ABSTRACTS

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BIOLOGICAL SCIENCES PAPER ABSTRACTS

SEVERE DROUGHT MAY ENHANCE OAK REPRODUCTION THROUGH EFFECTS ON ACORN WEEVIL POPULATIONS. *MALIA FINCHER*, ASHTON EDWARDS, MARISA GARRETT AND WESLEY WALTERS, SAMFORD UNIVERSITY.

Oak trees exhibit a reproductive behavior known as masting, in which they produce a large quantity of seeds in some years, interspersed with a periods of almost no seed production. This helps to conserve resources and combats against acorn predators, such as the acorn weevil. One popular hypothesis is the resource matching hypothesis, which states that masting is simply a version of all plants' ability to adapt to the abundance of resources, or lack thereof, in their environment (Perez-Ramos et. al 2010). This process can also be driven by environmental stress factors, such as drought. In summer-fall 2016, Alabama experienced a severe drought. It's probable that this drought could have inspired a subsequent stress masting event of Alabama's oak trees, in 2017. Simultaneously, very dry conditions in the leaflitter for pupating acorn weevils, which are important oak seed predators, may have decreased weevil populations in the year after the drought. We collected data from six cooccurring oak species at six sites in the Birmingham area and showed that weevil infestation rates of acorns were very low across all species. Since the frequency and severity of extreme drought events in the southeastern United States is expected to increase under most climate change models, this may actually benefit oak reproduction through suppression of acorn weevil populations.

PROTEIN AND LIPID PREFERENCES IN LYTECHINUS VARIEGATUS. *JACKSYN CLANTON*, UNIVERSITY OF ALABAMA AT BIRMINGHAM. BEN MCCAFFERTY,MARLEE HAYES,YUAN YUAN AND STEPHEN WATTS, UAB.

The sea urchin, *Lytechinus variegatus*, is an opportunistic omnivore that is innervated solely by a neural net. The urchin lacks a central brain, but we hypothesize that it prefers and targets specific quantities and qualities of both protein and lipid in its diet. In this study, 11 protein diets from various sources were prepared using an agar-based food cube. Each diet contained 1.5% agar, 10% of the respective pure protein source, and 32ppt of saltwater. Feed intake was found to be dependent on protein source. Feed intake was weakly correlated with the presence of higher essential and branched amino acids. These data suggest L. variegatus is able to qualitatively assess a protein source, presumably based on amino acid content. In addition, 10 additional agar-based diets with different lipid sources were provided using 2% agar, 2% of the respective lipid, and 32ppt of saltwater. Compared to a control diet (fish meal protein source), the experimental diets containing only lipids were consumed less, with phospholipids promoting the highest feed intake. These data along with previous studies suggest L. variegatus prefers food containing primarily protein and carbohydrate over lipid.

A CALL FOR SCIENCE EDUCATORS TO DISH OUT THE ART. ***SARAH ADKINS***, RACHEL ROCK AND JEFFREY MORRIS, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

Over 40% of American students who begin four to six-year degrees in Science, Technology, Engineering, or Math (STEM) fields do not graduate with those degrees. This is due in part to STEM education, especially in the laboratory classroom, often falling short in representing the true exploratory nature of these fields. Many evidence-based efforts, such as Course-Based Undergraduate Experiences (CUREs) attempt to bridge this gap. CUREs allow students to engage in authentic research that is of interest to communities beyond the classroom walls.

We reformed a semester-long traditional cookbook microbiology lab to a CURE which uniquely uses art - in the form of agar art - as a platform for scientific inquiry. Microbiology students paint personalized works of living agar art from environmental soil isolates. Students then use standard microbiology techniques to identify their isolates, self-generate hypothesis, and execute experiments based off observations they make from their agar art; mirroring the type of critical thinking which drives authentic scientific inquiry.

Using the Persistence in the Science questionnaire instrument developed by Hanauer et al. (2016), we found that 33 students in the agar-art CURE were significantly more likely than a similar control cohort of 15 microbiology students to affirm attitudes associated with retention in STEM. We discuss the implications of our study for education reform, and suggest future directions for the use of art in STEM education.

SINGLE CELL PROTEINS PROMOTE WEIGHT GAIN IN CULTURED SHRIMP. ***SOPHIE BRU***, YUAN YUAN, KAREN JENSEN, ROBERT BARRY, MICKIE POWELL, ADDISON LAWRENCE AND STEPHEN WATTS, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

Fish meal is a high-quality protein source for fish and shrimp feeds. World fisheries for fishmeal are at maximum sustainable yield and alternative protein sources are needed as both demand and price increase. Single cell proteins (SCP) have been identified as potential replacement ingredients for fish meal protein. This study reports a bacterial (MRD-Pro) and yeast based (DY-Pro) SCPs (from Meridian Biotech) as a fish meal protein (FP) replacement. Control diet using a commercial formulation contained 21.4% FP. Three experimental diets contained 6.9% DY-Pro and 15.3% FM, 6.9% MRD-Pro and 14.2% FM and 16.3% MRD-Pro and 4.35% FM with SCPs replacing FM on a protein equivalent basis. Groups of 20 shrimp (ca. 7 g) were stocked into separate tanks and tanks were assigned randomly into each treatment (n=3 tanks/diet treatment). Shrimp were fed an ad libitum ration and were weighed at the end of 38 days to quantify growth and feeding outcomes. Shrimp fed diets with MRD-Pro trended higher in weekly weight gain (2.6-2.9 g/week) than shrimp fed the FP control diet (2.4 g/week). Those fed DY-Pro showed weight gain equal to fish meal. Food conversion ratio trended lower in those fed MRD-Pro (2.18) compared to FP (2.52) and was equal to FP in those fed DY-Pro. These data indicate that SCPs can replace at least part of a quality FP in intensive culture.

