STEM
Posters at the Capitol

February 14, 2018

"It is essential, if we want to continue to reap the benefits of science, to commit as a nation to preparing more young people for extraordinary careers in science."

—Carol W. Greider, 2009 Nobel laureate in physiology & medicine

Highlights

- **Over 110 students**
- **From 12 Arkansas colleges and universities**
- **Presenting 70 different posters of original work**
- **Encompassing all aspects of natural science and math**


STATE
ARKANSAS STATE
UNIVERSITY


1871
UNIVERSITY OF
ARKANSAS


PHILANDER
SMITH COLLEGE
EST 1877


1876
HENDRIX


OUACHITA
BAPTIST UNIVERSITY


ARKANSAS
TECH
UNIVERSITY


UAM
The University of Arkansas at Monticello
Monticello • Crossett • McGehee


UALR
University of Arkansas
at Little Rock


1890
HENDERSON
STATE UNIVERSITY


LYON
COLLEGE


UNIVERSITY OF
CENTRAL
ARKANSAS


UNIVERSITY
of ARKANSAS
AT PINE BLUFF
1873

STEM Posters at the capitol

35 Posters Presented from 11 am—12 pm

11 am Poster number……..page for abstract

STEM Posters at the capitol

35 Posters Presented from 12 pm—1 pm

12 pm Poster number……..page for abstract

STEM Posters at the capitol

Student presenter (school) …..page with abstract

STEM Posters at the capitol

Student presenter (school) …..page with abstract

presenting
12 pm– 1 pm

Hometown: Searcy, AR

Effect of Elastic Bending Energy on protein-DNA interactions

Jack Freeland and Yong Wang

Department of Physics, University of Arkansas, Fayetteville, AR

Affecting millions of people around the world, heart disease, cancer, diabetes, and hemophilia are some of the largest killers and most frequently diagnosed cases in humans. These four diseases along with many more all share one thing in common; their origins of spawn are centered around a genomic error. There are specific proteins in the body that are responsible for making sure that such mistakes are recognized and fixed. It is when said proteins make a mistake and allow an unrepaired nucleotide error to pass through the cell cycle that cancer or other diseases form.

As a cell proceeds though the cell cycle, its DNA goes from a very loosely condensed state, called chromatin, to a very condensed state of chromosomes. The aim of this project is to see if the efficiency of an enzyme (restriction enzyme) to do its job is affected based on the configuration of the DNA ultimately leading to a higher chance of developing cancer.

presenting
12 pm--1 pm

Hometown: Conway, AR

Effect of Hind-Limb Suspension and X-Ray Irradiation on the Mechanical and Chemical Properties of Rat Femur and Tibia Bones†

S.G. Freyaldenhoven[1], B. Hill[2], R. Mehta1, J.S. Barajas[1], H.N. Heacox[1], M. Dobretsov[3], and P. Chowdhury[4]

[1]Department of Physics & Astronomy, University of Central Arkansas, Conway, AR; [2]Department of Biology, University of Central Arkansas, Conway, AR; [3]Department of Anesthesiology, University of Arkansas for Medical Sciences, Little Rock, AR; [4]Department of Physiology & Biophysics, University of Arkansas for Medical Sciences, Little Rock, AR

It is known that space conditions such as microgravity and cosmic radiation have detrimental effects on the skeletal system of humans, such as decreased bone mineral density. This research studies the changes in mechanical properties, elasticity, and chemical properties, calcium and phosphorus content, of rat femur and tibia bones when exposed to hind-limb suspension and x-ray irradiation, simulated microgravity and cosmic radiation. It is hypothesized that if microgravity and cosmic radiation lead to decreased bone mineral density, then these conditions will produce weakened bones, lower elastic moduli and abnormal concentrations of calcium and phosphorus, as compared to bones not subject to these conditions. A technique known as three-point bending was employed to estimate the Young's (elastic) modulus for the leg bones. To investigate the chemical nature of the bones, a Scanning Electron Microscope (SEM) was utilized to take cross-sectional images and to perform energy dispersive x-ray spectroscopy. Ultimately, the results produced by this research will aid in quantifying the effects of spaceflight and may be used in developing a treatment to counteract such effects.

† This work supported by a RID and CRP grant from Arkansas Space Grant Consortium.

presenting
12 pm—1 pm

Hometown: Beebe, AR

Microlens Array Laser-Ablation Spectroscopy for Measuring Elemental Composition of Solid Samples

Anna Anders and Jonathan Merten

Department of Chemistry and Physics, Arkansas State University, Jonesboro, AR

Laser-ablation laser-induced fluorescence has potential to measure arsenic and carbon without time-consuming and expensive sample preparation. However, the technique struggles to measure extremely low concentrations (parts-per-billion-level). Additionally, the technique only probes small (>1mm) portions of a sample surface. As a result, measurements on uneven or inhomogeneous surfaces generate low-quality, imprecise data. By splitting the ablating laser pulse with a microlens array to probe multiple points on the sample surface, we improve the reproducibility of the technique. The lens array generates a stripe of hot, miniature laser-induced plasmas. The thermal emission from these extremely hot (~8000 K) plasmas or laser-induced fluorescence (if an additional laser is used) can be collected and used to measure the elemental composition of the sample, though there are problems with the plasmas reabsorbing light emitted by adjacent plasmas (i.e. optical thickness). However, this new stripe geometry does improve the reproducibility and allows measurement of lower concentrations of arsenic and carbon, both of which are relevant to industries in Arkansas. Additionally, because the carbon atoms measured in the plasma are not in their lowest-energy quantum state, their measurement suffers from less reabsorption of light than the arsenic measurements.

presenting
12 pm—1 pm

Hometown: Kingman, AZ

Observing the 2017 Total Solar Eclipse from the Stratosphere

Patrick Tribbett and Ross Carroll

Department of Physics, Arkansas State University, Jonesboro, AR

Academic stratospheric ballooning is an inexpensive alternative for near-space probing and experimentation allowing researchers to study various celestial events, specifically the 2017 total solar eclipse. Arkansas BalloonSAT, as part of the Eclipse Ballooning Project initiated by Montana State University, released a high altitude balloon containing several imaging, tracking, and scientific payloads to fully document the eclipse and provide a public live video stream from a unique near- space perspective. In addition to the equipment provided by Montana State, the Arkansas BalloonSAT team designed and flew a custom 3D printed spherical panoramic image payload, and scientific payloads designed by students and faculty at the University of Central Arkansas and Pottsville High School. Ultimately, the payloads successfully streamed video until a connection loss after surpassing the modem's line-of-sight range, and the additional footage and data saved locally onboard the payloads was recovered after landing. Future flights will include modifications to the systems for more continuous public video during the flights, and more reliable and innovative methods for imaging and acquiring scientific data.

This work was funded by the Arkansas Space Grant Consortium and NASA Science Mission Directorate (NNX16AB84G).

presenting
11 am—12 pm

Hometown: Rockwall, TX

Passive Tracking of a Solar Panel with Shape Memory Alloys

Dillon Wester, Keeley Johnson, and Angela Douglass

Physics Department, Ouachita Baptist University, Arkadelphia, AR

This experiment seeks to achieve passive tracking of a solar panel through the use of unique metals called shape memory alloys (SMAs). SMAs were configured to rotate a solar panel without the consumption of energy from the solar system because of their ability to change shape when heated above their transformation temperature. The SMA can be activated by sunlight focused from a Fresnel lens. The advantages of SMA over other tracking methods include no maintenance, longevity, and two-way shape memory. The solar panel size, support stand, and electronics were optimized with the ultimate goal of powering an 11 W street light. Experiments were conducted to determine the pulling force and travel distance of various sizes of SMAs to determine optimal rotor design.

presenting
11 am—12 pm

Hometown: Bauxite, AR

Characteristics of Pattern Recognition Classifiers for EMG Signal Analysis

Shelby Wingate, Rajat Singh, and Kamran Iqbal

Systems Engineering-Mechanical, University of Arkansas at Little Rock, Little Rock, AR

Electromyography (EMG) is the recording of electrical signals in muscle tissues, produced when a motor neuron interacts with a muscle fiber. Using classification algorithms to interpret these myoelectric signals is one of the most efficient ways to control lower arm prosthesis for amputees. This study observed and compared two algorithms using several different features in an effort to find the most efficient set. The Multi-Layer Perceptron algorithm, an Artificial Neural Network, was observed, as well as Linear Discriminant Analysis facilitated through the BioPatRec research platform on Matlab. The algorithms were trained on data available on the BioPatRec repository, classifying 4 different arm movements. Pre-processing of the data involved filtering the signals using independent component analysis and contraction time percentage. Both algorithms performed adequately with impressive accuracies of 97.4% for Linear Discriminant Analysis and 98.3% for Multi-Layer Perceptron.

presenting
11 am—12 pm

Hometown: Star City, AR

Classification of Noise Color on Audio Signals via an Infinite-Valued Logic System and Neuro Network Learning

Allie Wynn and Lynn Fox

School of Mathematical and Natural Sciences, University of Arkansas at Monticello, Monticello, AR

Due to the inevitability of the unwanted modifications a signal suffers during capture and handling, noise removal and reduction are imperative in digital signal processing. The first step in developing such stratagems is to statistically classify the noise distorting the signal. By applying a Kaiser window to each overlapping segment of a non-stationary signal and concatenating the result of applying the short-time Fourier transform to each windowed segment, we are able to compute the time-dependent power spectrum. Through thorough analysis of the power components of numerous signals, a set of processing data is developed. The data is implemented by an infinite valued logic system using a learning algorithm derived from neural network theory. This system institutes parameters that are used as the basis for our computational system that classifies the distorting noise on altered audio signals using easily derived statistics.

presenting
11 am—12 pm

Hometowns: Jacksonville, AR (KG)
Texarkana, AR (WG)

Eye tracking and Calculus Videos

Kara Graham, Will Gloster, and Jason Martin

Department of Mathematics, University of Central Arkansas, Conway, AR

Understanding calculus is the first stepping-stone into STEM fields. As STEM continues to meet the needs of the modern world, it is important that instruction leverages technology to provide opportunities for learning that might not otherwise be achieved using more traditional approaches. Videos have become an essential part of "flipped" classrooms where videos present new material outside-of-class to support more active-learning during class. Yet little is known about how students watch these videos. This project is part of a NSF funded study investigating how students interact with calculus instructional videos by using eye-tracking to document aspects of the video to which students attend. In particular, we focus our analysis on a video about an essential calculus concept, derivative as a limit of average rates. Based on education research, this video introduces average rate by first developing student reasoning through representations of distance and time. Interviews were conducted with student volunteers from first-semester calculus courses from three institutions. Results demonstrate that students are indeed attending to these representations in different ways which can affect their performance. Results from this study can inform how to design better videos that promote an enhanced understanding of calculus for Arkansas students.

presenting
12 pm—1 pm

Hometown: Cave City, AR

A Length of Instructions with Technology in Teacher Training Programs: What Student Teachers Say?

