

**2019 Missouri Academy of Science  
Annual Meeting Abstracts  
Northwest Missouri State University  
April 12-13, 2019**

**Meeting Abstracts**

**AGRICULTURE SECTION**

**Oral Presentations**

E. Ernat, T. Zell, and O. Perez-Hernandez, School of Agricultural Sciences, Northwest Missouri State University. **OVERWINTERING BEHAVIOR AND END-OF-SEASON MORTALITY OF THE SOYBEAN LEAF BEETLE (*Cerotoma Trifucata Forster*) IN NORTHWEST MISSOURI.** The soybean leaf beetle (SLB, *Cerotoma trifurcata*) is the most economically important insect pest of soybeans in Missouri. Soybean leaf beetle adults are suggested to overwinter in soybean crop residue. However, little is known about the overwintering behavior and end-of-season mortality of SLB adults. The objective of this study was to characterize the overwintering habits and mortality of SLB in northwest Missouri. Adult SLBs were collected on September 26, 2018 from a soybean field near the Northwest Missouri State University campus in Maryville. Next, 25 beetles were carefully placed in each of four 12 x 12 x 12 inch collapsible mesh cages. To provide natural overwintering sites for the beetles, two 10 inch<sup>2</sup>, 1.5 to 2-inch deep, undisturbed soil portions were carefully excised, placed into plastic trays, and put inside each cage. Two cages were placed inside the laboratory and kept at room temperature while the other two were placed outside under normal end-of-season weather conditions. The activity and mortality of adult beetles was monitored every other day beginning September 26 and ending November 16. In the indoor cages, beetles were active for a few days, but most of them died or became lethargic within the first 17 days. In the outdoor cages, beetles became inactive or searched for refuges in plant debris as temperatures decreased. However, they remained alive longer than the ones kept indoor. Our study suggests that in northwest Missouri, SLB adult activity slows down by late October and beetles became inactive by middle November.

O. Pérez-Hernández, C. Olewunne, and N. Hoilett, School of Agricultural Sciences, Northwest Missouri State University, Maryville, Missouri. **PREDICTING INTENSITY LEVELS OF FROGEYE LEAF SPOT (*Cercospora sojina*) IN NORTHWEST MISSOURI.** Frogeye leaf spot (FLS; *Cercospora sojina*) is a late-season fungal disease that has become prevalent in northern U.S. states in recent years. Under favorable weather conditions, the disease can reduce yield up to 60% in susceptible soybean cultivars. Effective chemical control of FLS requires

sound knowledge of its epidemiology, especially timing when the disease attains certain intensity levels. This information is not clearly defined. The objective of this study was to determine intensity levels of FLS in northwest Missouri. Ten soybean rows in a soybean field were selected in Nodaway County, Missouri in the fall of 2017. In each row, four plants were identified and one trifoliolate leaf in the upper canopy was marked to monitor the progress of the disease, which was assessed as the number of lesions appearing on the leaf over time. The disease was monitored at four-day intervals starting on September 1 and ending on October 28. Varying intensity levels of the disease were determined using survival analysis. The results indicate that towards the end of the season, from initial lesion foci FLS can reach up to 50% severity in about 8 days. After that period, the epidemic rate decreases in a linear fashion.

## **AGRICULTURE SECTION**

### **Poster Presentations**

S.E. Svenson. Charles Nemanick Alternative Agriculture Garden, Department of Agriculture, Southeast Missouri State University. **NATIVE PERENNIALS FOR BUTTERFLY AND POLLINATOR GARDENS: FOURTH YEAR PERFORMANCE IN SOUTHEAST MISSOURI.** Perennials native to Missouri were evaluated for survival, growth, and flowering from forty to fifty-two months after planting into a compost-amended urban soil in Cape Girardeau, MO. Twenty-eight container-grown plants of each species were planted in late August 2014 in a butterfly-shaped garden under full sun growing conditions. Two plots per species were planted in each wing of the garden, providing four replicated plots of seven plants of each species for analysis. During the fourth full year after establishment, the following species had 100% survival, excellent growth, and 100% flowering: *Penstemon digitalis*, *Rudbeckia fulgida* var. *umbrosa*, and *Rudbeckia missouriensis*. Species having 75% to 86% survival, good growth, and 100% flowering during the fourth growing season included: *Eryngium yuccifolium*, *Eutrochium purpureum*, *Symphyotrichum oblongifolium*, and *Veronicastrum virginicum*. *Asclepias tuberosa*, *Echinacea pallida*, *Echinacea paradoxa*, *Echinacea purpurea*, *Glandularia canadensis* and *Zizia aurea* had less than 50% survival, poor growth, and 100% flowering of surviving plants. *Amorpha canescens* had less than 50% survival, but living plants had good growth and flowering. *Rudbeckia fulgida* var. *umbrosa*, *Rudbeckia missouriensis*, and *Eryngium yuccifolium* have seed propagated at the location, populating additional area in and around the experimental plots. Less than 75% of the original *Coreopsis lanceolata* specimens remained alive in the fourth growing season, but the species has aggressively populated near-by growing beds and gravel pathways. Two species planted in nearby secondary plots had 75% to 86% survival, excellent growth, 100% flowering, including: *Asclepias incarnata* and *Liatris spicata*. The data will help guide the selection of plant species used for urban or suburban butterfly and pollinator gardens in southeast Missouri.

S. Williams, A. Coy, N. Hoilett, and O. Perez-Hernandez. School of Agricultural Sciences, Northwest Missouri State University. **DO AGRICULTURAL BIOLOGICALS AFFECT CARBON DYNAMICS?** Increasing global populations dictate an increased efficiency in food, fiber, and fuel production techniques. The use of agricultural biologicals is a recent trend in production techniques to enhance crop productivity. The effect of agricultural biologicals on soluble soil carbon is little understood. Soluble soil carbon fractions have been associated with nutrient cycling and availability. Potassium permanganate oxidation provides a measure of labile carbon. The focus of this research is investigating the influence of soil biologicals on labile carbon as an indication soil response to management changes, specifically the introduction of agricultural biologicals. Labile soil organic carbon tends to respond very quickly to alterations in soil properties. For this study the potassium permanganate oxidation, cold-water extraction, and hot water extraction methods were used to measure soluble soil carbon. The information gathered from this project will provide valuable information on the influence of agricultural biologicals on soil carbon dynamics that could potentially influence soil microbial activity and nutrient cycling.

V. Singamreddy, C. Kipping, N. Hoilett, and O. Perez-Hernandez. **CHARACTERIZATION AND IDENTIFICATION OF MOLD FUNGI IN HARVESTED SOYBEAN SEED IN NORTHWEST MISSOURI.** Continuous rainfall at the end of the 2018 growing season in northwest Missouri favored the occurrence of field mold fungi on soybean grain in the region. Mold severity was exacerbated in fields infested by the soybean leaf beetle. Several species of fungi causing grain mold diseases are reported in the literature. However, the species that caused epidemics in harvested grain in northwest Missouri have not been characterized and their identity is unconfirmed. The objective of this survey was to characterize and identify the fungi associated to grain mold in the region in 2018. Twenty-two soybean grain samples were provided by two elevators in northwest Missouri for use in the study. The seeds were surface sterilized with 0.1% sodium hypochlorite and rinsed in sterile water for 1-2 minutes. Seven to ten seeds were plated in potato dextrose agar medium and incubated at 27 to 30°C for five to seven days. The fungal colonies that developed were transferred to new plates to isolate and purify the fungi and again they were kept in an incubator at 27 to 30°C for five to seven days. Based on colony morphology of microscopic observation of fungal sporulation, at least three genera have been identified to date: *Aspergillus*, *Penicillium* and *Fusarium*. These genera are believed to be associated with soybean seed mold in the collected samples. Pathogenicity seed tests and further morphological and molecular identification will substantiate the identity of the fungal species associated with mold diseases in this region.

V. Cloughley, K. Tharp, and O. Perez-Hernandez, School of Agricultural Sciences, Northwest Missouri State University. **EFFICACY OF A NUTRITIONAL SEED TREATMENT ON EARLY DEVELOPMENT OF SOYBEAN (*Glycine max*) IN CONTROLLED CONDITIONS.** Nutritional seed treatments constitute a new option in soybean production.

Their benefits include strong and rapid crop establishment, improved response to seedling diseases, and prevention of early-season crop nutrient deficiencies. However, their use is still limited and their benefits poorly recognized. This is mainly due to unavailability of nutrient-based products apt to be seed applied and to the lack of data on this treatment types. The objective of this study was to determine the efficacy of a nutritional seed treatment on early soybean development. Soybean seeds cv. Pioneer P37T09L were treated with a complex containing major elements, micronutrients and amino acids, or left untreated. The treatment was applied at a low, medium, and high commercial rates (4.0, 5.5, and 7 fl.oz. per 100 lbs of seeds, respectively) while the control was treated with sterile deionized water. The experimental units consisted of glass jars containing 50 grams of seed. All treatments were disposed in a completely randomized design with four replications. Four days after treatment, 20 seeds from each experimental unit were germinated in paper rolls and incubated for seven days at 25°C. Primary root length was measured in 12 seedlings selected systematically in two rolls from each of the four treatment replications. First run of the experiment indicated that treatment did not negatively affect germination and, compared with the control, it increased the length of the primary radicle of seedlings. No apparent treatment effect differences for dosages was observed. Repeat of the experiment is underway.

A. Coy, A. Kelly, S. Williams, N. Hoilett, and O. Perez-Hernandez. School of Agricultural Sciences, Northwest Missouri State University. **EVALUATING THE INFLUENCE OF AGRICULTURAL BIOLOGICALS ON RHIZOSPHERE ENZYME ACTIVITY.** Global demands for food, fiber, and fuel necessitate the use of innovative technology to increase agricultural productivity in an environmentally sound manner. A growing trend in crop production is the use of agricultural biologicals derived from microorganisms or plant extracts. The market for agricultural biological products is estimate to surpass US\$13 billion by 2022. The key concept behind the use of biologicals is their influence on crop productivity and soil health. However, the role of these biologicals in soil processes is not well understood. Questions arising from the use of biologicals include, how do biologicals influence soil microbial dynamics and function? One area of study that provides meaningful information on soil function is soil enzymology, due to the sensitivity of enzymes to management changes. This research hypothesizes the application of soil biologicals will stimulate soil microbial population within the rhizosphere zone, potentially increasing soil enzymatic activity. Four groups of soil enzymes, dehydrogenase (general microbial activity); carbon cycle enzymes ( $\beta$ -glycosidase); nitrogen cycle enzymes (urease) and phosphorus cycle enzymes (phosphomonoesterases) were assessed in this study. The information gathered from this project will valuable information on the effect of agricultural biologicals on soil microbial function and nutrient cycling.

H. Dudusola, P. Oruganti, S. Soman, S. Anuoluwa, N. Hoilett, O. Perez-Hernandez, and K. Royal. School of Agricultural Sciences, Northwest Missouri State University. **SPATIAL ANALYSIS OF COVER CROP INFLUENCE ON SOIL HEALTH USING KIRGING**

**GEOSTATISTICAL PROCEDURES.** Cover crops are an effective conservation management practice with the potential to improve soil health and crop yields. This study, conducted in Northwest Missouri uses kriging spatial interpolation technique to estimate field values based on observations collected from known sampling points. The objective of this study is assessing and analyze the effect of cover crops on soil health over a four-year period. Measured soil properties include characterizing soil biological community using phospholipid fatty acids (PLFA), soil enzyme activities (dehydrogenase, urease, phosphomonoesterase, and  $\beta$ -glucosidase), bulk density, water infiltration rates, and soil carbon dynamics. Field maps created from these discrete points will be presented.

P. Oruganti, H. Dudusola, S. Soman, S. Anuoluwa, N. Hoilett, and O. Perez-Hernandez. School of Agricultural Sciences, Northwest Missouri State University. **IMPACT OF INTRODUCING COVER CROPS IN A CORN – SOYBEAN ROTATION SYSTEM ON SOIL HEALTH AND SOIL ENZYME ACTIVITIES.** Cover crops have been proposed as a strategy to reduce soil erosion, prevent nutrient leaching, decrease nitrogen loss from fields, and improving soil physical, chemical, and biological conditions. Cover crops influences soil microbiology community via increased carbon (C) supply. The intent of this project is to track changes in soil enzyme activities over four years of including cover crops as part of the agronomic management practices. It is well established that soil enzymes are more agile in their response to management changes than other soil health indicators. In addition, enzyme activities are well-established indices of microbial biomass (dehydrogenase), carbon turnover ( $\beta$ -glucosidase), and nitrogen dynamics (urease). For this study, we measured the above-named enzymes for 20 fields in Northwestern Missouri. The results from this study will provide insight to farmers, soil conservationist, and other interested groups on the potential of soil enzymes as an indicator of soil health.

S. Anuoluwa, N. Hoilett, P. Oruganti, H. Dudusola, S. Soman, and K. Royal. School of Agricultural Sciences, Northwest Missouri State University. **ASSESSING THE INFLUENCE OF COVER CROPS ON SOIL COMMUNITY CHARACTERISTICS USING PHOSPHOLIPID FATTY ACID PROFILES.** The benefits of adding cover crops in agronomic systems include reducing soil erosion, relieving soil compaction, improving soil fertility, increasing water infiltration and storage, and promoting carbon sequestration. In addition, cover crops are reputed to influence soil biology. The intent of this project is to determine changes in soil biological profile of agronomic systems within the first four years of introducing cover crops. Soil biological assessment will include measuring active carbon using the potassium permanganate method; and characterizing soil biological community using phospholipids fatty acids (PLFA) profiles. The amount of active carbon in the soil is a good indicator of soil health, based on its association with soil organic matter readily available as food and energy sources for the soil microbial community. In addition, active carbon positively correlates with organic matter content, aggregate stability, and soil biological activities. PLFAs

are key components of the microbial cell membrane and has consistently been used to assess soil microbial response to management changes. Therefore, information from this project will provide insight to stakeholders on the response of soil health indicators to the introduction of cover crops in a crop management system.

S. Bugh and M. McGee, Department of Agricultural Science, Northwest Missouri State University. **SIGNIFICANCE OF ASSISTED REPRODUCTIVE TECHNOLOGY IN MODERN ANIMAL PRODUCTION SYSTEMS.** Assisted Reproductive Technology, also known as 'ART', is various techniques used to obtain genetics from superior animals and produce offspring from reproductively challenged candidates. ART has been a growing technique partner within the livestock industry to combat infertility issues among various species. As technology develops, techniques and instruments used within ART are developed further and instruments previously used are redesigned. Due to the strong relationship with technology, the ART industry is fast evolving and becoming more efficient. Techniques include multiple ovulations and embryo transfer (MOET), artificial insemination (AI) or even in-vitro fertilization. Similarly, technicians are able to select specific semen based off sex, or collect multiple embryos from one superior female to produce multiple offspring using surrogates or storing them for future use. Beyond combating infertility issues, ART also allow producers to swiftly increase genetic superiority as well as production levels in livestock systems compared to conventional methods. In this paper, ART's history and evolution will be explored demonstrating its importance in reproductive efforts.

E. Greeley and N. Hoilett, Department of Agricultural Sciences, Northwest Missouri State University. **UNDERSTANDING THE EFFECT OF FEEDING AND RUMINATION TIME ON PARTURITION TIME IN CATTLE TO DECREASE RISK OF DYSTOCIA.** Feeding and rumination time play key roles in determining the expected calving time in cattle. The purpose of this study is to examine the influence of feeding times on parturition process in cattle. The ability to observe pre-calving symptoms can help producers decrease calving loss. Studies have shown that there can be multiple causes for dystocia including environmental conditions, parity and age of the female, birth weight of calf and abnormal fetal positions. Other research observed relationships between feeding time, rumination time and calving time. This paper will review the body of research related to the impact of rumination times on parturition time and calving loss. Indications suggest strong correlations between rumination and feeding time with calving time. Understanding this idea and other factors related to dystocia can help producers monitor and more accurately predict the calving times of their cattle. This in return will decrease the economic impact that calf loss has on cattle productions and help producers become more efficient.

C. Mann, J. Steinkruger, A. Giri, and K.W. Lovercamp, School of Natural Sciences, University of Central Missouri. **EFFECT OF L-GLUTAMINE ON BOAR SPERM VIABILITY AND**

**QUALITY.** Previous studies have shown benefits of l-glutamine on sperm quality in livestock species. The purpose of this research was to determine the effects of l-glutamine on sperm motility and morphology in swine. Ejaculates from crossbred boars (n=4) were collected once per week for three consecutive weeks. Semen extender was prepared with concentrations of 0, 50 and 100 mM l-glutamine. Following semen collection and processing, the semen was extended to  $37.5 \times 10^6$  sperm/mL in each l-glutamine concentration for each boar. The semen samples were then stored in a semen cooler at 17°C in 15 mL conical tubes. Motility was evaluated on day 0 (day of collection), day 2 and day 6 of each week. On these days, 1 mL aliquots were placed into a warming well on a heating stage for 30 minutes at a consistent temperature of 39°C prior to analysis. The analysis showed that as l-glutamine increased in the extender solution, total and progressive motility decreased ( $P < 0.0001$ ). Motility also decreased from day 0 to day 6 which was expected. Following motility analysis, morphological analysis was performed through microscopy. There were no statistical differences ( $P > 0.05$ ) for normal morphological sperm cells between l-glutamine treatments. In conclusion, these results suggest that l-glutamine in concentrations of 50 and 100 mM adversely affects sperm motility, but have no effect on sperm morphology.

K. Clapp<sup>1</sup>, R. Sounders<sup>2</sup>, and N. Hoilett<sup>1</sup>. School of Agricultural Sciences, Northwest Missouri State University<sup>1</sup>; Natural Resource Conservation Services<sup>2</sup>. **EXPLORING CAREER**

#### **OPPORTUNITIES FOR STUDENTS THROUGH THE USDA PATHWAYS**

**INTERNSHIP PROGRAM.** The USDA Pathways Internship Program provides students enrolled in a wide variety of educational institutions, and recent graduates with opportunities to explore USDA careers. This program provides paid work experience to students currently enrolled in high school, or an accredited college or university. This includes Home-Schooling, certificate programs, and community colleges. Interns may work during the summer, fall, spring, or year-round. In order to be eligible for this internship the student must be a U.S. Citizen or U.S. Permanent Resident. They must be sixteen years or older. They must be enrolled in, or accepted for enrollment to, an accredited high school, community college, college or university; professional, technical, vocational, or trade school; advanced degree program; or other qualifying educational institution and pursuing a qualifying degree or certificate. The student must also be of good Academic standing with a 2.0 GPA or better. In order for the student to be placed into a permanent job position they must complete 640 hours of the internship, not including paid holidays. They must also have completed twelve credit hours or more of soil classes.