FEED INTAKE AS AN ESTIMATION OF ATTRACTABILITY IN SHRIMP. *YUAN YUAN*, SOPHIE BRU, KAREN JENSEN, ROBERT BARRY, ADELE FOWLER, ROBERT MAKOWSKY AND MICKIE POWELL, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

Immediate consumption of feed is important in commercial aquaculture, and leads to increased feed conversion and growth, reduced feed waste, reduced leaching of important and expensive nutrients, and improved water quality. We are testing single cell proteins (SCP) as protein sources for shrimp feeds. These include a bacterial SCP (MRD-Pro) and a yeast SCP (DY-Pro) provided by Meridian Technologies. Fish meal protein (FP) was replaced in part with two commercial SCPs and fed to the shrimp, *Litopenaeus vannamei*. These diets included a FP control diet containing no SCPs and three experimental diets with different levels of the two SCPs replacing FP. Groups of twenty shrimp were stocked into separate glass tanks in a recirculating aquaculture system. Tanks were assigned randomly into one of four treatments with three tanks/treatment. Forty feed pellets (ca. 1 g) were deposited into each tank at 9:00 am and 1:30 pm each day for three days. Pellets remaining in each tank were counted at three minute intervals for twenty-four minutes. Feed intake was calculated based on feed pellets remaining in the tank at each time point. Probability of consumption was determined by Cox Regression Analysis. Diets containing 6.9% DY-Pro or 6.9% MRD-Pro had significantly greater probability of 11.5% and 16.3%, respectively, of being consumed than the FP control diet. Diet containing 16.3% MRD-Pro had a significantly greater probability of 31.2% of being consumed than the FP control diet. These data indicate that SCPs enhance feed intake compared to FP and are effective attractants in shrimp diets.

VARIATIONS IN PATTERNS OF FEED INTAKE IN A SEA URCHIN. *MARLEE HAYES*, ROBERT MAKOWSKY, JESSICA M. HOFFMAN AND STEPHEN A. WATTS, UNIVERSITY OF ALABAMA AT BIRMINGHAM. JOHN M. LAWRENCE, UNIVERSITY OF SOUTH FLORIDA.

In sea urchins, feed intake is presumed to proceed until one or more requirements are met and satiation occurs. Feed intake targets may be a regulated on a daily basis, but mechanism(s) and plasticity of response that regulates food intake is unclear. Adult *L. variegatus* (25-35mm) were fed to excess an agar-based formulated diet that varied in both food and nutrient density. Each day for 11 days, agar cubes containing a formulated diet were weighed and placed in mesh cages housing a single individual. After 24 hours, each cube was removed, rinsed, blotted dry and weighed to determine the amount consumed daily per individual. Patterns and variability in feed intake over the experimental period were analyzed. Within and between individual variation was demonstrated in sea urchin feeding, with within individual variation comprising a greater portion of the total variability. This would suggest that day to day variation in feed intake in a single individual contributes more variation overall than when comparing variation among multiple individuals. For most treatment groups day to day patterns of feed intake were not changing from beginning to end of the experimental period. However, certain treatment groups exhibited patterns of feed intake that increased over the experimental period. These same groups were predicted by Akaike Information Criterion (AIC) statistical analysis to be greatly impacted by an effect of time (day). This variability illustrates the complexity of the factors regulating feed intake and satiety in the sea urchin despite the lack of an organized brain structure.

SINGLE CELL PROTEINS AS FISH MEAL REPLACEMENT IN ZEBRAFISH DIETS. *STEPHEN WATTS*, UNIVERSITY OF ALABAMA AT BIRMINGHAM. ROBERT BARRY,SOPHIE BRU,YUAN YUAN,LAUREN FOWLER,MICKIE POWELL AND ADDISON LAWRENCE, UAB.

Quality fish meal products are found in all commercially-formulated diets for most fish species, including zebrafish. Fish meal can sometimes be replaced in part by other animal or plant proteins; however, results are mixed. We are currently examining single cell protein (SCP) as candidates for use in animal feeds. We have replaced fish meal hydrolysate (FPH) with a commercial source of SCP from bacteria (MRD-Pro) or yeast (DY-Pro) provided by Meridian Biotech. Five experimental diets were prepared, including a control which contained 25% fish protein hydrolysate (FPH) by weight (as fed). Additionally, MRD-Pro and DY-Pro each replaced 50 or 100% of the protein provided by the FPH. Zebrafish larvae were reared on live diets until day 35, and then fed experimental diets for the next 8 weeks. Zebrafish received a daily ration split into two feedings equal to 10% of wet body weight, adjusted every two weeks. Fish were randomly assigned to 2.8-L tanks (n=14 fish per tank, n=8 tanks per diet treatment) for 8 weeks. Survival was higher than 99% for each treatment. Fish in all diet treatments showed weight gain. In males, highest weight gain was seen in fish fed MRD-Pro (317 mg), followed by DY-Pro (287 mg) and the FPH control (278 mg). These data indicate that SCPs show great promise to replace all or part of a fish meal product on a protein equivalent replacement basis and require further evaluation in supporting health and reproduction as a complete fish meal replacement.

THE REGULATION OF AN INTRACELLULAR CA2+ SIGNAL IN MOLTING GLANDS OF THE BLUE CRAB, CALLINECTES SAPIDUS, AND ITS ROLE IN ECDYSTEROID PRODUCTION. *MEGAN ROEGNER* AND WATSON R. DOUGLAS, UNIVERSITY OF ALABAMA AT BIRMINGHAM. HSIANG-YIN CHEN, NATIONAL TAIWAN OCEAN UNIVERSITY. ROBERT ROER, UNC WILMINGTON.