Ashley Green and Tharanga M. K. Wijetunge

Division of Mathematics and Science, Lyon College, Batesville, AR

Use of technology in teaching and learning in K-12 settings is increasing. Thus, teachers need to have a better understanding about these technologies to use them effectively in their classrooms. In-service teachers can acquire knowledge in the use of technology through professional development workshops or from other avenues. Pre-service teachers, on the other hand, have an advantage of learning these new technologies during their preparation to be a teacher. 1) How much should they learn about these new technologies? 2) How long should they learn about these new technologies? 3) Should they use these new technologies as a student? 4) Should they use these new technologies as a teacher? During this study, we are hoping to answer the aforementioned question 2. Two pre-service teacher groups were used in our study. One group used the student response system, as students, for 3 weeks and the other group used the system, as students, for 14 weeks. We are comparing the groups to investigate if there is a difference in identifying the potentials of this new technology between these two groups. What can we conclude based on the findings of the study? We are hoping to answer these research questions during this study.

presenting
11 am—12 pm

Hometown: MI

Application of machine learning algorithm on Voice Rehabilitation Dataset

Calvin Moten, Tia Barten, and Chuanlei Zhang

Division of Natural and Physical Sciences, Philander Smith College, Little Rock AR

Machine learning has been widely applied on medical field in recent decades, e.g. assist in diagnosis, biomarker identification, human genome analysis and etc. Differentiation between two groups of populations can be accomplished using binary classification algorithms. In this work, we investigate the application of a machine learning software, called WEKA on a published medical dataset - voice rehabilitation dataset. This high-dimensional dataset is divided into training data and testing data, where the training data labels are known while the testing data labels are set unknown. Classification algorithm from WEKA is applied on this dataset and classification performance is evaluated.

presenting
11 am—12 pm

Hometowns:

Automated Course Advising System for PSC: ACAS

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Department of Computer Science, Philander Smith College, Little Rock, AR

Course selection is an important process that is encounter unnecessary graduation delay. Students in Philander Smith College have faced problems such as, a lack of student's ability to find a good advice, inappropriate advising time schedules for advising, and awareness and experience of advisers, etc. Also, students are suffering with problems like, time conflicts with course selection, selecting unsuitable courses for specific semester, choosing less, too many, unnecessary, or incorrect courses if they are not advised fittingly. An Automated Course Advising System ACAS is devised to guide students in selecting appropriate courses suitable to register online. JAVA programming language will be used to develop ACAS software. The system will be friendly, and the courses selection will be stored and showed for each semester. ACAS software will be used by both student to select courses and administration to track and keep the records of each student up-to-date. ACAS software will guide PSC students to select appropriate courses to register with the online PSC registration system. The software will be mounted on PSC webserver for students to online access.

presenting
11 am—12 pm

Hometown: Monticello, AR

Adapting Snipe-It to Manage An Equipment Inventory System

Zaire Husband and Jim Winter

Computer Science Department, University of Arkansas at Little Rock, Little Rock, AR

Organizations often have huge inventories that are difficult to manage. Furthermore, there is no way for someone who is not a computer specialist to access the system. The problem that we face at the University of Arkansas at Little Rock is that we want scientists to be able to access a public database on research equipment available on campus. I decided to test an inventory management system that operates on the web, primarily through the script language (PHP) and Structured Query Language (SQL). At first, I wrote computer code to create a "cloak" over Snipe-It, an open source inventory management system, so the user could access the inventory but not manipulate the files. This method was unsuccessful because Snipe-It was incompatible with Hypertext Markup Language (HTML). Then, I used a server at University of Arkansas Little Rock and wrote additional code to allow Snipe-It to operate on that server. This effort was successful. Thus, my result was that the inventory can be accessed on the university system through a login function. In the future, I will create additional code to make the inventory available to the public through the inventory's website.

presenting
12 pm—1 pm

Hometowns: Dallas, TX (BH)
Little Rock, AR (DM & BW)
Boston, MA (AR)

Usability Evaluation of Mobile Apps: The Application of Usability Heuristics

Briana Heath, Dominique Mattlock, Andrea Rendel, Brittany Walker, and Samar Swaid

Department of Applied Math and Computer Science, Philander Smith College, Little Rock, AR

Mobile apps are software applications designed to run on smartphones, tablets and other mobile devices. The growth of mobile apps can be seen in just about every industry such as retail, media, travel, education, healthcare, finance and social. However, due to usability violations found in mobile apps, mobile user experience was found to be challenging. In this study we apply Nielsen's rules to test the usability of mobile apps for m-commerce apps. Based on our research, we extend the mode of Nielsen (1994) to include "Information Architecture" , "Performance", and "Efficient Interaction and Gesture Manipulation" to fit m-commerce mobile apps . We empirically test usability heuristics developed by this study using two mobile apps. Total of four usability evaluators participated in the study, applied mobile-heuristics to identify usability violations and suggest recommendations. As the space for mobile apps is growing, usability testing for mobile apps must rapidly evolve to keep up, and this is the main contribution of this study.

presenting
12 pm—1 pm

Hometowns: South Korea (KK)
Jonesboro, AR (JF)

The Analysis of Try-Catch Block Usages in Java open source projects

Kyoosik Kim, Jordan Freier, Phat Nguyen, and Donghoon Kim

Department of Computer Science, Arkansas State University, Jonesboro, AR

Try-Catch blocks are one of the most widely used exception handling features in the Java language. In this study, we analyze its overall usage in 7 different open source projects to determine if a pattern exists in the data and discuss what such patterns indicate the nature of exception handling as it is utilized for large projects with several independent contributors. We have observed that there does appear to exist (1) a trend among the usage of Try-Catch blocks based on the lifespan of the project, (2) the type of project in which it is used, and (3) Catch clauses compared to their respective Try statement. With a large portion of Try-Catch blocks in the beginning of each project, we inferred that a lot of exception handling is conducted at the front end of development indicating fewer new errors to occur as a project proceeds. We also have found that a project that requires frequent external interactions is likely to have more Try-Catch blocks from categorical analysis. Lastly, we have discovered that a Try statement mostly has a single Catch clause providing for a highly possible reason why the Multi-Catch feature failed to be popular.

presenting
12 pm—1 pm

Hometown: Fayetteville, AR

Arkansas Telemedicine Platform Design and Development for Dermatology: A Secure Cloud Based Skin Cancer Melanoma Detection System for Arkansas

Recep Erol and Sinan Kockara

Department of Computer Science, University of Central Arkansas, Conway, AR

In this study, we develop a system to help dermatologists to diagnose melanoma in its early stages. Accurate diagnoses of melanoma requires expertise, and the progress of the disease may not be noticed by naked eye examination. Computer systems can detect and analyze even minute details about skin lesions and notify physicians if any progress happens on a specific lesion by time. With this motivation, we develop a cloud-base skin cancer monitoring and diagnosis system to help doctors accurately diagnose skin cancers. We use machine learning and image processing techniques to recognize skin lesion images and algorithmically classify these lesions as malignant or benign melanoma. We create any time anywhere accessible a secure cloud based platform where images of patients stored and processed along with the patient specific unidentified information. Doctors and primary care professionals who use the system can collaborate with each other on patient specific data, and can help save more people's lives in Arkansas.

presenting
11 am—12 pm

Hometown: Valley Center, KS

Comparison of BMI, BMI-for-Age Percentile, Weight Status Category, and Z-Score between an Intervention Group and Control Group

Sydney Van Scyoc, Elizabeth Fast, and Detri Brech

Ouachita Baptist University, Nutrition and Dietetics Program, Arkadelphia, AR

The Centers for Disease Control and Prevention (CDC) report that 17% of American children 2-19 years old are obese; in Arkansas, 22% of school-aged children are obese. In Arkadelphia, Arkansas, childhood obesity rates are higher (24.1%) than national and state percentages. Therefore, programs to lower body mass index (BMI) and increase physical activity in children are needed. The purpose of the study was to determine the effectiveness of a nutrition and physical activity intervention in reducing the BMI of rural Arkansas children at risk for childhood obesity. The study consisted of an intervention group and a control group. Anthropometric data of participants 3-14 years old was collected at the beginning and end of the seven week program. It was used to calculate BMI, BMI-for-age percentile, weight status category, and BMI z-scores. The researchers visited the intervention group weekly and taught 30 minute lessons on nutrition and physical activity topics. The control group did not receive treatment. A total of 127 children were assessed and 73 were present at both assessments. The overall mean BMI for both groups increased over the summer, highlighting the need for more intensive, long-term nutrition and physical activity interventions for children to combat increasing adiposity.

presenting
11 am—12 pm

Hometown: Bolingbrook, IL

Ten Year Longitudinal Study Measuring Body Mass Index, Body Mass Index-for-Age Percentile and Weight Status Category of Children in a Rural Southwest Arkansas Community

Elizabeth Fast, Sydney Van Scyoc, and Detri Brech

Ouachita Baptist University, Nutrition and Dietetics Program, Arkadelphia, AR

Body mass index (BMI) is used to identify and track the prevalence of overweight and obesity in children which is important because of the increased health risks that are caused by obesity. The objective of this research was to track the BMI, BMI-for-age percentile, and weight status category of children in a rural Southwest Arkansas community over ten years. Participants in the study were children aged three to fourteen years who attended one of the summer child care programs in Arkadelphia. Individual children were followed and data analyzed for every year of their participation. A total of 738 children were measured. The number of males and females was 354 and 384, respectively. Ethnicities represented were White (n=406), African American (n=307), Hispanic (n=15), Asian (n=7), and other (n=3). Of the participants, a cohort of 273 (37%) were tracked for two or more years. Comparisons between starting and ending weight statuses showed statistical significance for children tracked over two years ($p=0.01$). The significance of the data comparisons for all other follow up periods were: three years $p=0.09$, four years $p=0.05$, five years $p=0.11$, six years $p=0.14$, and seven years $p=0.20$.

presenting
11 am—12 pm

Hometown: Bryant, AR

Validation of Insect Control Termination Timing in Arkansas Cotton

Haylee Campbell[1], Amanda Mann[1,2], Justin Chlapecka[3], and T.G. Teague[1,2]

[1]Arkansas State University, Jonesboro, AR; [2]University of Arkansas Agricultural Experiment Station, Jonesboro, AR;
[3]University of Arkansas Cooperative Extension Service, Harrisburg, AR

University recommendations for termination of insect pest control in late season cotton are based on maturity of the last economically significant boll (fruit) population. Cotton bolls have reduced susceptibility to damage from feeding by tarnished plant bugs (*Lygus lineolaris*) and Bollworms (*Helicoverpa zea*) by 250 DD60's and 350 DD60's, respectively, after flowering. Farmers sometimes make automatic insecticide applications in late season to ensure that all pest risks are eliminated. A study was conducted in 2017 in a 40 acre commercial cotton field in Poinsett County to compare use of integrated pest management (IPM) practices using scouting and plant monitoring compared to the practice of automatic insecticide application. The experiment had two treatments, replicated 6 times: 1.) automatic insecticide spray and 2.) untreated check. Plots were 100 ft wide and extended the length of the field. Pest numbers were monitored weekly before and after spray termination. Overall, pest densities and boll damage was low, and there were no significant differences between treatments in cotton yield or fiber quality. The late season application was unnecessary. Unwarranted pesticide use for crop protection may affect environment sustainability and farm profitability negatively. Use of IPM would be more beneficial than automatic sprays.

presenting
11 am—12 pm

Hometown: Little Rock, AR

Using Geological Facies to Estimate Chromate Sorption to Soils

Kennedy Smith[2], Victoria Smith[1], Daja Scurlock[2], Chauntilena Butler[3], Eddie Hollins[2], Tim Spearman[5], John Dickson[6], Daniel I. Kaplan[6], and Garriet Smith[7]

[1]Delaware State University; [2]LeMoyne-Owen College; [3]Savannah State University; [4]University of Arkansas at Pine Bluff; [5]Xavier University of Louisiana; [6]Savannah River National Laboratory; [7]University of South Carolina Aiken

Quantifying the extent to which contaminants bind to subsurface soils is important for risk assessment and developing environmental remediation strategies. Unfortunately, subsurface soils vary widely in their composition, which affects their tendency to bind contaminants. The hypothesis of this study was predicated on how a better understanding of geological facies would reduce uncertainty associated with contaminant sorption. Facies are expected to have similar assemblages of minerals, particle size distributions, origins of organic matter, and similar microbial population structures. The approach of this study was to collect 42 composite soil samples from a 5 m by 1.5 m grid outcrop in Graniteville, South Carolina and five end-member facies samples. The fraction of each of the five facies comprising the 42 composite soil samples were estimated. Particle size distribution, and iron coating content, were determined for each composite soil and the five end-member facies soils. Also, hexavalent chromium (Cr) was used as a model contaminant to provide a measure of contaminant sorption. Chromium distribution coefficients (Kd = Crsoil/Crwater) were measured. Significant correlations were identified between several soil chemical and microbial properties although large amount of inherent error characterized the calculated values. Additional work is needed to determine the applicability of this approach for remediation of contaminated sites.

presenting
11 am—12 pm

Hometown: Portland, Jamaica

The Regulation of CYP1B1 by Inflammation in Human Hepatocytes

Shamara S. Lawrencea[1], Hung-Chun Tungb, and Wen Xieb[2]

[1]University of Arkansas at Pine Bluff, Pine Bluff, AR; [2]Molecular Pharmacology, SURP, University of Pittsburgh, Pittsburgh, PA

