3.4 mm, and 4.0-4.6 mm) were removed from water and placed in plastic cups in the open air for various lengths of time (0 hours, 1 hour, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, and 48 hours) and then placed back into water and then assessed for survival. A preliminary analysis of the data suggests that there are significant differences in survival depending on size. Smaller snails tended to die by 12 hours out of water, while the largest size class survived significantly longer. These results suggest that even with visually inspecting gear, small snails that are likely to be overlooked can still be transported between water bodies for at least 12 hours. (143)

Young, Megan*, Jamie Atondo, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. *Characterization of Chryseobacterium gabrielii sp. nov., and reclassification of Chryseobacterium greenlandense as a junior synonym of Chryseobacterium aquaticum.* — As part of an undergraduate microbiology course, an aerobic, yellow pigmented, gram-negative, non-motile rod shaped bacterium designated JAH was isolated from the Loyalsock creek. The 16S rRNA gene sequence was 97.8-97.6% similar to those of *Chryseobacterium aquaticum*, *C. soldanellicola* and *C. greenlandense*. The genomes were sequenced for analysis the overall genome similarity indices of average nucleotide identity (ANI), average amino acid identity (AAI) and digital DNA-DNA hybridization (dDDH). It was observed that while strain JAH was different enough to be a separate species, *C. greenlandense* and *C. aquaticum* were similar enough to each other to be members of the same species. While analyzing the genome taxonomy database (GTDB) tree, *Chryseobacterium* sp. YR005 was found to belong to the species as strain JAH and *Chryseobacterium* sp. Hurlbut01 was found to be another strain of *C. aquaticum*. Finally, the whole genome tree also revealed that *C. piscicola* is a close relative despite relatively low 16S rRNA gene sequence similarity. (171)

Yu, Tracy*, Lara LaDage, and Pete Zani Penn State University-Altoona, Altoona, PA 16601. *Increased male sexual displays correlates with ventral posterior amygdala volume and cell volume in wild-caught side-blotched lizards Uta stansburiana.* — Variation in sexual display rate can induce variation in the ventral posterior amygdala (VPA), an area of the brain involved in reproductive behaviors. Specifically, increased sexual displays in the breeding season is correlated with increased VPA attributes. Previous research has demonstrated that higher rates of sexual displays, such as dewlap extensions in lizards, were associated with larger VPA volume and neuron soma size. However, it remains unclear if individuals residing in the field reflect results found within the laboratory, as there are likely many more selective pressures in the field with which to contend. Thus, in the current study, we examined variation in VPA attributes of wild-caught side-blotched lizards (*Uta stansburiana*) from two different states, Oregon and Nevada. In Nevada populations, males have lower display rates than that found in Oregon populations, likely due to increased predation pressures. Mirroring this, we found that Nevada populations exhibited decreased VPA volume and VPA cell volume suggesting that decreased display rates in the face of predation can downregulate VPA attributes in the field. (42)

Zakrzewski, Shelby*, Michael Tyree, Ellen Yerger, Timothy Tomon, and Carolyn Copenheaver Indiana University of Pennsylvania, Indiana, PA 15705. *Using tree-ring analysis to determine effectiveness and duration of biological treatments for hemlock woolly adelgid on eastern hemlocks.* — Since its introduction, hemlock woolly adelgid (HWA; *Adelges tsugae*) has caused widespread mortality in eastern hemlock (*Tsuga canadensis*). As a dominant, late-successional tree species, hemlocks provide unique and important habitats for a variety of organisms and its disappearance is disrupting these ecosystems. To combat HWA, the predatory beetle species *Laricobius nigrinus* has been released in many regions of infestation in the eastern United States. The primary focus of this study was to examine the effectiveness and duration of *L. nigrinus* releases on HWA populations using dendrochronology. During the summer of 2018, nine sites with known beetle releases in the Ridge and Valley region of Pennsylvania were selected for sampling. Within each site, cores were extracted from five hemlock and three non-target tree to be prepped for tree-ring analysis. Ring widths of all cores were measured following rigorous cross-dating to determine growth rates in the years prior to and following beetle releases. Based on average ring width data, both the eastern and western most sites saw dramatic declines in ring width following infestation of HWA with no apparent recovery following *L. nigrinus* releases. While no trends were observed in this initial dataset, five sites remain for further analysis. This study provides insight into the usefulness of predatory beetles as control agents for HWA and whether continued releases should be implemented. Future research should use tree-ring analysis to compare growth rates of chemically treated hemlocks to stands with biological controls. (184)

