November 6-7, 2015

Arkansas INBRE Research Conference

Arkansas IDeA Network of Biomedical Research Excellence

Schedule of Events

Friday, November 6, 2015

12:00 p.m. to 1:30 p.m.	Registration (Chancellor Hotel Atrium, 2nd floor). Graduate Program Information available from 12:00-1:30.
1:30 p.m.	Opening Session, chaired by Professor Wesley Stites, Chair, Department of Chemistry and Biochemistry, UA-Fayetteville (Chancellor Hotel, Eureka Springs Ballroom)
1:35 p.m. to 3:00 p.m.	Invited faculty presentations
3:00 p.m. to 3:15 p.m.	Set-up time for student orals
3:00 p.m.	Official hotel check in
3:15 p.m. to 5:00 p.m.	Undergraduate oral presentations (Chancellor Hotel, Biology – Eureka Springs Ballroom; Chemistry – Bella Vista Room; Physics – Petit Jean Room). (12 minute talks with 3 minutes for questions)
5:15 p.m. to 6:15 p.m.	Faculty Discussion Group and Reception (Chancellor Hotel, Lounge and White River Room)
5:15 p.m. to 6:15 p.m.	Student Discussion Group and Reception (Chancellor Hotel, Atrium)
6:30 p.m.	Banquet (Fayetteville Town Center)
7:15 p.m.	Featured Speaker Alex Badyaev, Ph.D.

Saturday, November 7, 2015

7:30 a.m. to 8:00 a.m.	Poster Set-up begins (Hillside Auditorium, Physics Building)
7:30 a.m. to 10:00 a.m.	Conference Registration (Upper Hillside Lobby)
7:45 a.m. to 9:30 a.m.	Continental breakfast (Upper Hillside Lobby, Physics Bldg.)
7:45 a.m.	Poster judges receive assignments (Hillside Auditorium for Biology and Chemistry, Physics Building for Physics judges)
8:00 a.m. to 9:00 a.m.	Poster Session A (Hillside and Physics)
9:00 a.m. to 9:15 a.m.	BREAK – Remove Session A posters (except Physics). Put up Session B posters.
9:15 a.m. to 10:15 a.m.	Poster Session B (Hillside and Physics)
10:30 a.m. to 11:45 a.m.	Workshops and Tours (UA Campus, various locations)
11:55 a.m.	Award presentations & conclusion, Hillside Auditorium 202

Registration Information

The INBRE registration desk will be open:

- Friday – 12:00 p.m. to 5:00 p.m., Chancellor Hotel Atrium (2nd floor)
- Saturday – 7:30 to 10:00 a.m., Hillside Auditorium, Upper Lobby

Travel Subsidies are no longer being given.

Lodging will be at the Chancellor Hotel,
70 N. East Avenue, Fayetteville, AR 72701.

Parking: Friday parking is complimentary in the Municipal Parking Garage, third level only (first level card access for registered guests of the Chancellor Hotel). Parking in the parking garage behind the Town Center is free all day Friday and Friday night.

Saturday parking is free on the UA campus in designated yellow-sign lots and parking decks. Please see the map at end of program.

Arkansas INBRE

The Arkansas IDeA Network of Biomedical Research Excellence (Arkansas INBRE) is funded by a grant from the National Institute of General Medical Sciences (NIGMS), under the Institutional Development Award (IDeA) Program of the National Institutes of Health (NIH). The IDeA program was established for the purpose of broadening the geographic distribution of NIH funding for biomedical and behavioral research. Currently NIGMS supports INBRE programs in 23 states and Puerto Rico.

The Arkansas INBRE builds on the successful Arkansas Biomedical Research Infrastructure Network (BRIN) program that was established in 2001 under a grant from NCRR. The Arkansas BRIN established a statewide network that links Arkansas institutions of higher education to establish and maintain a statewide infrastructure in support of growing efforts to build capacity for biomedical research in Arkansas. http://brin.uarms.edu/default.asp

Arkansas INBRE Research Conference

The Arkansas INBRE Research Conference is sponsored by Arkansas INBRE and is hosted by the departments of biological sciences, physics, and chemistry and biochemistry, Fulbright College of Arts and Sciences, University of Arkansas.

Conference Planning Committee

Denise Greathouse, chemistry and biochemistry
Ravi Barabote, biological sciences
Bill Durham, chemistry and biochemistry
Leslie Johnson, chemistry and biochemistry
Roger Koeppe, chemistry and biochemistry
Reeta Vyas, physics

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Joe Jeffers, Ouachita Baptist University
Roger Koeppe II, UAF
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Caroline Miller Robinson, UAMS, Business Manager
Linda Williams, UAMS, Research Liaison

Facility Leaders

Joshua Sakon, UAF
Alan Tackett, UAMS

Poster Session and Awards

Display

Poster set-up begins at 7:30 a.m. Saturday in Hillside Auditorium, Lower Level, and Physics Building.

Session A – 8:00 a.m. to 9:00 a.m.
9:00-9:15 BREAK. Biology and Chemistry Posters: Take down Session A posters. Put up Session B posters.
Session B – 9:15 a.m. to 10:15 a.m.

Presenters are expected to be present during the scheduled time. Business or business casual dress is encouraged. *See index and abstracts in this program for numbers and Session assignments.*

Awards

Prizes will be awarded to the top oral and poster presentations in the undergraduate category in each discipline. The awards will be presented Saturday at 11:55 a.m. in Hillside Auditorium Room 202. Presenters must be present at the awards presentation to receive an award.

Judging Rules

Each undergraduate oral presentation and poster will be judged by at least two judges, selected from various institutions. To avoid a possible conflict of interest, no judge will evaluate a presentation from his/her own institution.

Awards will be given in each of the three disciplines – physics, biology, and chemistry and biochemistry. Only oral/posters with undergraduate participation, and where the designated presenter is an undergraduate student, will qualify for awards.

Featured Speaker

Islands in the sea of possibilities: Making sense of biological diversity in the era of genomics

Alex Badyaev, Ph.D.

Alex Badyaev. Professor, Department of Ecology and Evolutionary Biology, University of Arizona.
Ph.D. in Organismal Biology and Ecology from the University of Montana, 1999.

The age of most genes exceeds the longevity of their current genomic and functional associations by many orders of magnitude. How do past associations among ancient genes bias contemporary biological diversity? For example, a metabolic network of carotenoids has evolved during the earliest 5% of the life existence on Earth and was fully in place a billion years prior to the origin of birds that now use carotenoids for plumage coloration. Did the structure of this ancient network direct color diversification in birds? If so, what fraction of this pre-existing network has already been explored in avian evolution? What fraction of this space and what colors are inaccessible to birds? And what would the world look like if such constraints did not exist?

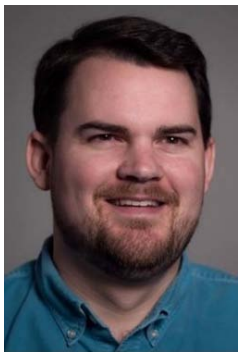
Alexander Badyaev joined the Department of Ecology and Evolutionary Biology at the University of Arizona in 2002. The central goal of his research is to understand the interplay of adaptation, contingency, and randomness in the evolution of complex organismal forms and functions. He received his B.S. and M.S. degrees in Comparative Anatomy and Population Ecology from Moscow State University in Russia; M.S. in Biological Sciences from the University of Arkansas in Fayetteville; and Ph.D. in Organismal Biology and Ecology from the University of Montana. Dr. Badyaev has been widely recognized for his research contributions. He is a recipient of the John Maynard Smith Prize (European Society for Evolutionary Biology) and the Theodosius Dobzhansky Prize (Society for the Study of Evolution), is a Packard Fellow in Science and Engineering (2005), a Fellow of the American Association for the Advancement of Science (2012), and a Kavli Foundation Fellow of the National Academy of Sciences (2013).

For more information on Dr. Badyaev, please visit www.u.arizona.edu/~abadyaev/

Invited Faculty Presentations

Friday from 1:30 p.m. to 3:00 p.m. (Chancellor Hotel, Eureka Springs Ballroom)

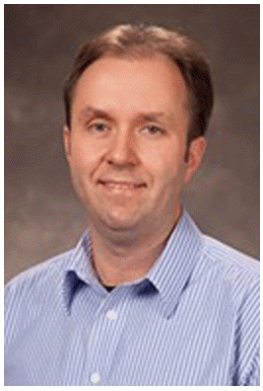
No registration required



Hugh Churchill
Assistant Professor
Department of Physics
UA-Fayetteville
(1:35 – 2:00)

TITLE: Building Electronic Devices with Atomically Thin Materials

Abstract: Two-dimensional crystals are materials only one to a few atoms thick. These materials are driving exciting developments in basic physics and technological applications of condensed matter in physics. Graphene, a one-atom thick membrane of carbon, was the first atomically thin material isolated when it was peeled from graphite over 10 years ago. The techniques used to isolate graphene have now been generalized to other materials so that the complete toolbox of properties – metals, insulators, and semiconductors – required for many electronic and optical devices is now available all with atomically thin materials. These materias can be picked up and stacked together to make a wide variety of devices composed entirely of atomically thin, transparent, and flexible materials. In this talk, I will present an overview of these developments and describe some of our contributions, including the demonstration of a photovoltaic device and light-emitting diode made from a three-atom thick sheet of WSe_2. I will also give an outlook of future plans for the new Churchill Lab in this rapidly developing research area.