Chronic inflammatory liver disease is associated with increased level of CYP1B1 in human liver. The objective of this study is to assess the contribution of CYP1B1 in human hepatocytes treated with pro-inflammatory cytokines, and to determine if NF-κB signaling pathway is responsible for the regulation of CYP1B1 in human hepatocytes under inflammatory condition. Real-time PCR and western blot analyses were performed to examine the expression of CYP1B1 in HuH7 cells and human primary hepatocytes (HPHs) treated with NF-κB activators, tumor necrosis factor alpha (TNF- α) and phorbol 12-myristate 13-acetate (PMA), for 24 hours. The regulation of CYP1B1 by NF-κB pathway was investigated by using NF-κB inhibitor, pyrrolidine dithiocarbamate (PDTC). The results show that CYP1B1 was induced in both Huh7 and HPHs treated with TNF-α and PMA. However, pharmacological inhibition of NF-κB signaling did not showed any significant decrease in CYP1B1 expression during inflammation. In conclusion, CYP1B1 expression is inducible in human hepatocytes treated with TNF- α and PMA, suggesting the relationship between CYP1B1 and hepatic parenchymal inflammation. However, the inflammatory activation of CYP1B1 is not mediated by NF-κB signaling pathway.

presenting
11 am—12 pm

Hometown: Pine Bluff, AR

Phenomics Study of Arabidopsis Lines Overexpressing Genes in Myo-Inositol Pathway to Ascorbate under Water Deficit Stress

Jordan Iverson[1], Jessica P. Yactayo-Chang[2], Nirman Nepal[2], Natalie Turner[2], Zachary Campbell[2], and Argelia Lorence[2]

[1]University Arkansas Pine Bluff, Pine Bluff, AR; [2]Arkansas State University, Jonesboro, AR

Vitamin C (L-ascorbic acid, ascorbate, AsA) is the most abundant water-soluble antioxidant found in plants. Ascorbate functions as an enzyme cofactor, a radical scavenger, and protects tissues against damage caused by reactive oxygen species produced from stresses such as water deficit, soil salinity, cold, and heat. There is a need to increase productivity of crops capable of thriving under challenging environmental conditions. A potential solution is development of genetically modified plants with enhanced nutritional value, improved tolerance to stresses, and superior yields. Our laboratory has studied four enzymes involved in AsA biosynthesis via myo-inositol pathway: myoinositol oxygenase (MIOX), glucuronate reductase (GlcUR), gulonolactonase (GNL), and L-gulono-1,4- lactone oxidase (GuILO). We studied effect of water limitation stress on the growth and health of Arabidopsis thaliana lines over-expressing AtMIOX, AtGNL, AtGuILO, and rGuILO enzymes. To measure plant growth and health, we used a high throughput phenotyping platform equipped with visible, fluorescence, and near infrared cameras. We complemented data with photosynthetic parameters measured using a hand-held fluorometer. Ascorbate measurements were done via an enzyme based spectrophotometric assay. Our findings show over-expressers had higher foliar AsA content, displayed healthier color, water content and chlorophyll fluorescence profiles, and higher linear electron flow than wild type controls.

presenting
11 am—12 pm

Hometown: Little Rock, AR

Isolating Exosomes Using Tumor-Specific Antibodies in the Serum and Ascites of Cancer Patients

Sylvia Szwedo[1] and Karen Abbott[2]

[1]Chemistry Department, University of Arkansas at Little Rock, Little Rock, AR; [2]Biochemistry Department, University of Arkansas for Medical Sciences, Little Rock, AR

Exosomes are small multifunctional vesicles that are rich in proteins and nucleic acids and occur in the budding stage of late endosomes. It has been suggested that the release of exosomes play a role in cell-cell communication in normal and pathological states such as cancer. Ovarian cancer is the leading cause of all gynecological malignancies and is the focus of our project. We analyzed the exosome proteins from normal patients and ovarian cancer patients using lectins and antibodies to determine the glycans that are changing in ovarian cancer exosomes. The overall aim is to use glycoproteomics to identify the glycoproteins present on the exosomes. In order to do so, the exosomes must be tagged and isolated from the serum and ascites samples of ovarian cancer cells using the provided antibodies. Western blot and mass spectrometry techniques are used to ensure the process. As a result, exosome extraction has shown promising outcomes to the project and will continue to be further investigated. Successful identification of the proteins found on exosomes may provide an efficient detective screening method for women with ovarian cancer.

presenting
11 am—12 pm

Hometown: Texarkana, TX

Use of cytosine-based tautomerically ambiguous nucleosides for induction of viral mutagenesis

Carlie Clem and Vincent Dunlap

Department of Chemistry and Biochemistry, Henderson State University, Arkadelphia, AR

Harmful viruses have posed a threat to the human race for generations. In particular, the human immunodeficiency virus (HIV) has been notably damaging to the individual and society alike. Although drugs to treat HIV exist, they are harsh and often result in negative side effects. The low fidelity replication enzymes that the virus replicates with contributes to the relative success of the virus's ability to evade antiviral medications, but can be exploited to develop new antiviral agents. This research focuses on viral mutagenesis, or the introduction of intentional errors in the genome of the virus. These resulting mutations will lead the DNA to reach error catastrophe and ablate. The method by which error will occur is the assimilation of synthesized cytosine based nucleosides with ambiguous hydrogen bonding faces resulting from tautomeric shift. These shifts will lead to the mispairing of DNA and a decrease in stability of the duplex molecule. Presented here are the details of the designed nucleosides' synthesis.

presenting
11 am—12 pm

Hometown: Hot Springs, AR

In pursuit of a family of Antimalarial medicines

Emily Williford and Martin Campbell

Department of Chemistry and Biochemistry, Henderson State University, Arkadelphia, AR

Malaria continues to be a major disease across much of Africa and Southeast Asia, resulting in an estimated 445,000 deaths from over 216 million individual cases. Although many control approaches are ongoing, there is a constant need for new medicines to treat those infected, especially the kids. Recently, GlaxoSmithKline, in combination with others, released a computer study of a variety of chemical structures predicted to be useful in treating malaria. One of the structures involved a series of three rings, held together by a fairly common organic linkage, an amide group. The structure appears to be fairly easy to assemble, although one of the components will be challenging. A variety of simple variations on the three rings should lead to make a number of similar compounds. Once prepared, these compounds will be tested for general toxicity, and specifically for effectiveness in killing the malaria parasite.

presenting
11 am—12 pm

Hometown: Little Rock, AR

Copper-Based Nanocatalyst for Hydrogen Production

Paloma Salazar, Sakr Elsaidi, Marina Avram, Daniel Nde, and Wei Zhao

Chemistry Department, University of Arkansas at Little Rock, Little Rock, AR

Using carbon-free energy sources (e.g., solar and wind) to split water and produce hydrogen fuel is a promising renewable and sustainable solution to reduce carbon pollution and global climate change. From volcano studies, our hypothesis is that a copper oxide-based nanocatalyst can efficiently perform the hydrogen evolution reaction, hence allowing us to obtain hydrogen that could be stored in fuel cells. Our methods first required carbonizing algae cells using a biotemplate approach. Our copper oxide nanocatalyst was then grown on the recovered cCells using a hydrothermal reaction. We examined the electrocatalytic properties of the catalyst using linear sweep voltammetry and cyclic voltammetry on glassy carbon and nickel foam electrodes. Our results were that the catalyst showed poor performance on glassy carbon (a potential of -0.68V compared to a Pt/C benchmark of -0.09V at a current of 10mA/cm^2). However, the catalyst performed better on the nickel foam electrode (a potential of -0.38V compared to a Pt/C of 0.21V at a current of 100 mA/cm^2). In conclusion, the copper oxide catalyst with modification shows promising performance for hydrogen evolution reaction. In the future, we will reduce the amount of oxides attached to the copper to enhance its performance for hydrogen productivity.

presenting
11 am—12 pm

Hometown: Little Rock, AR

Iron-Induced Decomposition of Greenhouse Gases with Significant Global Warming and Ozone Depleting Potentials

Christopher L. Emmerling, Angela B. Eden, and William S. Taylor

Department of Chemistry, University of Central Arkansas, Conway, AR

Ions of iron chloride, iron bromide, and iron iodide reacted with three greenhouse gases, namely: iodotrifluoromethane, bromotrifluoromethane (Halon 1301), and chlorotrifluoromethane (Freon R-13). These compounds have been widely used as refrigerants and fire-suppressants and have been shown to have negative impacts when released into the environment. The reactions examined here were carried out in the gas phase at room temperature and low pressure. The apparatus used in this work employs mass spectrometry (which reveals chemistry done based on mass and charge) to characterize reaction products. In the work reported here, the three iron-containing reactant ions initiated several distinct decomposition pathways with these environmentally unfriendly gases. By revealing the nature of these processes, this work seeks to gain insights that can be applied to the design of catalytic processes for remediation of these environmentally-suspect compounds. The economic impact of catalytic chemistry is substantial. Representing ~35% of world GDP annually, catalytic processes are involved in the production of an estimated 90% of all chemical products. As a catalyst, iron has certain advantages. It is inexpensive, abundant, and relatively non-toxic. Our results have revealed that by tuning the iron center with the appropriate substituents, its ability to initiate chemistry can be greatly enhanced.

presenting
12 pm—1 pm

Hometown: Little Rock, AR

Applying Nano Sensors Using Reduced Graphene Oxide to Detection Phosphate

Robert Rogers and Anahita Izadyar

Department of Chemistry and Physics, Arkansas State University, PO Box 419, State University, AR 72467, USA

The graphene- ion transfer stripping voltammetry (ITSV) phosphate analyzer will allow, for the first time, real-time monitoring of phosphate in the environment, water treatment and wastewater treatment. Until now, only time-consuming reagent-based colorimetric testing was the answer. Monitoring and controlling phosphorous in waters and in water treatment is central to fiscal efficacy in environmental degradation to our surface waters caused by nutrient loading. To monitor spatial and temporal changes in phosphorus concentration, one must be able to measure, in real time, its main constituent, orthophosphate. The sensor we propose will be the first analytical tool that can do this, and it is primed to be a disruptive innovation in all three areas of drinking water, wastewater and environmental monitoring. It will measure phosphorus based on ion transfer stripping voltammetry, a novel use of graphene embedded membrane, and an ionophore selective to phosphorus—tributyltin chloride. We expect ability to measure an unprecedented range of phosphate concentrations. It will pave the way for sensors that can measure a wide range of contaminants in surface waters, drinking water and wastewater, reducing reliance for water quality testing on expensive laboratory equipment such as GC-MS, IC, ICP-OES, ICP-MS and AA. Treatment plants and field scientists will be able to afford real time analysis.

presenting
12 pm—1 pm

Hometown: Conway, AR

Removal of an endocrine disrupting contaminant by clay-like oxides.

Kristiana Watson, Saeed Al-Ahmary, Bryant Fong, Ronnie Ruyonga, and Hashim Ali

Chemistry and Physics Department, Arkansas State University, Jonesboro, AR

4 nonylphenol (4-*n*-NP) is a contaminant that has been found to disrupt the functions of several (endocrine) glands in our bodies. It is a major component of cleaning agents, detergents, pesticides, plastic food packaging and other cosmetic products. The increase in the use of these commercial products, coupled with fatigued wastewater treatment plants have contributed to the observation of these contaminants in aquatic environments. Our research was aimed at finding ways in which we can remove these contaminants from waste water. Our studies have shown that for the two clay-like oxides studied, one of them (goethite) could remove the 4-*n*-NP from waste water at a faster rate, but with a low capacity. The other clay material (hematite), removes 4-*n*-NP at a slower rate, but can remove 3 times more 4-*n*-NP than goethite. We are continuing to find if a certain combination of these clays can lead to a faster removal process, without loss of capacity.