In crustaceans, cycles of growth and molting are triggered by cholesterol-derived molting hormones (ecdysteroids) released from paired endocrine glands (the Y-organs) located in the anterior cephalothorax. During much of the molting cycle, the levels of ecdysteroids in hemolymph are kept low by the action of a peptide molt-inhibiting hormone (MIH), produced in the eyestalks. While the removal of MIH suppression during pre-molt coincides with increased ecdysteroidogenesis, there is evidence that an additional positive stimulus in the form of an intracellular Ca2+ signal also plays a significant role. To better understand Ca2+ signaling in Y-organs, our lab investigated the proteins involved in regulation of intracellular Ca2+. We used a PCR-based cloning strategy (RT-PCR followed by 3'- and 5'-RACE) to clone a full-length cDNA encoding a putative sarco/endoplasmic reticulum Ca2+ ATPase (SERCA) protein from the Y-organs of the blue crab (*Callinectes sapidus*). SERCA transcript levels in Y-organs were then determined using quantitative PCR. Transcript abundance was assessed throughout a molting cycle, and compared to hemolymph ecdysteroid levels. The results are consistent with the hypothesis that stage-specific changes in SERCA expression occur in response to increased intracellular Ca2+, but are not a causative factor in promoting ecdysteroidogenesis. In order to identify the stimulus that drives the increase in intracellular Ca2+ we have pursued transcriptome analysis of C. sapidus Y-organs in search of differential gene expression patterns during times of high ecdysteroidogenesis. This work will elucidate the intracellular signaling pathways involved in increased ecdysteroid production and lead to a greater understanding of molting regulation.

URBAN TURTLE PROJECT. *ANDREW COLEMAN*, BIRMINGHAM AUDUBON SOCIETY.

Alabama is recognized as being home to the most species of turtles in the United States, mostly due to abundance of aquatic species. However, many of the state’s waterways flow through urban areas, and development and habitat degradation can negatively impact many of these populations. The Urban Turtle Project will be initiated in May 2018 and will be a long-term study to document urban populations of turtles around the Birmingham metro area. The initial study period will occur over a 3-day period in May 2018. Numerous field sites along several urban waterways (Cahaba River, Shades Creek, Village Creek, Valley Creek, and Five Mile Creek) will be sampled. Sampling will be lead by experienced field scientists, who will be assisted by trained citizen scientists. A suite of morphological measurements will be collected from each captured turtle and each turtle will be tagged for future identification. These data will elucidate relative abundances of various aquatic species at these sites, and future data will enable questions to be answered regarding health, survival, longevity, etc. This project also serves as an important outreach tool. The public will be invited to several of the sites to view the field work being executed. Their presence along with the assistance from the citizen scientists will provide education opportunities about the Alabama’s chelonian diversity and potential threats to their future survival.

INFLAMMATORY PAIN CAUSES MALE ZEBRAFISH TO SEEK COOLER WATER. *CHRIS TAYLOR*, UNIVERSITY OF ALABAMA AT BIRMINGHAM. WATTS STEPHEN AND SORGE ROBERT, UAB.

Previous studies in our lab suggest that the zebrafish *Danio rerio* is a good candidate as a high-throughput, inexpensive model for testing chronic pain treatments. However, reports that claim zebrafish suffer and feel pain like mammalian models have been met with skepticism. Our data suggests that zebrafish exhibit dose dependent behavioral changes in response to nociceptive stimuli. These responses are also affected by sex and nutritional history. However, these behaviors could be indicative of an acute nociceptive reflex rather than pain and suffering. Behavioral responses which are prolonged beyond the initial stimulus and behaviors which are adopted to alleviate pain are evidence of suffering. In mammals inflammatory pain is exacerbated by increasing temperature and alleviated by decreasing temperature of the inflamed tissue. In this study zebrafish were injected in the lips with 5% acetic acid solution to initiate an inflammatory response. These zebrafish were then placed in a novel fish tank which maintained a consistent temperature gradient across its length. Male zebrafish positioned themselves in cooler temperatures when they were injected with acetic acid as opposed to the control. We suggest this behavior is a purposeful decision by the fish to alleviate its suffering. As zebrafish become more common in preclinical research laboratories, it is critical to examine means to reduce pain following acute procedures. It appears that a decrease in system water temperature following such a procedure will alleviate suffering from an inflammatory stimulus.

ARABIDOPSIS BAX INHIBITOR 1 (ATBI-1) INTERACTS WITH ATIRE1A TO EXECUTE PRO-SURVIVAL FUNCTION. *XIAOYU LIU* AND KAROLINA MUKHTAR, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

The stress relief mechanism UPR can be initiated by ER stress sensor IRE1 upon the accumulation of misfolded or unfolded proteins. The output of UPR alleviates the ER stress; and if stress persists, cell will undergo cell death. However, the AtIRE1-dependent mechanisms that regulate bacterial-pathogen-triggered cell fate decision remains unclear. Here, we demonstrated that AtIRE1a interacts with a highly conserved cell death suppressor AtBI-1. The interaction of AtIRE1a and AtBI-1 appears to be tightly regulated by the phosphorylation status of two amino acids. The interaction of AtBI-1 with AtIRE1a directly promotes the AtIRE1a-dependent AtbZIP60 mRNA splicing in vitro. Our data also positions important roles of AtIRE1-AtbZIP60 and AtBI-1 in cell fate decision upon avirulent bacterial pathogen attack.

SING ANTIOXIDANT DRUG TEMPOL TO ENHANCE METABOLIC MODIFICATIONS OF GUT MICROBIOTA IN MICE. *DARNELLA COLE*, UNIVERSITY OF WEST ALABAMA. JINGWEI CAI,ROBERT NICHOLS AND DR. ANDREW PATTERSON, PENNSYLVANIA STATE UNIVERSITY.