P. Mayhood<sup>1</sup>, B. Mirza<sup>1</sup>, and M. Burton<sup>2</sup>, Department of Biology<sup>1</sup>, Department of Agriculture<sup>2</sup>, Missouri State University. **16S RDNA SEQUENCING OF RHIZOBIAL AND NON-RHIZOBIAL ENDOPHYTES WITHIN INDIVIDUAL ROOT NODULES OF SOYBEAN.** Soybean is a valuable crop that establishes a symbiotic association with nitrogen-fixing microorganisms. For a long time, culture-based methods suggested that members of the genus *Bradyrhizobium* are the only nitrogen-fixing inhabitants of soybean root nodules. However,

results from recent studies identified the presence of many other bacteria within soybean root nodules. Much of previous research is derived from culture-dependent methods, only estimated to account for 0.1% of microbes in agricultural soils, potentially misrepresenting community dynamics. This study investigated the presence and relative abundance of rhizobial and non-rhizobial endophytes (NREs), within different nodules on the same soybean plant. Three sites were selected on Kendrick Farm in Springfield, MO, where three plants and rhizosphere soil were collected at each (nine total plants). The microbiome of approximately 24 individual soybean root nodules from each plant were analyzed using next-generation 16s rDNA gene sequencing. Preliminary results suggest high abundance of *Bradyrhizobium* genera within root nodules. Two non-rhizobial endophytes that were consistently present in all root nodules, *Nitrobacter* and *Tardiphaga*. Other NREs were inconsistently present at low abundance, suggesting a lesser role in plant growth as endophytes. Investigation of *Tardiphaga* and *Nitrobacter* within root nodules are of high importance, as few studies have isolated *Tardiphaga* and none have isolated *Nitrobacter*.

## **BIOCHEMISTRY, BIOMEDICINE, & BIOTECHNOLOGY SECTION**

### **Oral Presentations**

C. Espinoza Patharkar<sup>1</sup> and O.R. Patharkar<sup>2</sup>, <sup>1</sup>Department of Science, Technology and Mathematics, Lincoln University, <sup>2</sup>Department of Biological Sciences, University of Missouri-Columbia. **USING FLUORESCENCE IMAGING IN UNDERGRADUATE RESEARCH-BASED COURSES TO STUDY PLANT-MICROBE SIGNALING PATHWAYS.** Inquiry-based and research-based laboratory pedagogies in undergraduate science are effective to increase student learning. We developed a semester-long research-based laboratory course of Cell Molecular Biology with the goal to provide a “real” research experience to motivate student learning. The research topic was the subcellular localization of Arabidopsis proteins involved in chitin signaling. Chitin, a main component of the fungal cell wall, is released when plants are attacked by fungal pathogens. Chitin is recognized by receptor proteins in plant cells leading to activation of the innate immune response in the whole plant. Students filled an exit survey and results showed that they found learning more interesting, encourage them to use scientific reasoning, and gave them a broader sense of purpose. More engaged students spent extra hours fixing problems encountered in the laboratory classes. Interestingly, a couple of students decided to go to graduate school and do research in Cell Biology or Genetics, instead of their initial idea of going to Medical School. Students presented their results at different local and regional conferences. More recently, we have developed a website (<https://rahulpatharkar.000webhostapp.com/>) that provides well tested reliable life science protocols in print and video form to be used as supplement in laboratory classes or for training of young researchers. We are currently working to develop laboratory courses syllabi using these video protocols to be readily available for higher education and high school teachers.



E. Suez, J.C. Smothers, O. Olson, and K. Kim, Department of Biology, Missouri State University. **NOVEL FUNCTION OF VPS1 ON MEMBRANE FUSION.** Cargo trafficking to the target organelle finishes its journey as the donor membrane fuses with the target. Dysregulation of the fusion as well as defects in its preceding steps is tightly associated with a diverse range of human disorders including cancers. We have established a successful protocol that can efficiently measure the extent of fusion between donor membranes carrying  $\nu$ -SNARE (Snc2) and target membranes with three  $t$ -SNAREs (Tlg1, Tlg2, and Vti1). Yeast dynamin-like protein Vps1 has been proposed to function in fusion of endosome-derived vesicles with the Golgi membrane. This prompted us to assess the potential fusion role of Vps1 with the in vitro fusion assay. Our data showed that Vps1, in the presence of GTP, robustly stimulated membrane fusion rates. However, membrane fusion rates dropped as Vps1's GTPase activity was compromised by the treatment of dynasore, a GTPase inhibitor. Ongoing research involves the testing of Vps1's effects on fusion between membranes containing PI3P or PI4P, which will be providing a significant insight toward the understanding of the mechanism of endosome fusion with the Golgi.

N. Nuthikattu and J. Ory, Department of Basic Sciences, St. Louis College of Pharmacy. **A SURVEY OF DISOMY AND MITOCHONDRIAL HETEROPLASMY IN 200 STRAINS OF THE HUMAN FUNGAL PATHOGEN *CRYPTOCOCCUS NEOFORMANS*.**

*Cryptococcus neoformans* is an encapsulated yeast that causes fungal meningitis and encephalitis. *C. neoformans* is acquired through inhalation and is engulfed by alveolar macrophages, where it is able to disseminate into the central nervous system. It survives for extended periods of time through a combination of latency and resistance to eradication by antifungal agents. It can also survive the hostile intracellular environment of macrophages by turning on the expression of genes for oxidative stress. Recent studies demonstrate that one mechanism of antifungal resistance in *C. neoformans* is the induction of disomy, where random chromosomes are duplicated in this normally haploid organism. To assess how common this phenomenon is, as well as the related phenomena of mitochondrial heteroplasmy, we have analyzed the genomes of over 200 isolates of *C. neoformans*.

A phylogenetic tree of the mitochondrial sequences shows a high degree of relatedness between most of the strains, with only three strains being clear outliers. Using short read mapping analysis, disomy occurs at least once for every one of the 14 chromosomes, being more common for the smaller chromosomes. Similarly, over 75% of the strains have at least one heteroplasmic site in their mitochondrial DNA, including the reference strain H99. We are currently growing the H99 strain in continuous culture with the goal of sequencing every 100 generations. We hope this will demonstrate both the basal rate of change as well as the stability of heteroplasmic sites.

Z. Ingram and A. Hulme, Department of Biomedical Sciences, Missouri State University. **CYCLOPHILIN A ENHANCES HIV-1 REVERSE TRANSCRIPTION IN MICROGLIAL**

**CELLS.** HIV-1 infection depends on a series of early replication steps. During cytoplasmic transit, viral RNA is reverse transcribed to DNA, initiating uncoating. Uncoating is the disassembly of the viral capsid and must be completed for nuclear import. The capsid also acts as an interface for host proteins that facilitate these early steps. Cyclophilin A (CypA), a cytoplasmic proline isomerase, binds capsid and alters infectivity in a cell dependent manner. Disruption of CypA-capsid interaction by CsA treatment enhances early replication steps in microglial cells. The interplay between reverse transcription, uncoating, and nuclear import suggests CypA may impact multiple steps. The effect of CypA on reverse transcription was indirectly quantified through synchronized infection of microglial cells with HIV-GFP in CsA or ethanol containing media. At 0, 1, 2, 3, 4, 6, and 8 hpi Nevirapine containing media was added to inhibit reverse transcription. Percentage of GFP positive cells were determined by flow cytometry. We found that reverse transcription was reduced when CypA-capsid binding was prevented. 2-LTR circles, a nuclear import marker, were measured using qPCR and showed a decrease at 12 and 24 hpi upon CypA-capsid disruption. As the nuclear import step is downstream of reverse transcription, these results suggest that CypA enhances reverse transcription for efficient replication in microglial cells. Elucidating CypA function in HIV replication will provide a better understanding of these early replication events.

K.A. Yusuf and K. Kim, Department of Biology, Missouri State University. **THE USE OF PALLADIUM (Pd) AND PLATINUM (Pt) CYANOXIMATES IN THE TREATMENT OF CANCER CELLS, INITIATING A NEW APPROACH TO CANCER**

**CHEMOTHERAPY.** The use of chemotherapy is the one of the most common treatments of cancer and the most effective and widely used are metal-containing anticancer drugs such as cisplatin, carboplatin, and all Platinum(II)-containing complexes. This research experiment is aimed at testing the effects of palladium (Pd) and platinum (Pt) cyanoximates in treatment of cancer cells (HeLa cervical cancer epithelial cells). The experiment is being conducted *in vitro* using novel Pd and Pt complexes from Dr. Nikolay Gerasimchuk of Chemistry department, Missouri State University. With Cisplatin as positive control, the study examined the effect of Pd(Deco) and Pt(Deco) on cell proliferation and cytotoxicity, using cell proliferation kit ii (XTT). The results obtained indicated that both Pd(Deco) and Pt(Deco) effectively inhibit cell proliferation at 0.25mM concentration with significant difference ( $p < 0.05$ ) when compared with non-treated control. Research is still ongoing in order to determine the effect of the chemicals on rate of cell apoptosis as well as taking measurements for reactive oxygen species. The ideal of this study is to decipher the more potent of the two cyanoximes providing evidence for why either or both can be used as a close substitute or replacement to the currently used cisplatin.

A. Ly, V. Nguyen, J. Smothers, S. Kottapalli, J. Villarreal and K. Kim. Department of Biology, Missouri State University. **TYPE 5 MYOSIN FOR TRAFFICKING OF SNC1 AND VPS10 CARGO.** Retrograde transport, a shipping of cargo towards the trans-Golgi network (TGN) from the endosome, is essential for cellular homeostasis. Its dysfunction is associated with pathogenesis of Alzheimer and Parkinson's diseases. Our hypothesis was that the retrograde

traffic is mediated by myosin family proteins, cellular motors walking along actin filaments using the chemical energy from ATP hydrolysis. We assessed the potential roles of all five yeast myosins in the recycling of two membrane cargo, Snc1 and Vps10. We found that all myosins except myo2 were not required for the Snc1 traffic, while myo1 and 2 play important roles in *Vps10 traffic towards the Golgi*. Multiple myo2 mutants including temperature sensitive strains, such as *myo2-16* and *myo2-66*, and several myo2 tail mutant strains displayed trafficking defects of those cargoes. Together, our data shed new insights into understanding the function of Myo-family proteins in protein retrograde pathway destined towards the TGN.

C. Nadeau, K. Clark, A. Green, and M. Fidler, Department of Natural Science and Mathematics, University of Central Missouri. **A COMPARISON OF HUMAN PAPILLOMAVIRUS RATES BETWEEN U.S. AND JAMAICAN LOW-INCOME AREAS.** *Human papillomavirus* (HPV) is one of the most prevalent sexually transmitted diseases around the world, and one of the most common causes for cervical cancer. HPV is usually preventable through vaccinations and routine screenings. Our study is comparing HPV rates between low-income areas in both Jamaica and the United States. The town of Falmouth does have a fully staffed hospital, but the expenses are too great for the common Jamaican so, most patients that come to clinic are likely of low-economic means. This clinic conducted preliminary diagnosis of patient concerns and disease as well as provided free medication and prescription refills. Results regarding the HPV rates in America were gathered through peer-reviewed sources. We predicted the rates of HPV may be higher in Jamaica due to low awareness of the virus as well as poor infrastructure to receive the vaccine, however our results seemed lower than expected. The majority of our data was gathered directly through an out-patient clinic ran out of the city of Falmouth, Jamaica. Our pap smears were ThinPrep tests, produced by Hologic. The tests were conducted in Jamaica and were sent back to LabCorp in the United States. Our results indicated that the rates for HPV were lower in Jamaica. This was likely due to the types of patients typically seen in the clinic, who opportunistically opted for a pap smear.

R. Islam, K. Ihenacho, J.W. Park, and S. Islam, Laboratory of Biochemistry, Northwest Missouri State University. **PLASMID DNA NICKING ACTIVITY OF SOYBEAN TRYPSIN INHIBITOR AND BOVINE APROTININ.** Protease inhibitors, such as trypsin inhibitor, serum alpha-1 antitrypsin, or liver aprotinin, are a class of proteins that competitively bind and block the catalytic activity of proteolytic enzymes with wide ranging biological functions. A significant number of protease inhibitors have also been shown to possess antimicrobial activity, presumed to contribute in defense against pathogenic microorganisms as plants with higher levels of protease inhibitors tend to exhibit increased resistance towards pathogens. Two proposed mechanisms for the antimicrobial activity are combating microbial proteases that play roles in disease development and disruption of microbial cell wall & membrane necessary for survival. Here we show for the first time a novel activity of soybean trypsin inhibitor and bovine aprotinin that they nick supercoiled, circular plasmid DNA. A number of experiments conducted

to demonstrate the observed DNA nicking activity is inherent, rather than a co-purified, contaminating nuclease. The nicking of the plasmid results in markedly reduced efficiencies in transformation of *E. coli* and transfection of HEK293T cells. Thus, this work reveals yet a new mechanism for the antimicrobial activity by protease inhibitors.

## **BIOCHEMISTRY, BIOMEDICINE, & BIOTECHNOLOGY SECTION**

### **Poster Presentations**

H. Marino, R. Ulbricht, and J. Wang, Department of Biomedical Sciences, Missouri State University. **ROLE OF THE P2Y<sub>2</sub> RECEPTOR IN GLUCOSE TOLERANCE.** Nucleotide receptor P2Y<sub>2</sub>R is an important mediator in vascular inflammation. Recent studies suggested involvement of P2Y<sub>2</sub>R in high fat diet-induced metabolic abnormality. However, physiological role of P2Y<sub>2</sub>R hasn't been clearly defined. The purpose of this study is to investigate P2Y<sub>2</sub>R's role in glucose metabolism under physiological conditions. Fasting glucose level and glucose tolerance were assessed in C57BL/6 (wild type) and P2Y<sub>2</sub>R<sup>-/-</sup> mice (ages 8-12 weeks, female, male, and littermates). Mice fasted for 5 hours, blood was obtained from the tail, glucose levels were measured using a glucometer and blood glucose test strips. Mice received an intraperitoneal injection of 20% dextrose at the dose of 2 g/kg body weight. Blood glucose levels were measured at 0 (fasting), 10, 20, 30, 45, 60, 75, and 90 minutes after dextrose administration. We found that there was no difference in fasting blood glucose levels between WT and P2Y<sub>2</sub>R<sup>-/-</sup> mice for both males and females. The fasting blood glucose levels differed between males (113.8 ± 8.4, n=5) and females (88.9 ± 5.7, n=9) in WT mice (P<0.05) while there was no significant sex-specific difference in P2Y<sub>2</sub>R<sup>-/-</sup> mice (P>0.05). The glucose tolerant test was comparable either between WT and P2Y<sub>2</sub>R<sup>-/-</sup> mice or between sexes. Overall, the findings indicate that P2Y<sub>2</sub>R is involved in sexual dimorphism of fasting glucose level. The corresponding insulin levels under the same conditions for the glucose tests remains to be determined.

S. Mahl and J. Baker, Department of Biology, Missouri Western State University. **DEVELOPMENT OF STRAIN-SPECIFIC REAL-TIME PCR TO EVALUATE GROWTH COMPETITION BETWEEN FOUR BRADYRHIZOBIUM JAPONICUM STRAINS.** Using previously designed strain-specific primer, we set out to optimize PCR conditions that would allow individual quantification of a mixed culture of four commercially important USDA strains of *Bradyrhizobium japonicum*. We found that an annealing temperature of 60 C eliminated primer non-specific binding between USDA 110, USDA 123, USDA 136, and USDA 138 strains. Quantification of the strain-specific DNA was not altered by the presence of DNA from the other strains for all except the USDA 138 strain. Additionally, strain growth was quantified by standard plating methods and DNA was quantitatively extracted. Preliminary equations have been developed relating strain-specific cell quantity to real-time PCR threshold cycle number. Knowledge from this study will allow for rapid quantification of strains grown in

culture competition as a means for *Rhizobium* fermentation industry to optimize production and strain ratios.

Z. McAdams, Department of Physical & Biological Sciences, Columbia College.

**DEVELOPMENT OF COMPETITIVE ENZYME-LINKED IMMUNOSORBENT ASSAY (ELISA) TO QUANTIFY LEVELS OF BENZOYLECGONINE IN NATURAL WATER SYSTEMS.** Cocaine is an illicit drug which functions as a dopamine reuptake inhibitor stimulating a pleasure sensation in the brain upon ingestion. The drug is spontaneously or enzymatically hydrolyzed into many metabolites, the prominent form being benzoylecgonine (BZE) - a biologically active molecule that serves as the most common target of cocaine drug testing. BZE has been detected in natural water, thus a method to monitor metabolite levels in these systems is needed. One fast and specific method to quantify concentrations of a target compound is an enzyme-linked immunosorbent assay (ELISA). A competitive ELISA to quantify BZE levels in an efficient manner is under development in the present study.

M. Ferrell and C. Espinoza Patharkar, Department of Science, Technology and Mathematics, Lincoln University. **INVESTIGATING THE ROLE OF SNAP33 IN CHITIN-TRIGGERED IMMUNE RESPONSES IN ARABIDOPSIS.** When plants are attacked by pathogenic fungi, plants defend themselves by "chewing" the fungal cell wall. Chitin, a main component of the fungal cell wall, is released and recognized by the chitin receptor complex (comprised by receptor proteins CERK1 and LYK5) in plant cells. This recognition leads to activation of the innate immune response in the whole plant. This study is investigating the role of *SNAP33* in chitin-triggered immune responses. *SNAP33* (soluble N-ethylmaleimide-sensitive factor adaptor protein 33) is an Arabidopsis homolog of the neuronal t-SNARE SNAP-25 involved in exocytosis. *SNAP33* expression is increased upon chitin treatment in Arabidopsis but no change in expression is found in the *cerk1* mutant plants, indicating that chitin-induced *SNAP33* expression is CERK1-dependant. *snap33* mutant plants exhibited altered response to chitin-triggered MAP kinase phosphorylation and showed enhanced resistance to the necrotrophic fungus *Alternaria brassicicola*. Transient expression of SNAP33-GFP fusion protein in tobacco epidermal cells indicated that SNAP33 is localized at the PM. We are currently testing the hypothesis that SNAP33 might play a role in early recognition of chitin through association with the chitin receptor CERK1 using BiFC studies.