Acknowledgments:
This research was done as part of the Arkansas State University Experiential Learning Fellowship (ELF) Program (NSF grant no. 1060209) research initiative (for Bryant Fong and Kristiana Watson) , ASTATE faculty research awards (for Saeed Al Ahmari and Ronnie Ruyonga) and the Arkansas Louise Stoke Alliance for Minority Participation (ARK_LSAMP, NSF grant: HRD-1304121).

presenting
12 pm—1 pm

Hometown: Conway, AR

FD&C Dye Content of Children's Beverages

Rachel Haislip and Robert Mauldin

Department of Chemistry & Biochemistry, University of Central Arkansas, Conway, AR

Historically, artificial dyes were added to food products in order to market substandard food products; today, however, they are added to food and drug products in order to make them more appealing to consumers. The safety of Food, Drug and Cosmetic (FD&C) dyes consumed by children and adolescent populations is of particular interest as some studies have linked these dyes with allergic reactions and attention problems (in fact, several FD&C dyes have been banned due to health concerns). Currently, American companies are required to list the identity of these dyes in food products, however, they are not required to disclose the amounts of these dyes in their products. This project seeks to determine the quantity of three of the most common food dyes – Red 40, Blue 1, and Yellow 5 – in popular beverages using UV-Visible Spectrophotometry. The development of the analytical methodology for quantitatively measuring these dyes in complex mixtures will be presented as well.

presenting
12 pm—1 pm

Hometown: Brinkley, AR

Producing and Studying Stilbenoids

Jeremiah Jeffers[1], Patrick Roberto[2], Abbas Karouni[2] and Fabricio Medina-Bolivar[2]

[1]University of Arkansas at Pine Bluff, Pine Bluff, AR; [2]Arkansas State University, Jonesboro, AR

Stilbenoids are inducible defense compounds produced by certain plants, including grapes and peanuts. In addition to their role in plant defense, they have potential applications in human health due to their antiviral, anticancer, neuroprotective, and anti-obesity properties. The peanut plant produces a unique class of stilbenoids, i.e. prenylated stilbenoids, upon fungal challenge. These compounds have shown higher metabolic stability than non prenylated stilbenoids and are potentially more bioavailable than their non prenylated analogues. In order to study the antioxidant properties of prenylated stilbenoids, peanut hairy roots were used as a bioproducion system for these compounds. The hairy roots were treated with elicitors for 48, 108 and 168 hours and the stilbenoids were extracted from the culture medium with ethyl acetate and analyzed by HPLC. The extracts contained the non-prenylated stilbenoids resveratrol and piceatannol and the prenylated stilbenoids arachidin-1, -2, -3 and -5. Higher levels of prenylated stilbenoids were obtained after 168 hours of elicitation. Antioxidant assays will be performed to determine if the antioxidant capacity is higher in the extracts than purified stilbenoids. These studies demonstrate the application of peanut hairy roots to produce bioactive compounds for human health.

presenting
12 pm—1 pm

Hometown: St. Louis, MO

Measurement of the activation parameters for fragmentation at penultimate proline in three tetrapeptides

Emma C. Sward[1], Chelbi A. Gilmore[1], Morgan I. Dasch[1], David A. Hales[1], Tarick J. El-Baba[2], Daniel R. Fuller[2], and David E. Clemmer[2]

[1]Department of Chemistry, Hendrix College, Conway, AR; [2]Department of Chemistry, Indiana University, Bloomington, IN

The function of a biological molecule depends on its shape. Changes in conformation cause changes in function, which can be related to disease. A molecule must overcome an energy barrier in order to change conformations. Higher barriers mean changes are less likely, and lower barriers make changes more likely. The peptides XxxProGlyGly (Xxx = His, Lys, Arg) were incubated in ethanol at various temperatures. A change of conformation at proline allows a proton transfer that results in cleavage of the Pro–Gly bond. Solution-phase fragmentation of the parent peptide to yield XxxPro was monitored by electrospray ionization-ion mobility spectrometry-mass spectrometry. The observed induction period indicates that some sequence of parent conformations is involved, but they are invisible in this experiment: electrosprayed XxxProGlyGly all yield the same conformation of $[XxxProGlyGly+H]^+$ in the gas phase. The data were fit by assuming a series of intermediates separated by activation barriers of equal height; the number of intermediates is optimized to give the best fitting statistics over all of the data. Arrhenius analysis of the rate constants thus determined yields transition state thermodynamics for fragmentation of each peptide. $\Delta H^{\ddagger}$ and $\Delta S^{\ddagger}$ vary, but $\Delta G^{\ddagger}$ values are remarkably consistent across all three peptides.

presenting
12 pm—1 pm

Hometowns: Fort Smith, AR (ET)
Barling, AR (KV)

The Synthesis of a Fluorophore for the Diagnosis of Neglected Tropical Diseases

Emily H. Trinh, Kayla B. Vinh, and Gregory R. Naumiec

Department of Chemistry, University of Central Arkansas, Conway, AR

Our research revolves around developing a cost-efficient and accurate method of diagnosing neglected tropical diseases (NTDs) by fluorescent emissions. “Neglected” refers to the prevalence of NTDs in the more impoverished parts of the world with inadequate sanitized water supply. NTDs are caused by parasites that are transmitted to humans by infectious vectors, such as malaria. When we attach a fluorophore to a drug used to treat the NTD, we can observe the effects of the drug on the disease live on a molecular level. Based on these observations, current drug therapies could be improved since there is a constant evolution of drug resistance in NTDs.

The synthesis of our research is based on the naturally-occurring fluorophore chlorin, a compound found in plants. These fluorophores play a significant role in collecting light in photosynthesis. Chlorins display a strong fluorescent emission in the near infrared region which makes it a good candidate to attach on drugs for the diagnosis of NTDs due to its permeability and safety. This fluorophore is synthesized in two discrete halves; a western half and an eastern half. Currently, the eastern half has been synthesized and significant progress has been made in the synthesis of the western half.

presenting
12 pm—1 pm

Hometown: Jonesboro, AR (NM)

Fighting Drug Resistant *Mycobacterium tuberculosis* with Modified Rifamycins

Natalie Milligan, Jordan Trant, LaShawana Miller, Zachary Hodge, Emerson Smith, and Irosha N. Nawarathne (PI)

Mathematics and Science Division, Lyon College, Batesville, AR

Tuberculosis, which is caused by the bacteria *Mycobacterium tuberculosis*, is a lung disease which kills roughly 1.5 million people a year. The most common family of antibiotics for this disease are rifamycins, which were developed 40 years ago. Rifamycins work by binding to the RNA polymerase (RNAP) and inhibiting RNA synthesis. The bacteria has since mutated in multiple ways that have decreased the effectiveness of rifamycins. Although there are many rifamycin resistant (Rif^R) strains of MTB, the mutations of three residues, D435V, H526Y, and S450L, account for 84% of the MTB Rif^R strains. Our research focused on S450L, which accounts for about 43% of the MTB Rif^R strains. The mutation causes the replacement of a serine amino acid with a leucine, which is both bulkier and more hydrophobic. This creates steric hindrances between drug molecule and RNAP, allowing the bacteria to continue RNA synthesis. We are attempting to change the structure of rifamycin so it will bind to the RNAP site better. We hypothesize that we can get the desired result by removing the hydroxy on the C-8 position through chemical deoxygenation or a fluorination. Being smaller and more hydrophobic, rifamycin analogue with the hydrogen or fluorine at C-8 will bind to the MTB RifR strains more effectively. Furthermore, fluorine incorporated rifamycins are proposed to be developed as an imaging agent tofacilitate diagnosis through TB screening, thus promoting prevention and/or early treatment of the disease. We have used this protocol on 1-hydroxyanthra-9,10-quinone to test the reaction efficiency. Then we continued the deoxygenation at C-8 position of rifamycin S with some measure of success that will be discussed in our presentation. The deoxygenated rifamycins are tested with mutated RNAP in an *in vitro* transcription assay that is based on rolling circle transcription technology.

presenting
12 pm—1 pm

Hometown: Newport, AR

Probing Interactions of Rifamycins and *Mycobacterium tuberculosis* RNA Polymerases

Brian Bumpous and Irosha N. Nawarathne (PI)

Mathematics and Science Division, Lyon College, Batesville, AR

Tuberculosis (TB), which is caused by the bacteria *Mycobacterium tuberculosis* (MTB), is a lung disease which kills roughly 1.5 million and infects over 9 million people every year. The most widely used group of antibiotics in treating TB are rifamycins. Rifamycins bind to RNA polymerase and block the RNA synthesis in MTB leading to the death of the organism. Mutations in the RNA polymerase change the polarity of the binding site and prevent the antibiotic from binding. TB evolved over the past 40 years; some strains are already resistant to many current antibiotic treatments. Among the rifamycin resistant (Rif^R) strains, 3 mutatons, D435V, H526Y, and S450L, create 84% of all Rif^R strains. The mutation D435V, makes a change in an amino acid at 435 of MTB RNAP, causing a slight rotation in the F514, phenylalanine, side chain. This rotation creates steric hindrances between the F514 side chain and the acetoxy at C-25. We hypothesize that by removing the acetoxy group (-OAc) and leaving behind a hydroxy group (OH) at the C-25 position (to better attract the D435V), rifamycin will bind better to RNAP of Rif^R strains. We are in the process of testing the developed modified rifamycins using rolling circle transcription assay. Development of modified rifamycins to combat Rif^R MTB strains will be discussed in this presentation.

This work is been supported by Arkansas IDeA Network of Biomedical Research Excellence (Arkansas INBRE) and Lyon College.

presenting
12 pm—1 pm

Hometown: Jonesboro, AR

Utilizing a Mutated *Taxus* Benzoyltransferase (*m*TBT) as a Biocatalyst

Tanner Duty, John Sifford and Irosha N. Nawarathne (PI)

Mathematics and Science Division, Lyon College, Batesville, AR

The antineoplastic agents paclitaxel (Taxol®) and docetaxel (Taxotere®) are currently supplied commercially by plant cell fermentations which rely on a biological source. While the plant cell fermentations may be a viable source for Taxol, a more biotechnological method would be more effective to make Taxol analogues. Structure-activity-relationship studies have led to the development of highly promising paclitaxel analogues compared to the parent molecule through acyl group modifications. Taxol pharmacophore includes all the acyl groups around the tricyclic core. Therefore, the acyl group modifications at C-10, C-2, C-4, and C-13 hydroxy-, and C-3' amino- positions are targets for developing efficacious paclitaxel analogues. The enzyme *m*TBT, has been observed to be able to catalytically produce several 7,13-*O*,*O*-diacetyl-2-*O*-acyl-2-*O*-debenzoylbaccatin III analogues. This shows the broad specificity of *m*TBT, suggesting that a plethora of 2-*O*-acyl variants of the antimitotic paclitaxel can be assembled through bio-catalytic sequences. By understanding the biosynthesis of these metabolites in detail, the production of paclitaxel and related compounds can therefore be improved. We intend to examine the modifications on the C-7 group of the substrate on the activity of *m*TBT. It has already been shown that an *O*-acetyl group on the C-7 is a more effective substrate over the substrate that has C- 7 hydroxylated. This could imply that either the *O*-acetyl group may play a role in *m*TBT reaction or that the hydroxy group may hinder the same reaction. The fact that the C-7 likely needs a moiety that is not a free hydroxyl group implies that the *m*TBT step occurs prior to the catalytic hydroxylation at C-7 in the biosynthetic pathway. By replacing the C-7 hydroxy group with hydrogen or fluorine and utilizing the resulting C-7 deoxygenated or fluorinated analogue as a *m*TBT substrate, more information could be discovered about the timing of the 2-*O*-benzoyltransferase reaction in Taxol biosynthesis and its importance in the biocatalytic production of Taxol analogues. Development of C-7 modified Baccatin III (a precursor of Taxol) analogues to test the above hypothesis will be discussed during this presentation.

presenting
12 pm—1 pm

Hometown: Cabot, AR

Analysis of Animal Kidney Stones Through Infrared Spectroscopy

Nathan Taylor[1] and Russ Summers[2]

[1]Chemistry Department, University of Arkansas at Little Rock, Little Rock, AR; [2]Arkansas Veterinary Diagnostic Laboratory, Little Rock, AR

The buildup of certain compounds and elements can produce kidney stones in some mammals that can be harmful if untreated. By learning how to change an animal's diet, we can potentially prevent additional stone formation. My project was to chemically analyze kidney stones from live dogs, cattle, and pigs. Using FT-IR spectroscopy, I analyzed the chemical structure of 50 different stones. I used four scans per stone. To begin, the stone was crushed into a fine powder and dried in an oven. It was then mixed with potassium bromide (KBr), and a spectrum was taken. I performed these analyses with a Perkin-Elmer Two FT-IR Spectrometer with DRIFT accessory (Diffuse Reflectance Infrared Fourier Transform). The results were analyzed and the type of stone was determined. Most of the stones were mainly composed of struvite, calcium oxalate, or oxalate. Next, the fingerprint region of the IR spectrum was read to decide if the animal's diet should be changed to increase or decrease necessary elements such as potassium, calcium, and/or sodium. Once this information was obtained, a detailed report was sent to the vet who sent in the stone so the vet could decide how to change the animal's diet.

presenting
11 am—12 pm

Hometowns: Hot Springs, AR (BJ)
Greenwood, AR (CG)
Bismarck, AR (BJ)
Malvern, AR (QG)

Metagenomic Analysis of Microbial Communities in Blanchard Springs Caverns, Arkansas and an Investigation of Low Temperature Tolerance in Cave-adapted Invertebrates