Andrew Schurko
Assistant Professor
Department of Biology
Hendrix College
(2:05 – 2:30)

TITLE: Piecing Together the Puzzle of DNA Repair in Bdelloid Rotifers

Abstract: Eukaryotic cells are under constant assault by exogenous stresses and endogenous sources that cause DNA damage. Inefficient DNA repair is associated with many disorders, including cancer, neurodegenerative diseases and immunodeficiency. Bdelloid rotifers are a remarkable group of aquatic microinvertebrates that possess an exceptional DNA repair system. In bdelloids, double-strand breaks (DSBs) induced by high doses of ionizing radiation are rapidly and efficiently repaired. This talk will describe our research characterizing DNA repair proteins in bdelloids. Gene expression studies are being used to distinguish genes that are differentially expressed following irradiation. We are also undertaking proteomic studies to identify protein interactions and investigate the

role of epigenetics during bdelloid DNA repair. Overall, this work will improve our understanding of DNA repair in bdelloids, which will have implications for understanding DSB repair in human cells.

Roger E. Koeppe II
Professor of Chemistry and Biochemistry,
UA-Fayetteville
(2:35 – 3:00)

TITLE: More Fun than Anything

Abstract: Toward the goal of understanding the ionization behavior of protein amino acid side chains when exposed directly to lipids, we have designed and developed a molecular framework to serve as a host for guest ionizable functional groups in lipid bilayer membranes. This talk will address the essential properties of the host molecular framework, the basis for detecting the outcomes of proton transfer reactions, and results from specific titration experiments conducted for arginine, lysine, histidine, aspartic acid or glutamic acid side chains held at defined ocations within the lipid-bilayer membrane environment. Initial results have been published in PNAS 110, 1692-95.

Participating Institutions

Arkansas State University
Arkansas Tech University
Central Baptist College
East Central University
Harding University
Henderson State University
Hendrix College
Heyoka Technical Consulting
John Brown University
Lyon College
Missouri Southern State University
Missouri State University
Northeastern State University
Northwest Arkansas Community College
Ouachita Baptist University
Philander Smith University
Pittsburg State University
Rhodes College
Southern Arkansas University
University of Arkansas at Fayetteville
University of Arkansas at Fort Smith
University of Arkansas at Little Rock
University of Arkansas at Monticello
University of Arkansas for Medical Sciences
University of Arkansas at Pine Bluff
University of Central Arkansas

Student Oral Presentations

Undergraduates will give 12-minute oral presentations from 3:15 p.m. to 5:00 p.m. on Friday. All talks will take place at the Chancellor Hotel. Students were chosen based on abstracts and willingness to present an oral platform talk. Additional information, authors, and footnotes can be found in the complete list of abstracts in this program.

Biology Oral Presentations

(Eureka Springs Ballroom)

Jace Bradshaw, Ouachita Baptist University
(3:20 p.m.) Biological Characterization of Mycobacteriophage Promoter and Terminator Identified through Bioinformatics

Cullen Shaffer, Southern Arkansas University
(3:35 p.m.) Radiation and Microgravity Induced Genomic Instability, Optimization of Cell Recovery

Olamide Alawoyin, Philander Smith College
(3:50 p.m.) Legos, Layouts and Lesions: Site-Specific DNA Lesion Analysis Method for Mammalian Cells

Morgan Tripod, Arkansas State University
(4:05 p.m.) RNA-Binding Protein Regulates the Cytokine Production in T Helper Cells

Quinton L. Anderson, Harding University
(4:20 p.m.) Mycobacterium Tuberculosis Cell Wall Fractions Induce Inflammatory Cytokines in Primary Mouse Macrophages and Fibroblasts

Sara Whitlock, John Brown University
(4:35 p.m.) Impact of MARCKS Inhibition on *Coxiella burnetii* Infections of Host Cells

Chemistry and Biochemistry Oral Presentations (Bella Vista Room)

Abby Ritter, Rhodes College
(3:20 p.m.) DFT Study of the Selectivity of DOPA-decarboxyalse

Duy Ha, Henderson State University
(3:35 p.m.) Design of Tautomerically Ambiguous Cytosine-Based Nucleosides as Potential Anti-HIV Agents

Nick Niggemann, Missouri Southern State University
(3:50 p.m.) Towards the synthesis of 1-arylethyl-4-arylmethanesulfonyl-piperazines as potential serotonin 2A/2C receptor antagonists

Katherine Demaree, University of Central Arkansas
(4:05 p.m.) Iron Heteroscorpionate Complexes

C. Skyler Cochrane, Rhodes College
(4:20 p.m.) Synthesis of Various Dopaminergic Compounds for Analysis in SULT1A3

Raynin Phomakay, University of Central Arkansas
(4:35 p.m.) The Effect of Retinoid Receptor Agonists on K562 Cellular Adhesion, Proliferation, and α5β1 Integrin Cell Surface Expression

Physics Oral Presentations
(Petit Jean Room)

Darryl Webb, Southern Arkansas University
(3:20 p.m.) Techniques to Enhance Endothelial Cells Attachment to Microcarrier Beads, Achieving Microgravity Treatment

James Thomas, Missouri State University
(3:35 p.m.) Molecular Dynamics Simulations of the Mechanical and Hydrothermal Properties of Mesoporous Silica and Aluminosilica

Gabrielle Rose Abraham, University of Arkansas at Fayetteville
(3:50 p.m.) Optical Characterization of CdSe Collodial Quantum Dots

Zach Leuty, Missouri State University
(4:05 p.m.) Aluminide Diffusion Coatings

Elizabeth Apala, East Central University
(4:20 p.m.) Gamma Ray Burst 150518a

Dan Jones, Missouri State University
(4:35 p.m.) Graphene-Biointerface for Biosensor Applications

Saturday Workshops

INBRE participants are expected to attend a workshop as part of the program. All workshops and tours will take place Saturday at 10:30 a.m., in various locations on the University of Arkansas Campus

Registration for Workshops will be at Conference Registration Table

Workshop 1 – Preparing for Graduate School
(Chemistry Building, Room 132)
Denise Greathouse, PhD, UAF
This workshop is targeted toward undergraduate students who are considering graduate school as part of a career path. Topics to be discussed will include graduate school expectations and how to prepare for and seect a graduate school and rogram. A panel of faculty and graduate students will be available to share their tips, strategies, insights, and practical advice. We will conclude with a "Question and Answer" session, with the possibility of breaking into smaller groups based on specific interests.
Panelists:
Colin Heyes, Assoc. Professor, Chemistry, UAF, Chair Graduate Studies Committee
Woodrow Shew, Asst. Professor, Physics, UAF
David McNabb, Assoc. Professor, Biology, UAF, Chair Graduate Studies Committee
Doug Rhoads, Univ. Professor, Biology, UAF, Director Cellular and Molecular Biology Program
Malathi Srivatsan, Professor, Neurobiology, and Director of Molecular

Biosciences, AR State, Director PhD Program
Ashley Henderson, Senior Graduate Student, UAF
Cameron Crane, Senior Graduate Student, UAF
Parker Cole, First Year Graduate Student, UAF

Workshop 2 – Introduction to Mass Spectrometry: Fundamental Principles and Applications

(Chemistry Building, Room 105)
Jennifer Gidden, PhD, UAF

John Fenn, the 2002 Nobel Laureate in Chemistry, wrote: "Mass spectrometry is the art of measuring atoms and molecules to determine their molecular weight. Such mass or weight information is sometimes sufficient, frequently necessary, and always useful in determining the identity of a species." While its roots are in particle physics, developments over the past decades have enabled mass spectrometry to become a vital tool in identifying/monitoring compounds that are important in biological sciences, environmental analyses, food science, forensics, medicine, and so many other areas. This talk will present an introduction to the basic elements of mass spectrometry – including the primary instrumental components of a mass spectrometer, interpretation of mass spectral data, and examples of questions answered using mass spectrometry resources available at the Arkansas Statewide Mass Spectrometry Facility.

Workshop 3 – Proteomic Data Acquisition and Analysis

(Chemistry Building, Room 144)
Stephanie Byrum, PhD., UAMS, Instructor of Biochemistry & Molecular Biology and **Alan Tackett, PhD,** UAMS, Professor of Biochemistry & Molecular Biology and Pathology, Director UAMS Proteomics Facility
In this workshop, we will outline the proteomic and bioinformatics applications available through the UAMS Proteomics Facility. Dr. Tackett will provide an overview of instrumentation and data collection capabilities. This will include data collected from a recently acquired Thermo Fusion Orbitrap mass spectrometer. Dr. Tackett will additionally provide details and recommendations for experimental design for quantitative proteomic applications including proteome analysis, protein-protein interactions and posttranslational modification mapping. Dr. Byrum will provide an overview of database searching, data analysis and associated bioinformatics. She will detail commonly used programs in the field and best practices for analyzing data. Quantitative strategies including label-free and isotope-based approaches will be presented.