Obesity rates have drastically increased in the past decade. About 72 million Americans are obese. Nonalcoholic fatty liver disease (NAFLD) is also a worldwide problem. NAFLD has been estimated to have affected 20 to 30 percent of people worldwide. This disease is directly related to obesity and excessive alcohol abuse. Tempol, an antioxidant drug, has been tested and demonstrated to prevent and decrease obesity in mice. Tempol prevents and decreases obesity in mice due to its ability to alter gut microbiota; the drug has also been tested and confirmed to kill the bacteria *lactobacillus*. Previous studies have not clearly determined exactly what is the relationship between how the drug modulates weight loss in the gut microbiome of mice and why it is happening, in conjunction with how bacterium in the mice's body is bio-transforming the drug into other substances, which, as a result, glucuronide and glucoside conjugates of the drug are being produced when injected into the mice. This study focuses on bacteria as it predominates in the gut of animals/humans to examine and determine how and why these transformations are being made, in conjunction with, underlining the relationship of how tempol is killing bacteria in mice. An anaerobic chamber is used as fecal samples are being prepared. Cell activity and cell damage of the fecal samples is determined using Flow Cytometry. Metabolomics data will include two methods: analyzing the samples via Nuclear Magnetic Spectroscopy (NMR) and a Principal Component Analysis (PCA). An examination of findings shows that there are three primary metabolites found in mice, which are Bacterial Acetate, Bacterial Propionate, and Bacterial Butyrate. For each primary metabolite, results show that with the control, the metabolism capability was high but when given increased amounts of tempol, the metabolism capability decreased, therefore, fermentation capability of the metabolites were low. The negative control, pH4, had the lowest metabolic activity, due to it making the cells inactive. In conclusion, now that methods of Flow Cytometry and Metabolomics have been optimized and the physiology and metabolic orders of the bacteria are known; the next approach would be testing several drugs to figure out if the drug has a primary or secondary effect on the bacteria. A primary effect will mean that the drug is directly effecting the microbes. Secondary effects will be expected if no results show from the primary effects, meaning the drug effects the host (mice) and the mice does something to the bacteria.

BIOLOGICAL SCIENCES POSTER ABSTRACTS

PHYLOGENETIC AND MORPHOLOGICAL ANALYSES OF THE EVERGLADES PYGMY SUNFISH (ELASSOMA EVERGLADEI). *ABBY HAWKINS*, JOHN LARRIMORE, JOSEPH SAMMONS, MICHAEL SANDEL AND KAYLA FAST, UNIVERSITY OF WEST ALABAMA.

Pygmy sunfishes are a group of morphologically distinctive, but poorly understood freshwater fishes of the southeastern United States. We investigated the taxonomic divisions within the species *Elassoma evergladei* using phylogenetic and morphological data. *E. evergladei*, known as the Everglades pygmy sunfish is commonly found in the Everglades and Atlantic coastal plain habitats. Environmental changes have recently led to concern within the fish's range because of fluctuations in population density and habitat loss. Recent changes could be leading to hybridization patterns with *Elassoma zonatum*, a closely related species within its range of the Atlantic coastal plain. Furthermore, geographical isolation north of the Everglades may be a mechanism driving diversity. We have collected representatives of the Everglades Pygmy Sunfish from all major watersheds and physiographic provinces within the species range. Morphological data include the number of dorsal spines, dorsal fin rays, caudal fin rays, pectoral fin rays, lateral series scales, and head scales. In conjunction, we have constructed a phylogenetic tree using mitochondrial data. This novel phylogeny revealed two well-supported and geographically restricted clades (North Carolina and Alabama). Morphometric analyses revealed wide variation in body shape, but no significant differences among the three groups. Head scale count distinguished populations from Alabama and extreme west Florida from all other populations. Morphological and molecular data provide evidence for a monophyletic clade within the range of *E. evergladei*. We propose a new species of Pygmy Sunfish, which is geographically restricted to the Mobile and Perdido River drainages of southern Alabama and western Florida.

PROSPECTING FOR ACTINOBACTERIOPHAGE PRESENCE IN HUMAN BREAST MILK AND NEONATE CHYLE. *MITCHELL DISHAROON*, MICHAEL SANDEL AND KAYLA FAST, UNIVERSITY OF WEST ALABAMA.

Breast milk is composed of crucial bacteria that aid in the development of a newborn's immune system. These bacteria are the building blocks of their intestinal flora. Babies fed strictly breast milk are healthier than babies that are fed formula, but the mechanisms for this are unknown. We hypothesize that bacteriophages from the breast milk are altering the microbiome in the gut that is beneficial to the baby. To test this hypothesis, we designed PCR primers for bacteriophages that infect *Staphylococcus aureus*. The genus Staphylococcus is one of the main bacterial components of breast milk, but S. aureus is a known human pathogen and a likely target of symbiotic bacteriophages. Primer design required three steps; 1) we ran DNA sequences through Bioedit to find the conserved regions across five S. aureus genomes, 2) we used the Primer3 program to design primers using the conserved regions, and 3) we used BLAST to identify putative gene functions. We found four viable primer sets corresponding to partial sequences of the dUTPase gene (x2), a repressor gene and a hypothetical gene with unknown function. We are using a custom PCR assay of S. aureus phage in milk and chyle. Bacteriophages recovered from this project could be used as a probiotic to prevent S. aureus infection in preterm neonates.

BIOINFORMATIC RESEARCH INTO PHAGE HOST SPECIFICITY. *RAKIM ALI*, KAYLA FAST AND MICHAEL SANDEL, UNIVERSITY OF WEST ALABAMA.

Bacteriophages are viruses that infect bacteria and are the most numerous biological entities on the planet, vastly outnumbering every form of life on earth. As pathogens of bacteria, bacteriophages are a driving force behind bacterial evolution, thus they are an extremely important part of our planet's ecosystem. In recent years, research into host-phage interaction has shed light on the mechanisms involved within phage infection and the phage lifecycle as a whole. However, there is still much that remains a mystery, such as the mechanisms responsible for host specificity among phages. I conducted an exploratory comparative genomics analysis of Actinobacteriophages to identify factors related to host specificity. Using *Gordonia* phages as a point of focus, a bioinformatic approach into host range specificity has uncovered a possible link between the Lysin A protein and host range. The Lysin A protein of *Gordonia* phages appear to be related through a known protein domain, the LGFP super family. This domain is known to alter interaction with mycolic acids, which are crucial for survival among members of *Gordonia* and closely related members of Corynebacteriales. Preliminary research points to the LGFP domain of Lysin A as a crucial piece in the puzzle responsible for host range specificity among bacteriophages.

