SECTION I – BIOLOGICAL SCIENCES
Paper Session I
Thursday Morning, 8:30 am – 11:30 am
Arthur J. Bond Hall Engineering Building – Room 136
Brad Bennett, Presiding

1. 8:30 **g INDIVIDUAL AND TEMPORAL VARIATION OF WINTERING WHOOPING CRANES AT WHEELER NATIONAL WILDLIFE REDUFE, ALABAMA. *Andrew Cantrell*, Yong Wang, Alabama A&M University.

Since the establishment of the whooping crane (*Grus americana*) eastern migratory population in 2001, more individual birds have been observed overwintering in novel areas across the eastern U.S. Having a novel population that utilizes novel areas coupled with limited knowledge of this population's overwintering ecology increases the need for understanding the mechanisms that influence habitat selection, use, and other behaviors. We examined the individual and temporal variation in whooping cranes during the wintering seasons of 2014-15 and 2015-16 at Wheeler National Wildlife Refuge in Alabama, a site that has experienced increased occupancy over the years. Using linear mixed models, we explored differences in occupancy times, habitats used, and co-occurrence with con- and heterospecifics while including individual life history information (e.g. breeding status, release method) and wetland availability. Individuals differed in their occupancy in wetlands ($p = 0.003$) and refuge crop shares (corn left unharvested; $p = 0.002$). Warmer temperatures and increased rainfall decreased wetland availability in 2015 ($p < 0.000$), contributing to temporal variations detected: shorter duration of stay ($p = 0.007$), and decreased wetland use ($p < 0.000$). Shared use with con- and heterospecifics was higher with non-mated individuals ($p = 0.004$ and $p = 0.002$, respectively), with whooping crane flock size increasing over the wintering season ($p < 0.000$), suggesting that social attraction could influence habitat selection. Due to variations observed, multiple management strategies would be needed for effective conservation, especially when considering how fluctuating conditions influence habitat availability and the use thereof.

2. 8:50 **g DETERMINING MERCURY CONCENTRATIONS IN TURTLES WHILE IDENTIFYING AREAS OF CONCERN AT WHEELER NATIONAL WILDLIFE REFUGE, ALABAMA. *Andrew Cantrell*, Yong Wang, and Irenus Tazisong, Alabama A&M University.

Turtles have been found to be good aquatic ecotoxicology study organisms because many species have large distribution ranges and have high longevity. The Wheeler National Wildlife Refuge (WNWR), located in north Alabama, has historical and current toxicology concerns due to nearby industrial activities and the refuge's shared boundaries with a superfund site. From 2014-16, we captured turtles to evaluate differences in mercury (Hg) concentrations across species and differences within species due to age, size, and presence of parasites. We also sought and to identify areas where turtles exhibited elevated Hg concentrations. Claw clippings were obtained from captured individuals and were analyzed using a Direct Mercury Analyzer. We found that out of nine species sampled *Apalone s. spinifera* and

Chelydra serpentina had the highest levels of Hg; however, only *Trachemys scripta* had large enough sample size for other analyses. We found that adult *T. scripta* showed higher concentrations of Hg than juveniles did ($p = 0.006$), females had higher concentrations than males had ($p < 0.001$), and individuals with parasites contained higher concentrations than those without parasites had ($p = 0.005$). Lastly, higher levels of methylmercury (MeHg) were found in turtles from two different areas showing levels of 0.58 mg/kg and 0.33 mg/kg within turtles ($p < 0.000$), warranting further investigation to determine if local contamination sources are contributing to the amount of MeHg within the respective turtles. Our study shows that turtles can be very good organisms to study ecotoxicology, with *T. scripta* being an optimal species for much of the habitat found in the southeast US due to their abundance in multiple wetland types.

3. 9:10 **g NOCICEPTION, STRESS, AND TEMPERATURE PREFERENCE IN THE ZEBRAFISH (DANIO RERIO). *Chris Taylor,* Stephen Watts, University of Alabama at Birmingham.

Zebrafish were tested as a suitable model for thermal hyperalgesia, wherein pain sensitivity is increased by noxious temperatures. Adult zebrafish were exposed either to alarm pheromone, system water, or injected in the lips with DDH_20 or acetic acid, followed by swimming in a (61 × 23 × 8 cm) trough with a thermal gradient ranging from 24-35℃. In all cases zebrafish spent the most time in the warmest zone of the tank. In response to a suggestion that the temperature gradient apparatus itself was a stressor, we measured whole body cortisol levels in fish that were acclimated to aquaria at different temperatures. Fish were injected in the lips with acetic acid or DDH_2O and allowed to acclimate in water that was 24℃ or 34℃ for fifteen minutes. Swimming behavior was recorded for the following fifteen minutes and fish were subsequently euthanized to be tested for levels of whole-body cortisol. No differences in swimming behavior were noted for any of the treatments. This finding contrasts with previous work wherein nociceptive responses at 28℃ decreased mobility. Male zebrafish had slightly lower whole-body cortisol at 34℃ than 24℃ ($p = 0.084$). We hypothesize that warmer environments may decrease the stress response in zebrafish; however, our data suggest that adult zebrafish have limited suitability as a model for thermal hyperalgesia.

4. 9:30 **u PRELIMINARY MEASUREMENTS OF ESTROGEN LEVELS DETECTED IN NORTHEAST ALABAMA WATERWAYS USING ELISA WITH IMAGEJ REDPLATE PLUGIN ANALYSIS. *Ansley Winter*, James Rayburn, Jacksonville State University.

Synthetic Estrogen (EE_2) is often found in waterway environments due to human waste or pharmaceutical disposal. An ELISA detection kit with an ImageJ Plugin was purchased for detection of EE_2 in the environment. ImageJ contains multiple plugins for processing and analyses. The particular plugin for this test is called ReadPlate. ReadPlate measures the absorbance of an image of a multi-well plate up to ninety six wells. ImageJ ReadPlate was used to read 96 well plates. This test is intended to detect how much EE_2 is in waterways of northeast Alabama. The water tested was from Germania Springs, Lake Heflin, Hane’s Branch Creek, Cane Creek, and Weaver’s Creek. A 100 mL bottle of water was collected above and below the water treatment plants at each location. Germania Springs is a natural underground spring and is being used as the control. To test the accuracy of the ImageJ Plugin for absorbances comparisons with a spectrophotometer were made using methylene blue and a Bradford protein analysis kit. The plate was placed in a light box and a picture of the plate was taken and analyzed using ImageJ. The data from ImageJ using the red channel was more consistent with the absorbances from the spectrophotometer than were the other channels on ImageJ.

5. 9:50 CULTURE CONDITIONS FOR PRODUCTION OF TRICHODERMA SG2 BIOMASS-HYDROLYZING ENZYMES FOR BIOMASS SACCHARIFICATION. *Benedict Okeke*, Auburn University in Montgomery; Ananda Nanjundaswamy, Auburn University at Montgomery and Alcorn State University.

Fossil fuels are non-renewable and cause environmental pollution. Lignocellulose biomass is the most plentiful renewable natural resource and is composed primarily of cellulose, hemicelluloses, and lignin. Using microbial catalysts and fermentation, lignocellulose biomass can be converted to biofuels and chemicals. Complete mixtures of cellulases and xylanases are required for efficient bioconversion of biomass. *Trichoderma* species SG2 produce a complete mixture of cellulolytic and xylanolytic enzymes for biomass conversion. *Trichoderma* SG2 produces more β-glucosidase than *Trichoderma* species RUT-C30 employed in industrial production of cellulase and coproduces amylase with cellulases and xylanases in lignocellulose medium. This study presents factors affecting enzyme production and lignocellulose biomass saccharification by *Trichoderma* sp. SG2. Cellulase and xylanase activities were much higher in solid substrate cultures than in liquid culture. Results indicate potential application of *Trichoderma* SG2 cellulolytic and xylanolytic enzymes in biomass conversion to saccharides for production of biofuels and chemicals.