Workshop 4 – Molecular Modeling

(Chemistry Building, Room 308)
Peter Pulay, PhD, Dept of Chemistry and Biochemistry. Limited to 12 participants or groups. If feasible, bring a computer, although this is optional.
Methods of molecular modeling on a personal computer will be addressed, with

software available for distribution to up to 12 individuals or cluster teams.

Workshop 5 – Cellular Mechanisms of Salt and Water Transport in Fish

(Ferritor Building, Room 317)

Christian Tipsmark, PhD, UAF

The goal of physiological research is to understand the function of living systems from the level of the whole organism and its organs to that of the single cells and bio-molecules. This workshop highlights mechanisms and regulation of salt and water transport in fish and demonstrates some of the methods used in physiology. It will cover experimentations with whole animals and isolated tissues. Tehcniques demonstrated will include enzyme assays, specific mRNA and protein quantification and cellular localization of specific proteins with immunofluorescence.

Workshop 6 – Machine Learning for Bioinformatics

(Ozark Hall, Room 101 computer lab)

Philip Hudson Williams, PhD, UALR

Limited to 30 articipants

Some bioinformatics solutions involve predictors and classifiers. Machine Learning is a method to train accurate predictors and classifiers. This workshop demonstrates C5.0, a decision tree method for training a predictive model. Different data types are used as examples in training. Validation methods are introduced. Using a trained model for prediction of unknown cases is demonstrated.

Workshop 7 – Physics of Cells

(Physics Building, Rooms 132 and 126)

Pradeep Kumar, Asst. Professor of Physics, UAF

Participants will have the opportunity to learn how concepts from physics can be used to gain a quantitative understanding of biological systems. The workshop will cover several topics including emergent properties of cellular systems, physics of motility, phenotypic changes in cells under stress, thermodynamics and random walk of molecular motors. Students will also be able to experiment with some of these cellular phenomena in the lab.

Workshop 8 – Kool Matters

(Physics Building, Room 133)

Jacques Chakhlian, Professor of Physics, UAF

Hands on show and tell workshop to reveal unusual properties of material one can routinely find in everyday life.

Workshop 9 – Nano Building Tour

(Nano Building Room 105)

Professor Greg Salamo and graduate student Tim Morgan

Students will have the opportunity to visit Nano Building facilities, learn about nanoscience and get hands-on experience on how to image a sample with nanoscale resolution using a scanning electron microscope (SEM).

Workshop 10 – Physics Lab Tours

- **Quantum Device Laboratory**
  Hugh Churchill, PHYS 129

We fabricate nanoscale electronic and optical devices with properties that are enabled or enhanced by quantum mechanical effects. Currently we are

making devices out of three-atom thick semiconductors to study how they behave at ultra-low temperatures, in strong electric and magnetic fields, and how they interact with light. Visiting students can learn about how these devices are made, find out what they may be good for, and look at atomically thin materials in a microscope.

- **Nano-Optics Lab**
  Joseph Herzog, PHYS 245

In the Nano-optics lab, students measure the optical properties of nanostructures both with computer simulations and an advanced, custom optical microscope and spectroscopic setup. In the computer models, students work on designing nanostructures with optimal optical properties. The experimental optical setup characterizes the optical properties of the nanostructures with dark-field spectroscopy, photo-luminescence, bright-field imaging, and Raman spectroscopy. Most of the nanostructures that are investigated are plasmonic structures. These structures can enhance and focus light at the nanoscale, below the diffraction limit of light. Other studies in the lab investigate the light interactions in biological structures and photonic crystals. Photonic crystals are nanoscale structures which can reflect, guide, and bend light very efficiently. Additionally, students in the Nano-Optics lab use other labs around campus to fabricate the optical nanostructures.

- **Nanofabrication, Nanoscale Materials Science, and Single DNA and Protein Detection**
  Jiali Li, PHYS 124
  1. How to make Molecular Size Solid Sate Nanopores in silicon nitride membranes.
  2. How a nanopore based single molecule detectors can detect single DNA and protein molecules.

- **Laser Physics/Quantum Optics Lab**
  Surendra Singh, PHYS 128/130

Investigations of polarization and phase properties of optical beams, optical vortices, statistical and dynamical properties of light generated in lasers and nonlinear optical systems, and light scattering studies of bio-molecules are being carried out.

- **Quantum/nonlinear Optics with Multi-level Systems**
  Min Xiao, PHYS 111

In our Quantum and Nonlinear Optics Laboratory, we experimentally investigate third-order Kerr nonlinearity in multi-level atomic systems. We study interactions between coherent atoms and an optical cavity, and have observed many interesting phenomena, including optical bistability, multistability, instability, chaos and stochastic resonance. Spatial-temporal interference between third-order and 5th order nonlinear wave-mixing processes has also been studied.

Abstracts

Presentations are posters, on Saturday, unless denoted as "**Oral**" for Friday afternoon.

Biological Sciences

Friday Oral Platform Session

ORAL – 3:20. **Biological Characterization of Mycobacteriophage Promoter and Terminator Identified Through Bioinformatics.**
Jace Bradshaw, AlleaBelle Gongola, Nathan Reyna. *Department of Biology, Ouachita Baptist University, Arkadelphia, AR 71998.*

Bioinformatics uses complex algorithms and computer software to make predictions about genetic material. However since this is done in silico, these predictions still need biological confirmation—a difficult and time-consuming process. The goal of this project is two fold: first, to examine characteristics of the regulatory elements found in mycobacteriophage using novel cloning techniques; second, to investigate the validity of commonly used algorithms to ensure that the data produced from genomic analysis can be properly interpreted. To accomplish this goal, fourteen putative promoters from mycobacteriophage Mendokysei were identified through bioinformatic analysis using DNA Master. Additionally, six terminators were identified using ARNOLD. Promoters were verified and quantified using the expression vector pClone Red (BBa_J119137). A novel construct for terminator analysis named PGR-Blue was developed to increase the efficiency and accuracy of terminator quantification. Both vectors utilize Golden Gate Assembly to allow for the rapid testing and selection of putative regulatory elements. Results show that mycobacteriophage Mendokysei has one strong promoter and several weak promoters. Our results will provide a more thorough understanding of the practicality of bioinformatic predictions.

ORAL – 3:35. Radiation and Microgravity Induced Genomic Instability, Optimization of Cell Recovery.
Cullen Shaffer, Rupak Pathak, Abdel Bachri, Sanchita P. Ghosh, Igor Koturbash, Marjan Boerma, Martin Hauer-Jensen. *Department of Biology, Southern Arkansas University, Magnolia, AR 71753.*

Chromosomal aberrations such as translocations and dicentric fragments can result from DNA double-strand breaks caused by radiation damage accrued from exposure to outer space environments. The effect of near-zero space gravity on radiation induced DNA damage is not well documented. Gamma Tocotrienol (GT3), an enhanced vitamin E analogue, has been shown to decrease the number of chromosomal aberrations in mouse lymphocytes. In order to test GT3 radioprotection capabilities we deliver a radiation dose to human umbilical endothelial vein cells (HUVEC) and subject them to microgravity episodes. To achieve microgravity free suspension while providing a growth surface we attach HUVEC to, and recover them from Cytodex 3 microcarrier beads. Cell recovery is essential in order to be able to create karyotype spreads that can be quantified with fluorescence in situ hybridization (FISH) and spectral karyotyping (SKY). By varying incubation times and concentrations of trypsin and dextranase we sought to standardize the trypsin treatment to detach cells from microcarrier beads and maximize cell recovery. Trypsin and dextranase are enzymes that work by digesting peptide bonds and the dextran core of the bead respectively. Ultimately 8ml per 30mg – 60mg dry weight of beads of trypsin with 7 minutes incubation yielded the highest cell recoveries. Dextranase treatment delivered low cell counts and created abundant debris due to beads destruction.

ORAL – 3:50. **Legos, Layouts and Lesions: Site-Specific DNA Lesion Analysis Method for Mammalian Cells.**
Olamide Olawoyin[1], Bogdan I. Fedeles[2], John M. Essigmann[2]. [1]Department of Biology, Philander Smith College, Little Rock, AR 72202. [2]Departments of Chemistry and Biological Engineering and the Center for Environmental Health Sciences, Massachusetts Institute of Technology, Cambridge, MA 02138.