S. Thomas, S. Sheravina, R. Ulbricht, and J. Wang. Cell and Molecular Biology Department, Biomedical Science Department, Missouri State University. **P2Y2 RECEPTOR-DEPENDENT CHANGES IN MICROVASCULAR LEUKOCYTE-ENDOTHELIAL INTERACTION.** Nucleotides (UTP, ATP) are released from cells in response to inflammation and act as extracellular signaling molecules through purinergic receptors. A hallmark of inflammation is increased leukocyte rolling and adhesion. Accumulating evidence suggests the purinergic P2Y2 receptor (P2Y2R) plays a role in pathological inflammation. In the current study, we

hypothesized that extracellular UTP would increase leukocyte rolling and adhesion mediated by P2Y2R. Microvascular hemodynamics and leukocyte-endothelial interaction of skeletal muscle cremaster venules were assessed in wild-type (C57BL/6; WT) and P2Y2R-deficient (P2Y2R<sup>-/-</sup>) mice. Leukocyte total flux, rolling flux, and adhesion were quantitatively analyzed using a semi-automatic leukocyte tracking methodology. Under basal conditions, P2Y2R<sup>-/-</sup> mice ( $n=7$ ) exhibited an increase in relative leukocyte rolling (WT,  $8\% \pm 1.7\%$ ; P2Y2R<sup>-/-</sup>,  $29\% \pm 5.7\%$ ;  $p<0.001$ ) and adhesion (WT,  $5\% \pm 1.8\%$ ; P2Y2R<sup>-/-</sup>,  $21\% \pm 5\%$ ;  $p<0.001$ ), compared to WT mice ( $n=12$ ). UTP concentration-response (10 nM-100  $\mu$ M) of WT mice ( $n=3$ ) revealed a concentration-dependent increase in leukocyte rolling and adhesion ( $p<0.05$ ). Following UTP treatment (10  $\mu$ M), WT ( $n=7$ ) and P2Y2R<sup>-/-</sup> ( $n=4$ ) mice both exhibited an increase in leukocyte adhesion, compared to baseline. Contrarily, the UTP-induced increase in leukocyte rolling observed in WT mice was abrogated in the P2Y2R<sup>-/-</sup> mice. Collectively, these data suggest that under normal physiological conditions, P2Y2R down-regulates leukocyte-endothelial interaction, and although extracellular UTP-induces leukocyte rolling and adhesion, only leukocyte rolling is P2Y2R-dependent.

J. Nguyen, S. Paudel, D. Westenberg, and J. Smith. Department of Biological Sciences, Missouri University of Science and Technology. **A SYNTHETIC BIOLOGY APPROACH FOR ANAEROBIC DIGESTION OF GLYCEROL TO MAKE ETHANOL.** Biofuels are an important economic driver in the state of Missouri. Biofuels provide an environmentally friendly and renewable energy. However, a considerable amount of glycerol, a waste product, is produced when making biofuels. This project aims at using the bacterium *E. coli* to metabolize glycerol into ethanol, a valuable commodity. *E. coli* naturally produce enzymes that convert glycerol into ethanol but only do so under very specific conditions. By synthetically producing many copies of the genes that make the enzyme and inserting them into plasmids, *E. coli* can be made to readily and consistently convert glycerol to ethanol.

R. DeWeerd and M. Manpadi, Department of Chemistry, Drury University. **NOVEL NAPHTHOQUINONE ANALOGS AND THE JAK/STAT PATHWAY.** Cancer cells proliferate by upregulating biochemical pathways and altering gene expression to avoid apoptosis. Compounds which target these pathways, such as the 1,4-naphthoquinone analog Plumbagin, are able to induce apoptosis in cancer cells. Plumbagin has been shown to inhibit the activation of the JAK/STAT pathway, a cytokine signaling pathway which is essential for proliferation, differentiation, migration, and apoptosis. Through Western blot, the compound demonstrated decreased levels of phosphorylation of JAK2 and STAT3 proteins. In this study, a library of novel naphthoquinone analogs was tested to determine effects on cell viability and the phosphorylation/activation of JAK2 proteins. In this poster, we'll disclose the cytotoxic effects of these compounds on cancer cells as established by MTT assay and protein phosphorylation by Western blot analysis.

W. Redler, Department of Chemistry, Northwest Missouri State University. **THE LINK BETWEEN HIGH DOSE B VITAMINS AND CANCER.** In 1998, The University of Tromsø sponsored The Norwegian Vitamin Trial or NORVIT, a study that involved 3750 men and women between the ages of 30-85 suffering from severe heart disease. The purpose was to see if administering the patients' treatments of vitamins B9, B12, B6, C, and D would lower blood homocysteine levels and treat cardiovascular disease. The results showed no promise in treating the disease but it did result in showing that the vitamin group had an increased mortality rate due to cancers particularly lung. These unfortunate results grabbed the attention of two researchers conducting a study at the Fred Hutchinson Cancer Research Center in Seattle that tracked the supplement intake of 77,000 people living in the state of Washington, Emily White and Theodore Brasky. The results showed that over years men who were taking daily 20mg doses of vitamin B6 showed an increased lung cancer risk 2x more than those who were not taking any, and showed increased lung cancer risk by 3x in male smokers. Smokers who daily took upwards of 55 micrograms of vitamin B12 showed a lung cancer risk increased 4x. Risk in the women were not apparent. It is recommended that individuals do not consume more than the recommended daily amount of B vitamins. Sources: <https://clinicaltrials.gov/ct2/show/NCT00266487>, <https://www.medicalnewstoday.com/articles/319083.php>.

C. Landewe and A. Slusarz Department of Science, Central Methodist University. **SALT VERSUS CHLORINE: THE EFFECTS OF POOL SANITIZERS ON WATER CHEMISTRY AND BACTERIA GROWTH.** The purpose of this research was to study the effects of different pool sanitizers on bacteria growth, water chemistry, and chemical costs in maintenance of residential swimming pools. Samples were collected from 15 different pools over a period of 4 weeks. There were 7 pools analyzed with salt systems and 8 pools analyzed with chlorine systems. Since chlorine pools still dominate the market, both residential and commercial, we expected these systems to be more efficient in maintaining bacteria-free water at a more affordable cost. Water samples were taken from each pool for 4 weeks for chemical analysis, before cleaning the pools and addition of chemicals. Another water sample was taken for 2 weeks and used for bacterial analysis. The chemicals added to each pool for 4 weeks were also recorded to calculate cost efficiency, as projected for a full season's use. The salt pools were able to maintain more stable water chemistry, therefore requiring less in chemical maintenance making them more cost effective. The salt pools also showed significantly lower bacteria growth over the chlorine pools.

## **BIOLOGY SECTION**

### **Oral Presentations**

T. Roy. Department of Biology, Missouri Western State University. **REVISITING THE NORTH AMERICAN AGALINIS (FAMILY: OROBANCHACEAE).** The genus *Agalinis*

(the “false foxgloves”), belonging to the family Orobanchaceae, is native to the Western Hemisphere, with around 40 species distributed across temperate North America, and a large group native to Missouri and the Midwestern United States. About 21 species of this genus warrant conservation measures. We utilized chloroplast and nuclear ribosomal ITS DNA sequence data, and bioinformatics tools, to further understand the phylogenetic relationships among the different species, taxonomical sections, and subsections within this group. Our study corroborates to previous studies and indicates the North American *Agalinis* to be a strongly supported, monophyletic group. Our study is also the first to investigate the biogeography of this genus in temperate North America. We utilized the computer programs BEAST and SDIVA and through secondary calibrations from previous studies, tried to understand the diversification timings and ancestral areas of this group. Our study points to south eastern United States as the center of diversity and place of origin of the *Agalinis* in temperate North America, from which they spread to the rest of the United States and even migrated to Canada, around the mid-Miocene period.

G. Dieringer and L. Cabrera R. Department of Natural Sciences, Northwest Missouri State University. **PHENOTYPIC SELECTION ON STAMINAL TRICHOMES OF *AGALINIS AURICULATA* (OROBANCHACEAE)**. Sexual selection theory predicts plant male reproductive success to be limited by its dispersion of pollen to other plants. Pollen presentation theory predicts that the best pollen dispensing strategy should evolve to match the abundance of pollinators and transfer of pollen to stigmas. When visitation is abundant, selection is expected to favor floral traits that cause pollen to be dispensed progressively over multiple visits to enhance the probability of siring seeds. The sonicating of anthers by bees represents a specialized behavior to dispense pollen as a floral reward. *Agalinis auriculata* is pollinated by *Bombus impatiens* and *B. pensylvanicus* and possesses long trichomes along the filament of the longer stamens. *Bombus impatiens* sonicates stamens while foraging sternotribically and *B. pensylvanicus* collects pollen while foraging nototribically. We conducted a field study to test whether trichome number influenced pollen removal. Experiments using single bee visits to virgin flowers were used estimate pollen removal from flowers and trichome number was quantified with the aid of scanning electron microscopy. Selection differentials were calculated for relative pollen removal versus standardized values of trichome number. We found statistically significant differentials for both types of foraging. Contrary to expectations, the number of trichomes along the filament had a significant positive effect on pollen removal for sternotribic, sonicating visits by *B. impatiens* but had a significant negative effect for nototribic visits by *B. pensylvanicus*. We conclude the contrasting influence trichomes had on pollen removal is most likely explained by the predominance of sternotribic visits to the short-lived flowers.

N. S. Remex<sup>1</sup>, J. F. Schaefer<sup>2</sup>, and D. D. Duvernell<sup>1</sup>. <sup>1</sup>Biological Sciences, Missouri University of Science and Technology. <sup>2</sup>Biological Sciences, University of Southern Mississippi.



## **CHARACTERIZATION OF CHROMOSOMAL TRANSLOCATIONS IN A GROUP OF KILLIFISHES USING GENOME-WIDE HIGH-DENSITY SNP MAPPING APPROACH.**

Chromosomal rearrangement is a common phenomenon among a variety of vertebrate species including human, chimpanzee, sheep, bovid, mouse, and fish. In heterozygous form, rearrangements may directly interrupt meiotic progression leading to partial sterility/subfertility or underdominance and also may suppress local meiotic segregation/recombination. Several human diseases are associated with this condition (e.g. familial down syndrome, mental retardation, and leukemia). Such unbalanced meiotic segregation may also result in reproductive isolation and play roles as a driving force of speciation. The objective of this study was to gain insight into the pattern of chromosomal rearrangements in a group of closely related killifish species in the genus *Fundulus* (*F. notatus*, *F. olivaceus*, and *F. euryzonus*) because of their changes in chromosome number both within and between species. Genetic linkage maps are excellent tools to understand genome-architecture and its difference between species. For this project, we constructed linkage maps using a high-resolution single nucleotide polymorphism (SNP) mapping of chromosomes. Markers associated with Robertsonian (Rb) translocations (already evident from karyotypic studies) were generated by high-throughput genotyping-by-sequencing method. Intra-specific SNPs were then aligned to contigs in a reference *Fundulus* genome (*F. olivaceus*) and contigs were mapped to linkage groups (corresponding to chromosomes) using an F2 controlled cross mapping approach. Species-diagnostic SNPs were finally aligned to mapped contigs to characterize chromosomal translocations. This SNP-based mapping approach revealed 24 linkage groups (LGs) in *F. olivaceus*, whereas, 20 LGs in *F. notatus* indicating that four of the groups in *F. notatus* resulted from Rb fusion.

K. Bradley, R. Galetti and P. Klawinski. Biology Department, William Jewell College. **FIELD TESTS WITH CLAY MODELS SHOW THAT APOSEMATISM IS MORE EFFECTIVE THAN BACKGROUND COLOR MATCHING IN CATERPILLARS.** Organisms have to accomplish many tasks in order to survive, but among the most important is avoiding predation. Aposematism and crypsis are among the most common methods to avoid predation. Aposematism occurs when an individual exhibits a signal to a predator that the individual is distasteful, toxic or dangerous. Crypsis occurs when an individual exhibits coloration that allows the organism to blend in to its background. While aposematism has been widely studied, few studies explicitly test the function of a color pattern assumed to be aposematic and fewer studies have tested the function of aposematic color patterns in caterpillars. We examined predation rates on two types of clay models: 1) banded patterns resembling the toxic caterpillar of the monarch butterfly and 2) the solid green, and presumptively cryptic, color pattern of the luna moth. We explicitly tested the aposematic function color pattern by placing half the models on a white background to remove the possibility of crypsis in both model types. The other half of the models were placed on camouflaged background that would allow crypsis to function. We found no difference in attack rates between banded models on white versus natural backgrounds, ruling out crypsis as a function of banded patterns. We found that banded models experienced fewer

attacks than green models indicating that banded patterns actively discouraged predatory attacks. We conclude that banded patterns function as aposematism in a group of organisms, lepidopteran larvae, where explicit tests of the anti-predator function of color pattern are rare.

C. Horstmann<sup>1</sup>, D.S. Kim<sup>2</sup> and K. Kim<sup>1</sup>. <sup>1</sup>Biology Department, Missouri State University.

<sup>2</sup>Kickapoo High School, Springfield, MO. **AN INVESTIGATION AND COMPARISON OF THE EFFECTS OF SILVER AND CADMIUM NANOMATERIAL ON BAKER'S YEAST.** The objective of this study is to determine and compare the toxicity of Ag nanoparticles and CdSe/ZnS quantum dots (QD) on yeast. We conducted a cell membrane stability assay, proliferation assay, and ROS assay to help determine each nanomaterial's relative mechanism of toxicity. In the cell membrane stability assay we determined that exposure to AgNPs caused a faster drop in yeast O.D. than CdSe/ZnS QD exposure. The proliferation assay determined that AgNPs had more of an effect of the growth curves of yeast, which can be visualized with decreasing concentrations of AgNPs. CdSe/ZnS QD exposure had little effect on the growth curves at varying concentrations. The ROS assay determined the amount of ROS present in yeast that were treated with AgNPs and CdSe/ZnSQDs and the percent ROS levels found were similar in both Ag and CdSe/ZnS treated samples. We also conducted an RNA Seq to identify differentially expressed genes in yeast treated with Ag and CdSe/ZnS nanomaterials. The RNA Seq helped us determine several up and down regulated genes in yeast treated with Ag and CdSe/ZnS. With the differentially expressed gene data gene ontology terms were generated using Gorilla.com, and major cellular processes connected to differentially expressed genes were identified. Upregulated genes were found to be involved in RNA processing and ribosomal biogenesis, and downregulated genes were found to be involved in metabolism and cell wall stability.

V. Brown<sup>1</sup>, A. Bagoly<sup>1</sup>, L. Mihindukulasooriya<sup>1</sup>, A. Campbell<sup>1</sup> and J.D. Ortiz<sup>2</sup>. Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>Department of Geology, Kent State University Kent. **COMPARING METHODS FOR QUANTIFYING HARMFUL ALGAL SPECIES IN OLD WOMAN CREEK NATIONAL ESTUARY.** Old Woman Creek National Estuary (OWC) is a freshwater estuary draining into Lake Erie and nutrient runoff into OWC frequently leads to algal blooms. Fifty-five water samples were collected from five sites within OWC during the week of July 16-26, 2018. Three different algal bloom-monitoring methods were used for comparison with environmental factors associated with the blooms in OWC. Reflectance spectra and environmental data were collected with every sample and extracted DNA was used in quantitative PCR (qPCR) assays to measure abundance of bacterial and archaeal 16S rRNA genes and 23S rRNA genes of eukaryotic algae plastids and cyanobacteria. Varimax Principal Component (VPCs) analysis was conducted on the reflectance data to identify, the major algae, cyanobacteria and/or pigment in the water. Four VPCs were found that correspond to a mixture of cyanobacteria and phycoerythrin; pigment present in some cyanobacteria and red algae (VPC1), chlorite+amphibole (clays in the water) and cyanobacteria (VPC2), fucoxanthin+chlorophyll-a

(VPC3), and calcite+ chlorophyll-a (VPC4). VPC 2 and 3 were negatively correlated with total suspended solids (TSS) and positively correlated to Secchi depth. VPC1 was positively correlated with maximum daily wind speed, while VPC3 and 4 were negatively correlated with maximum daily wind speed. Bacterial and archaeal 16S gene counts were positively correlated to each other but did not show any correlations with environmental data. Interestingly, neither VPC loadings nor qPCR gene counts correlated with temperature, salinity, nitrate concentration or oxidation-reduction potential. Bacterial and phytoplankton qPCR gene counts were significantly and negatively correlated.

K. Mellor, G. Hanrahan and G. Thornsberry. Department of Natural Sciences, Northwest Missouri State University. **THE EFFECT OF PEPPERMINT OIL ON BIOFILM PRODUCTION IN *STAPHYLOCOCCUS EPIDERMIDIS* ISOLATES.** As part of the human epidermal microbiota, *Staphylococcus epidermidis* can cause nosocomial infections, particularly if capable of producing a biofilm. This project investigates the ability of peppermint oil to decrease biofilm formation in *S. epidermidis*. Following an initial trial with five essential oils, peppermint oil was shown to decrease biofilm production and was selected for further study. Fourteen isolates previously characterized as moderate or high biofilm producers were chosen. Strains were grown overnight on tryptic soy agar, transferred to tubes of phosphate buffered saline (PBS), and standardized. Aliquots of *S. epidermidis* were transferred to 96-well plates containing tryptic soy broth supplemented with 1% glucose and then topped with aliquots of peppermint oil of varying concentrations. Four replicates of 12 wells were conducted for each strain at each oil concentration. Growth was determined using spectrophotometry. Wells were then emptied, washed with PBS, and dried. The biofilm was stained with crystal violet which was then solubilized with acetic acid before quantifying by spectrophotometry. The total growth and biofilm development for each concentration of oil was compared to the control. Biofilm production was also compared between moderate and high biofilm producing isolates at various oil concentrations. A significant difference in biofilm formation is observed at all concentrations of peppermint oil. A decrease in biofilm production is observed with 1% peppermint oil; however, both low (0.25% and 0.5%) and high concentrations (2%) show a significant increase in biofilm production when compared to the mineral oil control.

J. Winn<sup>1</sup>, E. McHugh<sup>1</sup>, D. Monismith<sup>2</sup>, Jr., J. Campbell<sup>1</sup> and A. Campbell<sup>1</sup>. <sup>1</sup>Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>559<sup>th</sup> Software Maintenance Squadron, Tinker Air Force Base. **PHYLOGENETIC COMPARISON OF CADMIUM RESISTANCE GENES IN *CUPRIAVIDUS* ISOLATES FROM PICHER, OK.** Mining operations in Picher, Oklahoma, left large piles of mine tailings and heavy metal contamination that ultimately led to the evacuation of the town and the creation of a DOE superfund site. Soil samples were collected from this site, and several distinct species of cadmium-resistant *Cupriavidus* were isolated. Sequenced genomic data from *Cupriavidus* sp. EM36 and composite assembly *Cupriavidus* sp. EM2223 all contain multiple copies of genes *czcABC*. The *czcABC* gene complex encodes an

efflux pump for cadmium, cobalt and zinc. EM2223 contains five copies of the *czcABC*. EM36 contains five copies of this complex, as well. The species most closely related to EM2223, *Cupriavidus alkaliphilus*, only contains three copies. These complexes were blasted against all *Cupriavidus* within JGI's Integrated Microbial Genome database, and it was concluded that two additional copies encoding efflux pumps within the EM2223 genome likely occurred through horizontal gene transfer within the *Cupriavidus* genus. Average Nucleotide Identity indicated that EM36 potentially represents a novel species with a diverse set of efflux pumps with top blast hits across the *Cupriavidus* genus.