6. 10:30 DIET, ANXIETY, AND GI QUALITY OF LIFE: IS THERE A LINK? *Mickie Powell*, Bijal Vashi, Rosianna Gray, Alan Whitehead, Chris Graham, Amandiy Liwo, Stephen Watts, and Gregory Kennedy, University of Alabama at Birmingham.

College life can be stressful, especially for freshman students living away from home for the first time. Students are often making food choices on their own, and many of the fast and convenience foods they consume are high in calories, fat, sugar, and salt. Studies have shown that under stress students gravitate to foods high in sugar, salt, and caffeine. As college instructors, we have observed an increase in self-reported student anxiety due to stress and gastrointestinal (GI) issues. Could the combination of stress and poor diet in college students manifest itself in the form of gastrointestinal issues? To better understand how diets, perceived student stress, and/or depression are impacting student GI health we have developed a survey for students in our introductory biology labs. This survey is designed to measure lifestyle factors such diet, stress, anxiety, and depression that may contribute to GI quality of life. Initial data from this survey suggests that students consuming chips, snacks, and sweets have an increase in bowel pain that negatively impacts their daily activities. This same trend was also observed in students who reported experiencing increased mental distress and anxiety. Students with gastrointestinal pain scored lower on the GI quality of life index. The results of this initial survey suggest that diet and stress may be important targets for intervention to help students improve their GI quality of life.

7. 10:50 **u IDENTIFICATION AND EXPRESSION OF NAD$^+$ SYNTHESIS SALVAGE PATHWAY ENZYMES IN *LACTOBACILLUS*. *Silvia Kinnebrew*, Bryce Pierce, and Brad Bennett, Samford University.

Vitamin B3 compounds can be converted into nicotinamide adenine dinucleotide (NAD+) and utilized in many metabolic processes. This project aims to identify, study, and compare enzymes within the NAD+ synthesis salvage pathway in probiotic species such as Lactobacillus. These microbes are critically important in the food fermentation industry. Using bioinformatics, four Lactobacillus species with known salvage pathway genes were found: *pncA, pncB, nadD, and nadE*. Although these enzymes have been characterized in several microbial species, there are many outstanding questions to their structure and function in Lactobacillus. For example, the substrate preference and oligomerization of the NAD synthetase (*nadE*) enzyme in any Lactobacillus species are still unknown. *nadD* and *nadE* genes from three of the Lactobacillus species were amplified by PCR, cloned into expression vector, and confirmed by DNA sequencing. To test for expression, the protein product of the *nadD* (*NaAD* synthetase) and *nadE* (NAD synthetase) genes from *Lactobacillus plantarum* were expressed in *E. coli* and the enzymes purified. These will be used for activity assays and structural characterization.

8. 11:10 **g IMPLEMENTATION OF DRONE-BASED TECHNOLOGY FOR SURVEYING SALTMARSH HABITAT FOR THE DIAMONDBACK TERRAPIN. *Nicole Conner*, Thane Wibbels, Ken Marion, and Catherine Sirgo, University of Alabama at Birmingham.

The diamondback terrapin (*Malaclemys terrapin*) is a medium-sized turtle found in estuaries on the Atlantic and Gulf Coasts of the United States. This once abundant species has an integral role in the saltmarsh ecosystem, but the Alabama population is currently considered by the Alabama Department of Conservation and Natural Resources to be of highest conservational concern. Diamondback terrapins have faced, and still face, many anthropogenic threats including reduction of saltmarsh habitat, drowning in fishing gear, hunting or commercial harvest, mortality by motorized vehicles, and nest depredation. Effective management of this species relies on accurate survey methods for documenting location and abundance in Alabama saltmarshes. In this study, we evaluated drone-based technology as a potential methodology. A DJI Phantom 3 Pro drone with 4K video capabilities was evaluated for surveying in the main tidal channel of Cedar Point Marsh (CPM) at the Mississippi Sound in Alabama. Flights were conducted using the Litchi Fly app, allowing us to generate standardized preprogrammed flight plans based on Google Maps. Surveys were flown at an altitude of ~15m and followed the tidal channel for ~2km for a total flight time of approximately twelve minutes. Periodic flights were flown over several nesting seasons, and this drone-based methodology proved to be a reliable system for standardizing surveys documenting both terrapins and birds in tidal channels. In 2020 we are conducting surveys every two weeks to document the occurrence and location of terrapins in the tidal channels at CPM before, during, and after nesting season.

9. 11:30 **g A NEW EUCRYPTODIRAN TURTLE (*TESTUDINES, MACROBAENIDAE*) FROM THE CAMPANIAN OF ALABAMA. *Andrew Gentry*, University of Alabama at Birmingham; James Parham, University of California at Fullerton.

A nearly complete turtle shell from the Campanian Mooreville Chalk of Alabama represents a new genus and species of Eucryptodire. *Bingemys tounotos* gen. et sp. nov. is referred to as *Macrobaenidae* based on its large size, lack of carapacial fontanelles, hexagonal neurals II-VII, and the proximal position of the sulcus between vertebral V and marginal XII. *B. tounotos* shares similarities with the coeval taxon *Judithemys sukhanovi*, such as a pronounced ridge on the visceral surface of the first costal, C-shaped bridge peripherals with only superficial insertion points for the thoracic ribs, a nearly rectangular eighth neural, and a lack of plastral fontanelles. *B. tounotos* can be distinguished from other species of *Macrobaenid* by the presence of a proportionally diminutive first costal and nine pairs of costals. *B. tounotos* is the first *Macrobaenid* described from southern Appalachia and only the second Eucryptodiran turtle described from the eastern United States. The occurrence of Eucryptodiran turtles on the eastern edge of Laramidia (*J. sukhanovi*), the southwestern edge of Appalachia (*B. tounotos*), and the northeastern edge of Appalachia (*Osteopygis emarginatus*) indicates that by the Campanian, Eucryptodires were widely distributed across present-day North America. Despite their widespread presence, fossil occurrence data indicate that individual species of *Macrobaenid* may have been regionally endemic. The discovery of *B. tounotos* in the Mooreville Chalk of Alabama illustrates the potential for new taxa even in purportedly well-known faunal assemblages.

***u* or ***g* Denotes presentation entered in student competition as an undergraduate or graduate student, respectively.

SECTION I – BIOLOGICAL SCIENCES
Paper Session II
Thursday Afternoon, 1:00 pm – 3:00 pm
Arthur J. Bond Hall Engineering Building – Room 136
Mary Anne Garner, Presiding

10. 1:00 **u THE PURSUIT OF LITTLE-KNOWN BIODIVERSITY: A SURVEY OF BRYOPHILOUS FUNGI IN AN ALABAMA WOODLOT. Brenn Schmittou, University of North Alabama; *Peter Döbbeler*, Ludwig Maximilian University of Munich; Paul Davison, University of North Alabama.