Brooke Johnson, Caitlyn Gosch, Brooke Jones, Quincy Gragg and James Engman

Department of Biological Sciences, Henderson State University, Arkadelphia

Caves provide examples of organisms adapted to extreme environments, making them excellent models for survival in such systems. We use molecular genetic techniques to survey the bacterial flora of Blanchard Springs Caverns, Arkansas. Recent work concentrates on the flora of the digestive system and exoskeleton of the cricket *Ceuthophilus gracilipes*, considered a keystone species in that ecosystem. Initial techniques involved growing bacteria on plates and sequencing the DNA of colonies that grew. Using metagenomic sequencing eliminates culturing. This has increased our bacterial species identified from 9 to over 200 per sample. We also identified bacteria from commercial grey crickets, for comparison. Observations revealed that the cave crickets have an unexpected tolerance to low temperatures. This seems at odds with the fact that they live in a thermally stable environment, constant at 12 C. A preliminary experiment suggests that cave crickets remain active for at least 18 hours at 0 C, while grey crickets rapidly become inactive. Many of these bacteria have unique adaptations and provide insight into the complexity of system traditionally considered simple. Some bacteria from our samples have DNA sequences distinct enough to be considered new species.

presenting
11 am—12 pm

Hometowns: Hot Springs, AR (DW)
Charleston, AR (MH)
White Hall, AR (SE)

Large Scale Expression of Ligated pGEX Vector with Sodium Toxin-654 in *Escherichia coli* Expression Cell Lines Rosetta, BL21, and Origami to Produce *Centruroides vittatus* Scorpion Sodium-Toxin 654

David R. Williams, Mallory E. Heft, Sara E. Eagle, and Tsunemi Yamashita

Biology Department, Arkansas Tech University, Russellville, Arkansas

Centruroides vittatus is found throughout the South Central United States and Northern Mexico. These scorpions produce a sodium toxin which interferes with the closure of neuronal sodium channels. If the sodium channels do not close the neuronal cell cannot open potassium channels to repolarize the cell in preparation for another action potential. Thus, the neuronal cell is stuck in an ionic imbalance preventing movement of the prey. The purpose of this research is to use *Escherichia coli* expression cells to produce a functional sodium toxin for further structural and physiological analysis. This was accomplished via the insertion of the Na654 toxin gene into a pGEX vector, then insertion of the vector into competent E. coli cells. After verifying proper insertion via DNA sequencing and gel electrophoresis, the plasmids containing the Na654 gene were extracted and transformed into *E. coli* expression cells. Proper insertion of the Na654 gene into expression cell lines BL21, Rosetta, and Origami were confirmed via DNA sequencing and gel electrophoresis. Small and large-scale expression experiments were performed and the production of Na654 toxin was analyzed via column chromatography and SDS-PAGE. Results indicated that the Na654 toxin was being produced in each cell line, however at lower concentrations than anticipated. Future research will be focused on procedural modification in hopes to increase the protein concentrations produced.

presenting
11 am—12 pm

Hometowns: Mesquite, TX (LH)
Star City, AR (JM)
Stuttgart, AR (BO)
Horatio, AR (FR)

Evaluating the Taxonomic Status of Arkansas Twistflower, *Streptanthus maculatus* subsp. *obtusifolius* and Clasping Jewel Flower, *Streptanthus maculatus* subsp. *maculatus* (Brassicaceae).

Leila M. Henning [1], Jose A. Magana [1], Vanessa Mendoza [1], Ben O' Neal III [1], Freddie Rivera [1] Brent Baker [2], Karen P. Fawley [1] and Marvin W. Fawley [1]

[1] University of Arkansas at Monticello, Monticello, AR; [2]Arkansas Natural Heritage Commission, Little Rock, AR

The objective of this study was to use DNA sequence data to determine if the Arkansas twistflower, *Streptanthus maculatus* subsp. *obtusifolius* and the clasping jewelflower, *S. maculatus* subsp. *maculatus* in the mustard family (Brassicaceae) are actually subspecies. The Arkansas twistflower is found in Arkansas, whereas the clasping jewelflower is found in a few counties in Oklahoma and Texas. This objective was evaluated by the 2017 UAM Research Program for Minority Students Research Experience class. The students produced nuclear ribosomal ITS DNA sequences from specimens of Arkansas twistflower, clasping jewelflower and two related species found in Arkansas, sandhill jewelflower, *S. hyacinthoides* and Ouachita jewelflower, *S. squamiformis*. Our results suggest that the Arkansas twistflower is intermediate between the Ouachita jewelflower and the published specimens of clasping jewelflower. Also, an Oklahoma specimen of clasping jewelflower is distinct from the published specimens of this subspecies, which are from a Texas population. Arkansas jewelflower may actually be a stable hybrid between the Oklahoma population of clasping jewelflower and an unknown parent.

presenting
11 am—12 pm

Hometown:

Plant Cell Secreted Growth Factors Targeted to Ex Vivo Production of Red Blood Cells from Hematopoietic Stem Cells

Taylor Hill[1], Xiaoting Wang[2], and Jianfeng Xu[2]

[1]University of Arkansas at Pine Bluff, Pine Bluff, AR, [2]Arkansas State University, Jonesboro, AR

Ex vivo production of red blood cells from hematopoietic stem cells represents one of the focuses in regenerative medicine. Production of red blood cells demands significant quantity and high quality of growth factors. Human stem cell factor is a key growth factor that stimulates the proliferation and differentiation of hematopoietic stem cells to red blood cells. The goal of this project is to produce the human stem cell factor plant cell culture technology, which has been presented to be a propitious bioproduction platform for therapeutic proteins. The human stem cell factor was expressed in plant cell with a hydroxyproline (Hyp)-Oglycosylated peptide (HypGP) that presumably functions as a molecular carrier in promoting efficient transport of the conjoined recombinant protein into the culture media and protecting the protein from proteolytic degradation, which ultimately boosts the secreted protein yield. In this study the human stem cell factor was expressed in tobacco BY-2 cells with a HypGP tag. The kinetics of plant cell growth and human stem cell factor accumulation in culture media and inside cells were determined. This research may provide a promising plant cell-based platform to produce large quantity of hematopoietic stem cells that assists the stem cell research and clinical applications.

presenting
11 am—12 pm

Hometowns: Monticello, AR (AG, CL)
Little Rock, AR (RK)

Soil Crust Algal Communities of Warren Prairie Natural Area

Ashton L. Gray [1], Rachel E. Knight [1], Caleb W. Lamb [1], Brent Baker [2], Marvin W. Fawley [1], and Karen P. Fawley [1]

[1] University of Arkansas at Monticello, Monticello, AR; [2]Arkansas Natural Heritage Commission, Little Rock, AR

Warren Prairie Natural Area (WPNA) in Bradley and Drew Counties, Arkansas, is a mosaic of saline slicks that form flat, crusty depressions. The edges of the saline slicks are home to the diminutive vascular plant, *Geocarpon minimum* (Caryophyllaceae), which is a federally protected species. The objective of this project was to characterize the soil eukaryotic algal communities in saline slicks from WPNA. We collected soil crust samples from two sites in WPNA in February 2016, one site where *Geocarpon minimum* was present and another where this plant was not found. Forty-five algal strains were isolated from the site without G. *minimum* and thirty-four strains were isolated from the site with *G. minimum*. We selected 20 strains from each site for molecular characterization based on initial microscopic examination. Ribosomal 18S, ribosomal ITS or *rbc*L DNA sequences were generated from the strains and BLASTN was used to identify each strain. We found algae from the Chlorophyta, Streptophyta and Eustigmatophyceae. Overall, the algal community resembled communities that inhabit desert crusts. Several of the strains are new species, with at least one new genus present. Our results show that the unusual soil chemistry of the WPNA harbors new and unusual algal species.

presenting
11 am—12 pm

Hometown: Toilette, AR

Water quality assessment at the Grand Prairie farming & water company irrigation system

Donae' Poindexter[1], Oluwayinka Iseyemi[2], Arlene Adviento-Borbe[2], Deborah Leslie[2], and Michele Reba[2]

[1]Department of Biology, University of Arkansas at Pine Bluff, Pine Bluff, AR; [2]Delta Water Management Research Unit, United States Department of Agriculture-Agricultural Research Service, Jonesboro, AR

Freshwater is imperative for the survival of all living organisms. Water quality monitoring is essential in recognizing any current or future harm to humans and the environment. Agronomic practices such as adequate fertilization and minimal soil disturbance aid in ensuring reduced environmental pollution. To assess water quality dynamics at the Grand Prairie (GP) Farms, Arkansas, grab water samples were collected from nine locations and analyzed for N concentrations, pH, hardness, alkalinity, turbidity, and electrical conductivity. Water samples were retrieved from the source inlet, water outlet, and seven commercial rice fields daily from 30 May to 21 June 2017. Ammonium (NH4+), nitrate (NO3-) and nitrite (NO2-) concentrations were measured using standard colorimetric methods for nitrogen. Other water quality parameters, pH, hardness, alkalinity, turbidity, and conductivity, were measured using lab instruments and standard methods. Concentrations of NH4+, NO32-, and NO2- across all locations and sampling dates were <4 mg L-1. Nitrogen concentrations were lower when compared to the regulated limit for ambient surface water. Water pH in all sites ranged between 6-6.9, while hardness and alkalinity were <50 mg L-1. Overall, these findings suggest that surface water moving through the GP farms is categorized as soft with a very low buffering capacity for potential pollution.

presenting
11 am—12 pm

Hometown: Little Rock, AR

Improving Aquaculture Catfish Health with a Novel Plant-Produced Therapeutic Protein

Madalyn Weiner[1,3], Lana Elkins[2,3], Maureen C. Dolan[1,2,3]

[1]Department of Biological Sciences; [2]Molecular Biosciences Program; [3]Arkansas Biosciences Institute, Arkansas State University, Jonesboro, Arkansas

Arkansas is the birthplace of aquaculture, which includes commercial farming of fish in ponds and tanks. Despite continuing improvements in fish health management, farmed fish remain susceptible to disease that result in economic loses to the farmer. Antibiotics are commonly used to manage disease outbreaks; however, increasing concerns of antibiotic resistance with negative consequences on humans and the environment have emerged. Our lab is working on technology for producing a catfish protein therapeutic as a safer alternative to antibiotics that when delivered by immersion or medicated feed could "naturally" boost the fish's immune system. Plants can be used as biofactories for producing complex proteins like catfish interleukin-22 (IL-22). However the natural instability of IL22 protein results in it quickly being degrading in the harsh aquaculture environment. Therefore this protein therapy was engineered with a partner protein, RTB, to enhance the stability and uptake of the IL22 therapeutic into fish gill epithelial cells. Preliminary data indicates IL22-RTB can be made in plants and successfully triggers an immune response in channel catfish cells used as a model system for testing. Catfish IL22-RTB therapeutic may provide a sustainable, alternative method for limiting disease in aquaculture, benefitting the state of Arkansas economically and ecologically.

presenting
11 am—12 pm

Hometown: Tulsa, OK

Quantitative Proteomic Analysis of Mice Kidney Reveals an Effect of High Fat Diet on Protein Expression

Damiesha Bryant [1], Rocio Zapata Bustos [2], Reginald Rayford [2], Paul Langlais [2], and Lawrence J. Mandarino[2]

[1]Philander Smith College, Little Rock, AR; [2]Division of Endocrinology, University of Arizona, College of Medicine, Tucson, AZ

As obesity remains prevalent in the western world, it is critical to understand how excess visceral adiposity alters the function of other organs. Obesity increases the risk of developing degenerative conditions such as hypertension and Chronic Kidney Disease. Dysfunctions in the regulation of the renin-angiotensin-aldosterone system has been shown to promote renal disorders. High fat diet induced obesity has also been shown to lead to hypertension due to both excessive visceral adipose tissue surrounding the kidneys and the elevation of renal tubular sodium reabsorption. Not only does a high fat diet promotes hypertension, but also it encourages an increased fatty acid oxidation and decreased fatty acid synthesis. In this study, using mass spectrometry based proteomic analysis, we evaluated the effects of high fat diet (HFD) induced obesity on the mouse kidney protein expression to gain insight into how obesity may lead to Chronic Kidney Disease. Our findings suggest that long-term consumption of a high fat diet may cause decreased expression of proteins in the kidney such as Acetyl Carboxylase I and II, Renin, and Fatty Acid Synthase while proteins such as CYP450 A410, CYP450 A414, and Angiotensinogen may increase in expression.