A. Allee<sup>1</sup>, E.L. Middleton<sup>2</sup> and A.G. Tipton<sup>1</sup>. <sup>1</sup>Department of Science, Technology, and Mathematics, Lincoln University. <sup>2</sup>Indiana Department of Conservation. **COVER CROPS AS TOOLS: HOW SOIL FUNGAL COMMUNITIES CAN BE PREPARED FOR SUCCESSFUL PRAIRIE RESTORATION.** Soil microbiomes significantly affect the structure of plant communities. This process is interdependent: every plant species can induce change in soil conditions, which can remain over time. These legacy effects can have long-term implications for plant-soil interactions and are especially important for the obligate-mutualistic symbiote arbuscular mycorrhizal fungi (AMF): a vital component in establishing native species during prairie restoration. Current land management utilizes tilled corn-soybean rotations prior to restoration to control for exotic weeds. Research suggests that these practices disrupt and alter soil biota, potentially making prairie restoration more difficult, but no-till and cover crop techniques can improve soil health and cause less disruptions to soil microbial communities. Here, we investigate whether incorporating no-till practices and different cover crop combinations prior to prairie restoration allow for more “prairie-like” AMF communities, thus supporting a more diverse prairie restoration. In preparation for this long-term project, we analyzed preliminary data to establish a baseline. We collected soil samples and assessed AMF communities using molecular techniques from plots within fields that will act as the site of future cover crop treatments along with remnant prairie, old field, and conventionally cropped fields as reference communities. We found that the community composition of the remnant prairie, conventional field, and the old field were distinct. AMF richness differed among field types but AMF diversity did not. Moving forward, we will monitor soil AMF and overall fungal community composition annually, measuring how cover crop treatments change soil biota and in time support a diverse native plant prairie restoration.

E. Everman, K. Cloud-Richardson and S.J. Macdonald. Department of Molecular Biology, University of Kansas. **DISSECTING THE GENETIC ARCHITECTURE OF COPPER RESISTANCE.** Metals have complex effects on organism physiology and function. Some metals are required for normal development and homeostasis, and deficiencies can result in disease, while metal poisoning poses risks of neurological and acute organ injury. Natural populations harbor genetic variation that influences resistance to metal poisoning, and toxicity is a genetically complex trait. Here, we treat copper as a model metal of interest to examine genetic

variation in resistance due to its critical requirement for normal cell function and similarities between copper metabolism and that of other essential and nonessential metals. Using quantitative trait locus (QTL) mapping in the *Drosophila* Synthetic Population Resource and whole animal RNA sequencing, we identify several candidate genes that are associated with variation in copper resistance including those that are involved in the detoxification (Catsup), transport (Zip42C.2), or homeostasis (Ccs) of metal ions. RNAi knockdown of these and other candidates strongly suggests these genes influence copper resistance. Pollution via metal-containing industrial wastes and leaching of metals into ground water presents a pervasive threat to environmental and human health; our study provides valuable insight into the genomic architecture of metal poisoning susceptibility, and provides candidates for future functional and mechanistic validation. Supported by K-INBRE (P20 GM103418) and the NIH (R01 OD010974).

## **BIOLOGY SECTION**

### **Poster Presentations**

B. Brommet<sup>1</sup>, K. Kolan<sup>2</sup>, S. Roberts<sup>2</sup>, L. Steen<sup>3</sup>, M. Leu<sup>2</sup> and J. Semon<sup>1</sup>. <sup>1</sup>Department of Biological Sciences, <sup>2</sup>Department of Mechanical and Aerospace Engineering, <sup>3</sup>Department of Material Sciences and Engineering, Missouri University of Science and Technology. **A NOVEL INK FOR 3D BIOPRINTING.** Borate bioactive glass (B3) has recently: (i) helped speed the healing of dermal wounds in > 90% of elderly patients, (ii) provided no signs of inflammation or infection surrounding the scaffolds, resulted in little to no scarring, demonstrated hair regrowth, and had complete healing of the dermatological wounds, and (iii) been administered safely in multiple applications. The goal of this study was to create a bio-ink with B3 bioactive glass and adipose stem cells (ASCs). For all experiments, ASCs were plated at 100 cells/cm<sup>2</sup>, grown until sub-confluent ( $\leq 70\%$  confluent), and used between passages 2-6. ASCs and B3 were incorporated in different approaches and evaluated by DNA amounts as well as live/dead assays at different timepoints. The results show that ASCs can be printed in conjunction with B3 bioactive glass and will survive for  $\geq 2$  weeks.

J. Hinsey. National Park Service, Heartland Inventory and Monitoring Network. **OUR DATA IS NOT OUR OWN – MANAGING NATURAL RESOURCE SCIENTIFIC DATA TO ENSURE DATA INTEGRITY.** Natural resource scientific data should be managed for perpetuity no matter how small the study. Given costs involved in collecting data while ensuring its integrity, it is imperative it be collected and managed throughout its life cycle (including field sheet design, equipment precision, data collection, data entry, data analysis, and data archival). Once archived, our data are no longer our own. At any time in the future, 5-50 years later, our data may be used for further analysis. To ensure our data are not misinterpreted, the methods, data organization, and means of conveyance should be clear and concise. Since 2005, the Heartland Inventory and Monitoring Network (HTLN) aquatic program has collected monitoring

data (fish, invertebrate, and aquatic vegetation) from 114 streams in 11 national parks resulting in over 200,000 field observation records. The average cost for collecting, processing, and identification of a single aquatic invertebrate sample is \$108, which totals over \$263,304 for the collection of 2,438 samples. This does not include additional costs for associated water quality/habitat data collection, equipment maintenance, data analysis, and data management. As scientists, we are in the data business and given the costs expended, we must make data integrity our number one priority through responsible data management. Key data management practices will be highlighted for different phases of development and implementation.

S. Templeton and P. Adam. Department of Natural Sciences, Northwest Missouri State University. **DIVERSITY OF SKULL MORPHOLOGY IN SEA TURTLES WITH CORRELATIONS TO DIET.** The seven living species of sea turtles are a small remnant of a lineage that was once, during the Cretaceous (80 million years ago), the most diverse group of marine reptiles ever to have existed. Although few in number, modern species still capture some of this past diversity, with species ranging in size from 30 kg (Ridley's sea turtle, *Lepidochelys kempii*) to 900 kg (leatherback sea turtle, *Dermochelys coriacea*) and with diets that vary and include species that specialize on sponges (hawksbill sea turtle, *Eretmochelys imbricata*), sea grasses (green sea turtle, *Chelonia mydas*), and jellyfish (leatherback sea turtle, *Dermochelys coriacea*), in addition to other, more generalized diets. Data used in my analyses include measurements taken directly from skulls combined with landmark data established from standardized photographs. Data were subjected to discriminant function analyses to ascertain validity of dietary groupings and to identify characteristics of skull morphology most indicative of each feeding type. The overarching objective of my study was to reveal functional differences in feeding structures of different sea turtles and to create tools that can be used to predict diet in extinct sea turtle species.

A. Ginsparg, E. Thibodeau and D. Duvernell. Department of Biological Sciences, Missouri University of Science and Technology. **FISH SPECIES IDENTIFICATION PROTOCOL FOR METABARCODED ENVIRONMENTAL DNA SEQUENCES.** Environmental DNA (eDNA) metabarcoding using universal mitochondrial DNA primers has become a viable alternative to traditional biodiversity sampling methods that rely on nets and electroshocking. One of the benefits of eDNA sampling is that samples can be bioinformatically identified to species quickly and efficiently. Our study focused on analyzing a 1.2kbp segment of the mitochondrial cytochrome B gene. Sequences were generated using the Oxford Nanopore MinION sequencer, which is a portable and affordable method for high throughput, parallel sequencing. A benefit of MinION sequencing is the ability to generate long reads of the entire cytochrome B gene. However, a disadvantage of the sequencing platform is high inherent sequencing error rates. The purpose of this study was to develop a bioinformatic analysis pipeline using available software, and an assessment of the accuracy of our pipeline to correctly identify DNA sequences to species. Using Usearch v.11, raw sequences were filtered to remove

low quality sequences with a predicted error rate threshold of 6% or greater. The remaining high quality sequences were aligned to a reference database of all Missouri fishes, and the highest scoring match was used to assign each sequence to species. We used MEGA X to perform a Neighbor-Joining analysis of a subset of identified sequences to evaluate the accuracy of Usearch species calls. We present results for shiners and darters with a discussion of sequence identification accuracy.

E. Thibodeau, A. Ginsparg and D. Duvernell. Department of Biological Sciences, Missouri University of Science and Technology. **EVALUATION OF ENVIRONMENTAL DNA VERSUS TRADITIONAL SAMPLING OF FISH COMMUNITIES.** Traditionally, sampling of fish communities has been done through the use of nets or via electrofishing. However, these techniques can come with inherent bias and are labor intensive. In this study, it was our goal to evaluate the effectiveness of environmental DNA (eDNA) as a potential sampling method. A set of universal fish cytB primers and sequencing with Nanopore MinION DNA sequencing were used to determine the efficacy of this process. The DNA sequences were compared to a reference database of cytB for all Missouri fishes. eDNA samples were collected from two drainages in the Ozarks. The Little Dry Fork is a tributary of the Meramec River, and Beaver Creek, a tributary of the Gasconade River. We compared our eDNA diversity samples from each drainage to each other as well as to reference data provided by the head MDC fish biologist for Phelps County. We have still found that we are able to detect the most abundant species found by traditional sampling techniques. Additionally, we were also able to detect new species, not found by traditional sampling methods. Further research must be conducted to verify that the new species found were identified correctly. We present our results, address technical issues with species determination, and contamination issues.

P. Keyser. Department of Natural Sciences, Northwest Missouri State University. **BENTHIC MACROINVERTEBRATE DIVERSITY IN THREE WATER BODIES.** Benthic macroinvertebrates are an important and often basal part of aquatic communities. Treatment of ponds with a variety of chemicals to discourage plant and algae growth could disrupt these communities. I compared the diversity of benthic macroinvertebrate populations of a stream, an untreated pond, and a pond treated with Dibrox® (herbicide), Mizzen® (algicide), SparKlear® (beneficial bacteria designed to lower dissolved nutrients), and a dye (inhibit UV penetration to limit algal growth) annually. The stream was sampled with three Hester-Dendy artificial substrates and the ponds were sampled with three Modified Hester-Dendy artificial substrates because of their muddy or silty substrates. Artificial substrates were left for one month (July 15<sup>th</sup> to August 15<sup>th</sup>), then benthic macroinvertebrates were collected and preserved with iodine tincture. Samples were identified to genus and a total count was taken. Diversity for each water body was assessed with a Shannon-Wiener diversity index. The Shannon-Wiener values were compared with a Hutcheson's t-test. Benthic macroinvertebrate diversity was significantly higher in the stream than in either pond and the diversity in treated and untreated ponds was not

significantly different. This suggests that while ponds have lower benthic macroinvertebrate diversity than streams treatment of ponds to discourage plant and algae growth does not significantly alter benthic macroinvertebrate diversity.

J. Cobb. Department of Science, University of Central Missouri. **EFFECTS OF SALT AND OTHER MELTS ON SALINITY OF AQUATIC ENVIROMENTS.** Pertle Springs in Warrensburg, Missouri contains four lakes named Race Horse, Mud, Cyna, and one unnamed. The excessive occurrence of snow and ice during late February and early March caused roadways in Warrensburg, MO, to be frequently treated using salt and other types of melts. Because they were directly across a roadway or downhill from one, both Cyna and the unnamed lake were susceptible to runoff of excess salts and melts. This study compared the salinity levels between the two lakes near roads (Cyna and unnamed) and the two lakes that were uphill or isolated from roadways (Race Horse and Mud) to determine if the runoff of salts and other types of melts into aquatic environments caused a significant difference. Water samples were collected from all four lakes on a bi-weekly basis (February 22-March 18, 2019). We recorded salinity by testing each samples conductivity by using a Labquest 2 and a Platinum-Cell Conductivity Probe. The average conductivity of the lakes near the roads was 444.7  $\mu\text{S}/\text{cm}$  while the average conductivities of lakes away from roads was 107.4  $\mu\text{S}/\text{cm}$ . A Welch two sample t-test assessing differences between lakes revealed that the lakes that received melt from roads had significantly higher measures of conductivity ( $t_{17.5} = -10.612$ ,  $P < 0.001$ ).

M. Haskins<sup>1</sup>, L. Bates<sup>2</sup>, L. Carter<sup>2</sup>, P. Clevenger<sup>2</sup>, R. Coffman<sup>2</sup>, L. Duncan<sup>2</sup>, T. Dunks<sup>2</sup>, S. Eckert<sup>2</sup>, D. Eddington<sup>2</sup>, S. Fossell<sup>2</sup>, B. Grant<sup>2</sup>, J. Grom<sup>2</sup>, C. Hargraves<sup>2</sup>, N. Hickman<sup>2</sup>, M. Ireland<sup>2</sup>, C. John<sup>2</sup>, S. Jones<sup>2</sup>, C. Jones<sup>2</sup>, J. Major<sup>2</sup>, A. Monteer<sup>2</sup>, E. Oldro<sup>2</sup>, B. Richards<sup>2</sup>, V. Roberts<sup>2</sup>, J. Sanders<sup>2</sup>, T. Schweder<sup>2</sup>, W. Selectman<sup>2</sup>, R. Siliven<sup>2</sup>, S. Simpson<sup>2</sup>, J. Smith<sup>2</sup>, L. Smith<sup>2</sup>, L. Suter<sup>2</sup>, J. Tate<sup>2</sup>, K. Troxel<sup>2</sup>, M. Via-Lockhart<sup>2</sup> and N. Yuille<sup>2</sup>. <sup>1</sup>Biology Department, Rockhurst University. <sup>2</sup>Chillicothe Correctional Center. **A COMPARISON OF BENTHIC ORGANISMS IN WINTER LEAF PACKS.** Abiotic and biotic tests were conducted on an unnamed perennial first-order tributary of Sni-A-Bar Creek in unincorporated eastern Jackson County, Missouri. Like many waterways in the area, the tributary exhibited both steep and severely undercut banks due to periodic localized flooding from the runoff of adjacent pastures and row crops. Despite the predominantly silt substrate the turbidity was a consistent 0 NTU, likely due to the normally sluggish current's inability to carry suspended particles. Benthic collection was accomplished by submerging six leaf pack LaMotte® mesh bags containing air-dried senescent leaves previously collected from trees on the tributary's banks. Individual bags of a single leaf type (Burr Oak, Paw Paw and Sycamore) were tied to cinder blocks and placed in 0.4 m of water on both east and west banks. Approximately seven weeks later, in January, bags were retrieved for analysis and yielded a total of 108 organisms representing 1b taxa. Burr Oak contained the highest taxon number (11), followed by Sycamore (8) and Paw Paw (7). In order of abundance, taxa present in all leaf types included: stoneflies, snails, midges, alderflies,



mayflies, sowbugs and scuds. Multiple indices indicated an overall rating of good, and nearly excellent, water quality.

E. Wedlock<sup>1</sup>, E. McHugh<sup>1</sup>, D. Monismith<sup>2</sup>, Jr., J. Campbell<sup>1</sup> and A. Campbell<sup>1</sup>. <sup>1</sup>Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>559<sup>th</sup> Software Maintenance Squadron, Tinker Air Force Base. **GENOME ANALYSIS OF THREE *CUPRIAVIDUS* ISOLATES FROM HEAVY-METAL CONTAMINATED SOILS FROM PICHER, OKLAHOMA.** The soils of Picher, OK, are contaminated with lead, zinc, and cadmium due to lead-mining operations decades ago. Cadmium-resistant bacteria were isolated from selected soils, and whole-genome sequencing was performed on three closely related *Cupriavidus* isolates. The *Bartik* compute cluster was used to assemble the sequence reads and optimize genome assemblies. Average nucleotide identity of all sequenced *Cupriavidus* isolates identified *C. plantarum* as the nearest relative. Functional annotations of the genomes have identified nine putative genetic markers for heavy-metal resistance, including efflux pumps and two-component systems. These mechanisms could be used to bioremediate or biotransform the contaminants in environments similar to Picher.

F. Manoj, M. Burton, S. McElveen and B. Mirza. Department of Biology, Missouri State University. **THE DIVERSITY OF *BRADYRHIZOBIUM* AND NON-RHIZOBIAL ENDOPHYTES WITHIN THE ROOT NODULES OF SOYBEAN.** Soybean serves as a food and feed crop, as well as an intercrop that may enhance soil fertility by establishing symbiotic associations with nitrogen-fixing bacteria of the genus *Bradyrhizobium*, which reside in the root nodules of the host plant. Culture-based methods have suggested that members of the genus *Bradyrhizobium* are the dominant occupants of soybean root nodules, while other studies have identified the presence of non-rhizobial endophytes. The extent and selection of non-rhizobial endophytic diversity within root nodules are unknown. The objective of this study is to assess the root nodule microbiome using NextGen DNA sequencing on root nodules from plants of differing genotypes, purple and white flowering cultivars. The 16S rRNA genes of the microbial community from all root nodules of each plant's root system were sequenced to assess the diversity of *Bradyrhizobium* and non-rhizobial endophytes of the total plant. Sequence analysis reveals that *Bradyrhizobium*-related sequences were the most abundant taxa in both soybean genotypes analyzed, followed in abundance by *Nitrobacter* and *Tradiphaga*. Relative abundances of these genera did not significantly differ between purple and white flowering soybean plants. Other non-rhizobial endophytes were found only inconsistently, and at far lower abundances in all nodules sampled. These results may suggest that soybean does not select growth-promoting bacteria for nodule occupancy. These results may inform strategies for the use of non-rhizobial bioinoculants in legumes.