Bryophilous ascomycetes are fungi that form tiny fruit bodies upon bryophytes and live as biotrophic or necrotrophic parasites upon their hosts (mosses and liverworts).These organisms are rarely, if ever, included in biodiversity studies. The goal of this study was to demonstrate the surprising abundance and diversity of these little-known organisms occurring in a 1.5-hectare woodlot in northwest Alabama. We focused primarily on B*ryophilous ascomycetes* parasitizing the liverwort, *Frullania*. Six species of *Frullania* occurred in the study site: *Frullania appalachiana, F. eboracensis*, *F. ericoides*, *F. inflata*, *F. kunzei*, and *F. virginica*. Of these, only two species (*F. inflata* and *F. virginica*) were locally abundant and were the only liverworts found to harbor B*ryophilous ascomycetes*. We observed known and unknown *ascomycetes*, which included *Bryonectria callicarpa* on both *F. inflata* and *F. virginica*, *Periantria frullaniae* on *F. virginica, Bryocentria lusor* on both *F. inflata* and *F. virginica*, and *Hypobryon bacillare* on *F. inflata*. The latter two species were recently named new to science, and the two former species were recently reported new for North America. Other fungi of uncertain taxonomic placement were also found fruiting upon bryophytes. Our documentation of these species in a small area indicates that the abundance of B*ryophilous fungi* is underappreciated. It is likely that many species of B*ryophilous fungi*, that are in fact common, are unknown to science.

11. 1:20 **u VARIED ENRICHMENT FOR AFRICAN LIONS (*Panthera leo*) AND CHEETAHS (*Acinonyx jubatus*). *Amanda Beddingfield*, Faulkner University.

This research project explored the idea of how enrichment can help to improve the overall well-being of animals in a captive environment and how this knowledge can help with the conservation and education of different species of animals. In order to improve the enrichment programs, empirical validation needed to be explored and associated with the enrichment techniques. There are many different types of enrichment, and they were given on a specific schedule or randomized. With many experiments, the focus was one type.Sometimes, the schedule was specific, but other times, it was randomized. This specific project combined different types of enrichment. It included a schedule that was somewhat specific and randomized to see if a combination was the best technique for enrichment programs. This study focused on two of the felids, lions and cheetahs, specifically at The Montgomery Zoo. It used scent, food, object, problem-solving, and associated-learning enrichment techniques. The study lasted for eighteen weeks with observations being made about the animals' behaviors. These scans represented the statistical data of the experiment which showed that varied enrichment decreased stereotypical behavior and improvesthe overall well-being of the animals. This result informs educational and conservation efforts.

12. 1:50 **g IMMUNOHISTOCHEMICAL ASSESMENT OF THE MECHANISMS BY WHICH CHEMICAL DISPERSANT (Corexit 9500A) AFFECTS THE STRUCTURE AND ION TRANSPORT FUNCTION OF BLUE CRAB (*Callinectes sapidus*) GILLS. *Amanda Weiner*, Joseph W. Palmer, and R. Douglas Watson, University of Alabama at Birmingham.

Chemical dispersants are commonly used in remediation of spilled oil. For example, an estimated 2.1 million gallons of chemical dispersant, mainly Corexit 9500A, were applied in remediation effortsfollowing the sinking of the Deepwater Horizon offshore drilling platform in the Gulf of Mexico in 2010. Our previous data showed that exposure of blue crabs (*Callinectes sapidus*) to Corexit 9500A negatively impacts both the structure and ion transport function of gills. Based on preliminary data, we hypothesize that Corexit 9500A induces NADPH oxidase (NOX)- and C-reactive protein (CRP)-mediated production of reactive oxygen species (ROS) in gill tissue, leading to caspase 3-dependent apoptosis. In studies reported here, we used immunohistochemical methods to assess NOX4, CRP, and cleaved caspase-3 in gills from control and Corexit 9500A-exposed *C. sapidus*. The results showed that exposure to Corexit 9500A (60-125ppm) produced an increase in NOX4-, CRP-, and cleaved caspase-3-immunoreactivity in gill tissue. The findings are consistent with the notion that exposure of blue crabs to Corexit 9500A triggers NOX- and CRP-mediated production of ROS leading to apoptosis that compromises the structural integrity and ion transport function of gills. [Research supported by the BP/Gulf of Mexico Research Initiative.]

13. 2:10 THE RETT-SYNDROME *MECP2* ALLELE IN MICE DOES NOT APPEAR TO INCREASE THE NUCLEAR OR MITOCHONDRIAL GENE MUTATION RATE. *Mary-Catherine Mitchell*, Hannah Olive, Katherine Wilson, Coleman Reeves, and David Johnson, Samford University.

Rett Syndrome is a human neurological disease caused by the mutant X-linked *MECP2* allele and resulting in physical and mental limitations . The wild-type allele produces a repressor which dampens transcription by binding to methylated DNA. Rett individuals lack this transcriptional dampening, with the brain being most affected. Rett-syndrome-model mice carry the mutant *MECP2* gene. We have undertaken an extensive study to test whether some of the effects of Rett might be caused by secondary mutations in *MECP2*-mutation-carrying individuals. Affected mice show progressive age-related deterioration in motor function. Although Rett-syndrome humans do not show pronounced later-age deterioration, there is definite progressive development of symptoms in early life, usually attributed to unregulated transcription. We were interested in determining if any of the developmental abnormalities might be attributed to the accumulation of secondary mutations in the presence of the mutant *MECP2* allele. We asked two questions: Has the mouse strain carrying the *MECP2* mutation accumulated more mutations since its creation than the strain from which it was created and do nuclear or mitochondrial mutations accumulate in circulating or brain cells of older *MECP2* mice at a higher rate than in older wild-type mice? To test for mitochondrial mutations, we sequenced the D-loop region of mitochondrial DNA, and for nuclear mutations, we used a ribosomal

RNA internal transcribed spacer sequence. Our sequence data shows no evidence in either study of significant increases in mutations in mutant-*MECP2*-bearing mice.

14. 2:30 SPACE USE AND ROOST-SITE SELECTION BY MALE CERULEAN IN ALABAMA DURING THE BREEDING SEASON. *Yong Wang*, Alabama A&M University; John Carpenter, Alabama A&M University; Callie Schweitzer, Southern Research Station, USDA Forest Service.

Detailed information about space use during the breeding season is limited for most Nearctic-Neotropical migratory species of songbirds because of their small size and often cryptic behaviors. We monitored male Cerulean Warblers (*Setophaga cerulea*), a species of conservation concern, using radio telemetry in northern Alabama to better understand their space use and habitat selection. We estimated diurnal home range and core areas using information theoretic criteriaWe also located nocturnal roost sites, and related day and evening locations to surrounding landscape habitat, including features representative of canopy disturbances. Mean home range size was 6.7 ha (N = 10), and home ranges included an average of two core areas encompassing 0.7 ha. We located fifty-three nocturnal roost sites that were an average 159 meters from the center of the nearest core area. More than one-third (36.6%) of roost sites were located outside the diurnal home ranges; only 13.6% were located in core areas. Male birds in our study moved much farther than reported in previous studies, with some singing in areas greater than 300 meters from previously used song perches. This behavior may suggest pursuit of extra-pair copulations. Cerulean Warblers in our study preferentially selected a heavily forested landscape composed of mesic, floodplain bottomlands with little man-made disturbance. Within their home ranges, diurnal locations in core areas were located significantly closer to a creek than locations outside of core areas. Our results suggest that male Cerulean Warblers require much larger areas than previously reported and underscore the importance of a predominately forested landscape in their habitat selection process. Although edge habitats appeared to influence space use by male Cerulean Warblers in our study, the extent to which this is an essential requirement is unclear. Our results, and those of previous studies, suggest that specific habitat requirements of this species can vary at the local scale throughout its breeding range.