Genetic information of living organisms is constantly altered by endogenous and exogenous agents that modify the chemical integrity of DNA. Despite the efficiency of several DNA repair systems that ensure high fidelity during replication, some lesions escape these repair mechanisms, leading to deleterious consequences. Although it has been elucidated that many lesions are structurally disruptive to ssDNA and mutagenic in bacterial cells, their biological consequences have not been well characterized in mammalian cells in vivo. In order to quantify and characterize the mutagenicity of DNA lesions in mammalian systems, we developed an assay that incorporates the construction of a modular plasmid with a versatile lesion cloning cassette and targeted homologous recombination sites for mammalian genome integration. For proof of principle, the AS52 (a Chinese Hamster Ovarian (CHO) cell line containing one copy of the bacterial gpt gene) was selected and recombination sites homologous to target gpt gene were designed and cloned. To stimulate recombination, CRISPR/Cas9 constructs targeting the gpt gene were also designed. Construction of the plasmid containing a site-specific lesion involved: a) introduction of a Golden Gate cloning site (featuring type II restriction enzyme

sites) through Site Directed Mutagenesis; b) introduction of a lesion cloning cassette using Golden Gate assembly; c) using nicking enzymes to create a specific gap on one DNA strand; d) annealing and ligation of an ODN containing the desired lesion. pUC 19 plasmid was used as background plasmid. Sanger DNA sequencing confirmed that restriction enzyme sites were successfully incorporated through Site Directed Mutagenesis. Incorporation of the lesion cassette by restriction and nicking enzymes through Golden Gate Assembly was confirmed through SDS-PAGE gel analysis which indicated a significant difference between our constructed plasmid and original pUC 19 plasmid. The properties and features of the lesion-containing vector were then validated using the REAP assay. After the lesion is introduced and replicated intrachromosomally within host cell, the neighboring DNA sequence will be amplified using PCR and analyzed to determine the base composition at the site, conveniently quantifying how mutagenic or toxic the lesion is. This assay will enable us to accurately and rapidly quantify the toxic and mutagenic effects of biologically important lesions such as N2, 3-ethenoguanine (cause by lipid peroxidation byproducts) and 5-chlorocytosine (caused by neutrophil-induced chlorination) that are believed to be functional inflammation biomarkers that could explain the link between inflammation and malignant transformation.

ORAL – 4:05. RNA-Binding Protein Regulates the Cytokine Production in T Helper Cells. Morgan Tripod, Jing Chen, Shiguang Yu. *Department of Biology, Arkansas State University, Jonesboro, AR 72401.*

Inflammatory bowel disease (IBD) is characterized by chronic inflammation of the intestinal mucosa. Current therapeutic treatments are less effective, which emphasizes the need to identify new therapeutic targets for the management of IBD. Mounting evidence has shown that interleukin-22 (IL-22) plays a protective role in IBD by enhancing epithelial cell proliferation and healing responses, as well as producing anti-microbe peptides. However, the regulation of IL-22 production by T helper cells remains unknown. Our preliminary data showed that a RNA-binding protein (RBP) negatively regulates IL-22 production in Th17 cells. Knockout of RBP increases IL-22 production in Th17 cells by reducing TGF-β-induced inhibition of IL-22. Further research is being executed using ELISA, quantitative PCR, and western blotting in order to better understand this pathway. Targeting RBP in T cells resulted in the up-regulation of IL-22 and may therefore represent a novel therapeutic intervention in IBD. (Supported by P20GM103429)

ORAL – 4:20. Mycobacterium tuberculosis cell wall fractions induce inflammatory cytokines in primary mouse macrophages and fibroblasts. Quinton L. Anderson, Jo M. Goy. *Department of Biology, Harding University, Searcy, AR 72143.*

Mycobacterium tuberculosis (Mtb) infects one third of the world's population resulting in either a latent or active disease. Mtb infects and grows within host macrophages, resulting in the recruitment of host immune cells via cytokines and chemokines to form a granuloma. A granuloma is a collection of immune cells that surround and block off an infected area with in a tissue which are formed in order to prevent the spread of the infection and to eradicate the infection. While in the granuloma, some Mtb will be degraded within the phagosome. Components of Mtb, along with live Mtb may be expelled from the host in aerosol form. These fractions of Mtb are likely to interact with the host respiratory tract and induce an inflammatory response. Here, we test the hypothesis that cell wall fractions taken from Mtb, will induce an inflammatory response when exposed to primary mouse macrophages and fibroblasts. Cell wall fractions were derived from the hyper virulent strain HN878 or the lab adapted strain H37Rv. Enzyme Linked Immunosorbent Assays (ELISA) were used to detect the production of inflammatory cytokines from treated cells. A multiplex assay was used to detect the presence of multiple inflammatory cytokines and chemokines in fibroblast samples. We found that the production of IL-1β in macrophages and in fibroblast is dependent on the strain of Mtb. The hyper virulent Mtb strain induces a more potent IL-1β response than the lab adapted Mtb strain which agrees with what has been published by Gopal et al 2013 with whole cell lysates. These findings not only support our hypothesis, but also offer novel opportunities for vaccine development against Mtb by allowing us to target the delivery of Mtb cell wall fractions as vaccine components.

ORAL – 4:35. Impact of MARCKS Inhibition on Coxiella burnetii Infections of Host Cells. Sara Whitlock, Joel Brown, Ryan Kinney, Joel Funk. *Biology Department, John Brown University, Siloam Springs, AR 72761.*

The human disease Q-fever is initiated as a respiratory tract infection by the bacterium Coxiella burnetii. Acute infections typically result in flu-like symptoms and can be treated with antibiotics, but untreated chronic infections can lead to severe conditions including endocarditis. Bacteria enter alveolar macrophages within a phagosome, but instead of being destroyed by cellular enzymes, bacterial cells induce the infected cells to develop a lysosome-like organelle called the parasitophorous vacuole (PV) where replication takes place. The PV starts small but grows in size to accommodate the increasing number of replicating cells. Manipulation of the host infection by C. burnetii includes activation of Protein Kinase C (PKC) isoforms that sequentially phosphorylate downstream

substrates. MARCKS is one of several PKC substrates phosphorylated during infections. The objective of this study was to localize MARCKS using antibodies and examine the role of MARCKS using inhibitors. Our results indicated that MARCKS localizes to the PV membrane and surrounding cytoplasm. The level of MARCKS protein was knocked-down using siRNA treatment of HeLa cells. Infected cells treated with MARCKS siRNA contained C. burnetii, but more PV's were larger in size than those of infected cells treated with control siRNA. A peptide inhibitor of MARCKS appeared to have a similar effect on infected THP-1 cells by causing the development of more enlarged PV's compared to control peptide treatments. These results show that MARCKS may have a role in regulating or controlling the size of C. burnetii-induced PV's.

Biological Sciences

A – Saturday 8:00 – 9:00 Posters

B – Saturday 9:15 – 10:15 Posters

(Posters designated "U" will be judged.)

1A. Regulation of the Chemokine expression by a RNA-binding protein on Th17 cells. Jing Chen[1,2], Carole Cramer[1], Ulus Atasoy[2], Paul Drew[3], Shiguang Yu[1]. *[1]Arkansas State University, State University, AR 72401, [2]University of Missouri, Columbia, MO 65211, [3]University of Arkansas for Med. Sci., Little Rock, AR 72205.*

The C-C chemokine receptor 6 (CCR6) is one of most critical chemokine for pathogenic Th17 cell migration to the central nervous system (CNS) in multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE). In the CNS of EAE, Th17 cells expressed CCR6 is attracted by the chemokine ligand 20 (CCL-20), which constitutively secreted by choroid-plexus epithelial cells. The gene expression in cells is regulated by both transcriptional and post-transcriptional mechanisms. Post-transcriptional regulation is required to mediate rapid responses to stimuli, and it is crucial to study post-transcriptional regulation of CCR6 expression in Th17 cells. Here we demonstrated that the RNA-binding protein HuR regulates CCR6 expression by binding to its mRNA using RNA immunoprecipitation (RIP) assay, and HuR stabilize its mRNA using RNA decay rate assay. Furthermore, the data showed knockout of HuR in Th17 cells impairs their migration. Indeed, CCR6 transcript in the CNS was significantly reduced in the recipients that received HuR knockout CD4+ T cells than that of WT CD4+ T cells. These studies suggest that HuR promotes CCR6 expression on Th17 cells, in turn, which contributes to the initiation of inflammatory encephalomyelitis. (NIH p20GM103429, R01AI119135).

1B-U. Identifying Enriched CDR3 Sequences in Systemic Lupus Erythematosus Patients. Judith A. James, Benjamin F. Bruner, Corbett S. Hall, Michael R. Eledge. *Biology Department, Harding University, Searcy, AR 72143.*

Systemic lupus erythematosus (SLE) is an autoimmune disorder which affects predominantly middle-aged women. Symptoms, which vary from malar rash to renal failure, are used to diagnose patients according to standard SLE Disease Activity Index (SLEDAI) criteria. One common SLE hallmark is increased antibody levels, and several studies have documented potential antigens: DNA, RNA, Ro, La, etc. Antibodies consist of 4 chains: 2 heavy (IGH) chains and either 2 κ (IGK) or 2 λ (IGL) chains. Within the IGH region, complementarity-determining-region 3 (CDR3) is primarily responsible for antigen recognition and represents a prime target for antigen-binding studies. Deep sequencing data obtained using an Illumina MiSeq instrument was analyzed for CDR3 sequences enriched in SLE flare. The patient population was screened for patients with a confirmed SLE diagnosis, at least one time point in flare (≥6 SLEDAI criteria), and a non-flare time point. The CDR3 sequences within this population were clustered using the CD-HIT web server's hierarchical clustering feature. A flare distribution calculation was developed to identify highly enriched sequences, and these target clusters were realigned using ClustalOmega and visualized in Jalview. These target clusters can be analyzed in the future for potential SLE-linked antigens and help identify novel SLE therapeutic targets.