E. Grimes<sup>1</sup>, E. McHugh<sup>1</sup>, D. Monismith<sup>2</sup>, Jr., A. Campbell<sup>1</sup> and J. Campbell<sup>1</sup>. <sup>1</sup>Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>559<sup>th</sup> Software Maintenance Squadron,

Tinker Air Force Base. **ANALYSIS OF GENOMES AND PHYLOGENETIC RELATIONSHIPS OF THREE *METHYLOBACTERIUM* ISOLATES FROM MINING SOILS OF PICHER, OK.** Cadmium has no known biological benefits; however, some bacteria are recorded to be able to persist in cadmium-contaminated environments. Heavy-metal-contaminated soils sampled in Picher, OK, yielded isolates showing cadmium resistance. Genomes from three isolates were sequenced to identify heavy-metal resistance genes, and learn about the biology and taxonomy of these isolates. Genomes sequences were quality controlled, assembled, and analyzed using the *Bartik* compute cluster, and JGI's IMG/ER online tools were used for bioinformatics. Nearest named relatives to our isolates were *M. soli* (EM06), *M. podarium* (EM12), and *M. aquaticum* (EM32). Average nucleotide identity analysis showed that each of the three isolates is distinct from established species of *Methylobacterium*. Isolates had a total of 29 genes related to cadmium efflux, most of which were related to those found in other *Methylobacterium* species. These analyses demonstrate the potential for the genus *Methylobacterium* to be used to biotransform soils contaminated through mining.

J. Kincaid and B. Mirza: Department of Biology, OEWRI, Missouri State University. **BACTERIAL SOURCE TRACKING OF HUMAN, BOVINE, DOG, AND GOOSE FECAL CONTAMINATION AND PATHOGENS IN GREENE AND POLK COUNTY STREAMS.** Due to urbanization and fast agricultural developments, impairment of water quality by fecal pollution is a global public health concern. In this study, we monitored the potential fecal contamination of human, bovine, dog, and goose in the Little Sac watershed in Greene and Polk Counties, as well as Pearson Creek in Greene county. Water samples were collected from five different locations of the Little Sac watershed and four sites along Pearson creek. Genomic DNA was extracted, and the abundance of *Bacteroidetes* specific markers associated with human, bovine, dog, and goose fecal material were quantified using real-time PCR. The qPCR results for the Little Sac locations indicated the presence of fecal contamination at four of the five sites for at least one marker gene. At sampling locations (PR\_102), adjacent to urban areas, and (PC\_SHYY), fecal contamination of human was found. Expanding this study, all samples were prepared for MiSeq sequencing and sent to Utah State University to be sequenced. These data are currently being analyzed for a correlation between pathogens at these sites with the fecal indicator microorganisms, as well as any other correlations between bacteria that are present in the stream community. In conclusion, the presence of fecal contamination suggests that continuous monitoring and continued testing of potential pathogens is needed at these sites.

S. Dolan<sup>1</sup>, E. McHugh<sup>1</sup>, D. Monismith<sup>2</sup>, Jr., A. Campbell<sup>1</sup> and J. Campbell<sup>1</sup>. <sup>1</sup>Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>559<sup>th</sup> Software Maintenance Squadron, Tinker Air Force Base. **GENOMICS OF SIX HEAVY-METAL RESISTANT *METHYLOBACTERIUM* ISOLATES FROM PICHER, OKLAHOMA.** Picher, OK is a DOE Superfund Site that was active in lead mining until the mid-1950s. High concentrations of

cadmium, zinc, and lead remain in these soils and have infiltrated the water system. Cultivation from soils collected near Picher yielded six closely related, cadmium-resistant isolates of *Methylobacterium*. Whole genome sequences from these isolates were optimally assembled using the *Bartik* High-Performance Compute Cluster. Average Nucleotide Identity analysis revealed that these isolates were most closely related to *M. brachiatum*. Genomic comparisons to close relatives annotated eight efflux-system proteins for cadmium and zinc, and two zinc-cadmium transporters. Additional genomic comparisons to *M. brachiatum*, *M. pseudosasicola* and *M. mesophilicum* are being used to elucidate shared metabolic capabilities and unique features of our Picher isolates.

M. Strecker, O. Rode and C. Scholes. Department of Biology, Rockhurst University. **WHICH BACTERIAL EPIPHYTES FROM MIDWESTERN TREES POSSESS NITROGEN FIXING GENES?** The phyllosphere is the entirety of the leaf surface of a plant that contains bacteria, fungi, protozoans, nematodes, and yeast. The organisms that inhabit this environment are epiphytes. Some rhizosphere bacteria appear in the phyllosphere. Therefore, there is the potential to find a nitrogen fixing gene in some species of phyllosphere bacteria, which is ecologically significant. Our goal was to identify epiphytes that reside on Midwestern trees and that possess genes that enable epiphytes to fix nitrogen. We swabbed leaves *in situ* during September and November, and stored swabs in sterile bags. Nutrient Agar plates were inoculated with swabs to culture, isolate, and Gram stain phyllosphere bacteria. We isolated and amplified rRNA DNA using quantitative PCR and sequenced the product to identify bacteria. Some of the bacteria genera found in the phyllosphere from 2018 include *Escherichia*, *Pseudomonas*, *Bacillus*, *Shigella*, and *Massilia*. Using degenerative primers, we identified phyllosphere bacteria that appear to possess the *nifH* gene.

A. Mann and B. Vohra. Department of Biology, William Jewell College. **THE POTENTIAL NEUROPROTECTIVE ROLE OF NICOTINAMIDE MONONUCLEOTIDE ADENYLYLTRANSFERASE, STERILE ALPHA AND TIR-MOTIF CONTAINING 1, AND NEUROSERPIN1 IN ALZHEIMER'S-LIKE TAU-ASSOCIATED AXONAL DEGENERATION.** Alzheimer's disease (AD) is a neurodegenerative disease that is typically associated with dementia, memory loss, and neuronal degradation. Two hallmarks of AD include extracellular aggregation of amyloid-beta ( $A\beta$ ) as well as the intracellular accumulation of hyperphosphorylated tau which results in neurofibrillary tangles (NFTs). Tau is usually associated with microtubule assembly and stabilization, which are necessary for effective mitochondrial transport in neurons. Protein phosphatases (PPs), especially PP2A, are responsible for balancing the phosphorylation levels of tau for a functional structure. Thus, we hypothesized that the inhibition of PP2A would disrupt the balance of phosphorylation required for proper tau function leading to axon degeneration characteristic of AD pathology. Furthermore, the naturally occurring proteins Nicotinamide mononucleotide adenylyltransferase (Nmnat), sterile alpha and TIR-motif containing 1 (SARM1), and Neuroserpin1 have all be implicated in axonal

degeneration mechanisms. Nmnat, particularly when localized in the cytosol, has been found to slow axonal degeneration and SARM1 has been found to have a pro-degenerative function. Serine proteases have been implicated in both neuronal degeneration and rescue due to potential excessive activity leading to axonal blebbing and activity aiding in protein aggregate breakdown respectively. In order to determine the role of these proteins in an AD-like pathway of axonal degeneration, we have successfully infected our primary neuron culture with lentiviruses that promote either the upregulation of Nmnat, the downregulation of SARM1, or the upregulation of Neuroserpin1 levels. Additionally, we have supported our hypothesis that the inhibition of PP2A, by way of the chemical inhibitors okadaic acid and cantharidin, promotes axonal degeneration. We now plan to expose our infected neurons to the PP2A inhibitors in order to determine whether these proteins of interest could act as putative molecular targets for AD treatment.

K. Bramwell\*, G. Hammack\*, S. Stadts, S. Farris and R.J. Ulbricht. Department of Biomedical Science, Missouri State University. \*Equal contribution of co-authors. **FLNA AND CAPS1 RNA EDITING IN INFLUENZA A INFECTED MICE.** The post-transcriptional process of adenosine-to-inosine RNA editing is catalyzed by adenosine deaminase acting on RNA (ADAR). ADAR1 has two isoforms; constitutively-expressed p110 and inducible p150. Using a viral agent, activation of the interferon pathway results in induction of the p150 isoform. Both ADAR1 isoforms are capable of editing the RNAs encoding Filamin A (FLNA) and calcium-dependent activator of secretion 1 (CAPS1), altering amino acids within their actin binding domain and vesicle binding domain, respectively. We determine if increasing levels of ADAR1 with an acute inflammatory response will increase RNA editing in CAPS1 and FLNA transcripts. Previous studies focusing on brain tissue in mice showed that increasing ADAR1 p150 does not result in changes in editing. For this study, we examined RNA from the brain, but also peripheral tissues (heart, pancreas, retina, pituitary, abdominal wall muscle, and kidney) of influenza A infected mice. FLNA and CAPS1 were amplified by RT-PCR and sequenced to determine the ratio of adenosine to inosine in both infected mice and uninfected mice. The presence of ADAR1 isoforms p110 and p150 were observed by RT-PCR and western blot. We expect that the uninfected tissues will only contain the ADAR1 p110 isoform and the infected tissues will contain both ADAR1 isoforms. The percentage of RNA editing will tell us if increased ADAR1 promotes increases in FLNA and CAPS1 editing. Our findings will determine if editing is regulated differently in brain and peripheral tissues, and if acute inflammation can regulate protein function through RNA editing.

C. Overmeyer, K. Jorgensen and B. Vohra. Department of Biology, William Jewell College. **INVESTIGATING THE ROLE OF TOM40 IN MITOCHONDRIAL FUNCTION AND NEURODEGENERATIVE PATHOLOGIES.** Alzheimer's disease pathology includes the presence of extracellular aggregation of amyloid-beta plaques while Parkinson's disease pathology includes the presence of Lewy bodies and nerve cell loss in the substantia nigra. Amyloid-beta protein is a necessary membrane forming protein while Lewy bodies are

composed of the protein alpha-synuclein that interacts at nerve endings with phospholipids and proteins. Neurodegenerative disorders like Alzheimer's disease and Parkinson's disease vary greatly in pathology, but can be linked by some proteins. One of these proteins, TOM40, is a crucial component of the outer mitochondrial membrane involved in the transport of proteins into the mitochondria. The mitochondria plays an integral role in the maintenance of healthy axons. TOM40 mutations resulting in a truncated protein might be linked to multiple neurological disorders, including Alzheimer's and Parkinson's disease. However, the mechanisms that may lead to neurodegeneration due to dysfunctional TOM40 protein are currently unknown. We hypothesize that TOM40 dysfunction leads to mitochondrial abnormalities and, thus, neurodegeneration. In Alzheimer's and Parkinson's pathology, it is believed that TOM40 dysfunction leads to production of oxidative stress by disrupting complex I of the mitochondrial electron transport chain. However, it is not known what role TOM40 plays in preserving normal neuron structure or whether it works in conjunction with other mutations to alter penetrance of either disease. Proteins such as Nicotinamide mononucleotide adenylyltransferase (Nmnat) have been implicated to protect against axonal degeneration. To determine whether the downregulation of TOM40 can be prevented by a transferase like NMNAT, this protein will also be upregulated and downregulated. We are proposing experiments to investigate the importance of TOM40 in mitochondrial function and investigate the mechanism of neurodegeneration in the TOM40 depleted neurons. Data from these experiments could provide us the new molecular target to prevent clinical symptoms in TOM40 related neurological disorders.

D. Ehie and K. Kim. Department of Biology and Chemistry, Missouri State University. **TEAB AND TEPB: GENE THERAPY ALTERNATIVES.** Current gene therapy techniques used for chemotherapy can be toxic to the cells. Many studies have shown the effectiveness of chitin and chitosan on drug delivery to these cancer cells. The problem at hand lies in the solubility of chitin and chitosan in the cells. A long-term goal of my study involves the use of two derivatives of Chitosan, triethylphosphonium butamide-chitosan (TEPB-CS) and triethylammonium butamide-chitosan (TEAB-CS) for gene therapy and drug delivery on cancer cells. This study presents the efficacy of these chemicals on cell proliferation and cytotoxicity in HeLa cells. It was found that the chitosan derivatives display negligible effects on cell proliferation with their concentrations ranging from 0 to 0.2 mg/mL, pointing to their non-toxicity on cells. Further, the measurement of reactive oxygen species (ROS) with Dihydrorhodamine123 (DHR123) resulted in reduced oxidative stress in cell groups treated with these chemicals. Overall, these chitosan derivatives are considered safe agents for gene delivery experiments.

K. Sewell and C. Lupfer. Department of Biology, Missouri State University. **INVESTIGATING NOVEL PROTEIN INTERACTIONS IN NLRP3.** NOD-Like receptors (NLRs) are intracellular proteins that play an important role in the regulation of the innate immune response to pathogens. There are 22 NLR proteins encoded in the human genome. Specifically, NLRP3

can detect the presence of pathogens by recognizing cellular damage leading to the formation of a multi-protein complex known as the inflammasome. The inflammasome is responsible for activation of the Caspase-1 protein that ultimately leads to the activation of inflammatory cytokines IL-1 $\beta$  and IL-18. Mutations to the NLRP3 gene lead to autoinflammatory diseases. Even though we know the function of NLRP3, how it is activated and the proteins that it interacts with are still unknown. By creating a yeast two-hybrid system, we can discover novel proteins that interact with NLRP3. Determining these novel proteins will allow us to learn more about how NLRP3 is regulated and how the immune system works to fight off infection. We have previously discovered seven potential interacting proteins (such as PLSCR4) using this method and are currently in the process of examining the strength of their interactions with NLRP3.

L. McKinney, A. Mann and B. Vohra. Department of Biology, William Jewell College.

**INVESTIGATING THE POTENTIAL EFFECTS OF TRYPSIN-LIKE AND CHYMOTRYPSIN-LIKE INHIBITORS ON AXONAL DEGENERATION.** Alzheimer's disease (AD) is a debilitating condition that often affects memory and behavior. It is characterized by early axon degeneration, followed by neuronal cell death and eventually the onset of clinical symptoms associated with neurodegenerative diseases. Previous research has indicated that the regulation of several proteins, such as up regulation of Nicotinamide Mononucleotide Adenylyl Transferase (NMNAT) and knockdown of Sterile Alpha And TIR-Motif Containing 1 (Sarm1), has protective effects against axon degeneration although the pathway by which these effects are offered has yet to be elucidated. Chymotrypsin-like inhibitors such as tosyl-L-phenylalanine chloromethyl ketone (TPCK) and trypsin-like inhibitors such as tosyl-L-lysine chloromethyl ketone (TLCK) are known serine protease inhibitors involved in an apoptotic cell degradation pathway. In addition, each are known to inhibit other proteases involved in these cell-death pathways. Thus, we plan to investigate the effects of trypsin-like and chymotrypsin-like inhibitors on axonal degeneration pathway in the hopes of determining the pathway(s) by which axons degenerate and, potentially, the mechanisms by which certain proteins offer their protective effects. We hypothesize that the inhibition of these proteases will lead to protective effects in our axons. We will accomplish this by creating a dorsal root ganglia (DRG) culture and infecting it with lentiviruses containing the gene that encodes our protein of interest. To produce a DRG culture, the spinal cords from 12.5-day old murine embryos are isolated, followed by the removal and culture of DRG from the spinal cords. Fluorescence microscopy was used to determine whether our gene of interest has infected our culture. We have successfully infected our neurons with lentiviruses which upregulate NMNAT and downregulate Sarm1, each of which have been shown offer neuronal protection; thus, we next plan to add TPCK and TLCK in order to determine their roles in neuron degeneration. Mechanical (axotomy) and chemical (rotenone) treatments will be used to induce axon degeneration and observation of neuron death, or lack thereof, will be monitored.

O. Olson, J. Smothers, E. Suez, S. Rallabandi and K. Kim. Department of Biology, Missouri State University. **DYNAMIN-ASSISTED PROTEOLIPOSOME FUSION.** SNARE proteins mediate membrane fusion between the Endosome and Golgi. The vesicular SNARE (v-SNARE) Snc2 combines with the target SNARE (t-SNARE) complex composed of Tlg2, Tlg1, and Vti1 to create an active SNARE multiplex. The “zippering” of the assembled SNARE complex is thought to provide the force necessary to draw two opposing membranes into close enough proximity to destabilize and fuse the separate bilayers into one membrane. While many types of SNARE containing liposomes have been able to effectively recreate fusion events *in vitro*, inter Golgi and Endosome-to-Golgi SNAREs have been shown to require additional factors for fusion. We utilized an *in vitro* fusion assay using FRET techniques to measure the fusion efficiency of Endo-TGN SNAREs in the presence of Vps1, a dynamin like protein. For this, recombinant SNARE proteins were purified and reconstituted into liposomes containing fluorescent NBD and Liss-Rhodamine lipids. Dynamin is a GTPase that plays an important role in clathrin-dependent endocytosis as well as possible vesicle trafficking to and from the Golgi. To test GTP requirement, Vps1 and GTP were incubated together along with SNARE proteins, resulting in an increase in fusion compared to tests without added GTP. Dynasore, a dynamin GTPase inhibitor, when incubated with Vps1 and GTP, caused a decrease of fusion in comparison to runs with Vps1 and GTP alone. Future direction of measuring fusion efficiency will be discussed in the subsequent presentation.

P. Carroll and J. Dyer. Department of Biology, Rockhurst University. **IDENTIFYING LETHAL GENETIC MUTATIONS IN *DROSOPHILA MELANOGASTER*.** Though many genes are known to be required for viability in the fruit fly *Drosophila melanogaster*, more than 1,500 lethal mutant stocks have yet to be characterized in terms of the lethal genetic mutations. Therefore, the overall objective of our research is to map unknown lethal mutations in *Drosophila* to their respective genes. Previous genetic crosses performed with this project narrowed down the location of several unknown lethal mutations to specific regions of chromosome 2 in the fruit fly. Subsequently, complementation testing was used to identify the genes mutated in three unknown lethal mutant stocks. The results from these experiments suggested that the *Snap29* gene, which is involved in exocytosis, is mutated in each of these stocks. DNA sequencing confirmed our initial results by determining the nature of the mutations present in the *Snap29* gene. Currently, rescue experiment crosses are being conducted to confirm that the *Snap29* mutations in these stocks are responsible for lethality. Due to the high degree of similarity between genes found in *Drosophila* and humans, genes required for viability in *Drosophila* could be essential for human development. The findings of this ongoing project might provide a better understanding of the molecular requirements for viability in humans.

L. Lamey, S.T. Boss, B. Bashaw and T. Roy. Department of Biology, Missouri Western State University. **INVESTIGATING THE HISTORICAL BIOGEOGRAPHY OF THE NORTH AMERICAN FALSE FOXGLOVES (*AGALINIS SP.*; FAMILY: OROBANCHACEAE).**

The genus *Agalinis*, belonging to the family Orobanchaceae, is native to the Western Hemisphere, with around 40 species distributed across temperate North America, and a large group native to Missouri and the Midwestern United States. About 21 species of this genus warrant conservation measures. Our study is the first to investigate the biogeography of this genus in temperate North America. We utilized molecular methods, bioinformatics tools, and fossil calibrations to understand the diversification timings and ancestral areas of this group. Our study points to south eastern United States as the place where the *Agalinis* clade had their center of diversity in temperate North America, from which they spread to the rest of the United States and even migrated to Canada, around the mid- Miocene period.