15. 2:50 **g ABIOTIC FACTORS THAT INFLUENCE CAVE USE BY SALAMANDERS. *Joseph Lamb*, Andrew Cantrell, and Yong Wang, Alabama A&M University; Matthew Niemiller, University of Alabama Huntsville.

Lungless salamanders (family *Plethodontidae*) rely on cutaneous and buccopharyngeal gas exchange, which strongly influences temperature and moisture regimes that can be inhabited. While many *plethodontid* salamanders have been documented to use caves for at least part of their life cycles, few studies have examined the factors that affect the abundance and diversity of salamanders in caves. No such studies have been conducted on salamander communities in caves of northern Alabama. This study aims to determine a relationship between salamander diversity and abundance among northeastern Alabama caves and environmental variables. Surveys are being conducted in fifteen caves every season from July 2018 through June 2020, documenting salamanders along transects from entrance to found within the first 160 meters into the dark zone. Environmental variables, such as air temperature, humidity, and wind speed, are being characterized along study transects, and climatological and landscape data around cave locations, such as rainfall, surface temperature, slope, and land cover, are being recorded to determine relationships between these variables and salamanders' diversity and abundance among seasons. We will be presenting the preliminary data on the use of caves by salamanders, displaying seasonal preference, species abundance, and spatial preferences.

SECTION I – BIOLOGICAL SCIENCES
SECTION VIII – ENVIRONMENTAL AND EARTH SCIENCES
Concurrent Poster Session
Thursday Afternoon
Arthur J. Bond Hall Engineering Building – Auditorium

Authors Set-up: Begins at 12:00 pm
Authors Present: 3:00 pm– 5:00 pm
Brad Bennett, Presiding (Biological Sciences)
Malia Fincher, Presiding (Environmental and Earth Sciences)

SECTION I – BIOLOGICAL SCIENCES
Posters

16. **g GROWTH AND PRODUCTIVITY OF LOBLOLLY PINE IN RESPONSE TO BARK BEETLE ASSOCIATED FUNGI. *John Mensah*, Auburn University; Mary Sword Sayer, USDA Forest Service, Southern Research Station, Pineville, LA.; Ryan Nadel, Auburn University; George Matusick, New York City Department of Environmental Protection, Bureau of Water Supply, Natural Resources Division.; Zhaofei Fan, Auburn University; Lori Eckhardt, Auburn University.

    Loblolly pine (*Pinus taeda L.*) is a predominant and economically important timber species in the southeastern United States, but it suffers from growth decline and mortality. Root-feeding bark beetles and their associated *ophiostomatoid* fungi (OPF) have been hypothesized to contribute to loblolly pine decline. Nonetheless, the role of the fungi in southern pine decline remains unresolved. We evaluated varying inoculum density of *Leptographium terebrantis* on thirteen-year-old loblolly pine growth and productivity at Eufaula, Alabama. Artificial inoculations were done using sterilized and *L. terebrantis* colonized toothpicks to simulate the natural feeding habits of bark beetles. Thirty-three months post-inoculation treatment, the high inoculum and control treatment caused 50% and 19% reduction in relative basal area increment respectively;growth decline resulted in a 30% mortality among the high inoculum trees. The results demonstrate that the OPF, *L. terebrantis*, contributes to loblolly pine decline and mortality at high inoculum density.

17. **g COMPARATIVE TRANSCRIPTOME AND EPIGENOME ANALYSES OF SALT-TOLERANT AND SALT-SUSCEPTIBLE GENOTYPES OF SOYBEAN. *LaMont Croom*, Zachary Gossett, Govind Sharma, and Venkateswara Sripathi, Alabama A&M University.

    Salinity stress is a known abiotic constraint that impedes the vegetative growth, yield, and quality of crop plants. Soybean (*Glycine max*) as a commercially important staple crop whichserves as food, feed, and fuel, commercial production, and health is vital to the growing populations of the global community. This is the first genome-wide DNA transcription profiling study in salt-sensitive (Dare) and salt-tolerant (Lee-68) genotypes of soybean using RNA-Sequencing (RNA-Seq) approach. This study includes two genotypes (Dare and Lee-68); three NaCl treatments (0 mM, 75 mM, and 150 mM); three collection time points (0 Days After Treatment (DAT); 7 DAT; and 14 DAT) with three replications (R1, R2, R3), which is equivalent to fifty-four [2x3x3x3] samples each for isolating DNA and RNA. Later, RNA Sequencing and Whole Genome Bisulfite Sequencing (WGBS or BS-Seq) libraries were prepared and sequenced on NextSeq 550 (Illumina), with an estimated yield of ~900 million reads. Quality reads were pre-processed (trimming and filtering), mapped to the reference genome, assembled, and annotated to identify differentially expressed genes (DEGs) and differentially methylated regions (DMRs). Using bioinformatics analysis on our experimental permutations in soybean, the comparative transcriptome analyses identified over 1,000 DEGs and ~100 DMRs that were significantly expressed in the salt-tolerant and salt-susceptible genotypes of soybean. In conclusion, the comparative unstressed and salt-stressed gene expression analysis of Lee-68 and Dare soybean genotypes will aid in identifying critical genes and pathways involved in combating the harmful physiological effects associated with salinity stress.

18. **g TRANSCRIPTOME ANALYSES OF FOUR *GOSSYPIUM* SPECIES USING RNA SEQUENCING. *Shalini Priya Etukuri*, Zachary B. Gossett, Manish Jakka, Govind C. Sharma, Venkateswara R. Sripathi, Alabama A&M University.

Cotton is valued as the world's leading natural textile fiber and a prominent oilseed crop. The cotton genus *Gossypium* consists of 45 diploid and six tetraploid species. Although it contains more than 50 species, only four species produce spinnable fiber, of which two are considered as diploid (2n=26) and two are tetraploids (2n=52). Among them, upland cotton (*Gossypium hirsutum* [AADD]) is the most widely cultivated cotton species. It has likely evolved from two wild ancestral genomes A&D: the A genome donor being *G. herbaceum* (A1) or *G. arboreum* (A2), and the D genome contributor being *G. raimondii* (D5). In this study, transcriptome analyses of four *Gossypium* species (*G. hirsutum* cv. TM-1, *G. herbaceum*, A1-141, *G. arboreum*, A2-44, and *G. raimondii*, D5-24) were conducted from seed and root tissues by using RNA sequencing. Delinted cotton seeds were ground in liquid nitrogen and total RNA was isolated. Then RNA was quality-tested and used for sequencing and bioinformatics analyses. The transcriptome analysis of four species identified over twenty thousand differentially expressed genes (DEGs) when compared to the control plants. Among these, ten significant DEGs (Log2FC>2) with a prominent role in biotic and abiotic stresses, about 50 transcription factors with a possible role in gene regulation and cellular processes, and ten genes associated with R-proteins were identified. Additional work is required to validate the predicted DEGs related to biotic/abiotic stress tolerance.

19. **u THE EFFECTS OF SALINITY STRESS ON SENSITIVE AND SALT-TOLERANT GENOTYPES OF SOYBEAN *Kindrea Gibbons*, LaMont Croom, Govind C. Sharma, Venkateswara R. Sripathi, Alabama A&M University.

Salinity stress is a known abiotic constraint that decreases the vegetative growth, yield, and quality of crop plants. *Glycine max*’s (soybean) commercial production and health is central to sustaining the increase of the global community due to its multifaceted use as food, feed, and fuel. This is the first phenotypic profiling study in salt-sensitive (Union) and salt-tolerant (S-100) genotypes of soybean for downstream next-generation sequencing (NGS) applications.