IMPACTS OF SEVERE DROUGHT ON REMNANT MONTANE LONGLEAF PINE COMMUNITIES AT OAK MOUNTAIN STATE PARK. *MALIA FINCHER*, SAMFORD UNIVERSITY. EMILY REPAS, ELMIRA COLLEGE.

Longleaf pine is a fire dependent species that once dominated the forests of the southeastern portion of the United States. Frequent fires, both natural and manmade, maintain the longleaf pine community structure and composition, while fire suppression results in increasing dominance by hardwoods and other pine species in many areas. Stressful habitats and stress events, such as intense drought, may allow longleaf pine to persist and maintain dominance in fire suppressed communities. We examined ecological differences between ridge and foothill habitats within Oak Mountain State Park and how these differences affected the survival of remnant longleaf pines and competing hardwoods and other pine species, in the summer after the severe drought of 2016. Ecological factors included slope, soil depth, canopy cover/light availability, soil nutrient availability, and temperature. The impacts of stress, as measured by these ecological variables in the year following a severe drought, were determined by comparing the percent mortality of longleaf pine, other pine species, and hardwood species across habitats varying in measures of potential stress. We found that while environmental conditions vary between the ridge and foothills, with greater potential for stress on the ridge, this does not correspond to mortality. Drivers of drought mortality may vary on a very fine spatial scale, reflecting the microclimate of individual trees.

CATALSE PRODUCTION AND FUTURE MUTAGENESIS OF V. FISCHERI. *JULIAN JACKSON*, RACHEL ROCK AND JEFFREY MORRIS, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

Oxygen is an essential element that mainly comes from a micro alga in the ocean called *Prochlorococcus*. *Prochlorococcus* is responsible for producing over 70% of the oxygen that we breathe in every day, but it is also is dying off due to the excess carbon emission that exist in our air. Excess carbon that is responsible for climate change also causes oxidative damage to *Prochlorococcus*. Oxidative damage occurs when alga cannot protect itself because it lacks the enzyme catalase which causes the reduction of hydrogen peroxide, the main culprit of cause of oxidative damage. *Vibrio* fischeri is a species of symbiotic bacteria that help protect *Prochlorococcus* by producing catalase. These bacteria are virulent pathogens that live within the Bobtail Squid but also processes the ability to produce catalase both intracellularly and extracellularly. Former explorations suggested that this pathogen could only be produced intracellularly, but current research challenges this notion. In our experiments, four strains of *Vibrio* were grown in a medium and centrifuged. The supernatant was then filtered to make sure no other nutrients could be in the media. Hydrogen Peroxide was added to the supernatant and bubbles were formed proving that *Vibrio* could excrete catalase extracellularly. If a mutant gene could be found through mutagenesis, then there is a bright future for *Prochlorococcus,* as it would no longer have to depend on symbionts to protect itself from hydrogen peroxide, and in turn provide the environment more oxygen.

ISOLATION, PURIFICATION, MODELING, AND BINDING SITE ANALYSIS OF THE SALMONELLA BACTERIOPHAGE ε34 REPRESSOR FOR SUBSEQUENT CRYSTALLIZATION AND STRUCTURE-FUNCTION STUDIES. *RICHARDRIA GOODSON*, DOBA JACKSON, MILAN BRANCH, MEAGAN CLAUSELL AND LOGAN GILDEA, HUNTINGDON COLLEGE. ROBERT VILLAFANE, ALABAMA STATE UNIVERSITY.

The bacteriophage ε34 is one of many phages that infect the bacteria *Salmonella* which is the main cause of salmonellosis (food poisoning). The bacteriophage ε34 encodes a protein called the cI repressor that is like other phage repressors. It has a C-terminal protease domain which is about 80% identical to the repressors of phage λ (which infects *E. coli*), but its DNA binding N-terminal portion is only about 50% identical to its closest known relatives in phages λ, and Lex A. This means that the ε34 repressor may have the same pathway for inactivation as phage λ, but probably has a different operator binding specificity due to lower sequence homology of its DNA-binding domain. The N-terminal DNA-binding domain is homologous to the Helix-Turn-Helix family of DNA-binding domains.

The main goal of this project was to initiate a structure-function study on the repressor protein of phage ε34. The ε34 Bacteriophage DNA was first isolated and purified. The gene encoding the bacteriophage ε34 repressor was amplified by PCR and cloned into a pET11a vector. The cI repressor, was overexpressed and purified by immobilized metal affinity chromatography and ion exchange chromatography. We also generated a homology model of this protein using the bacteriophage λ as a template in the SWISS-MODEL homology modelling server. Our models predict a unique structure for the N-terminal Helix-Turn-Helix domain. Finally, we have identified several potential binding sites upstream of the cI gene on the Bacteriophage λ DNA. We will present new models for the binding modes for the cI repressor/DNA complex. Crystallization trials are currently in progress. This project was done as a collaborative venture between two laboratories, Huntingdon College (Dr. Doba Jackson) and Alabama State University (laboratory of Dr. Robert Villafane). This project is in line with Dr. Robert Villafane's research into the Genomic analysis of bacteriophage ε34 of *Salmonella* enteric serovar Anatum.