S. Boss, L. Lamey, B. Bashaw and T. Roy. Department of Biology, Missouri Western State University. **INVESTIGATING PHYLOGENETIC RELATIONSHIPS WITHIN THE NORTH AMERICAN FALSE FOXGLOVES (*AGALINIS SP.*; FAMILY: OROBANCHACEAE).** The genus *Agalinis*, belonging to the family Orobanchaceae is native to the Western Hemisphere, with around 40 species distributed across temperate North America, and a large group native to Missouri and the Midwestern United states. About 21 species of this genus warrant conservation measures. We utilized molecular methods, and bioinformatics tools, to understand the evolutionary (phylogenetic) relationships among the different species, taxonomical sections, and subsections within this group. Our study corroborates to previous studies and indicates the North American *Agalinis* to be a strongly supported, monophyletic group.

C. Barta, B. Jenkins, D. Lindstrom, J. Reynolds, N. Karns, W. Constable, J. Phelan, M. Helsel, R. Prawitz, J. Brown, K. Moore, M. Moore, and C. Thammarat. Department of Biology, Missouri Western State University. **PHYTOHORMONE TREATMENT ALLEVIATES THE NEGATIVE ALLELOPATHIC EFFECTS OF AMUR HONEYSUCKLE (*LONICERA MAACKII*) LEAF EXTRACTS ON SEED GERMINATION AND GROWTH.** Invasive species are a threat to biodiversity and a relevant concern for species conservation and restoration. These species may employ a large array of strategies, through which they negatively impact the germination, growth, survival or reproduction of native species. One such strategy is the synthesis and release of a variety of allelopathic chemicals into the environment, which directly or indirectly affect native species. Decomposing leaves of Amur honeysuckle (*Lonicera maackii*), a shrub rapidly invading the Midwestern US have been shown to leach a variety of phenolic molecules into the soil, with devastating inhibitory effects on native species in the region. Nevertheless, the action mechanism of inhibition has not been studied to date. In this work we explored the mechanism of inhibition by honeysuckle leaf extracts in germinating field mustard in a bioassay. The extracts significantly decreased the germination of mustard seeds. While the inhibitory effect was dose-dependent, stronger with increasing extract concentrations, we found that high endogenous or exogenous gibberellic acid (GA) phytohormone treatment can relieve the inhibition. We hypothesize, that the allelochemicals in the honeysuckle leaf extract alter the hormonal balance in



germinating seeds, effect which however, can be alleviated by elevated GA concentrations. Ultimately, a better understanding of the inhibition mechanism by allelopathic chemicals is expected to contribute to developing effective invasive species management approaches in the future. Supported by MWSU-PORTAL and the MWSU-Department of Biology.

D. Lindstrom, B. Jenkins, R. Prawitz, M. Helsel, W. Constable, N. Karns, J. Phelan, R. Brown, A. Jones, M. Moore, K. Moore, B. Bolander, S. Bilby, J. Brown, A. Duryee, D. Edelman, C. Gray, C. Gossett, A. Haddock, M. Klingseis, K. Leslie, E. Miles and C. Barta. Department of Biology, Missouri Western State University. **THE IDENTIFICATION OF PARTIAL PIN OAK (*QUERCUS PALUSTRIS*) AND POST OAK (*Q. STELLATA*) ISOPRENE SYNTHASE (*ISPS*) GENE SEQUENCES.** Isoprene released from leaves of many, but not all plant species contributes to tropospheric ozone formation and may increase the lifetime of methane—a greenhouse gas—in the atmosphere with positive feedbacks on a warming climate. To gain a better understanding of the evolution of the isoprene synthesis capacity in the Plant Kingdom, sequences of the gene(s) encoding for isoprene synthase (IspS) and/or the isoprene synthase protein have been isolated from a variety of emitter species, including poplars (*Populus* spp.), willows (*Salix* spp.), figs (*Ficus* spp.), black locust (*Robinia pseudoacacia*), kudzu (*Pueraria montana*) and more recently *Arundo donax*, a herbaceous species. However, to date, no information is available on the isoprene synthase genomic or protein sequences of any oak species (*Quercus* spp.), regardless of their global relevance and extensive land coverage. In this work, we amplified, sequenced, and identified segments of the pin oak (*Q. palustris*) and post oak (*Q. stellata*) isoprene synthase (*IspS*) genes, and used the sequence information for a phylogenetic study. Phylograms revealed the highest homology between oak, the Australian pine tree (*Casuarina equisetifolia*) and fig (*Ficus* spp.) isoprene synthases, but also significant differences between oak and other isoprene synthases deriving from woody species, such as *Populus* spp., *Salix* spp., or herbaceous taxa, to which kudzu (*Pueraria montana*) or velvet bean (*Mucuna pruriens*) belong to. Our data support prior hypotheses on the potential independent evolution of the isoprene emission trait in different clades as a result of convergent evolution driven by environmental constraints.

R. Prawitz, M. Helsel, D. Lindstrom, B. Jenkins, W. Constable, N. Karns, J. Phelan, B. Bolander, S. Bilby, J. Brown, R. Brown, A. Duryee, D. Edelman, C. Gray, C. Gossett, A. Haddock, A. Jones, M. Klingseis, K. Leslie, E. Miles, K. Moore, M. Moore and C. Barta. Department of Biology, Missouri Western State University. **IN SITU DARK ADAPTATION INCREASES THE EFFICIENCY OF DNA EXTRACTION FROM MATURE PIN OAK (*QUERCUS PALUSTRIS*) LEAVES, FACILITATING GENE IDENTIFICATION STUDIES.** Mature oak (*Quercus* spp.) leaves are rarely exploited as viable sources of genomic DNA, as they are rich in metabolites difficult to remove during standard DNA purification, interfering with downstream molecular genetics applications. In the current study we tested whether *in situ* dark adaptation, to deplete sugar reserves and inhibit secondary metabolite synthesis, could alleviate

the difficulties encountered when isolating DNA from mature leaves rich in secondary metabolites. We optimized a rapid, commercial kit-based method to extract genomic DNA from dark- and light-adapted leaves. The results showed that *in situ* dark adaptation increases the yield and quality of genomic DNA obtained from mature oak leaves, yielding templates of sufficiently high quality for direct downstream applications, such as PCR amplification and gene identification. The quality of templates isolated from dark-adapted pin oak leaves particularly improved the amplification of larger fragments in our experiments. To validate the suitability of DNA extracted from mature pin oak (*Q. palustris*) leaves in gene discovery applications, we isolated and sequenced, for the first time, a partial segment of the 18S rRNA gene [Accession # MF360746], using template DNA extracted from dark-adapted mature leaves.

## CHEMISTRY SECTION

### Oral Presentations

M. McCarthy and V. Merker. Department of Natural Sciences, Northwest Missouri State University. **SYNTHESIS AND EVALUATION OF TYLENOL DERIVATIVES.** Tylenol is an over-the-counter analgesic with several side effects. The purpose of this research work is to find the best form of Tylenol's active ingredient (acetaminophen) that may reduce the negative health impact concerning toxicity and liver health. The acid-catalyzed reaction of acetaminophen at 60°C, 80°C, and 100°C with acetone, betulin, and vanillin in variable molar ratios affords products in high yield. These products were characterized using NMR, and melting point data. Modified acetaminophen compounds are interesting since they increase the design potential of analgesics and hence represent an unexplored strategy for therapeutic compound discovery. A series of modified acetaminophen derivatives was synthesized and assessed for physical, chemical, and medicinal properties.

G. Fernando<sup>a</sup>, B. Ross<sup>a</sup>, Y. Ndambakuwa<sup>a</sup>, S. Santra<sup>b</sup>. <sup>a</sup>Department of Chemistry, Cottey College, <sup>b</sup>Department of Chemistry, Pittsburg State University, KS. **INVESTIGATING ANTIOXIDANTS OF AERVA LANATA AND SIMILAR HERBAL TEAS AVAILABLE IN THE SRI LANKAN, INDIAN AND US MARKETS.** Flavonoids are an important class of natural products for their biological activities including antioxidant, UV-protection, antiparasitic, anti-inflammatory, and antifungal. Various studies have shown that a high dietary intake of natural flavonoids is strongly associated with longer life expectancy, reduced risk of developing some chronic diseases, various types of cancer, diabetes, obesity and reduced blood pressure. Flavonoids are most common in citrus fruits, vegetables as well as in herbs. In this research, the total flavonoid content of Chamomile (*Matricaria chamomilla*), Polpala (*Aerva Lanata*), Lavender (*Lavandula*) and Peppermint (*Mentha piperita*) were analysed using UV-Vis Spectroscopy according to Zhizen method. Both organic soluble and water-soluble flavonoids were extracted and identified using MALDI-ToF Mass Spectrometry. The flavonoids identified

were myricetin, catechin, quercetin, apigenin, maldivin, hesperetin and kaempferol. Quercetin was found to be in high concentration in all of the tea extracts analysed. Peppermint contained the highest amount of total flavonoids. Most of the flavonoids analysed in chamomile, lavender and peppermint were water soluble while most flavonoids analysed in Polpala were water insoluble.

A. Patel, H. Shrestha, M. J. Meziari, and J. H. Campbell. Department of Natural Sciences, Northwest Missouri State University. **A FACILE STRATEGY FOR THE PREPARATION OF COMPOSITE RESIN INCORPORATING SILVER AND MAGNETIC NANOPARTICLES WITH ENHANCED ANTIBACTERIAL PROPERTIES.** A novel and facile route for the immobilization of silver and magnetic nanoparticles in anion exchange resin-beads with different loading is proposed. Morphology and structure of the resulting resin nanocomposites were characterized by X-ray diffraction (XRD), scanning electron microscope (SEM), energy dispersive spectroscopy (EDS), Fourier-transform infrared spectroscopy (FTIR), and Thermogravimetric analysis (TGA). The results confirmed the presence of smaller diameter Ag NPs and Fe<sub>3</sub>O<sub>4</sub> incorporated into the resin beads having an average diameter on the order of 10 nm with a few nanoclusters of 20-100 nm. The Ag-loaded resins were tested for antibacterial activity *in vitro* against *Escherichia coli* (*E. coli*) as a model microbial contaminant in water, and results showed excellent bacterial inhibition. The resin form offers greater ease of handling, long term storage at room temperature, reusability in repeated reactions, and reduces the risk of environmental contamination.

C.R. Scholtz, J.D. Steinkruger, C. Zhou. School of Natural Sciences, University of Central Missouri. **ZWITTERIONIC THIOLATED GOLD NANOPARTICLES AS SENSORS FOR METAL IONS IN AQUEOUS SOLUTION USING FLUORESCENT SPECTROSCOPY.** Metal ions play vital roles in biological environments. Detection of metal ions in aqueous environments is traditionally completed using fluorescence spectroscopy due to assay simplicity and low cost. Fluorescent gold nanoparticles (AuNPs) have emerged as effective tools for the probing of metal ions with high selectivity and sensitivity. Significantly, AuNPs can be customized by changing the thiolated ligand(s) chosen to synthesize the luminescent AuNPs. We have completed a gram-scale synthesis of a thiolated dipeptide (tDP) containing a Lysine residue. Molecule tDP was combined with 11-mercaptouanoic acid (11-MUA) in a 1:1 ligand ratio to prepare luminescent gold nanoparticles under mildly reducing conditions. Transmission Electronic Microscopy (TEM) of the resulting AuNPs revealed a gold core size of  $1.6 \pm 0.3$  nm. Fluorescent spectroscopy of AuNPs in water displayed a 25 nm red-shifted emission maximum compared to single-ligand 11-MUA AuNPs. The observed red-shifted fluorescence emission provides indirect evidence of dual-ligand AuNPs. Preliminary studies using the synthesized luminescent AuNPs as sensors for toxic metal ions using fluorescence spectroscopy will be discussed.

## CHEMISTRY SECTION

### Poster Presentations

J. Ballay, B. Gunsaru, and C. Roberts. Department of Chemical and Physical Sciences, Missouri Southern State University. **SYNTHESIS OF MODIFIED DIMERS OF QUINOLINE RING ANTIMALARIAL COMPOUNDS.** Chloroquine resistance in malaria is now so widespread that chloroquine has lost efficacy in many parts of the world. Several drugs which have the quinoline ring moiety have been used to fight malaria. However, because the *P. falciparum* parasite has become resistant to chloroquine, it is imperative that new drug routes are explored. In recent studies testing the efficacy of the quinoline ring moiety, it has been shown that the retention of the quinoline ring alongside the addition of an amine group are effective against *P. falciparum* malaria. Based on these studies, newly synthesized molecules that retain the quinoline ring and the new addition of a six-membered ring containing two amine groups are expected to exhibit positive results against the *P. falciparum* parasite. If the two moieties (the quinoline ring and the six-membered ring containing two amine groups) are joined, then it is expected that they will have a stronger potency against *P. falciparum*, than the current antimalarial drug, Chloroquine.

W-J. Choi, A. Patel, N. Collins, and M. J. Meziari. Department of Natural Sciences, Northwest Missouri State University. **RAPID AND DIRECT EXFOLIATION OF BORON NITRIDE SHEETS BY SUPERCRITICAL FLUID PROCESSING.** Boron nitride nanosheets (BNNs) have attracted great deal of attention in recent years due to their unique electronic, mechanical, and thermal properties and their promising applications in future optoelectronics. Exploiting their properties in a variety of applications requires a chemical approach for high quality and scalable preparation of few-layer BNNs, which has remained a challenge. Herein, we report a simple, rapid, and one-pot exfoliation of BNNs using supercritical processing. Morphology and structure of the resulting BNNs were characterized by X-ray diffraction (XRD), scanning and Transmission electron microscope (SEM and TEM), fourier transform infra-red (FTIR), and thermogravimetry analysis (TGA).

P. Corn, and S. Burchett. Department of Chemical and Physical Sciences, Missouri Southern State University. **QUANTITATIVE ALCOHOL DETERMINATION USING INFRARED SPECTROSCOPY FOR INDUSTRIAL AND EDUCATIONAL USE.** Infrared spectrophotometers are traditionally qualitative instruments. The exploration of quantitative use has not been well documented and has potential in both industrial and educational applications. In the educational setting, this technique will provide students the opportunity to investigate multiple applications of FT-IR. The technique will support investigations on product yield evaluation which allows students to evaluate the success of reactions. As a concentration quantification tool, the method will offer a validation for traditional techniques. In the industrial setting, alcohol concentration quantification is highly regulated for the wine, beer,

pharmaceutical, and hygiene product industries. The standard tools for measuring alcohol content are hydrometers and refractometers. Both tools are highly subjective to temperature, other constituents, and user proficiency. The development of a procedure that provides non-subjective numerical data is highly desired. This presentation will offer promising results on the use of an infrared spectrophotometer as a quantitative tool for measuring alcohol content in a solution.

L. Hedges and C. Babayco. Department of Physical and Biological Sciences, Columbia College. **QUANTIFICATION OF WIDESPREAD COCAINE CONTAMINATION ACROSS ONE-DOLLAR BILLS IN THE SOUTHERN MIDWEST.** Previous research has identified cocaine contamination on banknotes around the world, including more locally in Chicago, IL and Kansas City, KS. This study examines the contamination of cocaine on bills from Kansas City, MO along Interstate 70 to Saint Louis, MO and then along Interstate 64 to Evansville, IN. Three one-dollar bills were collected at each of 30 locations at 20 to 40-mile intervals along the interstates and more frequently within urban areas. Cocaine was extracted from each bill by acid extraction followed by concentration using solid-phase extraction and analysis by gas chromatography-mass spectrometry. Quantifiable amounts of cocaine were detected on all 90 bills with concentrations ranging from 0.02  $\mu\text{g}/\text{bill}$  to 40.5  $\mu\text{g}/\text{bill}$ . When bills were grouped into urban and rural regions, higher concentrations were observed in the more urban areas and also exhibited greater variability in the measured concentrations. Compared to previous studies, these results show greater cocaine contamination on paper currency both in the relative number of bills contaminated and the total concentrations found on bills.

A. Malkawi, C. True, and A. Bailey. Department of Chemistry, Northwest Missouri State University. **EFFECT OF SELENIUM NUTRITION ON GIBBERELIC ACID ACCUMULATION IN SPINACH PLANTS GROWN UNDER VARIABLE ENVIRONMENTAL CONDITIONS.** Selenium is an essential micronutrient for humans. Agricultural crops fortified with selenium provide a practical approach to increase the amount of selenium in the human diet. The three-fold objectives of the present study were, first, to isolate and identify gibberellic acid present in spinach tissues grown in the presence of selenium, second, to quantify levels of this compound during the ontogeny of flower induction, and third, to study the effect of selenium on the levels of endogenous gibberellic acid. Plants were initially grown under non-inducing conditions and then half of the plants were transferred to inducing conditions. Harvest of plants began 48 hours later and over a period of 12 days with 2-day intervals. Gibberellic acid was isolated and quantified using preparatory solvent partitioning, reversed-phase high-performance liquid chromatography and combined gas chromatography-mass spectrometry. When plants were transferred from floral non-inducing to inducing conditions, the gibberellic acid content increased with increasing levels of selenium treatment. Two additional experiments were performed in which the above photoperiodic regime was employed and the temperature was kept constant at 30°C and 20°C. These experiments showed

similar trends of decreasing gibberellic acid content under non-inducing conditions and, conversely, increasing under flower inducing conditions. Our study establishes a correlation between increased gibberellic acid levels with the flowering of spinach grown in soil supplied with selenium.

F. Weng, M. Whalen, A. Sengypta, and M. Manpadi. Department of Chemistry and Physics, Drury University. **SYNTHESIS AND BIOLOGICAL EVALUATION OF NOVEL UNSYMMETRICAL ANALOGUES OF CURCUMIN.** Curcumin, the active component of turmeric has been long associated with promising anti-inflammatory and anti-cancer activity against various cancers. However, the therapeutic benefits are limited by its rapid metabolism and excretion from the body, which results in the low bioavailability of the compound. Our research focuses on synthesis of novel unsymmetrical analogues of Curcumin designed to decrease the rate of glucuronidation and thereby increasing the effective concentration in the cells. We will present the synthesis of new analogues based on Aldol condensation and their cytotoxic abilities on Colon Cancer cells.

D. Dan<sup>a</sup>, A. Patel<sup>a</sup>, W-J. Choi<sup>a</sup>, Z. Wang<sup>b</sup>, M. J. Meziari<sup>a</sup>, and Y-P. Sun<sup>b</sup>. <sup>a</sup>Department of Natural Sciences, Northwest Missouri State University, <sup>b</sup>Department of Chemistry and Laboratory for Emerging Materials and Technology, Clemson University, Clemson, SC. **EXFOLIATION OF BORON NITRIDE SHEETS USING VARIOUS LIQUID-PHASE STRATEGIES.** There are growing technological needs for materials and systems of the high thermal conductivity decoupled from electrical conductivity and high-quality boron nitride nanosheets (BNNs) represent an excellent platform for this purpose. These unique materials are known to have broad and important applications ranging from ultrahigh-performance electronics to high-speed vehicles and to systems operated under some extreme conditions (taking advantage of the high stability of boron nitride). In this work, we examined various solvent systems and experimental conditions for the exfoliation of commercially acquired hexagonal boron nitride into BNNs and their ability to form relatively stable dispersions. The more stable dispersions were used for the fabrication of polymeric nanocomposites. Morphology and structure of the resulting BNNs and their based nanocomposites were characterized by powder X-ray diffraction (XRD), field-emission scanning and transmission electron microscopy (SEM and TEM), FT-IR, and thermal conductivity.