2A-U. **Autoantibody Profiling and Immunosuppressive Medications in Systemic Lupus Erythematosus and Incomplete Syndromes.** Michael Eledge, Corbett S. Hall, BF Bruner, JA James. *Biology Department, Harding University, Searcy, AR 72143.*

Autoantibody Profiling and Immunosuppressive Medications in Systemic Lupus Erythematosus and Incomplete Syndromes Article Abstract Systemic Lupus Erythematosus is an autoimmune disorder currently affecting 5-7% of the population; this is more likely an approximation due to the difficulty of diagnosis in a clinical setting. In some sub populations, for example females, this rate increases exponentially. In order to receive a "diagnosis", one must meet 4 or more of 11 ACR criteria. A specific and sensitive clinical test has yet to be developed due to system wide manifestations, varying disease activity, and unpredictable flare-ups. The purpose of this study is to investigate the clinical prevalence of autoantibodies of incomplete lupus-like syndromes and confirmed lupus individuals in means of developing a more specific diagnosis in future studies. A protein microarray composed of 77 possible targets of autoantigens was used to profile autoantibodies from 33 patients blood sera; SLE(n=18), ILE(n=15). Median

fluorescent values were obtained and subsequently used for analysis. Blood samples were taken at two different time points and clinical diagnosis was recorded as either SLE or ILE. Analysis revealed a great number of outliers within ILE individuals and a general trend of having a higher autoantibody level than SLE. Additional information regarding immunosuppressant medications were obtained and conclusions of medication effectiveness were made in regards to lowering disease related autoantibody levels in SLE patients.

2B-U. Using NF-κB pro-inflammatory pathway to predict response to therapy in an equine model of naturally occurring osteoarthritis. Angela Eichhorn, Kathie Ferbas, Monet McNally. *Biology Department, Harding University, Searcy, AR 72143.*

Osteoarthritis (OA) is the most common form of arthritis characterized by alterations in the chondrocytes and loss of cartilage extracellular matrix, which leads to biomechanical failure of articular cartilage. OA is an important cause of pain, disability and economic loss in humans. OA is similarly important in other species, such as horses (4). This study sought to test the hypothesis that pretreatment synovial fluid (SF) cytokine profiles can be used as biomarkers to predict whether or not routine injections of equine joints with steroids or autologous conditioned serum (ACS) will be effective. A total of nine horse SF samples were analyzed to measure and compare cytokine concentrations in horses undergoing joint treatment. The Nuclear Factor kappa-light-chain-enhancer of activated B-cells (NF-κB) pathway was used in order to identify activator and effector cytokines that may act as biomarkers of OA. Cytokine concentrations of Interleukins 1a, 2, 4, 8, 10, and 15, Interleukin 1 Recepor Antagonist (Il-1RA), Monocyte Chemoattractant Protein-1 (MCP-1), and Interferon gamma (IFN-g) were measured using a Quantibody Equine Cytokine Array. Real Time Quantitative Reverse Transcription Polymerase Chain Reaction (qRT-PCR) was used to measure transcription of MCP-1 RNA. Based on the results, IL-8 and MCP-1 levels were elevated in horses that did not respond to treatment. All horse samples were positive for MCP-1 RNA and the fold changes were consistent with the MCP-1 levels detected in the Quantibody Equine Cytokine Array.

3A. **Genetic Predictors of Exemestane Pharmacokinetics in Healthy Human Volunteers.** Bryana Gregory, M.A. Murphy, L.K. Kamdem. *Harding University College of Pharmacy and Physician Assistant Program, Searcy AR 72143.*

BACKGROUND: Exemestane is an aromatase inhibitor used for the prevention and treatment of hormone-dependent breast cancers and it works by blocking the aromatase enzyme in the final step of estrogen synthesis. Data suggests that there is inter-individual variability in the clinical response to exemestane. Since not all patients are candidates for exemestane therapy, we hypothesize that heredity may help identify the proper patient profile of those who should receive exemestane. The aim of this study was to determine the genetic predictors of exemestane metabolism. METHODS: 14 healthy postmenopausal women were enrolled into our study. They received a single dose of 25mg oral exemestane and plasma concentrations were measured from 0-8 hours. We determined the genotypes for 35 candidate polymorphisms in genes previously linked to the absorption, distribution, metabolism and excretion of drugs. The areas under the plasma concentration vs. time curves (AUC) were determined by the linear trapezoidal method. The AUC of exemestane were compared with the subjects' genotypes using either a two-sided Student's t-test or Mann-Whitney U Test. RESULTS: Among the polymorphisms genotyped, we identified three genes (SLCO1B1, UGT2B7 and CYP1A2) containing variants that were associated with exemestane metabolism. Significant P values (≤ .05) ranged from 0.0049-0.0455 for exemestane metabolism. CONCLUSION: Our results indicate that the genetically polymorphic enzymes SLCO1B1, UGT2B7, and CYP1A2 influence the metabolism of exemestane in healthy human volunteers following a single oral administration of 25mg exemestane. Genetic variants residing within the SLCO1B1, UGT2B7, and CYP1A2 gene loci could be important in determining the appropriate patient profile for exemestane therapy. ACKNOWLEDGEMENT: This work was made possible by the 2011 Young Investigator Award supported by grant funding from the American Society for Clinical Pharmacology and Therapeutics (ASCPT) and by the Arkansas INBRE program, supported by grant funding from the National Institute of Health (NIH) National Institute of General Medical Sciences (NIGMS) (P20 GM103429).

3B-U. **Anticancer activity of XMD8-87 (DCLK1 inhibitor) in Neuroblastoma.** Jeffrey Boakye, Nathan Moore, Fleur M. Ferguson, Nathanael S. Gray, Rani E. George. *Pediatric Oncology, Philander Smith College, Little Rock, AR 72202.*

Doublecortinlike-kinase-1 (DCLK1) along with its splice variants, DCLK-long and DCL has an oncogenic role in cancer, contributing to spindle fiber formation at mitosis and the Epithelial-Mesenchymal Transition (EMT). Although there is high expression of DCLK1in neuroblastoma (NB), a cancer of the sympathetic nervous system, the therapeutic potential for inhibition of DCLK1 in NB is unknown. XMD8-87 is a first-in-class ATP competitive inhibitor with 50nM selectivity against DCLK1 in vitro. Treatment of established neuroblastoma cell lines (Kelly, CHLA-20 and IMR32) with XMD8-87 showed little effect on cell viability at doses ranging

from 0.313μM to 5uM for 72hrs using the Cell Titer-Glo viability assay(TM). A significant effect on cell viability was observed at only 10 μM, suggesting potential therapeutic efficacy for XMD8-87 only at high doses. Immunoblotting and qRT-PCR of E-cadherin, Twist2 and Vimentin, markers of EMT, did not show any significant variation in the expression of these proteins or their mRNA after 24hrs of treatment. Cell cycle analysis did not show a mitotic-phase arrest. In summary, these findings suggest that DCLK1 inhibition is not cytotoxic, does not induce cell cycle arrest and does not promote an epithelial cell phenotype in neuroblastoma Cells.

4A-U. **External and Internal Bacterial Flora Survey of Ceuthophilus gracilipes from Blanchard Springs Caverns, Arkansas.** Taylor Lee, Itzela Cruz, Leah Efird, Caitlyn Gosch. *Biology Department, Henderson State University, Arkadelphia, AR 71999.*

This project is using molecular genetic techniques to survey the bacterial flora of Ceuthophilus gracilipes, from Blanchard Springs Caverns, Arkansas, considered the most biologically diverse cave in the Ozark Plateau. A survey of cave organisms' bacterial flora has the potential to identify previously unreported/undescribed bacteria. Our goal is to further the understanding of life in this cave system by identifying bacteria from cave crickets through DNA sequencing. Cave crickets were obtained from various locations in the cave and taken to the lab, where bacterial samples were collected from their body surfaces and digestive tracts. These samples were plated on selective media, with resulting cultures stored at -80 degrees Celsius. A conserved region of ribosomal DNA (16S subunit) from these colonies was amplified by polymerase chain reaction (PCR) and sequenced using universal bacterial primers. Sequences were compared with those in the GenBank database, which is an archive of DNA sequences, allowing identification to genus and species level. Initial work has identified Pseudomonas protegens and Serratia proteamaculans, from the digestive tract. Species of Serratia fonticola, Hafnia alvei, Chryseobacterium sp., Flavobacterium sp., Acinetobacter sp., and Vitreoscilla sp have been found on the external surface. The identification of other samples is ongoing.

4B-U. **Preparation of an MSP-1 tetramer for the identification and tracking of B cell populations in mice infected with Plasmodium yoelii.** Susie Brown, Jason Stumhofer. *Department of Biology, Henderson State University, Arkadelphia, AR 71999 and University of Arkansas for Medical Sciences, Little Rock, AR 72205.*

Malaria, caused by protozoa in the genus Plasmodium, kills over a million people each year. Effective vaccines are not currently available for malaria. In large part, this is due to the way immunity develops to the disease. It takes multiple exposures over many years for humans to develop immunity. Antibodies, made by B cells, are known to play a crucial role in the development of prolonged immunity in humans, but it takes repeated exposure to the parasite to develop these protective antibodies and maintain high titers. In order to gain a better understanding of how a protective antibody response is generated and maintained after Plasmodium infection it is critical to understand the events taking place on a cellular level during the B cell response. The goal of this project is to develop a merozoite surface protein-1 (MSP-1) tetramer that will act as a tool to allow individual B cells to be tracked during a primary as well as secondary infections in mice, using the rodent parasite Plasmodium yoelii. Currently, we have successfully expressed a 42-kilodalton portion of the P. yoelii MSP-1 (PyMSP-1) protein in transformed BL21 E. coli. After purification and refolding, PyMSP-1 was biotinylated and prepared for thrombin cleavage of the C-terminal 6xHis-tag prior to binding phycoerythrin-conjugated streptavidin to form the tetramer complex. Upon completion the MSP-1 tetramer will be utilized to bind and identify MSP-1-specific B cells after infection of mice with P. yoelii. This B cell tetramer will allow the MSP-1-specific B cells to be analyzed and sorted using flow cytometry. Once sorted, the cells can be used for further study.