presenting
11 am—12 pm

Hometown: East End, AR

Analysis of a Drosophila melanogaster Ribosomal Protein Gene

John Mitchell and Mary Stewart

Mathematical and Natural Sciences, University of Arkansas at Monticello, Monticello, AR

In humans, mutations in genes coding for ribosomal proteins or in genes involved in ribosome biogenesis can cause conditions known as ribosomopathies. These conditions cause symptoms such as anemia, craniofacial abnormalities and abnormal blood cell production, which may be associated with decreased rates of protein synthesis. With some ribosomopathies, patients have a higher risk of some cancer types. Likewise, mutations in ribosomal protein genes in *Drosophila melanogaster* (fruit fly) cause phenotypes consistent with reduced protein synthesis such as delayed development and short, thin bristles in adult flies. Mutation of the *D. melanogaster ribosomal protein S6* gene (*RpS6*), cause tumors in developing animals. The *RpS6* gene codes for ribosomal protein S6 (RpS6). In addition, the first intron of this gene contains information for a small non-coding RNA thought to function as a small nulceolar RNA (snoRNA). We are working with a mutant strain of *D. melanogaster* that is known to reduce *RpS6* mRNA expression, but we do not know how RpS6 protein expression is affected in these flies nor do we know if the mutation affects expression of the snoRNA. Our current work is aimed at comparing RpS6 protein expression in the mutant flies and in wild-type flies.

presenting
11 am—12 pm

Hometown: El Dorado, AR

Effects of Hypobaria with Added O_2 and CO_2 Concentrations on *Arabidopsis thaliana* Development

Mason Clay and Jim Taylor

Ouachita Baptist University, Biology Department, Arkadelphia, AR

This study addressed the effects of hypobaric conditions as well as increased O_2 and CO_2 concentrations on plant growth of *Arabidopsis thaliana*. This research can be beneficial to increasing the capability of establishing a system for long term space travel. In this study, three groups of plants were grown, two experimental groups and a control group. Both experimental groups contained 30 wells with 2 seeds per well and were grown in a hypobaric chamber with a constant pressure of 20 inHg, approximately 33% of atmospheric pressure, and had a 24-hour light intensity of approximately 28-33 $\mu M/M^2$. The control group contained 18 wells with 2 seeds per well and was grown in a chamber at normal atmospheric pressure and had a 24-hour light intensity of approximately 38 -43 $\mu M/M^2$. All three plant groups were grown on a Rockwool substrate. The first experimental group was grown in a hypobaric chamber with no added gases. The second experimental group was grown in a hypobaric chamber and received added oxygen for the first week, and added CO_2 from the second week to the end of the experiment. The plants were allowed to grow for 6 weeks and were then harvested in order to collect data on their growth and development. The control, first, and second experimental groups experienced germination in all wells and little to no plant death throughout the duration of the experiment. The plants in each group were evaluated for their overall growth as well as the size and color of their leaves. The second experimental group which received added O_2 and CO_2 experienced more growth and larger, greener leaves compared to the first experimental group. The second experimental group had an average leaf area of 113.36 mm^2 compared to the first experimental group having an average leaf area of 60.35 mm^2. The control group grew much more quickly and much larger than the experimental groups which was expected with an average leaf area of 199.43 mm^2. The lack of vertical growth of the experimental groups could have been caused by the decreased pressure in the hypobaric chambers as wells as an inability to distribute water effectively throughout the Rockwool. The different treatments exhibited similar photosynthetic rates of electron transport (0.784, 0.787, and 0.789 respectively) as measured by Pulse Amplitude Modulated (PAM) fluorescence. This indicates that the photosynthetic ability of the leaves was not compromised when placed in hypobaric conditions and the addition of CO_2 and O_2 in future scenarios of space flying will benefit plant growth at low atmospheric pressure.

presenting
11 am—12 pm

Hometown: Jacksonville, AR

Investigations into the Effects of Caffeine on Cell Death in *Dictyostelium discoideum*

Kristen Gregory, Azure Yarbrough, and John Bush

Department of Biology, University of Arkansas at Little Rock, Little Rock, AR

Dictyostelium discoideum is a haploid amoeba that is found in the wild and used as a model organism in different applications. The purpose of this study was to look at cell death with and without caffeine to see where death is inhibited. Caffeine is used in commercial and medical applications in today's world and studying caffeine will help in understanding what happens and how it affects us when it goes through our bodies. In *D. discoideum,* it has been shown to block the binding site of cAMP. I tested three different cell lines with and without caffeine. Each experiment was completed in triplicate and statistical analysis was completed. One cell line was ddRab32c which is the protein that is being studied in this experiment. In this cell line, calcium is overexpressed and it is known that caffeine affects the absorption of calcium. Caffeine increased cell death, blocked early development of cells. The ddRab32c cell line acted differently than the other cell lines. Future work includes investigating the role of calcium in programmed cell death and looking for a possible connection, functional characterization of the ddRab32c protein, and studying the role of ddRab32c in programmed cell death.

presenting
11 am—12 pm

Hometown: Pine Bluff, AR

Thymoquinone induces apoptosis in murine squamous cell carcinoma (SCC VII) cells through ROS induction and glutathione depletion

Malcolm Anderson and Selma Dagtas

University of Arkansas at Pine Bluff, Pine Bluff, AR

Oral cancer is a challenging medical problem with disappointing survival rates. Despite the successful treatment of the initial lesion, new lesions appear under the influence of the same predisposing factors that anti-oxidant effects. In our laboratory, a water-based whole N. sativa seed extract was found to inhibit cell viability in murine squamous cell carcinoma (SCC VII) cells in vitro. Among the known bioactive compounds N. sativa contains, α-hederin was found to be the effective compound in the water extract. However, IC50 of α- hederin was considerably higher than what is reported in the literature on different cell types. In this study, we compared the IC50 of α-hederin in the presence and absence of serum in murine squamous cell carcinoma (SCC VII) cells. IC50 of α-hederin in the absence of serum was about 10 times lower suggesting that α-hederin is bound by serum proteins.

presenting
11 am—12 pm

Hometown: Malvern, AR

Incorporation of SNP Mutations in Integrin's Alpha Subunit to Alter Function

Quincy Gragg[1], Billy G. Hudson[3], and Kyle Brown[2]

[1]ASPIRNAUT Research Program,Vanderbilt University Medical Center, Nashville, TN; [2]Henderson State University, Arkadelphia, AR; [3]Nephrology and Hypertension Department, Vanderbilt University Medical Center, Nashville, TN

The excess accumulation of extracellular proteins, like collagen, in the extracellular matrix (ECM) of the kidney can lead to the scaring of healthy tissues and ultimately kidney fibrosis. The binding of collagen IV throughout the kidney is mediated in part by integrins, a class of transmembrane protein receptors. Specifically, integrin alpha1 beta1 plays the vital role of downregulating the production of collagen IV in the kidneys. This research project focuses on the alpha subunit of integrin alpha1 beta1 with a goal to understand its mechanism of function. We hypothesize that a single nucleotide polymorphism (SNP) in the alpha subunit will affect this integrins function. Using the National Center for Biotechnology Information's (NCBI) SNP database we selected from roughly 522 SNPs based on amino changes most likely to deleteriously affect the integrins function according to structural models and what we know about integrin activation. These SNP selections distorted the charges, functional groups, polarity, and overall relationship between amino acids in the integrins structure. The insertion of a N-terminal FLAGG-affinity tag into plasmids expressing wild-type integrin a1, followed by the introduction of SNP mutations through site-directed mutagenesis, lead to the subsequent expression of recombinant integrin subunits in human embryonic kidney cells. Unexpectedly, we discovered that Q5 site directed mutagenesis improved the incorporation of mutations. We structurally analyzed these mutated integrins by placing them in lipid bilayer Nano disks and using negative stain electron microscopy. We then compared the conformations of several integrins and concluded that our mutation indeed influenced our integrin's structure. Research supported by: NIH R01 DK18381 to B.G.H, This work was also supported by the Aspirnaut Program through the National Institute of Diabetes and Digestive and Kidney Diseases of the National Institutes of Health, R25 DK09699 to B.G.H.

presenting
11 am—12 pm

Hometown: Hot Springs, AR

Improving the Health Benefits of Muscadine Grape through Genetic Engineering

Parker Knapp[1], Mohammad Azim[1], Tianhong Yang[1], and Fabricio Medina-Bolivar[1,2]

[1]Arkansas Biosciences Institute; [2]Department of Biological Sciences, Arkansas State University, Jonesboro, Arkansas

Muscadine grape is a native species of the southeastern United States which produces resveratrol, a compound that has shown several biological effects with potential applications in human health. However, one major limitation of resveratrol's use in humans is its low bioavailability due to its rapid metabolism. Interestingly, the peanut plant can produce arachidin-2. The latter is a derivative of resveratrol which is prenylated and exhibits favorable metabolic profiles. Importantly, a recent study proposed arachidin-2 as a lead compound for the treatment of Alzheimer's disease. Our laboratory identified the peanut prenyltransferase gene responsible for the prenylation of resveratrol to produce arachidin-2. To this end, we are developing tissue culture conditions to express this prenyltransferase in muscadine grape. Plants of two cultivars of muscadine grape (i.e. cultivars Fry and Noble) were grown in the greenhouse. Cuttings were taken from these plants and sterilized to start shoot cultures *in vitro*. Plantlets are being propagated *in vitro* and explants from these plantlets are used for genetic transformation with the ultimate goal of producing arachidin-2 in muscadine grape and thereby increasing the health benefits of this important Arkansas plant.

presenting
11 am—12 pm

Hometown: El Dorado, AR

Exosomes and their role in Neuron Differentiation

Alyson Cole[1], Rachel Bacon[1], Madison Crosby[1], Nathan Reyna[1], Raj Kore[2], and Rob Griffin[2]

[1]Ouachita Baptist University, Arkadelphia, Arkansas; [2]University of Arkansas for Medical Sciences

Unlike other cells in our body, when neurons are damaged they cannot be replaced, and the result is a loss of feeling or in some cases paralysis. Through AR-EPSCoR funded Center for Advanced Surface Engineering (CASE) grant**,** research at Ouachita Baptist University has focused on understanding the role exosomes play in repairing damaged neurons. While many aspects of exosomes are unknown, they have been shown to play a role in cell growth, communication, and differentiation. Recent by our team has shown the ability of exosomes to induce neurite differentiation in the absence of Neural Growth Factor. Elucidating the role of exosomes in cell signaling may provide novel approaches for regenerative medicine in relation to spinal cord injuries. Additionally, this project is unique in that it incorporates undergraduates into all phases of the project and as a result connects our students directly with graduate programs in Arkansas and increases the State's research infrastructure. Funding is provided by the Center for Advanced Surface Engineering, under the National Science Foundation Grant No. OIA-1457888 and the Arkansas EPSCoR Program, ASSET III.

presenting
11 am—12 pm

Hometown: Monticello, AR

Neuronal Differentiation For Transplantation Therapy: Role of Matrix Components

Shontiara Johnson[1], Chetan Pandanaboina[2], Dustin Rhoads[2], Malathi Srivatsan[2]

[1]University of Arkansas at Pine Bluff, Pine Bluff, AR; [2]Arkansas Biosciences Institute, Arkansas State University, Jonesboro, AR

Neurodegenerative diseases and brain injuries affect millions of people worldwide when functional units of the nervous system, neurons, are unable to function and die. Since neurons do not divide, unlike other cells in the body, and cannot replace themselves once they are lost, cell transplantation therapy is being proposed as a cure for these diseases. However, transplantation therapy requires a large number of neurons and neural stem cells (NSCs) which have the potential to differentiate into neural cells such as neurons, astrocytes, and oligodendrocytes. Mesenchymal stem cells (MSCs) are multipotent stem cells that give rise to extracellular matrix (ECM), blood vessels, cartilage, bone, and muscle. To test this hypothesis, conditioned medium was collected from mesenchymal stem cell culture and exosomes were isolated from the conditioned medium. Rat neural stem cells were then differentiated using (1) Conditioned medium (2) Isolated exosomes (3) Conditioned medium depleted of exosomes for one week to see if beneficial components obtained from different conditions would promote neuronal differentiation. Our initial results suggested that the medium of mesenchymal stem cells consists of neuronal differentiation promoting as well as inhibitory molecules and exosomes isolated from mesenchymal stem cells help promote differentiation of more neurons.

presenting
11 am—12 pm

Hometown: North Little Rock, AR

Bottom-up vs. Top-down Processing in Individuals with Autism Spectrum Disorder

Taylor Dague[1], Kenith Sobel[2], Kami Koldewyn[3], and Amrita Puri[1]