## COMPUTER SCIENCE AND MATH SECTION

### Oral Presentations

A. Hasanbasri and Y. Liu, College of Arts and Science, Maryville University. **PREDICTING AND TESTING THE CHICAGO TAXI FARE.** Using the data of the Chicago taxi trips from January to December of 2016, we predict taxi fare using several models: linear regression, tree,

and random forest. In addition, we also tested the data on the k-mean clustering method to find the best number of clusters by looking at the cost and silhouette values. We then choose the best model to predict the Chicago fare based on the root-mean-squared error (RMSE). Due to the largeness of the dataset, we used Spark Apache in our big data analysis.

I. Shields, M. Tsai, R. Patel, and Y. Liu Department of Actuarial Science, Data Science and Mathematics, Maryville University of St. Louis. **OPINION MINING USING DEEP LEARNING WITH PRE-TRAINED MODELS.** Due to the rise of digitalization in business, vast amounts of text data are generated every day. The text data have significant potential economic value. Utilizing text mining techniques such as opinion mining can help business understand customers' experience which is important for businesses to better their services and products. In this study, an Opinion Mining Model for Yelp reviews was built using Deep Learning with pre-trained models GloVe, Word2Vec, FastText, and Universal Sentence Encoder. We also summarize, compare and contrast the various models.

## **COMPUTER SCIENCE AND MATH SECTION**

### **Poster Presentation**

N. Kempf, K. Slater, D. Urban, and J. Mutua, Department of Computer Science, Mathematics, and Physics, Missouri Western State University. **A MATHEMATICAL MODEL TO EVALUATE THE EFFECTS OF VARYING ANTIBODY CONCENTRATIONS ON HIV DYNAMICS.** HIV (Human Immunodeficiency Virus) remains a major public health challenge and one of the leading causes of death worldwide with over 36 million people living with the virus. HIV attacks the body's CD4 T cells in the immune system, thus making the body more susceptible to disease and other HIV related infections. The major challenge about HIV is that no effective cure for the virus currently exists. This fact has prompted the emergence of studies which look at ways to control the virus. As such, it is important to study the effects that antibodies have on the spread of HIV. In this study, we develop a mathematical model that incorporates the effects of antibody concentrations on the HIV dynamics. Using our model, we quantitatively describe how varying antibody concentrations affect virus infection rates, infected cell deaths, virus clearance, CD4 T cell count, and the basic reproduction number. We found that high levels of antibody concentration result to decreased virus infectivity, increased virus clearance, and death of infected cells. Our results also show that high levels of antibody concentration result in a low basic reproduction number suggesting that HIV may be controlled if effective measures such as development of vaccines which boost antibody levels are explored.

## CONSERVATION SECTION

### Oral Presentations

K. Hill and M. Kilmer, Department of Biology and Environmental Health, Missouri Southern State University. **COLLECTION AND IDENTIFICATION OF POLLEN COLLECTED FROM BEEHIVES (*APIS MELLIFERA*) ON THE MISSOURI SOUTHERN STATE UNIVERSITY PRAIRIE.** Honeybee populations in the United States have been in decline for several years, due to a combination of factors, including loss of habitat, use of pesticides and infestation by a various pests and parasites. An important part of habitat restoration for these insects is to determine which native plants provide an optimal food source, generally in the form of nectar or pollen. Collecting pollen directly from beehives can provide information on preferred food sources. The goal of this pilot study was to collect and identify pollen from beehives and determine the viability of the process. Pollen was collected from two beehives located on the Missouri Southern State University prairie using bottom-mounted Sundance pollen traps. Monthly pollen collections were planned for May-August 2018, however, a severe drought in the latter half of the season limited availability of pollen and reduced collected amounts. Collected pollen was sorted by size and color, then weighed to quantify relative amounts collected. Prior to mounting, pollen was washed using a 20% isopropyl alcohol solution, then mounted using a fuchsin jelly technique. Mounted pollen was analyzed microscopically using pollen identification keys and compared to known pollen samples for confirmation. Although samples were limited, at least six distinct types of pollen were found with pollen types varying by date of collection. Despite environmental limitations, the success of collection and identification indicates the potential usefulness of this method. This information can be valuable to landowners and land managers seeking to restore habitat specifically for pollinating insects.

M. Kilmer and K. Hill, Department of Biology and Environmental Health, Missouri Southern State University. **BUILDING A POLLEN LIBRARY FOR MICROSCOPIC IDENTIFICATION OF LOCAL POLLEN.** While palynology has historically been performed on fossilized pollen samples to help reconstruct past vegetative conditions, a new use has emerged, in light of the population declines of many pollinating insects. Analysis of pollen collected by pollinating species can illuminate preferred plant species that can then be used in restoration of pollinator-friendly habitat. However, online pollen databases have limited image availability, with most images being from species in the southwestern or northeastern United States. Here we describe steps taken to construct a pollen image library for plant species found in the Midwestern United States, particularly from grassland/prairie species. 30 species of flowering plants were identified on the Missouri Southern State University Prairie in May and June 2018. Flowers were collected from blooming plants and frozen until analysis occurred. Upon thawing, anthers were collected from flowers and pollen was extracted from anthers using a 20% isopropyl alcohol solution. Anthers from the same flower were used to make side-by-side



mounts of pollen, one stained with fuchsin jelly, the other with unstained glycerin jelly. Images of mounted pollen were taken using a Leica microscope and viewing software. Images were used to construct an initial pollen library, for comparison to environmentally collected samples. Images of pollen will also be digitized and uploaded to the Global Pollen Project, a database for pollen collected worldwide. Currently, this database has no images of pollen from species collected in this study. Thus, construction of this library represents both a local and global resource to the scientific community.

P. Klawinski, Department of Biology, William Jewell College. **STRANGERS IN A STRANGE LAND: 27 YEARS OF COMPETITION AMONG EXOTIC GECKOS.** Interspecific competition can lead to resource partitioning by competing species. Testing whether interspecific differences in resource utilization develop as a result of competition is difficult because observing resource utilization of the interacting species in sympatry *and* allopatry is often difficult. Klawinski et al. (1994) utilized the introduction of two species of exotic geckos in Galveston, TX to test whether the two species partition resources differently in allopatry and sympatry. Based on stomach contents, the two species had different diets in sympatry but similar diets in allopatry. In addition, the diet of *Cyrtopodion scabrum* was similar in allopatry and sympatry while *Hemidactylus turcicus* experienced a dietary shift from allopatry to sympatry. In 2018, I repeated the 1994 study to map the progress of the spread of *C. scabrum* into Galveston and to determine if the asymmetry of competitive interactions has led to further displacement of *H. turcicus*. In the last 27 years, *C. scabrum* has advanced only 150 meters and has not displaced *H. turcicus*. I found that all categories of geckos were different from one another but the differences in sympatry were greater than differences in allopatry and the competitive asymmetry observed in the 1994 study remained. *H. turcicus* had fewer prey items per stomach (compared to *C. scabrum*) and had even fewer prey items in sympatry with *C. scabrum* while *C. scabrum* did not differ from allopatry to sympatry. I conclude that competitive interactions remain important in Galveston but that species turnover is occurring more slowly than expected.

J. McGhee, Department of Natural Sciences, Northwest Missouri State University. **ASSESSING SUMMER POND AND LAKE INLET USE BY COPE'S GRAY TREE FROGS USING PVC PIPE TRAPS.** The need to develop rigorous conservation strategies for amphibians means reliable monitoring methods are required. I investigated the use of PVC pipe traps as a monitoring method for a Cope's Gray Tree frog (*Hyla chrysoscelis*) population in Nodaway County, Missouri. PVC pipes were placed as four arrays of four pipes at each of three ponds and two inlets of Mazingo Lake. Arrays were centered on a randomly selected tree within 50 m of a pond. Tree frogs were monitored during the summers of 2016–18, to determine if ponds and pipes within ponds were used differentially, using contingency table analysis. We also assessed and compared sex ratios at each pond or inlet using an ANOVA. We found that tree frogs were detected in pipes more commonly at inlets rather than breeding ponds, but found no significant difference between ponds or between inlets, respectively. Pipe location relative to trees within

a pond also showed no significant difference in use by tree frogs. Mean sex ratios tended to favor males, ranging from 0.6 to 6.3 males per female. These sex ratios did not differ significantly between ponds. Despite inherent variability, monitoring using PVC pipes seems suitable for our study site. There is no indication of a need to focus on or drop particular ponds or inlets in the study or modify pipe placement.

M. Mills<sup>1</sup>, C. Watson<sup>1</sup>, H. Mills<sup>1</sup>, S. Brown<sup>1</sup>, B. Robertson<sup>1</sup>, M. DeShazo<sup>1</sup>, J. Herron<sup>1</sup>, J. Jedlicka<sup>1</sup>, and T. Quedensley<sup>2</sup>, <sup>1</sup>Department of Biology, Missouri Western State University, <sup>2</sup>Botanical Research Institute of Texas. **BIODIVERSITY AND MANAGEMENT OF MISSOURI OZARK GLADES WITH AN EMPHASIS ON AMPHIBIANS AND REPTILES.** Glades are threatened ecosystems in the Ozark Highlands of Missouri. These communities typically occur in isolated patches on South/Southwest slopes among the oak-hickory forests of the Ozarks. Glades are dry with rocky outcrops and thin soils and therefore are dominated by prairie species, species adapted to arid environments, and endemics. Over two years, we sampled 55 glades located on Missouri Department of Conservation (MDC) land throughout the Ozarks for plants, amphibians, reptiles, and birds. Using a Community Health Index (CHI) developed by MDC and a variety of ecological factors, we attempted to assess or rate the relative quality of each site and relate this to site management (e.g., the use of prescribed burning). Of the 55 glade sites, 6% had CHI scores above 80, indicating healthy glade ecosystems. CHI scores were positively correlated with frequency of prescribed burns, reinforcing the importance of fire as a management tool for these habitats. Here we report on the overall results of our surveys with emphasis placed on the amphibians and reptiles of these unique ecosystems.

D. Ashley<sup>1</sup>, T. Aley<sup>2</sup>, C. Aley<sup>2</sup> and P. McKenzie<sup>3</sup>, <sup>1</sup>Department of Biology, Missouri Western State University, <sup>2</sup>Ozark Underground Laboratory, <sup>3</sup>United States Fish and Wildlife Service.

**OBSERVATIONS ON THE USE OF ARTIFICIAL SUBSTRATES TO MONITOR POPULATIONS OF THE ENDANGERED TUMBLING CREEK CAVE SNAIL**

**(*ANTROBIA CULVERI*).** The Tumbling Creek Cave snail (*Antrobia culveri*) is federally listed as an endangered species and is endemic to a single cave (Tumbling Creek Cave) in Taney County, Missouri. Tumbling Creek Cave is a registered National Natural Landmark and contains the highest biodiversity of any North American cave west of the Mississippi River. Several additional species of conservation concern are also found in this important habitat. Regular trips (starting in 1996) have been scheduled into Tumbling Creek Cave to a transect area where we monitor the cave snail population following a standardized protocol. This protocol involves lifting and examining cobble and rocks from the stream substrate and allows us to estimate the current number of snails found within the transect area. In 2006, we initiated an additional monitoring approach by placing unglazed ceramic tiles in a separate area of the cave where snails were found. This report describes this monitoring approach and presents data obtained over the past decade. We will compare this approach to our standard protocol and discuss advantages and disadvantages of using the tiles as artificial substrate when monitoring species of conservation concern.

J. Willand<sup>1</sup> and S. Baer<sup>2</sup>, <sup>1</sup>Department of Biology and Environmental Health, Missouri Southern State University, <sup>2</sup>Department of Plant Biology, Southern Illinois University. **RESOURCE AVAILABILITY AND THE POTENTIAL FOR BISON INTRODUCTION IN RESTORED TALLGRASS PRAIRIE.** The tallgrass prairie ecosystem was historically maintained through the interaction of climate, fire, and grazing by large ungulates. Efforts are being made to return bison back into prairie landscapes, but successful introductions can be constrained by suitable habitat as determined by resource availability (plant biomass, forage quality of the plant biomass, and soil carbon and nitrogen). The objective of this study was to quantify whether plant biomass (available forage) differs between prairie types, if forage quality varies across native prairie remnants and restored prairies, and if this is related to carbon and nitrogen storage in soil. We sampled native prairie remnants, low seeded-diversity older restored prairies, and high seeded-diversity younger restored prairies at Nachusa Grasslands, Illinois. Total plant biomass differed between the three prairie types, with the high seeded-diversity younger-restored prairies having almost twice that of the low seeded-diversity older-restored prairies and more than twice that of the remnant prairies. In regards to forage quality, the percentage of crude protein in dry matter was greater in the remnant prairies compared to both of the restored prairie types. The high seeded-diversity younger restored prairies had the highest fat content and lignin concentration in the forage. Total soil carbon and nitrogen did not differ between the three prairie types at either the 0-10 cm or 10-20 cm depth. The preliminary findings of this study suggest bison grazing within the introduction unit at Nachusa Grasslands may be more intensive within restored prairies compared to remnants.

## **CONSERVATION SECTION**

### **Poster Presentations**

L. Germeroth, B. McLaughlin, J. Hinson, M. Long, and R. Verble. Department of Biological Sciences, Missouri University of Science and Technology. **THERMAL ENVIRONMENTS OF OZARK HIGHLANDS LEAF LITTER.** We examined the thermal environment of oak-hickory leaf litter at varying depths in the Mill Creek Watershed as a first step toward understanding the regulation of the structure, diversity, and composition of soil surface-active arthropod communities. We predicted that deep leaf litter would result in cooler and more insulated (e.g., slower to change) soil surface temperatures than shallow leaf litter. Leaf litter depth was measured among 100 0.25 m<sup>2</sup> quadrats, and we selected plots that represented the median, 10th and 90th percentiles of that range (control = bare ground, shallow, medium, deep, for N = 12 total). I-Button data loggers were placed on the soil surface of each plot and left in place for five days. Data loggers recorded temperature hourly on a 24-hour cycle. We plotted our data against ambient temperatures as recorded by an i-Button data logger placed on bare soil. We used ANOVA to compare differences in hourly mean temperature across all sites, grouped by treatment. Data suggest that thermal environments differ among sites; however, this relationship is likely influenced by other environmental factors.

K. B. Nowack and J. D. McGhee, Department of Natural Sciences, Northwest Missouri State University. **WADING POOL USAGE BY TERRESTRIAL VERTEBRATES AS AN ADDITIONAL WATER SOURCE DURING DROUGHT CONDITIONS AT MOZINGO LAKE IN NORTHWEST MISSOURI.** Supplemental water sources may be important to vertebrate wildlife during periods of drought, and may in turn provide opportunities for monitoring. We examined the use of small wading pools by terrestrial vertebrates during a season of drought in conjunction with a population study on Cope's Gray tree frogs, at Mozingo Lake, Nodaway County, Missouri. Pools were in 10 different locations near 5 different ponds and lake inlets. Usage of pools was examined from May through August of 2018 using trail cameras, which were checked weekly. Pictures were examined for the three most commonly caught species: Gray Catbird (*Dumetella carolinensis*), Raccoon (*Procyon lotor*), and White-tailed Deer (*Odocoileus virginianus*). We found that pool activity was highest in July for all three species. Pictures suggest high re-use of pools by deer and raccoons. We conclude that supplemental water sources, even near large lakes, are beneficial to wildlife during drought and may be used heavily by certain species. This in turn may provide useful opportunities for monitoring and assessing vertebrate diversity at a given site.

J. Porter, Department of Natural Sciences, Northwest Missouri State University. **COMPARISON OF WATERFOWL DIVERSITY BETWEEN NATURAL WETLANDS AND FLOODED AGRICULTURE FIELDS IN NORTHWEST MISSOURI.** Studies have shown that waterfowl show a preference between natural wetlands and flooded agriculture fields during the fall migration. This hypothesis was tested in this study done across Northwest Missouri by randomly selecting five sites within four different wetland habitats and conducting point-count surveys at each site. It was determined there was a higher species richness within flooded agriculture wetland habitats than within natural wetlands. Natural wetlands did produce a higher number of species but lacked in species diversity as compared to flooded agriculture fields. In conclusion, flooded agriculture fields which likely provide a higher density of food attract a higher diversity of species of waterfowl than do natural wetlands.

A. Reuter, M. Andres, R. J. Arndt and J. D. McGhee, Department of Natural Sciences, Northwest Missouri State University. **COMPARISON OF *Anchoa mitchilli* DIET COMPOSITION AT BACK BAY, EAST PASCAGOULA AND CENTRAL MISSISSIPPI SOUND.** Bay Anchovy (*Anchoa mitchilli*) is the most abundant fish in the estuaries of the Gulf of Mexico. As an important species in the diets of larger commercial and recreational fish, they are a key link in the food web for the local biotic community, and the local diet of this species is therefore of interest. We collected samples of *A. mitchilli* from random locations in Back Bay, East Pascagoula, and Central Mississippi Sound. The samples were taken back to the lab where their stomach contents were sorted and counted. We used a One-way ANOVA to assess if zooplankton distribution differed by location for 3 taxa: Calanoidea, Cyclozoidea, and Diatom.

We found a significant difference in the amount of all zooplankton by location. We conclude zooplankton amounts likely vary by regional habitat, possibly affecting the distribution of *A. mitchilli*.

T. R. Sutton and J. D. McGhee, Department of Natural Sciences, Northwest Missouri State University. **NAIVE METAMORPHOSIS RATES FOR A COPE'S GRAY TREE FROG POPULATION AT MOZINGO LAKE, NODAWAY COUNTY, MISSOURI.** To better understand Cope's Gray tree frog (*Hyla chrysoscelis*) reproduction, we assessed tadpole metamorphosis rates at Mozingo Lake, Nodaway County, Missouri. We placed plastic wading pools at random locations at ponds and lake inlets to act as sites for tree frogs to deposit eggs. We collected a subset of tadpoles at pools where eggs were laid to observe in the lab to estimate metamorphosis rates. Only 3 out of 10 pools were used by frogs. For the cohort, metamorphosis occurred over a short period of time, with high survival. This information can help monitor the reproductive vital rates of Gray tree frog populations within the Mozingo Lake ecosystem.