5A-U. **Developmental Lineage Tracing in the Mouse Dorsal Root Ganglion.** Alan Umfress, Richard C. Murray. *Biology Department, Hendrix College, Conway, AR 72032.*

The dorsal root ganglia (DRG) are paired structures that flank each vertebrae along the spinal cord and contain the sensory neurons that detect touch, temperature, pain, and body position in space. In the developing embryo, these sensory neurons, as well as the glial cells of the DRG, are derived from neural crest stem cells. These neural crest stem cells first commit to a glial or neural lineage and form glial or neural progenitors. These lineage specific progenitors then differentiate into specific subtypes of cells including the different types of sensory neurons. To learn more about the genetic regulation of these developmental decisions, we are studying the role of the neurogenin1 (ngn1) gene in the development of the DRG since one subtype of neuron is missing from the DRG in ngn1 knockouts. While this result shows that ngn1 is required for normal DRG development, it does not indicate where ngn1 acts in the developmental decision process. Based on data from a homologous gene, we hypothesize that it is involved in the neural vs glial fate determination decision. If ngn1 is involved in neural fate determination, it should be expressed in the last common progenitor cell to the neural and glial lineages. To test whether ngn1 is expressed in the last common progenitor, we are attempting to genetically label these cells in early development and then detect neural and

glial cells derived from them at a later time. We used an inducible cre-loxP approach to genetically label the cells, which relies on crossing mice expressing a tamoxifen-inducible creER transgene from ngn1 promoter elements to a reporter strain containing a Rosa26 lacZ gene that is inactivated by a floxed stop signal. We have successfully labeled ngn1-expressing progenitors in the DRG at E11.5 and have detected neural cells derived from these progenitors at E16.5. We are currently trying to detect cells that express the reporter and glial markers at E16.5 and P21. Supported by the Arkansas INBRE program and the Hendrix Odyssey Program.

5B-U. Assessing the relationship between histone H2A variants and DNA repair in bdelloid rotifers. Miracline Ebijoyeldhas[1], Alexander C. Jones[1], Marjan Boerma[2], Alan J. Tackett[3], Andrew M. Schurko[1]. [1]*Department of Biology, Hendrix College, Conway, AR 72032,* [2]*Department of Pharmaceutical Sciences,* [3]*Department of Biochemistry and Molecular Biology, UAMS, Little Rock, AR 72205.*

Bdelloid rotifers are aquatic, asexual micro-invertebrates that have the ability to effectively repair DNA double-strand breaks (DSBs) induced by high doses (>1000 Gray) of ionizing radiation. In eukaryotes, C-terminal phosphorylation of the histone variant H2AX serves as a marker for DNA damage and links damaged chromatin to DNA repair proteins. In bdelloids, since histone H2A variants possess C-terminal tails that are significantly longer than those in other eukaryotes, these have the potential to act as targets for post-translational modifications (PTMs). The objective of this project was to investigate PTMs associated with the C-terminal tails of H2A variants during DNA repair and to identify proteins that bind to H2A variants in bdelloids. We induced DSBs by irradiating the bdelloid Adineta vaga with 280 Gray of ionizing radiation, and histones were isolated at different time points post-irradiation. High-resolution mass spectrometry was used to identify the five H2A variants in A. vaga along with several PTMs in irradiated and non-irradiated treatments. We then produced 6xHis-tagged proteins representing H2A variants in A. vaga. These recombinant proteins are being used in pulldown assays to identify binding partners to each of the histone variants. We also designed antibodies against each of the five bdelloid H2A variants. These antibodies were used in western blots to confirm the identities of the 6xHis-tagged proteins. Pulldowns will also be performed with irradiated A. vaga to characterize proteins that bind specifically to histones during DNA repair. Overall, these findings will evaluate the relationship among histones, epigenetics and DNA repair in bdelloids. Information gained will guide future projects investigating the role of H2A variants in DNA repair in bdelloids and other eukaryotes, which could have biomedical implications.

6A-U. The role of the Dlk-1 Gene in the Developing Mouse Vomeronasal Organ. Jarrett Wann, Richard Murray. *Department of Biology, Hendrix College, Conway, AR 72032.*

In mice, the vomeronasal organ (VNO) is a small, cigar-shaped organ located on either side of the nasal septum just above the roof of the mouth. The VNO, which detects inhaled pheromones, is connected to the nasal cavity and sensory neurons in the surface epithelium. The sensory neurons of the VNO are derived from the olfactory placode which forms the nasal cavity containing both the main olfactory epithelium and the VNO. The VNO separates from the rest of the olfactory epithelium beginning around embryonic day (E) 10.5 in the mouse when it invaginates toward the nasal septum. Currently, little is known about the genetic regulation of the invagination process or the specification of neural stem cells in this organ. Preliminary work in the lab found that the Dlk-1 gene is expressed in a ventral subset of cells in the developing VNO at E10.5. This pattern of expression suggests that it may be involved in either the invagination of the epithelium or the specification of neural stem cells during VNO development. To determine if the Dlk-1 gene is required for either of these processes, we obtained and bred mice that contain a null allele of the Dlk-1 gene to compare the development of the VNO in wild-type and Dlk-1 knockout embryos. We have found that the VNO invaginates properly in the absence of Dlk-1 function in the knockout embryos, but the development of VNO sensory neurons appears to be altered. This indicates that Dlk-1 is involved in neural determination or differentiation in the VNO. Supported by the Hendrix Odyssey Program.

6B-U. Optimization of a Double Label in situ Hybridization Protocol in the Mouse Dorsal Root Ganglion. Jeffrey A. May II, Richard C. Murray. *Department of Biology, Hendrix College, Conway, AR 72032.*

The dorsal root ganglia (DRG) are pairs of sensory ganglia located adjacent to the spinal cord at the level of each vertebrae. Neurons within the DRG provide sensory input to the nervous system regarding touch, temperature, pain, and limb position in space. During embryonic development, these neurons are generated from neural crest stem cells that give rise to both neurons and glia within the DRG. Little is known about the genetic regulation of the differentiation decisions made by neural crest stem cells to give rise to specific types of neurons and glia within the DRG. One gene that has been shown to be involved in the differentiation of DRG neurons is the neurogenin1 (ngn1) gene. Ngn1 is expressed in neural progenitor cells in the DRG, and knockout animals that lack ngn1 function do not develop pain-sensing neurons. We hypothesize that

ngn1 is involved in early progenitors as they decide between a neural or a glial fate. We are testing this hypothesis by characterizing the fate of progenitor cells in the DRG of ngn1 knockout embryos. We approach this by comparing the expression of genetic markers of specific cell types between wild-type and knockout DRG. To ensure that the genetic marker we use are being faithfully expressed in specific cell types, we are optimizing a double label in situ hybridization protocol that will allow us to visualize two distinct genetic markers on the same tissue section. The protocol involves two differentially labeled complementary RNA probes that can be used to generate differently colored fluorescent signals. Optimization of this protocol will allow us to dissect the intricate relationship between different cell types during the development of the DRG. Supported by the Arkansas INBRE program (NCRR (P20RR016460) and NIGMS (P20 GM103429) at NIH) and the Hendrix Odyssey Program.

7A-U. Meiotic Proteins and Their Potential Role during DNA Repair in Bdelloid Rotifers. Jeanita McReynolds, Lauren Dickinson, Andrew Schurko. *Department of Biology, Hendrix College, Conway, AR 72032.*

Bdelloid rotifers are ancient asexual microinvertebrates that have survived without males, meiosis, and sex for over 40 million years. The long-term survival of bdelloids without the advantages of sex and recombination is partly attributed to their ability to recover from desiccation and to repair the resulting DNA double-strand breaks (DSBs) with an efficiency unparalleled in other eukaryotes. Despite the long-standing absence of meiosis in bdelloids, their genomes contain four genes that encode proteins (HOP1, SPO11, MSH4, and MSH5) known to be specific to meiosis in other eukaryotes. Following exposure to ionizing radiation (which induces DSBs), genes encoding HOP1 and SPO11 are upregulated in the bdelloid Adineta vaga. Since bdelloids lack meiosis yet possess a noteworthy DNA repair system, the objective is to investigate the potential role of meiotic genes during DNA repair. Western blots using antibodies against HOP1, SPO11, MSH4, and MSH5 from A. vaga revealed that these proteins are produced in bdelloids. Western blot assays using these antibodies with irradiated rotifers will then be done to quantify protein abundance during DNA repair. We have also generated 6xHis-tagged copies of these meiotic proteins from A. vaga that will be used in pull-down assays to characterize binding partners of these proteins in irradiated and non-irradiated bdelloids. Identifying proteins that interact with HOP1, SPO11, MSH4, and MSH5 during DNA repair will shed light on the functional significance of these meiotic proteins in bdelloids. Overall, this study seeks to determine if meiotic genes in bdelloids have evolved a novel function in DNA repair, which could justify the maintenance of these genes in an ameiotic lineage. Data supporting a role for "meiotic proteins" in DNA repair would be the first evidence of a non-meiotic function for these genes and could be used to further our understanding of DNA repair in eukaryotes.