[1]Department of Biology, University of Central Arkansas ,Conway, AR; [2]Department of Psychology & Counseling, University of Central Arkansas, Conway, AR; [3]School of Psychology, Bangor University, Bangor Wales

Previous research on Autism Spectrum Disorder (ASD) has emphasized the importance of identifying components of perceptual and sensory processing that differ between individuals with ASD and typically developing individuals (Dakin & Frith, 2005). Perceptual processing theories attribute these differences to abnormalities in bottom-up (sensory stimuli) or topdown (expectations) processing. Here, a visual search task was used to determine if individuals with ASD differ from NT individuals in their utilization of top-down strategies versus bottom-up information. Participants completed a task in which they searched for a red horizontal target among red tilted and green horizontal distractors. To manipulate the salience of bottom-up features, we varied the ratio of distractor types. The "distractor ratio effect" predicts that when either distractor group is small, reaction times are fastest (Bacon & Egeth, 1997). Both ASD and NT participants exhibited the "distractor ratio effect" and seemed to favor searching by color when the difference between the target and distractor orientation was small, indicating similar utilization of a top-down strategy by both groups. Our results are consistent with Happe and Frith (2006) who suggest that bottomup signals are stronger than normal in individuals with ASD.

presenting
12pm—1 pm

Hometown: Greenbrier, AR

How to fingerprint a lizard by mapping unique patterns of scalation

Garrett R. Lawson, Chris J. Kellner, Sarah A. Tomke, and James H. Noble

Department of Biology, Arkansas Tech University, Russellville, AR

Investigations into the ecology of lizards often require that individuals be marked for identification so that demography and life history traits can be evaluated. Toe-clipping is the most common method of marking lizards. However, photographic identification is an attractive alternative to toe-clipping, which may reduce survival and is sometimes unreliable. Our objective was to determine whether scalation patterns on the heads of prairie lizards, (*Sceloporus consobrinus*), could be used to identify individuals. We used a sample of alcohol-preserved lizards and the photographic identification software Interactive Individual Identification Systems (I^3S) to identify individuals based on their scale intersections. The I^3S software produces a fingerprint of each individual based on the spatial relationship among a series of points, in our case, scale intersections. First, two of us independently marked scale intersections on a random sample of 30 lizards. All of the 30 lizards were correctly matched by I^3S in this trial. The second trial simulated a capture-mark-recapture study. In our second trial we had an average error rate of 7.4%. We concluded that the pattern of scale intersections in prairie lizards is unique to each individual and that I^3S is a suitable alternative to toe-clipping to identify individual prairie lizards.

presenting
12 pm—1 pm

Hometown: Conway, AR

Response of riffle fish communities to stream morphology changes resulting from stream degradation

Chance Garrett, Ginny Adams, and Reid Adams

College of Natural Science and Mathematics, University of Central Arkansas, Conway, AR

The streams of the Arkansas Ozarks have experienced extensive erosion and gravel intrusion due to changing land use. As a result, modifications to instream habitat have resulted in an increase in transverse and diagonal gravel bars along with associated shallow, low flow riffles. This study was conducted to determine if variation in riffle habitat (depth, velocity, substrate size) affects the riffle fish community. Understanding how fishes are using different riffle habitats is crucial to ensuring restoration efforts provide the necessary habitats for fishes throughout their various life history stages. For this study 22 riffles were sampled in the King's River, Arkansas using seines and kick set methods. Fishes were preserved in 10% formalin and identified in lab; standard lengths of benthic fishes were taken. Habitat data were taken at each riffle including velocity, pebble count, depth, and water quality. The King's River exhibited a gradient in available riffle habitat with two extremes being shallower, slower, wider riffles with smaller substrate (transient riffles) and deeper, faster, narrower riffles with larger substrate (stable riffles). Results of community and species level analyses in relation to habitat will be discussed.

presenting
12 pm—1 pm

Hometowns: Jonesboro, AR (KV)
Beebe, AR (KS)

Peanut Hairy Roots: A Sustainable Production Platform of Bioactive Compounds for Agriculture and Human Health

Krishna Vellanki[1], Kennith Swafford[1], Abbas Karouni[1], Patrick Roberto[1], Tianhong Yang[1], and Fabricio Medina Bolivar[1,2]

[1]Arkansas Biosciences Institute; [2]Department of Biological Sciences, Arkansas State University, Jonesboro, Arkansas

Hairy roots are "immortalized" tissue cultures that can reproduce the biosynthetic potential of the entire plant. Our laboratory has developed peanut hairy roots as a bioproduction system of stilbenoids, These compounds have shown a wide range of biological effects and potential benefits to agriculture and human health. For instance due to their antioxidant properties the stilbenoids may provide resistance to different abiotic stresses in the plant. In addition, stilbenoids have shown several bioactivities including anticancer and anti-obesity properties. To produce the stilbenoids, peanut hairy root cultures were co-treated with multiple elicitors for 168 hours. Ethyl acetate extracts were prepared from the culture medium of the elicited cultures. HPLC analyses of the extracts showed the presence of non-prenylated stilbenoids (resveratrol and piceatannol) and prenylated stilbenoids (arachidin-1, arachidin-2, arachidin-3 and arachidin-5). Ongoing studies are focused on optimizing the extraction procedure of the stilbenoids in order to obtain the highest levels of these bioactive compounds. The ultimate goal of this project is to identify and functionally characterize new compounds that could benefit the health and agriculture in Arkansas.

presenting
12 pm—1 pm

Hometowns: Dardanelle, AR (EF)
Russellville, AR (CC, TS)
Greenwood, AR (CS)

How Many Lives Can We Save? Isolation of Antibiotic Enhancing Microbes and New Antibiotics from Soil

Elvys Ferrufino-Mejia, Cody Campbell, Thomas Spencer, Courtney Stockton, Thomas Rolniak, Blake Wilson, Newton Hilliard, and Scott Kirkconnell

Biology Department, Arkansas Tech University, Russellville, AR.

Bacterial antibiotic resistance has been a developing problem recognized since the early 1940's with 2 million in the U.S. falling ill, 23,000 dying, and 700,000 dying worldwide in 2013 from infection by such microbes. The British government predicts this figure will soon rise above 10 million worldwide deaths annually. Our studies are directed at using novel techniques (iChips) employed by others to isolate and identify soil microbes yielding new antibiotics such as Teixobactin. We also developed creative approaches designed to identify antibiotic altering microbes which may enable isolation of substances that restore effectiveness of existing antibiotics against resistant bacteria. Progressively higher resistance levels were established in *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Serratia marcescens* in order to test for soil microbes that enhance the effectiveness of streptomycin against the resistant strains we created.

presenting
12 pm—1 pm

Hometown: Conway, AR

Characterizing Environmental Health Risks in Kanembwe, Rwanda

Mason Rostollan and Leah Horton

University of Central Arkansas, Conway, Arkansas

The burning of biofuels for cooking is particularly common worldwide in regions with low socioeconomic status and can lead to respiratory illness or mortality. This problem is worsened by lack of affordable healthcare and poor environmental health conditions. However, the use of rocket stoves may help lower the negative health impacts by reducing smoke production. In Kanembwe, Rwanda in 2015 ten families were introduced to rocket stoves. The stoves' users report a reduction of smoke production and reduced sinus irritation. In a pilot study, we measured lung function in some of the residents of Kanembwe using the peak expiratory flow rate (PEFR) and the Tiffeneau-Pinelli index along with data on height and age. For the preliminary data, two groups were used: those who already utilize a rocket stove and those who still cook on the traditional three-stone fire. There was no significant difference detected between individuals cooking over rocket stoves versus those who cook over traditional fires for either test of lung function. There was, however, a significant difference in PEFR value based on gender. Future work includes increasing the sample size of this study, identifying suspended particles in the smoke while cooking, and analyzing risks in the drinking water.

presenting
12 pm—1 pm

Hometowns: Plano, TX (AK)
North Little Rock, AR (CF)
Pottsville, AR (AT)

Relative Gene Expression Study on *Centruroides vittatus* Investigating Sodium Toxin Gene Activity

Chloe Fitzgerald [1], Ashlyn Tedder [1], Alyssa Kool [1], Taylor Bishop [1], Aimee Bowman [1], Cody Chivers [1], and Tsunemi Yamashita[1,2]

[1]Arkansas Tech University, Russellville, AR; [2]INBRE

Scorpions release neurotoxins in their venom when capturing prey or fighting off predators, from an area in the tail called the telson gland. The neurotoxins produced are mostly composed of a combination of different sodium toxins which alter the kinetics of sodium channel gating in the cells where they have been injected. This exploratory study on the sodium β toxin gene activity for the only scorpion known to inhabit Arkansas, the striped bark scorpion, *Centruroides vittatus*, specifically focused on gathering relative gene expression data for six neurotoxin variants in particular: Na668, Na667, Na1210, CsBeta, CvAlpha, and Na3066. This was accomplished by quantitative real-time polymerase chain reaction, or qRT-PCR. Preliminary experiments have been conducted on both male and female organisms by which threshold values yielded from these have been statistically analyzed within biological replicates as well as computationally analyzed through the ΔΔCt method, which has generated a tentative ratio of activity for these gene variants. The goal of this study was to determine the level of expression for the different sodium β toxin genes in the telson gland relative to body tissue in male and female scorpions of the eastern population. This information may one day be used to help develop therapeutic compounds for medical use.

presenting
12 pm—1 pm

Hometown: Vilonia, AR

A comparison of Japanese and American children's diets, and a literature review of diet and disease.

Malynn McKay and Robin Jamie Dalton

Department of Biological Sciences, Arkansas Tech University, Russellville, AR

The popular belief is that Japanese have a healthier diet than Americans. My goal was to determine if this belief is scientifically founded. The diets of Japanese and American children (ages 6-10) of similar socio-economic backgrounds, and living in similar rural environments were compared. A survey was conducted in Ofunato, Japan, as well as in Vilonia, Arkansas. This survey asked children what they ate for dinner the previous night, including the number of servings that the children had. Each student's meal was organized by what percentage of each biomolecule (saturated fat, unsaturated fat, high fructose corn syrup, cane sugar, protein, and fiber) was in the meal. The results were analyzed using ANOVA statistical analysis to determine if any significant differences exists between the two group's diets, and a Tukey Post-Hoc to determine between which biomolecules the differences exists. Next, a literature review of previous research was done to analyze the health benefits or detriments of each biomolecule. The top five death-causing chronic illnesses were identified for each country, and the aspects of the diet that are believed to influence the probability of developing each illness were discussed.

presenting
12 pm—1 pm

Hometown: Cabot, AR

Cognitive and Motor Task Switching Networks in Parkinson's Disease

Kori Maloy[1], Amrita Puri[1], Elizabeth Disbrow[2], and Christina Ledbetter[2]

[1]Department of Biology, University of Central Arkansas, Conway, AR; [2]Department of Neurology, LSU Health Sciences Center, Shreveport, Louisiana

Parkinson's Disease (PD) is well-known to impair motor movements due to the loss of neurons in the substantia nigra. Set switching deficits, or impairments in the ability to shift focus between one task and another, have been described in PD patients in relation to both motor and cognitive tasks. We used fMRI to explore the brain networks involved in motor and cognitive switching in participants with PD in comparison to a healthy control group. In the control group, the fMRI activity revealed activity in the superior and middle frontal gyri, right inferior frontal gyrus and the caudate nucleus. However, the PD group presented reduced activity in the left insula for motor switching. In PD, activity was decreased in the left insula, similar to the motor switching condition, as well as in the ACC and caudate nucleus. Our results suggest that motor and cognitive switching engage partially overlapping neural networks involving frontal and striatal regions. The PD group showed relative underactivation in the insula, a region known to be involved in task switching, for both types of switching. This underactivation in the PD group may reflect deficits in cognitive control networks involved in task switching and response selection.

presenting
12 pm—1 pm

Hometown: Fort Smith, AR

Regulation of Symbiotic Gene Expression in Rice

Randall Rainwater[1], Jacklyn Thomas[1], Yasir Rahmatallah[2], Galina Glazko[2], Ha Ram Kim[1], Grant Wiggins[1], Qingqing Yang[1], and Arijit Mukherjee[1]

[1]Department of Biology, University of Central Arkansas, AR; [2]Department of Biomedical Informatics, University of Arkansas for Medical Sciences, AR

Plants can form beneficial associations with microbes that aid in biological nitrogen fixation for the host. For instance, major food crops (e.g., rice, corn, etc.) can form beneficial associations with nitrogen-fixing bacteria like *Azospirillum* and *Herbaspirillum*. Our current understanding of the molecular aspects and signaling that occur between crops like rice and nitrogen-fixing bacteria is limited. Our long-term goal is to characterize the genetic pathways controlling these interactions. We established an experimental system where the bacteria could colonize the plant roots and then used this colonization model to identify several host pathways that could be potentially involved in symbiosis. Using RNA sequencing, we identified hundreds of differentially expressed genes during both interactions. Further analysis revealed that our dataset was highly enriched in genes involved in nitrate assimilation, nitrate metabolic processes, carbohydrate transport, etc. during rice-*Azospirillum* interactions. We identified genes involved in similar processes during rice-*Herbaspirillum* interactions suggesting that nitrogen fixation is ongoing and the plant is responding transcriptionally. This dataset serves as an excellent resource for genetic analyses of the host pathway involved in these interactions. These findings will have important implications towards improving nitrogen fixation in crops and will benefit agriculture in Arkansas, in the US and beyond.

presenting
12 pm—1 pm

Hometown: Portland, OR

Understanding the Mechanisms that Regulate the Dissociation of FACT from Genes Following Transcription

Graham Harris and Andrea Duina

Biology Department, Hendrix College, Conway, AR.