C. Yocom-Russell and R. Verble, Department of Biological Sciences, Missouri University of Science and Technology. **USING CAMERA TRAPS TO DETECT SPECIES ON THE OZARK BIOLOGICAL RESEARCH FIELD STATION.** Using camera traps has proven to be a successful technique to assess the presence of species on the Ozark Biological Research Station. The Ozark Biological Research Station is a 9-acre field station enclosed in the Bohigian Conservation Area, an approximately 400 acre Missouri Department of Conservation Area in the Mill Creek Watershed, Phelps County, Missouri. In late winter 2019, camera traps were placed in five randomly selected areas to assess wildlife presence on the site. Traps were deployed for a total of 16 continuous trap nights, recording photo data 24 hours per day. At the end of the trapping session, photos were analyzed and the species were recorded. Traps detected >14 species, ranging in size from white-tail deer to field mice. Camera traps have extended our knowledge of cryptic and nocturnal wildlife presence near the field station and provided a method to catalog species that may be less detectable by active survey teams.

E. Grimes<sup>1</sup>, J. McGhee<sup>1</sup> and D. Welchert<sup>2</sup>. <sup>1</sup>Department of Natural Sciences, Northwest Missouri State University. <sup>2</sup>Loess Bluffs National Wildlife Refuge. **ROAD MORTALITY OF SNAKES AT LOESS BLUFFS NATIONAL WILDLIFE REFUGE.** A common detriment to local wildlife populations is the anthropogenic effect of automobile traffic. Despite the strong protective measures of National Wildlife Refuges, sites with auto-tour roads subject the same pressures of collisions on refuge inhabitants. The primary objective of this survey was to quantify the number of snakes hit by automobiles on the Loess Bluffs National Wildlife Refuge auto tour route. Secondarily, the study attempts to correlate the relative rate of mortality (RRM) with multiple characteristics including species, age class, and location. I drove 220.3 km of the auto-tour loop on days with favorable weather conditions for snake activity. I measured snout to

vent length (SVL), identified the species, and took a geotagged picture at each encounter. After seven survey days from April to October 2018, I recorded 96 resident snakes from 10 native species. The three most prevalent species were *Storeria dekayi*, *Thamnophis sirtalis*, and *Nerodia sipedon*. Sixty snakes were immature and 36 were mature. Of the 96 total snakes, 62 were found dead on road (DOR) and 34 were found alive. Immatures were found DOR more often than matures. *Nerodia rhombifer* had the highest RRM at 0.88, and 6 out of 10 species had an RRM value greater than 0.50. I was able to determine three primary crossing points where snake movement and collisions were highest. These areas of high snake-traffic would be good starting points for refuge management measures, especially for common native species that are more active during this time of the year.

T. Aley<sup>1</sup>, C. Aley<sup>1</sup> and D. Ashley<sup>2</sup>, <sup>1</sup>Ozark Underground Laboratory, <sup>2</sup>Department of Biology, Missouri Western State University. **THE OZARK UNDERGROUND LABORATORY AND THE TUMBLING CREEK CAVE FOUNDATION COLLABORATE TO ADVANCE KARST CONSERVATION, MANAGEMENT AND EDUCATION.** Staff of The Ozark Underground Laboratory have participated as environmental consultants in karst topography for more than 60 years. Tumbling Creek Cave is located near Protem, MO at the site of the OUL. Tumbling Creek Cave is a registered National Natural Landmark and contains the highest biodiversity of any North American cave west of the Mississippi River. Tumbling Creek Cave has been a major feature in karst educational programs provided by OUL. The not-for-profit Tumbling Creek Cave Foundation was formed in 2009 to partner in efforts to conserve and manage Tumbling Creek Cave and to continue educational outreach related to karst regions. This presentation will describe the facilities and surface features at the site and overview conservation, management, and educational activities of the OUL.

## **GEOLOGY & GEOSCIENCES SECTION**

### **Oral Presentations**

S. Muttel, and M. McKay, Department of Geology, Geography, and Planning, Missouri State University. **SEDIMENTARY PETROCHRONOLOGY FOR DETRITAL PROVENANCE ANALYSIS: U-PB AND RARE-EARTH ELEMENT COMPOSITIONS IN ZIRCON FROM THE MODERN MISSISSIPPI/MISSOURI RIVER DRAINAGE BASIN.** Zircon geochronology is often paired with rare-earth elemental analysis to investigate the petrogenetic history of igneous and metamorphic rocks. The application of petrochronology has not been widely explored to decipher the sedimentary record due to the complexity of mixed-source detrital systems. To investigate the potential applications of detrital petrochronology, we present *in situ* rare-earth element compositions and U-Pb ages of zircon from the modern channel and bank sediment from the river systems that drain into the Gulf of Mexico. Samples of river sediment were taken from the Upper Missouri, Yellowstone, Platte, Kansas, Red, and Lower Mississippi

Rivers. The current extent of North American drainages is well constrained; therefore, we can directly correlate our observations to known sediment sources in the headwaters of the Mississippi River and its tributaries. We hypothesize that large orogenic systems have distinct chemical-age signatures, demonstrating the utility of detrital petrochronology.

D. Spurgeon<sup>a</sup>, M. McKay<sup>b</sup>, J. Fosdick<sup>c</sup>, and W. Jackson Jr.<sup>d</sup>, <sup>a,b</sup>Geography, Geology and Planning, Missouri State University, <sup>c</sup>Center for Integrative Geosciences, University of Connecticut, <sup>d</sup>Department of Earth Sciences, University of South Alabama. **U-PB AND (U-TH)/HE ZIRCON DOUBLE DATING OF PALEOZOIC APPALACHIAN VALLEY AND RIDGE STRATA: SEDIMENT ROUTING AND OROGENIC UPLIFT.** The Southern Appalachian Mountains were formed by multiple collisional events, culminating in the Pennsylvanian-Permian Alleghanian Orogeny. Today, this complex collisional history is recorded in the fold and thrust belt of Alabama. While age relationships of deformation within the Southern Appalachian fold and thrust belt have been investigated, fault cross-cutting relationships suggest a complex sequence of out-of-sequence and/or breaking backward thrust faulting; thereby resulting in the timing and duration of Alleghanian deformation to be poorly understood. Along a cross-strike transect spanning the Southern Appalachian fold and thrust belt, sandstone units located near major thrust faults constrained through recent geologic mapping were sampled to investigate the sequence of thrust faulting. Zircon (U-Th)/He thermochronology of sandstone units may provide low-temperature thermal information for respective thrust sheets, which serves as a proxy from thrust sheet uplift and exhumation during orogenesis. New thermochronology ages will (a) test the relative ages for faulting and (b) provide a duration for thrust fault exhumation of thrust sheets during the Alleghanian Orogeny in the Southern Appalachian fold and thrust belt. If Alleghanian deformation was prolonged, individual thrust sheet deformation may be resolvable. In contrast, if deformation occurred over a brief period, such that cooling ages are all within uncertainty, the results will provide a control on thrust belt deformation as a whole. Our results will allow a temporal correlation of deformation in upper crustal rocks of the fold and thrust belt with the mid-crustal metamorphic rocks in the Appalachian Piedmont to the southeast.

## PHYSICS & ENGINEERING SECTION

### Oral Presentations

C. Sailor, Department of Mathematical Science and Physics, Westminster College. **THE BIG BANG THEORY — GEOMETRY OF THE EXPANDING UNIVERSE.** The expansion of the spatially homogeneous and isotropic universe is described by Friedmann models in which Einstein's equations take the form of one single ordinary differential equation. Differential geometry is used to study the curvature of spacetime equipped with the Robertson-Walker metric:  $ds^2 = -dt^2 + a^2(t)(dL^2)$ . Here,  $a^2(t)dL^2$  denotes the metric of the homogeneous and

isotropic spatial slice with  $a(t)$  being the scale factor. The shape of the evolving universe is determined by the solutions of Einstein's equations for the scale factor. These include constant positive, zero, and constant negative spatial curvature respectively. In the case with negative or zero curvature, the universe expands forever. In the case with positive curvature, the universe collapses back to a singularity after a maximum radius is reached.

Dakota Shields<sup>a</sup>, Ruma De<sup>a</sup>, Himadri Chakraborty<sup>a</sup>, Mohamed Madjet<sup>b</sup>, and Steven Manson<sup>c</sup>,  
<sup>a</sup>Department of Natural Sciences, Northwest Missouri State University, <sup>b</sup>QEERI, Hamad Bin Khalifa University, <sup>c</sup>Department of Physics and Astronomy, Georgia State University.

**PHOTOEMISSIONS FROM HYBRID STATES IN METASTABLE HALOGEN-ENDOFULLERENE MOLECULES.** For the Cl@C<sub>60</sub> endofullerene we consider the transfer of a C<sub>60</sub>  $\pi$  electron of  $p$  angular character to the outer  $3p$  shell of confined Cl forming a metastable molecule Cl<sup>-</sup>@C<sub>60</sub><sup>+</sup>. The ground state of this molecule is modeled in a spherical local density approximation (LDA) augmented by the Leeuwen and Baerends exchange-correlation functional [1] where the core of sixty C<sup>4+</sup> ions is jelliumized [2]. A time-dependent LDA (TDLDA) method [3] is subsequently applied to calculate the dipole photoionization parameters of the molecule. Cross sections for the photoemission from levels hybridized between the C<sub>60</sub> level containing the  $p$  hole and the Cl<sup>-</sup>  $3p$  level show the coherence between C<sub>60</sub> plasmonic and atomic Coulomb dynamics. At higher energies, the mixing of confinement and cavity oscillations [4] determines the structures in the spectra. Calculations are also extended to similar hybrid levels of metastable Br<sup>-</sup>@C<sub>60</sub><sup>+</sup> and I<sup>-</sup>@C<sub>60</sub><sup>+</sup>. Detailed comparison among the results provides deeper insights into the role of evolving halogen structures to influence the molecular photoionization. This work is supported by the US NSF and the US DOE. [1] R. van Leeuwen et al, Phys. Rev. A 49, 2421 (1994); [2] M. E. Madjet et al., Phys. Rev. A 81, 013202 (2010); [3] Choi et al., Phys. Rev. A 95, 023404 (2017); [4] Potter et al., Phys. Rev. A 82, 033201 (2010).

J. Shaw<sup>a</sup>, D. Monismith<sup>b</sup>, Y. Zhang<sup>a</sup>, D. Doerr<sup>a</sup> and H. S. Chakraborty<sup>a</sup>, <sup>a</sup>Department of Natural Sciences, Northwest Missouri State University, <sup>b</sup>Software Maintenance Group, Tinker AFB, Oklahoma. **WAVEPACKET DYNAMICS IN THE SCATTERING OF HYDROGEN ANIONS OFF VICINALLY NANO-STEPPED METAL SURFACES.** We study the electron dynamics in monocrystalline Cu, Au and Pd surfaces with stepped vicinal structures modeled in a Kronig-Penney scheme. The unoccupied bands of the surface are resonantly excited *via* the charge transfer interaction of the surface with a moving hydrogen anion. The interaction dynamics are simulated in a quantum mechanical wavepacket propagation approach [1,2] that used parallel computations. The survival probability of the interacting ion is calculated as well as the electron probability density at all times during the interaction. Animated videos are produced of the electron



probability density which show that, when the electron is transferred to the metal, the first image state and surface state are the most likely locations of the electron as it evolves through the superlattice. The survival probability shows peaks at those energies that produce standing waves between the steps on the surface when the electron is in the image state subbands. The relative survival probabilities between the metals are shown to be related to relative positions of the band gaps, first image state energy and surface state energy. The work is supported by the XSEDE allocation grant for high performance computation and partly by NSF Grant No. PHY-1806206.

References:

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## PHYSICS & ENGINEERING SECTION

### Poster Presentations

J. Sundararajan, M. Cruzan, T. Pederson, M. Yang, C. Ames, G. Cornwell, and S. Beebe, Chemical and Physical Sciences, Missouri Southern State University. **STRATEGIC APPROACH TO ACTIVE LEARNING TECHNIQUES AND EFFECTIVE PARTICIPATION IN INTERMEDIATE PHYSICS LABS.** The main aim of intermediate physics lab course is to expose students to experiments in modern physics, optics, photoelectric effect, wave phenomena and circuits. Every experiment in this course demonstrate specific concepts and deliberate approach in performing the lab. The structure of the course was framed as follows. Every student was assigned two labs for the semester, expected to approach them in a scientific way, develop hypothesis, present the concept behind the experiment, history and background to the class. The student clearly explained the importance of the experiment and the actual experiment performed initially, planned the course of experiment and framed the data sheet. The students took primary role in conducting the lab and guiding fellow classmates towards successful completion of the lab. Implications of the results of the newly adopted strategy of intermediate physics lab activities will be presented in the poster. Supported by the department of chemical and physical sciences.

A. Sithole, J. Mutua, and G. Lack, Department of Computer Science, Mathematics, and Physics. **NON-PARAMETRIC TREND TESTS AND CHANGE-POINT DETECTION FOR RADIOACTIVE IODINE LEVELS IN DRINKING WATER IN THE U.S. MIDWEST.** Radioiodine (I-131) is one of the most feared and hazardous byproducts from the nuclear fission of Uranium-235 or the neutron capture by Tellarium-130. Iodine-131 is radioactive, and its nuclear decay to Xenon produces ionizing beta ( $\beta^-$ ) particles and gamma ( $\gamma$ ) radiation. Human exposure to ionizing radiation can have short and long-term health effects. The purpose of this study was to perform trend tests and change-point detection of Iodine-131 times series data. In this study, the longitudinal data (1979 -2017) from the EPA database, comprising

Iodine-131 concentrations in drinking water measured in the Midwestern part of the United States (EPA Region 7) were analyzed. The Gaussian kernel (G-k) smoothing was performed to separate long-trends from the random noise in the data. The Mann-Kendall (M-K) rank correlation and Theil-Sen's (T-S) tests indicated the existence of positive trends on the data. The Pettitt's Homogeneity (P-H) tests indicated statistically significant increases ( $\alpha = 0.05$ ,  $p < 0.0001$ ) in Iodine-131 radiation levels for the periods 1978-1995 and 1995-2017. Jefferson (MO) and Lincoln (NE) had higher average concentrations of Iodine-131 than Cedar Rapids (IA) and Topeka (KS). The implications of this study will be discussed in detail in this paper. The determination of the existence of seasonal variations in the I-131 data require future investigation.

E. Bereyso, N. Thorsen, and S. Tewari, Cooperative Engineering Program, Missouri State University in association with Missouri University of Science and Technology. **EXPLORING VARIATION IN WATER CLARITY AND FLOW RATE OF LAB-SCALE SAND FILTERS.** The purpose of this preliminary study is to explore variation in water clarity and flow rates of lab-scale sand filters. These filters are composed of up to two layers varying thicknesses consisting of sand particles separated by physical sieving. The particle sizes are 1.18mm for the large particles and 0.3mm for the small particles. The study consists of five filters having various layers of these particles - 100% large particles, 75% large particles with 25% small particles, 50% of each, 25% large and 75% small, and 100% small particles. Titration tubes were used as containers for the filtering medium. The volume of the sample water used for each filter was 30 ml. The height of the total filtering medium was about 25.4 cm. The initial average turbidity of the dirty water samples was 713 NTU. The percent removal of turbidity ranged from 77% to 97%. The flow rate varied from 0.05 to 0.46 ml/s/cm<sup>2</sup>. There is a definite trend in filtering efficiency and the volumetric flow rate per unit area of these filters. This kind of study could be used to determine particle sizes and the ratio of depths of filtering media composed of these particles to have a certain water quality and optimized flow rate.

## SCIENCE EDUCATION

### Oral Presentation

M. Yang, N. Cook, and R. Bajracharya, Chemical and Physical Sciences Department, Missouri Southern State University. **STUDENT UNDERSTANDING OF THE INVERSE-SQUARE LAW USING MULTIPLE REPRESENTATIONS.** The inverse-square law is a mathematical concept that come across various physical contexts, such as gravitational, electrostatic, and magnetic forces/fields, intensities of sound and light. The law could be presented in numerous representations, such as in words, graphs, symbols, and numbers (tables). In my research, we designed two survey versions, one without any physical context and the other with physical contexts. The questions aimed to probe whether or not students can identify an algebraic

expression, a graph, and a table that represent the inverse-square law and the reasoning they provide to justify their responses. We administered the version without any physics context in several introductory mathematics courses including college algebra, single and multivariable calculus. The version with physical contexts was administered in second semester algebra and calculus-based introductory physics courses. The survey results revealed that students have several difficulties with the inverse-square law with or without physical contexts. Our results indicated that student difficulties with the inverse-square law in physics stem from their lack of deep understanding of the inverse-square function in mathematics. We also found that the majority of students struggled with the graphical representation of the inverse-square law even when they had clear understanding of the inverse-square function. Many students were also unable to distinguish between the inverse and inverse-square functions. In addition to the results, I will also discuss about the instructional implications in my presentations.

## **SOCIAL AND BEHAVIORAL SCIENCES SECTION**

### **Oral Presentations**

B. C. Gerhard. Department of Social and Behavioral Sciences, Lincoln University. **THE RELATIONSHIP BETWEEN DEPRESSION, SLEEP, AND DREAM CONTENT AMONG COLLEGE STUDENTS.** This study examined any correlation linking depression with the sleep and dream content of college students. A survey was given to Social and Behavioral Science college students at Lincoln University. The survey contained self-report questions on their level of depression, sleep habits, dream content, exercise habits, and basic demographic information. Based on prior research, we expect students who report high levels of depression to have poor sleep quality. We also expect depressed students to report a higher frequency of dreaming, and “bad” dream content than non-depressed students. Results indicating there is a relationship between depression and sleep will serve as a basis to conduct future research to narrow down the potential link.

M.S. Aruguete, P.M. Hardy, and E. Kaganda, Department of Social and Behavioral Sciences, Lincoln University. **WHY HISTORICALLY BLACK COLLEGES AND UNIVERSITIES MATTER.** This study compared Historically Black Colleges and Universities (HBCUs) to Predominantly White Institutions (PWIs) on student outcome variables, precollege characteristics (e.g., SAT scores), and college ranking scores. We collected data on HBCUs and PWIs matched by size and location using the US Department of Education’s College Scorecard, US News and World Report Best College Rankings, and CollegeNET Social Mobility Index. When compared to PWIs, HBCU ranks tend to be lower on US News and World Reports, but higher on the Social Mobility Index. HBCUs showed more favorable first year retention and graduate salary than PWIs once precollege characteristics were controlled. Results suggest that HBCUs serve a higher proportion of low-income students than PWIs, which can affect the public

perception of their performance. We will discuss the importance of HBCUs' demonstrated success in promoting social mobility of students in a society marked by increasing income inequalities.