7B-U. Impact of MARCKS inhibition on Coxiella burnetii infections of host cells. Joel Brown, Ryan Kinney, Sara Whitlock, Joel Funk. *Biology Department, John Brown University, Siloam Springs, AR 72761.*

The human disease Q-fever is initiated as a respiratory tract infection by the bacterium Coxiella burnetii. Acute infections typically result in flu-like symptoms and can be treated with antibiotics, but untreated chronic infections can lead to severe conditions including endocarditis. Bacteria enter alveolar macrophages within a phagosome, but instead of being destroyed by cellular enzymes, bacterial cells induce the infected cells to develop a lysosome-like organelle called the parasitophorous vacuole (PV) where replication takes place. The PV starts small but grows in size to accommodate the increasing number of replicating cells. Manipulation of the host infection by C. burnetii includes activation of Protein Kinase C (PKC) isoforms that sequentially phosphorylate downstream substrates. MARCKS is one of several PKC substrates phosphorylated during infections. The objective of this study was to localize MARCKS using antibodies and examine the role of MARCKS using inhibitors. Our results indicated that MARCKS localizes to the PV membrane and surrounding cytoplasm. The level of MARCKS protein was knocked-down using siRNA treatment of HeLa cells. Infected cells treated with MARCKS siRNA contained C. burnetii, but more PV's were larger in size than those of infected cells treated with control siRNA. A peptide inhibitor of MARCKS appeared to have a similar effect on infected THP-1 cells by causing the development of more enlarged PV's compared to control peptide treatments. These results show that MARCKS may have a role in regulating or controlling the size of C. burnetii-induced PV's.

8A-U. **Association Study of Ascites at Chromosome 2 of Chickens.** Ryan Kinney[1], Douglas D. Rhoads[2] and Shatovisha Dey. 1*Biology Department, John Brown University, Siloam Springs, AR 72761 and [2]Cell and Molecular Biology, University of Arkansas, Fayetteville, AR 72701.*

This project has focused on development of a reliable genotyping assay for determining the genetic association of a region on chicken chromosome 2 with development of ascites. Ascites is the buildup of fluid in the peritoneal cavity resulting in a swollen "water belly." Ascites is not only a problem in the poultry industry, but also in human health. Our group at the University of Arkansas has been identifying the genetic

factors of ascites in chickens. Through a genome wide association study several regions of the chicken genome have been shown to have a mild correlation with ascites. Extending these analyses to hundreds of samples allows for stronger elucidation of association. We have developed and validated a TaqMan qPCR assay for a SNP at 71.32 megabase pairs (Mbp) on chromosome 2. Genotype data for the SUS, REL and RES lines do not show a shift in genotype frequencies accompanying selection for ascites phenotype. Upon initial examination my data show that the CC homozygous females at this locus are more susceptible to ascites and are more susceptible to cardiac hypertrophy. However upon further investigations and other methods of analysis. There does not seem to be a direct connection with ascites.

8B. Yeast dynamin interacts with subunits of ESCRT complexes and with novel binding proteins. Bryan Banh, Hyoeun McDermott, Shiva Kumar Goud Gadila. *Biology Department, Missouri State University, Springfield, MO 65897.*

Vacuolar protein sorting 1 (Vps1) is a dynamin-like GTPase involved in multiple cellular trafficking pathways. Vps1 is a membrane peripheral protein that interacts with an array of intracellular organelles, including peroxisomes, endosomes, vacuoles, and the late Golgi. It appears that Vps1 functions together with a selective group of proteins that reside at each organelle. Though Vps1's implication in membrane remodeling has been well recognized, the mechanisms by which it interacts with its functional partners remain poorly understood. Our yeast two-hybrid assay revealed that Vps1 interacts with at least 4 endosomal proteins, including subunits of ESCRT II and III complexes; Vps22, Vps36, Vps24, and Vps2. Interestingly, Vps1 interacts primarily with the helical domain (HD) at the N-terminal region of Vps22 and Vps36. The investigation of precise domains of Vps24 and Vps2 that bind to Vps1 is in progress. ESCRT II and III complexes are directly involved in the sorting of Cps1 at the endosome for its final delivery to the vacuolar lumen. Upon loss of each subunit of these ESCRT complexes, Cps1 was found to be located at the rim of vacuole or at the E compartment. vps1Δ cells displayed a similar defect, albeit less significant compared with ESCRT mutants, suggesting Vps1 being a potential member for Cps1 sorting, possibly functioning together with the above-mentioned binding partners at the endosome. In addition, we have performed a screen for novel Vps1 binding partners in Saccharomyces cerevisiae using a Yeast two-hybrid library system. Our results show seventeen as-yet-unidentified Vps1 binding proteins. To validate our results, we have selected two proteins to undergo more stringent assays. Our research may provide more insight into Vps1's diverse roles by understanding its partners at each organelle.

9A. Lipid Homeostasis Required for Proper Protein Recycling. Sara Woodman, Justin Conover, Chris Trousdale, Kyoungtae Kim. *Biology Department, Missouri State University, Springfield, MO 65897.*

Protein recycling is an essential cellular process that involves endocytosis, intracellular trafficking, and exocytosis. It has been shown in mammalian systems that membrane lipids, including cholesterol, sphingolipids, and phospholipids, play a pivotal role in protein recycling. In order to address the roles of yeast plasma membrane lipid components on protein recycling, we utilized GFP-Snc1, a v-SNARE protein serving as a fluorescent marker for faithfully reporting the recycling pathway. Here we show results that display moderate to significant GFP-Snc1 recycling defects upon overexpression or deletion of phospholipid biosynthesis enzymes, as well as defects upon deletion of ergosterol biosynthesis enzymes. We also report the severity of GFP-Snc1 recycling in the presence of myriocin, a sphingolipid synthesis inhibitor. Together, the homeostasis of membrane lipid levels is prerequisite for proper protein recycling. Through using a truncated version of GFP-Snc1 that cannot be recycled from the plasma membrane, we determined that abnormalities in Snc1 localization in membrane lipid overexpression or underexpression mutants are not due to defects in the synthetic/secretory pathway, but rather in the recycling pathway. Snc1 recycling is currently being studied in ergosterol and sphingolipid overexpression mutants.

9B. Physical interaction between the scission protein Dynamin and the coat protein Clathrin at the TGN in saccharomyces cerevisiae. Shiva Kumar Goud Gadila, Michelle Williams, Hyoeun McDermott, John Short, Mariel Delgado Cruz, Kyoungtae Kim. *Biology Department, Missouri State University, Springfield, MO 65897.*

Vps1 (Vacuole protein sorting 1), a dynamin-like protein in yeast, is implicated in diverse membrane trafficking pathways and localized to many organelles, including Golgi. Payne lab from California previously showed that Vps1's physiological function is linked to clathrin. Our working hypothesis is that Vps1 physically interacts with clathrin and functions as a membrane remodeling agent at the trans-Golgi network (TGN). In agreement with this hypothesis, our yeast-two hybrid assay revealed that Vps1 binds to the C-terminal region of clathrin. Through a colocalization assay, we also found that Vps1 partially overlaps with clathrin and other late Golgi markers, including Sec7. Loss of Vps1 resulted in a mislocalization of clathrin, but not Gga1 adaptor, to the late endosome and to the vacuolar rim, suggesting Vps1 is required for clathrin recruitment to the Golgi. It was found that Vps1's targeting to the Golgi requires either MID or GED domains, but each of these domains showed less efficient targeting to the Golgi. In addition, we found

that the mean number of the late Golgi in vps1 mutant cells was drastically increased, probably due to Vps1's involvement in the homotypic fusion at the TGN.

10A-U. The effect of blood flow on vascular smooth muscle cell coverage of embryonic blood vessels. Shilpa Mohite, R. Padget, T. Hoog, S. Fredrickson, M. Wickham, R. Udan. *Biology Department, Missouri State University, Springfield, MO 65897.*

During embryonic development, blood vessels are formed (from endothelial cells) by a process called vasculogenesis. These early vessels further remodel to form a hierarchy during angiogenesis—creating large-diameter arteries that branch into small-diameter capillaries. Next, the vessels respond to local signals (like PDGF or Notch signaling) which act to cover the vessels with an outer tissue layer comprised of vascular smooth muscle cells (vSMCs) in a process called maturation. What remains unclear is why large-diameter arteries have a thicker vSMC layer than small-diameter capillaries (which are sometimes missing vSMCs). Since previous studies have implicated that mechanical forces provided by blood flow control the formation of arteries over capillaries, we hypothesize that these same mechanical forces may also determine the extent of vSMC coverage. To test the hypothesis, we compared the extent of vSMC coverage in arteries from normal-flow embryos (wild type) with arteries from reduced-flow embryos (Myl7-/- mutant embryos having reduced heart contractility). We observed less vSMC coverage around both extraembryonic and intraembryonic arteries in the reduced-flow embryos. To determine how flow could promote changes in vSMC coverage, we investigated changes in PDGF and Notch signaling. Our qRT-PCR data showed that Hey1 (a Notch target gene) was downregulated in reduced flow vessels. This suggests that Notch is activated by high flow to increase vSMC coverage of arteries, and supports the combined evidence that mechanical forces provided by blood flow initiate a maturation program.