Zangakis, Reannon*, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. *Repeated emergence counts at a little brown bat (*Myotis lucifugus*) maternity roost in the Delaware Water Gap National Recreation Area.* — The emergence of White-nose Syndrome (WNS) in 2006 has prompted monitoring of bat populations affected by this new disease. Little brown bats (*Myotis lucifugus*) have suffered drastic population declines due to WNS. Since 2012, East Stroudsburg University students have conducted summer emergence counts at a maternity colony of little brown bats in an old church in the Delaware Water Gap National Recreation Area in eastern Pennsylvania. After severe declines following the appearance of WNS in the area, the number of bats at this roost increased from 2012 to 2014 and has since remained relatively stable. However, estimates of reproduction in the colony were unreliable due to infrequent monitoring. In 2018, we tried to improve our estimates of population size and reproduction in this roost and also establish more precisely the date that young began to fly. We conducted emergence counts for up to 3 days in a row during multiple weeks throughout the summer. We counted the number of bats coming out of the church each night and recorded data on temperature and sky and wind conditions. The 2018 counts were compared to previous years for each stage of the summer: pre-volant, peak volant, and post-volant. The early summer counts of emerging female bats averaged 125 in 2018, similar to past years. However, there was an increase of 87 bats in mid-summer, during the volant stage, suggesting a 62% reproductive rate, considerably higher than the 2017 estimate of 29%. Variation in the numbers of individuals counted for each stage was also reduced by performing more frequent counts. We conclude that regular emergence counts provided a more accurate count of colony size and a better estimate of reproduction in the colony. (169)

Zhang, Chenyu*, and Robert Kurt Lafayette College, Easton, PA 18042. *Characterizing metabolic reprogramming in early innate immune response of myeloid cells to murine mammary carcinoma in BALB/c mice.* — We used three different murine mammary carcinoma to study the early anti-tumor immune response. Initial analysis showed that the number of cells at the tumor sites almost doubled between 12-72 hours going from about 3e5 cells at 12 hours to about 6e5 cells at 72 hours. Surface staining revealed that the immune response during this period was predominated by Gr1+ and F4/80+ cells, representing neutrophils and macrophages (Mφ) respectively. Strikingly, similar cell numbers and cell types were recruited to control sites suggesting non-specific cell recruitment. However, closer examination revealed significant differences not only between the control and tumor-injected sites, but also among different tumor sites. At 24 hours post-injection there were significantly more Mφ at the EMT6 tumor site than at the 4T1, 168 and control-injected sites, and at 72 hours post-injection there were significantly more Mφ at the EMT6 tumor site compared to the 4T1 and 168 tumor sites. Using qRT-PCR we found that Mφ from the EMT6 site

expressed more MMP-9 and TNF- α than M ϕ from the 4T1 and 168 tumor sites. By performing Seahorse glycolytic rate and ATP production assays, we found differences in metabolic preferences and energy production. The M ϕ collected from 168 tumor sites showed the greatest reliance on OXPHOS, while those from 4T1 tumor sites showed the largest increase in OXPHOS from 24 to 72 hours. By 72 hours, as compared to the control, M ϕ from all three tumors had lower ATP production, with the most significant difference being at 4T1 tumor site. M ϕ from the EMT6 tumor site showed a reduction in ATP production from 24 to 72 hours, while an increase and no change were observed for the M ϕ from 168 and 4T1 sites respectively. Collectively, these data indicated that a unique anti-tumor immune response was evident within hours of tumor delivery. (202)

Zimmerman, Courtney*, Jean-Francois Therrien, and Allison Cornell Cedar Crest College, Allentown, PA 18104. *Diet composition and sex ratio of American kestrel chicks.* — American kestrels (*Falco sparverius*) are sexually dimorphic birds, with females being about 9% larger than males. Kestrels feed on a diversity of prey, including, but not limited to small mammals, songbirds, and insects. Due to their size differences, female chicks may need a different diet during development than male chicks. Like most raptors, kestrels regurgitate pellets of indigestible material which can then be dissected to assess diet composition. The goal of this study was to identify prey from nine kestrel nests from the 2018 breeding season, and to test for a correlation between the sex ratio of chicks and the composition of diet. Pellets were collected after chicks had left the nest from broods ranging from 100% female offspring to 100% male offspring. Each nest box pellet was sorted in the lab and its contents were then tallied in twelve different prey categories. A total of 5,629 prey items were found, including songbird, rodent, beetle, cricket/grasshopper, and bat prey. By comparing the pellet contents and chick sex ratios of each nest, we tested the hypothesis that nests with predominantly female (larger sex) chicks would have a higher proportion of larger prey items (such as mammalian prey) compared to nests with predominantly male chicks. Preliminary results show no clear relationship between offspring sex ratio and diet composition, despite the variation in the composition of diet across nests. (151)