This study included two genotypes (Union and S-100); three NaCl treatments (0 mM, 75 mM, and 150 mM); three collection time points (0 days after treatment, 7 DAT; 14 DAT; and 21 DAT) with three replicates (R1, R2, R3), or 54 [2x3x3x3] biological independent samples. Biomass, leaf scorch score (LSS: 1-9; 1 = no chlorosis; 9 = necrosis), and DNA and RNA quality (A260/230 ranged between 1.8-2.1) were assessed under greenhouse conditions on salt-sensitive and salt-tolerant genotypes of soybean to characterize the salt-tolerant phenotype in soybean. The increase in salinity concentrations led to a rise in LSS and resulted in a decrease in biomass, RNA, and DNA quality. A non-saline (control) and two saline (75 mM and 150 mM NaCl) conditions were used to monitor change in morphology and biomolecule quality and quantity. A single leaf was procured at 0 DAT, 3 DAT, and 7 DAT from the most mature trifoliate, from each biological replicate, to assess phenotypic, quantitative, and qualitative aspects of the tissue. Preliminary results show that Union, the salt-sensitive cultivar, has a more observable change in leaf color and reduction in biomass when compared to the salt-tolerant, S-100. The complete set of results are in progress and will be reported at the time of the conference. However, it is key to note implications from this study could confirm the degree of tolerance and or susceptibility of salinity stress in two contrasting cultivars of soybean. The morphological and physiological data generated can augment the downstream NGS applications.

20. **u THE LESSER OF TWO WEEVILS: WEEVIL INFESTED WHITE OAK ACORNS HAVE A HIGHER MICROBIAL RICHNESS. *Hannah Harper*, Abigail Collins, Frank Gonzalez, Malia Fincher, Samford University.

White oak (*Quercus alba*) acorns are susceptible to pre-dispersal seed predation by acorn weevils (*Curculio spp*.), which often consume much of the cotyledons, decreasing germination and seedling success. Adult female weevils chew a small hole in the acorn, oviposit, and then seal the oviposition site with feces. The eggs hatch and the juvenile weevils complete their larval development inside of the acorn. After chewing a small exit hole through the fruit wall, the weevil pupates over the winter in the leaflitter. Both oviposition and the larval exit hole present opportunities for microbes to enter the acorn. Vertebrates, including rodents, deer, and birds, also consume acorns, resulting in damage that may be associated with microbial growth in the acorns as well. We hypothesized that weevil infestation and vertebrate attack would increase internal microbial species richness in *Quercus alba* acorns in Oak Mountain State Park. Acorns were externally sterilized and cut in half. Inner cotyledon was inoculated on nutrient agar plates with a sterile loop and incubated at 25-30 ℃. The microbial colonies were pure inoculated and incubated at 25-30 ℃. Microbial morphospecies were described based on morphological characteristics. Weevil infested acorns had a higher number of microbial morphospecies compared to uninfested acorns. This research raises questions about whether weevils intentionally deposit beneficial microbes when they oviposit in developing acorns.

21. **u THE K(3) HERBICIDE ALLIDOCHLOR CAN CAUSE VARIATIONS IN THE BIOSYNTHESIS OF ALKENONES IN *EMILIANIA HUXLEYI* STRAIN 1516. *Frank Gonzalez,* Samford University; Betsy Read, California State University of San Marcos.

Emiliania huxleyi, also known as *E. hux*, is one of the most abundant phytoplankton on earth and has attracted the attention of biogeochemists, oceanographers, climatologists, and those in the biotech industry. *E. hux* is characterized by its unique calcium carbonate cell covering and is also one of only five species in the world to produce long-chain lipids known as alkenones. These alkenones are exceptional because they have long carbon chain lengths between 36-41, and they have the potential to be used for renewable petroleum products and are already being used as a paleothermometer. The aim of this research was to characterize neutral lipid profiles from three spontaneous mutants exposed to the long-chain fatty acid elongase inhibitor, allidichlor, which will be used to determine the genetic lesion and its effects on gene expression. We found that the mutants resulting from allidichlor exposure exhibited different neutral lipid profiles compared to the wild type, *Emiliania huxleyi* strain 1516. They also produced fewer alkenones, and the types of alkenone profiles differed to that of the wild type. These results can be used to identify the genetic lesion resulting in different neutral lipid profiles and survivability of the mutants, determine the impact of said lesion on gene expression, and discern whether the wild-type phenotype can be restored upon repairing the genetic lesion.

22. **g A COMPREHENSIVE IDENTIFICATION OF GLUTATHIONE-BINDING PROTEINS IN *ARABIDOPSIS THALIANA*. *Anna Moye*, Sang Wook Park, Skylar Wilson, Auburn University.

Tripeptide glutathione (GSH) is the most abundant, small thiol molecule in plants, animals, and microbes. Until recently it has been characterized as a nonspecific antioxidant that detoxifies a broad range of toxic peroxides and peroxynitriles. We, however, have uncovered novel activity of GSH, directly binding and modulating the functional state of redox-sensitive enzymes (e.g., peroxiredoxins), which in turn activates redox signaling cascades in maintaining cell growth and metabolisms. To further understand a mode of GSH-mediated post-translational modification, the present study has attempted the comprehensive identification of *Arabidopsis thaliana* GSH-binding proteins (AtGBPs), utilizing a batch affinity chromatography technique. Total extracts prepared from *A. thaliana* were subjected to a GSH-agarose resin and washed with 50 mM Tris buffer containing 50 mM NaCl (pH 7.5). The column was further washed with 0.1 mM GSSG to remove nonspecifically bound proteins, and column-bound proteins were eluted with 10 mM GSH. Both GSSG and GSH eluates were then fractionated by SDS-PAGE and identified by MS analyses. Thus far, three independent purifications have carried out and identified 66 AtGBP candidates. The next step is to clone these proteins into the *E. coli* expression system for the subsequent validation of their GSH-binding affinity, which will assist us to elucidate more specific functions of GSH in the cellular regulations and mechanisms.

23. **g GLUTATHIONE ACTIVATES AUTONOMOUS REDUCTANT SIGNALING CASCADES INDEPENDENTLY FROM OXIDATIVE STRESS SIGNALING. *Pratima Subedi*, Sang Wook Park, Auburn University.

Glutathione (GSH; γ-L-glutamyl-L-cysteinyl-glycine) is the most abundant nonprotein thiol in plants, acting as a major reducing agent transmitting oxidative stress signaling. GSH acts as a major antioxidant that prevents damages to a variety of important cellular components. It reduces reactive oxygen species and other peroxides by donating its electron (H+, e-) and is subsequently oxidized to a disulfide form (GSSG). 2-cysteine peroxiredoxins (2CPA) are key proteins possessed by plants that are able to detoxify hydrogen peroxide molecules. Here we demonstrate a unique, regulatory reaction of GSH that operates autonomous metabolic and signaling pathways. Our preparatory pull-down assays showed that *Arabidopsis* 2CPA can directly bind to GSH-agarose beads underpinning the potential S-glutathionylation of 2CP-family proteins. A series of redox mobility assays demonstrated a unique activity of GSH where it oxidizes and directly binds to the sulfhydryl group of cysteine residues, modifying the quaternary structure of 2CPs, which in turn determines and protects their structure-function against enzymatic reductions and various ecological constraints that cause pH flux and/or oxidative stresses. The GSH-binding kinetics of 2CPs is coordinated by systematic regulations of GSH synthesis and attendant reduction capacity, occurring independently of free radicals and oxidant generations. Thus, we conclude that GSH can also act as a signal activating redox and enzymatic cascades, besides a general antioxidant (electron donor).