DIETARY SATURATED FAT SOURCE DIFFERENTIALLY AFFECTS WEIGHT GAIN IN ZEBRAFISH. ***AUDREY D. POWERS***, **L. ADELE FOWLER, R. JEFF BARRY, MICHAEL B. WILLIAMS, LOUIS A. D'ABRAMO AND STEPHEN A. WATTS, UNIVERSITY OF ALABAMA AT BIRMINGHAM.**

Current guidelines for saturated fat intake lack the support of conclusive research; therefore, the effects of saturated fat on human health remain controversial. Defining the effects of specific saturated fat sources will help establish more accurate nutritional guidelines. Zebrafish share many of the same pathophysiological pathways as humans and have been established as a powerful model for lipid metabolism studies to provide insights into the effects of dietary lipid on adiposity and nutrient allocation. The goal of the present study was to assess the effects of three different saturated fat sources (milk fat, palm oil, and coconut oil) on weight gain and growth in adult zebrafish. Each saturated fat source had one low- and two high-fat diets. A low fat and high fat reference diet were also included in the study as control diets, resulting in 11 total treatments. Zebrafish larvae were raised on live feeds until 28 days, and then fed a maintenance diet until they reached 3 months of age. Zebrafish were then fed the experimental diets for an eight-week period. At the termination of the experimental phase, each treatment was evaluated based on body weight and length. For all saturated fats the largest fish were found in those fed low fat diets (and highest protein: energy rations). Smallest fish were found in those fed the high fat coconut oil diets. We hypothesized that sources of saturated fat affect nutrient allocation. Our data support this hypothesis and indicate that current nutritional guidelines should be re-evaluated.

RARE EARTH METAL OXIDES: SYNTHESIS, CHARACTERIZATION, AND ANTIMICROBIAL ACTIVITY. ***AFEF JANEN***, **MOHAN AGGARWAL AND KADIATOU KEITA, ALABAMA A&M UNIVERSITY.**

KUZHIVELIL JOSEPH ARUN, SREE KERALA VARMA COLLEGE, INDIA.

In this work, we report the synthesis of silver oxide (AgO), lanthanum oxide (LaO), samarium oxide (SmO), and neodymium oxide (NdO) nanoparticles that was carried out by the hydrothermal method. The prepared nanoparticles were characterized using X-ray diffraction (XRD), scanning electron microscopy (SEM), energy dispersive X-ray spectroscopy (EDS), transmission electron microscopy (TEM), Fourier transform infrared spectroscopy (FTIR), and ultraviolet visible spectroscopy (UV-vis spectroscopy). XRD analyses confirmed the crystalline structure and size distribution of SmO nanoparticles and their average particle size was 15.16 nm, LaO nanoparticles results were 30-40 nm in width and 150-200 nm in length, and NdO nanoparticles average size was 30 nm. In addition, the bioactivity of AgO, LaO, SmO, and NdO nanoparticles was assessed against *Escherichia coli* and *Pseudomonas aeruginosa* (Gram-negative organisms); *Streptococcus pyogenes, Listeria monocytogenes,* and *Bacillus subtilis* (Gram-positive organisms), and *Candida albicans* by using Bioscreen C which is a Growth Curve Analyzer. The results showed that at concentrations of 10 and 25 µl, AgO nanoparticles had the highest inhibiting effect on *Pseudomonas aeruginosa, Listeria monocytogenes*, and *Candida albicans* compared to LaO, SmO, and NdO nanoparticles. At 25 µl, LaO nanoparticles had a higher antibacterial effect on Listeria and at 10 µl on Pseudomonas and Candida compared to SmO, and NdO nanoparticles. Therefore, our results suggest that these nanoparticles have antimicrobial effects.

A RAPID METHOD FOR THE IDENTIFICATION OF ALABAMA CUSCUTA USING PCR-RFLP. *DAVID JOHNSON*, SAMFORD UNIVERSITY. JAVIER CARRILLO-CORTEZ, HUMBOLDT STATE UNIVERSITY.

Members of the genus *Cuscuta* are parasitic plants that feed on host plants, limiting growth and lifespan. Individual species identification of *Cuscuta* is difficult. The aim of our project was to develop a rapid method for identifying the species of *Cuscuta* found in North-Central Alabama using the polymerase chain (PCR) and restriction fragment length polymorphisms (RFLP). We developed a protocol using the a trnL/trnF primer sets followed by Mbol1 restriction enzyme digestion.

EFFECTS OF CHEMICAL DISPERSANT (COREXIT 9500A) ON THE STRUCTURE AND ION TRANSPORT FUNCTION OF BLUE CRAB (CALLINECTES SAPIDUS) GILLS. *AMANDA WEINER*, MEGAN ROEGNER AND R. DOUGLAS WATSON, UNIVERSITY OF ALABAMA AT BIRMINGHAM.

Chemical dispersants are widely used in the remediation of spilled oil. When applied to an oil spill, such dispersants move to the oil/water interface and break the oil into small micelles, facilitating its dispersion through the water column. The several life cycle stages and broad distribution of blue crabs (*Callinectes sapidus*) increases the likelihood of their exposure to chemical dispersants used in remediation of spilled oil. Crustacean gills have multiple functions, including respiration and ion transport. Despite the economic and ecological significance of blue crabs in the western Atlantic and Gulf of Mexico, the effects of chemical dispersant on the structure and function of blue crab gills have not been adequately investigated. In studies reported here, adult blue crabs were exposed to the chemical dispersant Corexit 9500A (60-125ppm) under static conditions in glass aquaria containing artificial sea water. Effects of dispersant on gill structure were assessed using conventional histological methods. Preliminary results indicate exposure to Corexit 9500A resulted in an increase in gill epithelial edema. Effects of Corexit 9500A on gill ion transport function were assessed by quantifying the abundance in gills of transcripts encoding two Ca2+ transport proteins, plasma membrane Ca2+ ATPase (PMCA) and sarco/endoplasmic reticulum Ca2+ ATPase (SERCA). Results of quantitative PCR showed PMCA and SERCA transcript abundance was significantly lower in gills of dispersant-exposed crabs than in gills of control crabs. The combined results are consistent with the hypothesis that exposure of blue crabs to Corexit 9500A significantly impacts the structure and ion transport function of gill tissue.