In eukaryotic cells, histone chaperones can manipulate chromatin to facilitate a variety of processes that occur on DNA, such as transcription and DNA replication. The FACT complex (FAcilitates Chromatin Transcription) is a highly conserved histone chaperone that plays important roles during transcription initiation and elongation by interacting directly with histones. Previous research from our laboratory has identified a region on the nucleosome – which we refer to as the CSGI (Control Spt16-Gene Interactions) region – that is required for proper dissociation of FACT from the 3' ends of genes at the end of the transcription process. We have recently initiated a series of studies to further investigate the mechanisms that regulate FACT dissociation from genes. Specifically, we are looking for proteins and histone modifications that might be involved in this process. For this purpose, we are employing a biochemical approach using the *Saccharomyces cerevisiae* model system. We describe experiments that utilize the CRISPR-ChAP-MS system previously published by the laboratory of Dr. Alan Tackett at UAMS. These experiments will allow us to assess the chromatin environments at the 3' end of a transcribed gene in wild-type cells and cells in which FACT does not dissociate normally due to a mutation within the CSGI region. Subsequent comparisons of the two chromatin environments may then lead to the identification of proteins and histone modifications that regulate FACT dissociation from genes. Potential hits from this screen may represent genes whose protein products are involved in promoting FACT dissociation from genes, increasing our understanding of this highly conserved process.

presenting
12 pm—1 pm

Hometown: Vilonia, AR

The Role of DNA Sequences in Controlling Interaction Between a Transcription Factor and Genes in Budding Yeast

Heather Prowse, Daniel Habenicht, Jennifer Harper, Sydney Ozersky, Claire Turkal, Alex Crocker, and Andrea A. Duina

Biology Department, Hendrix College, Conway, AR

Our studies focus on how basic genetic processes are regulated in cells. Transcription, the process in cells in which a DNA segment is transcribed into a RNA template, leads to expression of genes. Nucleosomes are present throughout the genome, including along the transcribed units of genes – nucleosomes can present barriers to the transcription process and DNA replication. To promote transcription elongation, the Facilitates Chromatin Transcription (FACT) complex, made up of the Spt16 and Pob3 proteins, works in parallel with RNA polymerase II (Pol II) by disassembling and assembling nucleosomes while moving toward the 3' end of genes. In previous studies from our laboratory using the Saccharomyces cerevisiae model system, we identified a region on the side of the nucleosome that is required for proper dissociation of FACT from the 3' ends of transcribed genes. Here we present our strategy to assess a possible role for DNA sequences in promoting FACT dissociation from the ends of genes. Together, these experiments will lead to a better understanding of the mechanisms that contribute to the dissociation of FACT from genes at the end of the transcription process.

presenting
12 pm—1 pm

Hometowns: Russellville, AR (AB)
Strawberry, AR (LS)

Generation of a loss of function mutant library by error prone PCR and gap repair to aid in structure-function studies of the Yvh1p protein in *Saccharomyces cerevisiae*.

Alice Bewley, Luke Shackelford, and Alexander Beeser

Department of Biology, Lyon College, Batesville, Arkansas

Protein structure-function studies are aided by the generation of a large panel of mutants that can be evaluated phenotypically. We are interested in a protein in the budding yeast Saccharomyces cerevisiae called Yvh1p that regulates ribosome assembly, and thus is a key regulator of global protein expression. Previous work had demonstrated that yeast cells engineered to lack this protein display ribosome assembly defects leading to a pronounced slow growth phenotype. What is currently unknown however is how Yvh1p mechanistically promotes faithful ribosome assembly? To address this question we have made a large library of mutants by error prone PCR and have used two different phenotypic assays to isolate cells that now re-express these mutated variants but which continue to fail to promote faithful ribosome assembly. We intend to sequence these mutated variants in order to identify amino acid(s) critical to Yvh1p's cellular function. These studies expose evolutionarily conserved residues/domains/functions of the human ortholog of Yvh1p, (Dusp12), a protein implicated in the development of aggressive liposarcomas.

presenting
12 pm—1 pm

Hometown: Little Rock, AR

Collagen Increases Proliferation and Drug Resistance of Papillary Thyroid Cancer Cells Harboring BRAFV600E Mutations

Anna Sharabura, Jonathan Jenkins, and Laura J. MacDonald

Biology Department, Hendrix College, Conway, AR

Thyroid cancer is the most common endocrine cancer, and incidence is increasing worldwide. Thyroid cancer can be classified as either well-differentiated or poorly differentiated. Of well-differentiated thyroid cancers, papillary thyroid cancer is most common, and is associated with activating BRAF mutations. While our understanding of the genetic basis for thyroid cancer is fairly extensive, less is known about how the tumor microenvironment alters tumorigenic characteristics of thyroid tumor cells. Recently, Jolly et al. reported that papillary thyroid tumors derived from cells harboring activating BRAFV600E mutations and PTEN deletions are enriched with fibrillar collagen which is associated with decreased survival. In this study, we investigated whether growth on collagen enhanced tumorigenic characteristics of papillary thyroid cancer cell lines with BRAFV600E mutations. Three distinct cell lines derived from mouse papillary thyroid cancer tumors were grown in the presence and absence of collagen. Morphology was assessed using brightfield microscopy. Proliferation was assessed by trypan blue staining and ATP concentration, while growth inhibition assays were used to assess response to chemotherapy drug resistance. Interestingly, our results suggest that growth on collagen contributes to a more mesenchymal morphology, increased proliferation, and decreased sensitivity to chemotherapy drugs. These and other results implicate an important role for collagen in the progression of thyroid cancer.

presenting
12 pm—1 pm

Hometowns: Havana, AR (NL)
Harrison, AR (CF)
Monticello, AR (MH)

Potential Coexpression of Heterodimeric Thiosulfate Dehydrogenase in *Halothiobacillus neapolitanus*

Nicholas LaRoe, Christopher Fleming, Megan Hand, and Newton Hilliard

Department of Physical Science, Arkansas Tech University, Russellville, AR

Halothiobacillus neapolitanus is an obligate chemolithoautotroph capable of utilizing the extracytoplasmic oxidation of inorganic sulfur compounds as its sole source of metabolic energy. Unlike other sulfur oxidizing microbes capable of utilizing thiosulfate as an energy source, genomics data has shown the presence of a gene for a potentially heterodimeric thiosulfate dehydrogenase (tsdAB). The putative fused gene, comprised of Hneap_1476 and Hneap_1477, contains an ATGA motif indicating potential for coexpression of the two genes with a 1:1 stoichiometry. In addition, the ATGA sequence is accompanied by a putative Shine-Delgarno region that exists between 7 and 12 bases upstream of the ATGA sequence. Also, sequence alignment of the Hneap tsdAB gene against genes from species reported to produce a monomeric thiosulfate dehydrogenase indicates the presence of a 'spacer' of bases between the end of the 'monomeric genes' and the Shine-Delgarno sequence i n the fused gene. These features together lend support to the hypothesis that the two genes are coexpressed. In order to verify the tsdAB subunit stoichiometry, PCR primers were designed to amplify the entire Hneap_1476/1477 gene coding region including the region surrounding the gene fusion site. All PCR amplicons indicate a fragment near the predicted size of ~1638 bases. Mutagenic primers have been designed to remove/ modify the Shine-Delgarno region.

presenting
12 pm—1 pm

Hometown: Batesville, AR

Fiber-type composition of bearded seal (*Erignathus barbatus*) locomotor muscle

Lindsey M. Barrett[1], Jennifer L. Dearolf[1], Nicole M. Thometz[2], Anna Bryan[3], Colleen Reichmuth[4]

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Bearded seals are ice-associated pinnipeds (seals, sea lions, and walruses) that forage benthically. These animals are vulnerable to sea ice loss caused by global climate change. As such, understanding more about the unique physiology of this seal compared to other pinnipeds is important. One approach is to examine the construction of their swimming muscles. In this study, we examine the fiber-type profile of one of the bearded seals' locomotor muscles, the longissimus dorsi (LD). Sections of bearded seal LDs were cut using a cryostat and stained for their myosin ATPase activity after basic pre-incubation, as well as for their reaction to myosin heavy chain antibodies. The stained sections were imaged, and the fibers on the ATPase images were placed into three categories: dark, intermediate, and light. The numbers of fibers in each category were counted, and these abundance data were used to calculate the average fiber-type profile of the bearded seal LD. Additionally, the diameters of fibers in each of the three categories were measured using ImageJ. These properties of bearded seal swimming muscles will be compared to those of the locomotor muscles of other seals, to enable an improved understanding of the species-specific characteristics of bearded seal muscle.

presenting
12 pm—1 pm

Hometown: Jonesboro, AR

Does frequently visiting a bluebird nest increase predation risk?

Amanda Trusty and Virginie Rolland

Arkansas State University, Jonesboro, AR

Monitoring avian nest success requires visiting nests regularly, but visits create disturbance and may attract predators. Therefore, our objective was to determine the impact of visit frequency on nest predation. Between March and September 2017, we monitored 115 nest boxes occupied by Eastern Bluebirds (*Sialia sialis*), about 10 km north of Jonesboro, Arkansas. We recorded the nest status every 1-6 days from the first egg to fledging or nest failure. Fifteen days after hatching, chicks may fledge prematurely if disturbed. Therefore, we also randomly divided nests with 15-day-old chicks in two groups: checked daily or at the estimated fledging date. We excluded nests abandoned or of unknown fate, and of the remaining 195 nesting attempts, 44 were depredated. Specifically, we found that the more frequent the visits, the more likely a nest was to be depredated. However, all chicks successfully fledged from the nests checked daily after day 15, indicating that nests may be most vulnerable at a younger stage. We recommend that bluebird monitors of Arkansas and elsewhere record nest status at a 3-day or longer interval. With caution, monitors may visit nests daily after day 15 without jeopardizing nest success, allowing them to accurately determine nest fate.

presenting
12 pm—1 pm

Hometown: Jonesboro, AR

Does axle grease effectively protect bluebird nests from predators?

Michael Trusty and Virginie Rolland

Arkansas State University, Jonesboro, AR

Bird conservation organizations have long promoted the use of predator guards, such as the Kingston stovepipe baffle, to protect nest boxes and increase nest success of birds nesting in cavities. A recent large-scale study showed that predator guards effectively reduce nest predation. However, the effectiveness of axle grease as a common predator deterrent was not tested. Therefore, our objective was to determine the effectiveness of axle grease at increasing nest success. From March to September 2017, we monitored 148 nest boxes at a site 10 km north of Jonesboro, Arkansas, but we focused our study on the 115 nest boxes used by Eastern Bluebirds (*Sialia sialis*). We divided these nest boxes evenly among three groups: baffle, grease, and no guard. Bluebirds made 238 nesting attempts, 44 of which were depredated, primarily by snakes (48%) followed by raccoons/cats (28%), squirrels (13%), and unidentified predators (11%). Our models indicate that grease and baffles equally improved bluebird nest success by about 40%. Though not significantly, grease tended to yield a higher nest success than baffles. To conclude, axle grease is a cheap and effective alternative to baffles that owners of bluebird boxes in Arkansas and elsewhere can use to further bluebird conservation.

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