24. **g MICROBIAL DIVERSITY ASSOCIATED WITH THE ORAL AND FECAL SAMPLES OF WHITE-NOSE SYNDROME (WNS) INFECTED GRAY BATS AND TRICOLORED BATS. *Kristina Burns*, Venkateswara R. Sripathi, William Stone, Jeanette Jones, Leopold Nyochembeng, Govind Sharma, Alabama A&M University.

White-nose syndrome (WNS) has spread rapidly across the eastern United States and Canada since it was first documented in New York over a decade ago. The causative organism for WNS in bats is *Pseudogymnoascus destructans*, and it has accounted for 5.7 million deaths of bats in the United States. Molecular mechanisms associated with the WNS and the resultant shift in the microbial diversity are underexplored. Species identification was achieved by using both field-based methods and molecular techniques. This study included two bat species (gray, *Myotis grisescens* and tricolored, *Perimyotis subflavus*); one condition (WNS-infected); two populations (males and females); and two sample types (oral and fecal swabs) with six replicates (R1–R6). In total, 48 microbiome samples (2x1x2x2x6) were selected for microbial DNA extraction (ZymoBIOMICS). The DNA isolated from two sample types (oral and fecal) was compared using two different methods (spectrophotometer-based and quantitative PCR) and three different preservation media (ethanol, NaCl-saturated dimethyl sulfoxide-DMSO, and silica desiccant) compared. The results showed that fecal samples and silica yielded more DNA. Microbial diversity was assessed by sequencing single-end libraries of amplified 16S rDNA genes from respective microbiomes and analyzed using QIIME 2. The readings were clustered into operational taxonomic units (OTUs), and phylogenetic trees were constructed with closely related bacterial species to compare microbiomes. Preliminary results indicated that the majority of OTUs identified belonged to the phylum Spirochaetes with *Leptospira* being the dominant genus. Further, with bats being a mammalian system, the knowledge generated here can be applied to humans.

25. **u THE INFLUENCE OF pH ON BACTERIAL COMMUNITY COMPOSITION OF SOILS FROM THE WINFRED THOMAS AGRICULTURAL RESEARCH STATION. *Jayla Pettway,* Elica Moss, Alabama A&M University.

There is considerable variability in the abundance of different phyla in soils; however, it is not clear to what extent variations are in response to conditions in soil environments. Proteobacteria, Acidobacteria, and Actinobacteria are most abundant in soils as Bacteroidetes, Firmicutes, and Planctomycetes are generally less abundant. The factors that may influence the abundance of these bacterial phyla could be large. Research suggests the abundance of Verrucomicrobia is influenced by soil moisture and Acidobacteria by soil pH. The Winfred Thomas Agricultural Research Station at Alabama A&M University contains a variety of agricultural soils used for the growth of industrial hemp, switchgrass, sweetgum, soybean, biochar infused soil and pasture soils. For this study, samples were collected to assess the influence of soil pH on differences in bacterial community composition using metagenomic approaches. DNA was extracted using the ZymoBIOMICS®-96 MagBead DNA Kit and sequenced on Illumina MiSeqTM. Results identified the abundance of bacteria phylum, such as Proteobacteria, Actinobacteria, and Acidobacteria, patterns of their distribution within each soil community and the overall diversity among the soils. Biochar soil, the most acidic, pH 4.5, seemed to contribute to the abundance of Actinobacteria (62.78 %) whereas Actinobacteria in Industrial Hemp, pH 7.84, comprised only 27.75 % of the community. Consequently, Acidobacteria was least abundant (5.7%) in biochar and greater (17.35%) in hemp. Additionally, industrial hemp soil was more diverse than any other soil community. Further research will aid in identifying other factors that may contribute to the variability in soil bacterial community composition.

26. **g UNCOVERING THE DIRT ON NORTH BIRMINGHAM. *Sarah Adkins*, Qutia Roberts, Robert Aksycn, Sam Gregory, Kathryn Aler, Alex Dawson, University of Alabama at Birmingham; and Brad Bennett, Samford University.

Environmental injustice by way of heavy metal pollution from large-scale industry has plagued the north Birmingham 35207 zip code for decades. Former research has shown that residents in the 35207 zip code face almost double the risk of respiratory disease compared to residents in neighboring zip codes like 35214. Considering that bacteria, which confer resistance to heavy metals, can use those same resistance pumps to resist antibiotics, it may also be possible that bacteria in the soil in 35207 has increased levels of antibiotic resistance compared to the 35214 zip code. To test this, we collected six homogenized soil samples from public areas in both zip codes. DNA was subsequently extracted with the Qiagen PowerSoil Kit, analyzed using Illumina MiSeq, and processed using ordination analysis from mothur. With the help of student course-based undergraduate researchers at three Birmingham universities, we found significant effects of metal concentration on the microbial community structure. Now that this has been confirmed, ongoing work will compare these trends to the antibiotic resistance, using culture-based methods and sequencing of plasmids. Local north Birmingham stakeholders, like those from the coalition People Against Neighborhood Industrial Contamination (PANIC), have asked for more direct evidence between the pollution and health problems to which this work makes an important contribution.

27. **u ENVIRONMENTAL IMPACT ASSESSMENT OF PROPERTY TRENDS TO STIMULATE REVITALIZATION IN AFRICATOWN IN MOBILE, ALABAMA, USING ARC GIS. *Sameerah Rice,* Elica Moss, Alabama A&M University.

Vacant and abandoned property is increasingly recognized as a significant barrier to the revitalization of cities. This type of property affects aspects of community life, including housing/neighborhood vitality, crime prevention, and commercial district vitality. Africatown is a historic community three miles north of downtown Mobile, Alabama. It was formed by a group of 32 West Africans brought to the United States on the last known slave ship, the Clotilda. Once home to around 10,000, Africatown's population has decreased to ~3,000. Abandoned houses line the town, and residents consider them a significant problem. With the recent discovery of the Clotilda, the community has an opportunity to leverage international interest in its extremely unique history for economic development and improvement in health and educational benchmarks for their youth. To assess the impact of the discovery on heritage tourism development within the area, the Africatown Housing Assessment Project recognizes the need to collect and analyze available data related to home ownership, rent, condemnation, and tax assessment. The goal of the project was to analyze the past 5 years of available data of 450 homes and apply it to ArcGis, which generated a map of the properties. The trends documented existing and changing home ownership patterns, property tax rates, and housing condemnation and destruction within Africatown. This study serves as the genesis to combat the issue of vacant and abandoned property problem in Africatown that could lead to aggressive code enforcement, tax foreclosure, eminent domain, and cosmetic improvements, thereby stimulating economic development.

28. **g EVALUATING THE ROLE OF INNATE IMMUNE GENE EXPRESSION IN MELANOCYTE BIOLOGY. *Alex Dawson*, Melissa Harris, Joseph Palmer, University of Alabama at Birmingham.