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THE EFFECT OF α2A ADRENERGIC RECEPTOR ON ALZHEIMER'S DISEASE (AD) PATHOLOGY IN AN AD MOUSE MODEL. *ITZEL MENDOZA*, SAMFORD UNIVERSITY. MARY GANNON AND QIN WANG, DEPARTMENT OF CELL, DEVELOPMENTAL, & INTEGRATIVE BIOLOGY. YIN PING AND KAI JIAO, DEPARTMENT OF GENETICS. UZMA NUR, SUMMER SCIENCE INSTITUTE: STUDENT RESEARCH INTERNSHIP PROGRAM.

Alzheimer's Disease (AD) is a neurological disease that affects the patient's motor skills and cognitive functions. Unfortunately, AD cannot be prevented, cured, or slowed. Two neuropathological hallmarks of AD are excess deposition of amyloid β (Aβ) peptides, generated from the processing of amyloid precursor protein (APP), and hyperphosphorylation of the tau protein, which creates tau tangles. Research from our lab has shown that activation of the α2A adrenergic receptor (α2AAR) promotes β-secretase cleavage of APP, thus increasing Aβ generation. Further, we have found that blocking the α2AAR improves several of AD's cognitive symptoms and decreases Aβ plaque load in the brain of AD model mice. In this study, treatment of AD mice with idazoxan, an antagonist of the α2AAR, even when begun after profound Aβ plaque load, improved AD pathology and reduced APP plaque load. In conclusion, idazoxan is able to reduce AD pathology in an AD mouse model, even when treatment is not begun until after AD pathology is already present in the mice.

GONAD GROWTH IN SEA URCHIN LYTECHINUS VARIEGATUS EXPOSED TO VIBRIO NATRIEGENS. *AMY SEYMOUR* AND UDUAK AFANGIDEH, FAULKNER UNIVERSITY.

A four-week rearing trial was carried out on the sea urchin species *Lytechinus variegatus* in order to determine the relationship between microbes and nutrient uptake. *Lytechinus variegatus* is commonly known as the green or variegated sea urchin. This species can be found in the warm waters of the Western Atlantic Ocean. Although L. variegatus has no commercial importance, sea urchin gonads are known as a delicacy in Japan and other countries (Norris 2008). The gonads of various species of sea urchins are enjoyed in many parts of Europe, especially in France and southern Italy (Fabbrocini and D'Adamo 2010). The roles of various microbial taxa in both the digestive health of the host, as well as the ecological importance of those bacteria to the host's community has become a large focus in research (Hakim et al. 2015) with suggestions that microbial digestive support could potentially increase gonad size through nutrient uptake. The objective of this research was therefore to investigate the relationship between the microbial community and nutrient intake as it affects gonad growth in L. variegatus. The gram-negative marine bacterium *Vibrio natriegens* was administered to the experimental group and the effect on survival rate and gonad size were observed. Although the initial weight was directly correlated with the initial test diameters of the sea urchins ($r = 0.99$), the final weights and diameters were not highly correlated with a correlation coefficient of ($r = 0.37$). There was an increase in mortality rate and the various factors that contributed to the high mortality rate was also investigated.

SOUTHERN PORCINI: A PUTATIVE NEW VARIETY IN THE GENUS BOLETUS. *SAHAR DELGHANDI* AND JUAN L MATA, UNIVERSITY OF SOUTH ALABAMA.

Porcini is the name given to edible mushrooms in the genus *Boletus* whose type species is *B. edulis*. Besides their economic importance porcini are vital symbionts with plants. Porcini are distinctive in that they exhibit a tubed hymenium, instead of gills, with white pores becoming yellowish olive in age. Their stipes develop distinctive apical reticulations and their caps display a broad range of brown colors that don't change when cut. *B. variipes* is one of several look-alikes reported in the Southeastern United States that is most similar to specimens observed in the Gulf Coast of the United States. The goal of this study was to characterize and determine species identity of commonly found edible porcini in Mobile County which exhibit great variation in size, shape, and colors. Collections were first morphologically described. Results indicate we have *B. variipes* based on overall mushroom appearance but spore range is more akin to *B. atkinsonii*. DNA from 17 mushrooms was amplified to perform a restriction enzyme digest. Results indicate we have only one species. A handful of DNAs were selected for sequencing and blast-searching for matches in GenBank. Results suggest we have a taxon akin to *B. variipes* with only 85-92% identity based on the ITS region. In the phylogenetic tree our sequences come out as a distinct clade suggesting a unique and divergent variety among *B. edulis*, *B. variipes*, and other porcini. We recognize additional specimens from a broader geographical spectrum need to be collected and examined to corroborate our findings.

A PRELIMINARY INVESTIGATION OF THE VASCULAR FLORA OF GENEVA COUNTY, ALABAMA. *CAMERON BYRD* AND ALVIN DIAMOND, TROY UNIVERSITY.

A survey of the vascular flora of the Geneva County Alabama was undertaken in August 2016. Geneva County has an area of 1,500 km2 and lies in southeastern Alabama approximately 77 km north of the Gulf of Mexico. It lies entirely within the Dougherty Plain Ecoregion, and is drained by the Pea-Choctawhatchee River system. Major habitats found within the county include mesic hardwood forests, fire managed Longleaf Pine forests, farm land, river banks, ephemeral ponds and cypress swamps. As of the end of 2017, 648 species of vascular plants had been collected during this study. Two hundred twelve of these species (32.72%) had not been previously reported from Geneva County. Twenty-six species (4.01%) documented during the study appear on the Alabama Natural Heritage Program's list of rare, threatened, or endangered plants of Alabama. All voucher specimens will be deposited in the Troy University Herbarium (TROY), with duplicates to the University of West Alabama Herbarium (UWAL).

INVESTIGATING HISTONE DEACETYLATION DURING CHORION GENE AMPLIFICATION IN DROSOPHILA OOGENESIS. *ERIN BROWN* AND KRISTOPHER MCCONNELL, JUDSON COLLEGE.

During oogenesis of the fruit fly *Drosophila melanogaster*, the oocyte is surrounded by a population of somatic follicle cells, which are responsible for eggshell assembly. These follicle cells undergo characteristic transitions in the cell cycle during egg development. At oogenesis stage 10B, follicle cells exit the cell cycle and begin amplification, a process of DNA re-replication. Amplification serves to increase the copy number of the chorion genes, and is necessary for eggshell synthesis. The histones at the amplifying origins of DNA replication are hyperacetylated. This hyperacetylation is removed after amplification, prior to transcription of the chorion genes. Typically, histone acetylation is associated with active transcription of genes. Thus, removal of acetylation prior to transcription is unusual. We propose that acetylation is replaced with an additional activating histone modification. One candidate for this additional modification is crotonylation, which is also associated with active transcription. Here we use fluorescence microscopy to test for the presence of histone crotonylation at amplification origins. We further propose that if the removal of acetylation is necessary for chorion gene transcription, then a histone deacetylase (HDAC) must be required. We use Flp:FRT recombination to express dsRNA constructs against candidate HDACs in clonal patches of follicle cells, in order to knockdown these candidate HDACs by RNA interference. We then tested these clonal patches for disruptions in acetylation and amplification. Studying this developmental transition can provide key insights into the regulation of DNA replication – an important cellular process often at the center of focus in cancer research.

EFFECTS OF HEAT SHOCK AND GAL4 ON DROSOPHILA OOGENESIS. *KATIE OWENS* AND KRISTOPHER MCCONNELL, JUDSON COLLEGE.

Oogenesis in the fruit fly *Drosophila melanogaster* is an ideal model for studying cellular processes such as DNA replication and cell death. Investigations into the molecular pathways involved in these processes have informed our understanding of cancer and the disruptions that lead to cancer. A common tool used by fruit fly geneticists is the *Gal4:UAS* system that allows researchers to express transgenes using the transcriptional activator Gal4. This tool is widely used because Gal4 generally has no detrimental effects on normal fruit fly biological processes. However, it has been shown that Gal4 expression disrupts oogenesis when combined with heat shock. These disruptions include increased cell death, altered patterns of DNA replication, and an inability to lay eggs. We set out to characterize the defects in Drosophila oogenesis by determining the extent and timing of each defect. In addition, we also used various transgenic constructs to express inhibitors of cell death in an attempt to rescue these defects.

MUSKOGEE MEDICINE: NATIVE PLANTS COMMONLY USED IN MUSKOGEE CEREMONIES AND HEALING. *ALVIN DIAMOND* AND ROBERT PULLEN, TROY UNIVERSITY.

Alabama is home to over 4,100 species of plants, many of which were used by indigenous peoples and early settlers for a variety of purposes. Ceremonial leaders and medical practitioners in the Muskogee/Creek Nation continue to use many of these same plants in the pursuit of community wholeness and individual healing. This report is based upon fieldwork with three Muskogee plant specialists and review of relevant literature that describes the medical practices of the contemporary Muskogee Heles Haya (Medicine Makers). It identifies 12 commonly used medicine plants, gives their Muskogee name and how they are used in ceremonies or in healing work. Plants were collected during fieldwork at the Tuckabatchee site, one of four mother towns of the Muscogee Creek Confederacy, and capital of the Upper Creeks. Voucher specimens were deposited in the Troy University Herbarium (TROY).

LIMNODRILUS SP. LIVING IN TOXIC HYDROGEN SULFIDE. *SHELBY LAUZON,* JUDSON COLLEGE. DAVID JOHNSON, SAMFORD UNIVERSITY.

Very few Annelid species live in Sulfur-rich environments. Little is known about the physiology of these few organisms that allows them to survive in toxic environments. An Annelid species belonging to the genus Limnodrilus was discovered in 2016 thriving in a highly toxic sulfur spring. The aim of our research was to identify the main mechanisms by which the *Limnodrilus sp.* detoxify themselves of hydrogen sulfide. Our data suggests that the *Limnodrilus sp.* exhibits two detoxification mechanisms via a sulfur dioxygenase enzyme and a sulfur-oxidizing bacterial symbiont. We used primers from other sulfur-rich environment annelids and the 16S rDNA to find these mechanisms. Our study will help inform how these mechanisms play a major role in the longevity of this organism.

DIFFERENCES IN FREQUENCY AND INTENSITY OF CANOPY DISTURBANCE ACROSS THE RANGE OF EASTERN HEMLOCK. ***ISAIAH BYRD*, UNIVERSITY OF WEST ALABAMA. CAROLYN COPENHEAVER, VIRGINIA TECH. KETIA SHUMAKER, THE UNIVERSITY OF WEST ALABAMA.**

Eastern hemlock (*Tsuga canadensis* (L.) Carriere) is a long-lived conifer in old-growth forests in eastern North America. This tree can be a valuable record of historical disturbance. In this study, tree-ring chronologies from eight eastern hemlock stands were used to determine differences in canopy disturbances using the radial-growth averaging criteria. We hypothesized that across the range of eastern hemlock, canopy disturbance would be similar in intensity and frequency. We rejected our hypothesis because this study showed a diversity of disturbance patterns across stands. This heterogeneity is likely due to extreme weather events, logging, insects or pathogens. Eastern hemlock is a foundational species that provides habitat for wildlife, aquatic species, and later successional plants and our results imply old-growth forests are highly diverse which makes conservation efforts difficult.