The convergence theory of vitiligo, the most accepted theory of vitiligo pathogenesis, states that vitiligo is the contribution of multiple factors, such as oxidative stress, innate immune dysregulation, and autoantigenicity, which causes T-cell infiltration. However, it is currently unknown if a particular innate immune signature could be predictive of melanocyte fragility that could trigger the onset of vitiligo. In order to test whether gene expression changes in the melanocyte are sufficient to cause melanocyte fragility, we will employ a transgenic mouse line, C57B6/J.Tg(Dct-Sox10). Tg(Dct-Sox10) mice conditionally over-express transcription factor SOX10 in the melanocyte. SOX10 is necessary for melanoblast development, melanocyte stem cell retention, differentiation, and normal pigment production. Tg(Dct-Sox10) mice exhibit elevated sensitivity to viral activation, which is expressed through acute graying in the subsequent hair cycle. RNA-seq performed on skin samples of Tg(Dct-Sox10) mice shows upregulation of innate immune genes related to viral reception compared to WT C57/B6J mice, and we hypothesize that innate immune dysregulation is causing the loss of melanocyte stem cells in the transgenic mice. We will attempt to elucidate the mechanism that causes increased sensitivity to viral reception and melanocyte loss. We will be determining whether the sensitivity to viral reception is due to the transgenic insertion location, gene regulation by SOX10, or due to increased cellular stress from increased pigment production. It is expected that we will see changes in innate immune gene expression following changes to the cellular pigment production, denoting it as the primary factor in causing gene expression changes.

29. **u EFFECTS OF NITROTYROSINE ON DOPAMINERGIC SH-SY5Y CELLS: IMPLICATIONS FOR PARKINSON’S DISEASE. *Allie Smith*, Mary Anne Garner, Judson College.

Parkinson’s disease is one of the most common neurodegenerative diseases in the world. The disease is characterized by the death of dopaminergic neurons in the substantia nigra. The death of these neurons can lead to the development of tremors, bradykinesia, and memory disorders. The exact mechanism behind Parkinson’s disease is unknown. However, reactive oxygen species and reactive nitrogen species have been implicated in most neurodegenerative diseases, including Parkinson’s disease, amyotrophic lateral sclerosis, and Alzheimer’s disease. This study utilizes the SH-SY5Y neuroblastoma cell line, which can be differentiated into dopaminergic, neuron-like cells when treated with brain-derived neurotrophic factor and retinoic acid. In this presentation, we describe the effects of 3-nitrotyrosine on cell growth, cell differentiation, and cell death in the SH-SY5Y cell line. Nitrotyrosine is formed as the result of the interaction between reactive oxygen and nitrogen species. It is found in diseased tissues of animal models and human patients suffering with neurodegenerative diseases. These experiments investigate the effects of nitrotyrosine on the cell pathways involved in cell division, cell differentiation, and apoptosis, in an effort to identify points of intervention for potential treatments for these diseases.

30. **g ESTABLISHING THE EFFICACY, ACCURACY, AND REPRODUCTIBILITY OF A BRAIN METABOLITE ISOLATION PROTOCOL. *Victoria McConnell*, Bernhard Vogler, Sharifa Love-Rutledge, University of Alabama in Huntsville.

Proton nuclear magnetic resonance metabolomics can provide novel information about changes occurring during disease onset. The first objective of our research is to establish the efficacy, accuracy, and reproducibility of a brain metabolite isolation protocol in extracting water-soluble metabolites. We will then use it to discover differences in the brains of two aged rat groups with and without glucose intolerance. The initial protocol/equipment was tested by using only known standard solutions of beta-alanine to see how much was recovered for normalization. Filtration caused a 24% loss of beta-alanine, so filtration was eliminated. The improved protocol, also using beta-alanine in solution, was applied to the brains of young rats, aged to 10 weeks on a standard diet. Beta-alanine recovery was lower than expected, but additional pure solvent rinses increased its recovery rate. In addition, we discovered that the premixed beta-alanine degrades over time. To account for loss of the beta-alanine in the standard solution, it is now tested separately in parallel to its addition to brain samples. Double-stranded DNA concentration was measured to use as an internal normalization standard. Total protein concentration was determined with the Lowry method on the remaining tissue pellet for a second internal normalization factor and to show the adequacy of tissue extraction. This protocol can now be applied to aged rat models with and without glucose intolerance. We expect brain metabolites in glucose intolerant rats with elevated serum insulin will establish a unique signature of altered metabolism around the onset of brain insulin resistance.

31. **g TROUBLE WITH THE TIGHT JUNCTION: THE EFFECTS OF TGF- β IN PAH. *Alyssa Pace-Patterson*, Jonathan Brown, Caleb Hamilton, Adam Morrow, Audrey Vasauskas, Rebekah Morrow, Alabama College of Osteopathic Medicine.

    Pulmonary arterial hypertension (PAH) is an incurable disease causing premature death. Remodeling the pulmonary arteries increases vascular resistance. The increased resistance is partly due to endothelial to mesenchymal transition (EndMT), which changes endothelial cells (EC) to a muscular, fibroblast-like lining. EC function depends on cell-to-cell junction and cell-to-ECM proteins. We explored EndMT and the specific effects of TGF-β on various EC proteins in PAH. Control cells (FR6) and diseased cells (SPAC and SPAD) were treated with TGF-β or a vehicle for 24 hours. Supernatants and whole cell lysates were collected, RNA was isolated, and western blots and RT-PCR were run. The data shows signs of a cellular transition, including decreases in cell-to-cell adhesion. Our findings suggest cells change in structure with the addition of TGF-β. Cell-to-cell adhesion molecules in the disease state decreased with the addition of TGF-β. This suggests a structural change, which may allow more leakage and a less concentric lining to protect from edema and pathogens. In addition to the potential loss of barrier function, we found a reduction of proteins involved in leukocyte trafficking, which could alter appropriate immune responses, further supporting functional changes in the endothelial cells. The work was supported by 1 R15 HL137135-01A1.

32. **u INTERFACE-ORIENTED BEHAVIORS IN THE COASTAL LOBATE CTENOPHORE *MNEMIOPSIS LEIDYI*. *Angeline Lawson*, Anthony Moss, Auburn University.

    Mnemiopsis leidyi, a common coastal lobate ctenophore from the northern Gulf of Mexico, exhibits a complex behavior. We confirmed data from animals in Apalachicola Bay, Florida, (collected in 2004) and extended our ctenophore behavior knowledge base with improved imaging. Animals from Mobile Bay, Alabama, were dipped during July 2019 and transferred to a 15-gallon tank illuminated by LED strip lights (SMD 5050M, Daybetter). 19 adults were followed over 5 days with 1080p images recorded at 5- second intervals (Everio camcorder GZ-M300, JVC). Most behaviors involved interactions with interfaces. Interface behaviors included: a) Looping -- transient backward swimming with geotaxis change; b) Pulsing -- listlobe clap and return to substrate; c) Skipping – repeated #2 w/lateral displacement; d) Stationary – straightened auricular lobes and oral lobes contacting substrate; e) Hovering-- 1) horizontal, 2) mouth down, and 3) mouth up; f) Rolling – midwater rotation around any axis or across axes (yawing); g) Spiraling – helical swimming, lobes-up ascent; h) Pivoting – one lobe touches substrate while swimming, animal rotates around lobe; and i) Deceleration – animal slows and may stop before contacting the surface, in which both oral and auricular lobes are spread. In all studies, approximately 40% of behaviors involved direct substrate contact. This result is in general agreement with earlier work where animals spent 38% of their time on substrate. Rolling and hovering displayed a strong sequential correlation (R2=0.945). In contrast, looping and pulsing showed very weak correlation (R2=0.427). Looping was the predominant benthic behavior in all studies. Funding NSF EPSCoR EPS-047675 to R Henry and F Bartol, NSF MIP MCB-0348327 to AGM.

33. **g CONTRASTING DIFFERENTIAL GENE EXPRESSIONS TO HEAT OR FIRE ANT ENVENOMATION IN *SCELOPORUS UNDULATUS*. *Dasia Simpson*, Auburn University; Rory Telemeco, California State University, Fresno; Tracey Langklide, Penn State University; Tonia Schwartz, Auburn University.

Environmental stressors--such as extreme temperature change, invasive predators, and other disturbances--can negatively affect an organism's performance, survival, growth rate, and, ultimately, its fitness. The underlying molecular mechanisms of how organisms respond to diverse stressors are still poorly understood. *Sceloporus undulatus*, the eastern fence lizard, has become an ecological model organism for addressing questions in eco-physiology and life history evolution. Recently, we have developed a high-quality reference genome that furthers its utility for investigating molecular and physiological mechanisms. We are interested in understanding how stress responses may vary when an organism is exposed to diverse environmental stressors--such as an extreme heat event (as predicted by climate change), or an attack by an invasive predator, such as a fire ant. In this study, we test whether stress response to either acute heat or fire ant attack diverges at the endocrine level (plasma corticosterone levels) or at the gene expression level. We found that male *S. undulatus* (n = 24) which were either exposed to heat (43C) for up to 3 hours or fire ant envenomation (receiving ~10 stings) each had the same response in corticosterone levels, with an increase relative to the control. Liver RNA seq data are being analyzed to test whether the gene expression response to acute heat and fire ant envenomation is highly similar or is divergent. These results will bring further insight into the similarity of molecular responses to ecologically relevant stressors.

34. **u CREEPER ANTS TAKE THE BAIT. *Olivia Rice*, Jacob Dittel, Paul Davison, University of North Alabama.

Ants (*Hymenoptera, Formicidae*) are well-recognized as ecologically important and are famously one of "the little things that run the world" (Wilson 1987, Del Toro et al. 2012). Alabama is home to approximately 175 species of ants, yet for many species, little is known of their biology beyond taxonomic descriptions and spotty distributional data. *Temnothorax schaumii*, an arboreal species nesting in trees in open forests and suburban areas (Deyrup 2016), is a common ant whose biology is poorly known. In an effort to learn more about this elusive species, we tested the efficacy three types of bait (cat food, jelly, and peanut butter; n=140 for each bait) to recruit foraging workers in an upland oak-hickory forest in Northwest Alabama. We performed a generalized linear model (GLM) with a binomial distribution to detect if the type of bait influenced the presence of *T. schaumii* foragers. We found a significant difference among bait types (= 13.2, df = 3, P = 0.004), and, using Tukey's honest significance test, we were able to determine that peanut butter recruited *T. schaumii* foragers better than cat food. There was no significant difference between peanut butter and jelly (P >

0.05); however, our data suggests that peanut butter may be the best bait and worthy of further comparison with jelly and other baits, with the additional aim of following foragers to their nest.

35. **g EVALUATING THE IMPACT OF PREDATORS AGAINST DIAMONDBACK TERRAPIN NESTS IN ALABAMA. *Catherine Sirgo*, Thane Wibbels, Nicole Conner, Ken Marion, University of Alabama at Birmingham.

The diamondback terrapin (*Malaclemys terrapin*) inhabits saltmarshes throughout the southern and eastern United States. This species was a valuable economic resource in Alabama during the 1800s, when tens of thousands of terrapins were farmed and shipped to the northeastern U.S. as an ingredient for terrapin stew. One of the largest farms in the U.S. was located on Cedar Point Marsh, Alabama, a major nesting beach of the terrapins. Although the terrapin was once abundant in Alabama saltmarshes, it declined significantly over the past century due to major threats, such as commercial crab fishery and increased coastal development. Now, the terrapin is a protected species in Alabama and listed as “a species of highest conservation concern”. A major problem associated with the increased coastal development is an increased number of predators such as raccoons, which prey on terrapin nests. The purpose of the current study is evaluating predator depredation of terrapin nests at the Cedar Point Marsh nesting beach during the 2019 nesting season. These areas were surveyed several times a week throughout the season to document depredated terrapin nests. Additionally, infrared wildlife cameras and wide-angle GoPro cameras were placed in experiment plots along the beach, approximately twice a week for 24-hour sampling periods, to document the presence of predators. The results indicate that raccoons are significantly impacting the survival of terrapin nests at the Cedar Point Marsh nesting beach and that their impact represents a major threat, limiting the recovery of the terrapins in Alabama.

SECTION VIII – ENVIRONMENTAL AND EARTH SCIENCES
Posters
Malia Fincher, Presiding

1. **g . THERMOREGULATORY GENE VARIATION IN THE EASTERN FENCE LIZARD (*SCELOPORUS UNDULATUS*) IN RESPONSE TO SULVICULTURE TREATMENTS IN A SOUTHEASTERN HARDWOOD FOREST. Thomas *Haltigan*, Alabama A&M University; Yong Wang, Alabama A&M University; William Sutton, Tennessee State University; Venkateswara Sripathi, Alabama A&M University.

Understanding the impacts of forest management practices on habitat and wildlife community composition is essential for long-term biological conservation. The life history traits of ectothermic vertebrates, such as *Sceloporus undulatus*, are dependent on the thermal environment these organisms inhabit and thus alteration due to anthropomorphic change may influence the expression of genes that are functionally associated with thermoregulation. A large-scale field experiment, consisting of “before-after control-impact” and factorial complete block design was implemented in 2005 at Bankhead National Forest, Alabama, to evaluate the effects of prescribed fire and thinning regimes on the forest ecosystem. As an ongoing research project evaluating the responses of herpetofaunal communities, my study will evaluate both the abundance dynamics of *S. undulatus* during the thirteen years and genetic variations of *S.*

undulatus after thirteen years of the initial prescribed burning and thinning treatments. *S. undulatus* will be sampled throughout the active season which ranges from May to October each field year. Two-way analysis of variance (ANOVA) will be conducted to test treatment after x year(s) effect of the abundance of *S. undulatus*. DNA will be extracted from toe and tail clippings of *S. undulatus* collected in 2017 and 2018 using the QIAGEN DNeasy Kit and amplified via Polymerase Chain Reaction (PCR). Primer Pairs will be obtained from NCIB Primer-BLAST. Ten genes associated with thermoregulation will be sequenced and aligned with MUSCLE.

2. **u BACTERIAL COMMUNITY COMPOSITION OF BIOCHAR AMENDED SOIL. *Autumn Hill*, Elica Moss, Alabama A&M University.

Climate change is one of the most critical issues concerning the modern world. The recent practice of amending soil with biochar, a carbon rich product derived from the pyrolysis of organic material at relatively low temperatures, has become a promising method to minimize atmospheric CO2 emissions (carbon sequestration), mitigate global warming, and improve plant productivity and nutrient cycling. Biochar affects physiochemical processes and has the ability to alter microbial community composition. This study observed the predicted carbon sequestration potential of four soils amended with biochar (0 mg/ha, 5mg/h, 12.5 mg/h, 30.02 mg/h). Our study reflects a shift in microbial community structure and diversity with added biochar. Specifically, the higher bacteria diversity, increase in copiotrophic bacteria (Actinobacteria), and decrease in oligotrophic bacteria (Acidobacteria) align with the theory of enhanced copiotrophic bacteria and reduced oligotrophic bacteria contributing to an increase in C02 emissions. However, our study also showed that with increased biochar amendment, there was a decrease in copiotrophic (Proteobacteria, Gemmatimonadetes and Fermicutes) bacteria, which would signal a decrease in CO2 emissions. The results reflected here confirm that biochar alters microbial communities. However, there is a contradiction in terms of whether this addition indicates the role of oligotrophic and copiotrophic bacteria in carbon sequestration and thus deems further review and analysis.

***u* or ***g* Denotes presentation entered in student competition as an undergraduate or graduate student, respectively.