10B. Physical Interaction between Vps1 and GARP Vps51 at the Golgi in Saccharomyces cerevisiae. Uma Saimani, Ashley Smock, Kyoungtae Kim. *Biology Department, Missouri State University, Springfield, MO 65897.*

Physical Interaction between Vps1 and GARP Vps51 at the Golgi in Saccharomyces cerevisiae Uma Saimani, Ashley Smock and Kyoungtae Kim Missouri State University, Springfield, Missouri – 65897 Vacuolar Protein Sorting 1 (Vps1), a yeast homolog to human dynamin, displays an important role in the recycling traffic from the early endosome to the Golgi network. Previous research has shown a genetic interaction of Vps1 with Vps51, a component of the GARP tethering complex that functions at the late Golgi mediating the fusion between endosome-derived vesicles and the Golgi. In order to elucidate the functional relationship between Vps1 and Vps51, we performed a yeast two-hybrid assay and found that Vps1 interacts with Vps51 physically. Vps1 consists of a N-terminal GTPase domain, a Middle, and a C-terminal GED domain, and thus we wanted to narrow down the domain of Vps1 that binds to Vps51. Surprisingly, we found that all these domains interact with Vps51. In order to check the interdependency between these proteins we introduced Vps51 tagged with GFP into a vps1Δ cell and found that there was a three-fold increase in the GFP-puncta number when compared to wild-type yeast cell. For determining if the increased puncta number was due to loss of Vps1, we exogenously expressed mRFP-Vps1 in the vps1Δ cells and this rescued the puncta number similar to a wild-type cell. Currently, we are working on proving in-vitro interaction of Vps1 and Vps51 using a GST pulldown assay and are also checking expression of Vps1 in a vps51Δ cell to assess interdependency.

11A. MDM2 Case Study: Improved Binding Site Predictions with protein flexibility using AutoDock and AutoDock Vina. Anthony Ascone, Ridwan Sakidja. *Physics, Astronomy and Materials Science, Missouri State University, Springfield, MO 65897.*

Recovery of the p53 tumor suppressor pathway via small molecule inhibitors of oncoprotein MDM2 highlights the critical role of computational methodologies in targeted cancer therapies. Molecular docking programs in particular, provide a quantitative ranking of predicted binding geometries of ligands to proteins based on binding free energy, and allows for the screening of large chemical libraries in search of lead compounds for cancer therapeutics. AutoDock and AutoDock Vina are often cited docking programs shown to be reasonably accurate predicting the binding sites of ligands with 6 or fewer rotatable bonds. However, accuracy decreases with increased ligand flexibility due to the exponential increase in conformational search area. Therefore, standard docking protocol will hold the receptor rigid to allow for a manageable 3D search space. Here, we test a protocol designed to improve binding site predictions of small medicinal compounds to the p53 binding site of MDM2 based on RMSD values using AutoDock and a reliable, faster alternative, AutoDock Vina. Four complexes representing small molecule inhibitors bound to MDM2 were selected from the protein data bank. A total of 12 rotatable bonds was supplied to each complex and distributed systematically between the ligand and the binding site residues of MDM2. A docking run was performed for each configuration and evaluated in terms of binding free energy and RMSD. Our results show lowest RMSD values coincide with the ligand having one or no rotatable bonds, while transferring the majority of flexibility to the protein, and in each of the four

complexes, these RMSD values are within 2 angstroms of the experimentally known binding site. Further, we found AutoDock Vina mirrored these results while requiring less computational time.

11B. Rab GTPase and Dynamin Function Together at the Late Golgi in Yeast. Pelin Makaraci, Hyoeun McDermott. *Biology Department, Missouri State University, Springfield, MO 65897.*

Membrane recycling is an important cellular process required for proper maintenance of the cell. Though lines of evidence showed that Vps1 is implicated in protein recycling from the early endosome to the late Golgi, the detailed function of Vps1 in this pathway remains elusive. By using the yeast-two hybrid assay, the present study reveals that Vps1 physically interacts with Ypt6, a master GTPase protein in this pathway, and that Ypt6 binds to the N-terminal and the middle domains of Vps1. In addition, we found that presumable GTP non-hydrolyzable Ypt6 mutants (Ypt6 G139E and Ypt6 T24N) and GDP-bound inactive mutant (Ypt6 Q69L) interact with Vps1 with a similar binding affinity when compared with WT Ypt6. In light of our observation that the overexpression of Vps1 rescued the abnormal recycling phenotype caused by loss of Ypt6, but not vice versa, it is likely that Vps1 functions downstream of Ypt6. Furthermore, the overexpression of the N-terminal half of Vps1 that carries the GTPase domain was sufficient enough to rescue the abnormal phenotype in ypt6Δ, suggesting that Vps1's active role in the recycling pathway relies on its intrinsic ability to hydrolyze GTP. Kim lab recently demonstrated Vps1 interaction with Vps51, a GARP subunit (see the Poster by Uma Saimani) implicating that Vps1 might link Ypt6 to the GARP tether and then to the SNAREs at the Golgi. The possibility of Vps1's interaction with SNAREs at the event of vesicle fusion at the late Golgi is under investigation.

12A. Investigating the Effects of High and Low Resistance to Blood Flow on Mouse Embryonic Heart Development. Samantha Fredrickson, Tanner Hoog, Ryan Udan. *Biology Department, Missouri State University, Springfield, MO 65897.*

The most common type of birth defects are congenital heart defects (or CHDs) (National Institutes of Health). Though a few cases of CHDs have been attributed to genetic defects specific to the heart, or to maternal disease (eg. diabetes), the cause of most CHDs is unknown (American Heart Association). Thus, further research is needed to determine how CHDs form. Very few studies have investigated how physiological factors like perturbations of blood flow can affect normal heart development. For instance, increasing or decreasing the resistance to blood flow can change the morphology and function of the heart in both zebrafish and chicken embryos (Culver and Dickinson, 2010). This could be one way to explain how CHDs form, but further investigation in a mammalian system is needed. To examine this idea, we plan to experimentally manipulate cultured mouse embryos and test the effects of increasing or decreasing blood viscosity (to create high or low resistance to flow). To determine any effects on heart development, we will prepare the embryos for 3D imaging by optical projection tomography (OPT), and perform morphometric analysis to compare heart morphologies. Further, we will determine if high or low resistance to flow will also alter the expression of heart genes by RNA sequence analysis. As of now, we have successfully prepared cultured embryos for imaging by OPT, and we will soon begin to manipulate the embryos.

12B. Surface display for improved and novel production by the industrially important acetic acid bacterium Gluconobacter oxydans. Marshal Blank, Kaleb Pearson, Paul Schweiger. *Biology Department, Missouri State University, Springfield, MO 65897.*

Acetic acid bacteria (AAB) are incomplete oxidation specialists and the natural ability of AAB to produce enantiopure chiral molecules is used for the combined microbial-chemical synthesis of industrial sugar derivatives that would otherwise require complex and expensive chemistry (e.g. L-ascorbic acid (vitamin C) and the anti-diabetic drug, Miglitol). The genome sequences of many species in this genera are known; however, few molecular tools are available for metabolic engineering and strain improvement. Foreign enzymes are expected to be perfectly incorporated into the metabolism of AAB, as they expresses many periplasmically-oriented dehydrogenases that produce a variety of value-added chiral products in nearly quantitative yields. To integrate these enzymes without competing for cytoplasmic membrane space, a library of surface display anchor proteins was examined for the ability to deliver a translationally-fused reporter alkaline phosphatase, PhoA, to the outer membrane of the model acetic acid bacterium, Gluconobacter oxydans. Display of enzymes at the cell surface is advantageous over cytoplasmic expression because it avoids translocation of substrates and products across the inner cell membrane, allowing for simple product extraction and increased yields. Phosphatase activity was observed in whole-cell reactions when using a truncated version of the major nonspecific porin from Pseudomonas aeruginosa, OprF188, as the surface anchor protein. PhoA only forms active dimers outside the cell, and is inactive when in the reducing environment of the cytoplasm. Thus, this activity suggests that OprF was successfully localized to the outer membrane in G. oxydans. This display system will be used to exploit and expand the natural ability of AAB to produce value-added compounds by whole-cell biocatalysis.

13A-U. Ammonium salt toxicity in various crops with pathogen pressure grown in hydroponic conditions. Jose Hernandez, Matthew Thompson, Brynna Pruett, Gary Bates, LaShall Bates. *Biology Department, Northwest Arkansas Community College, Bentonvile, AR 72712.*

High salinity soils are becoming a problem for crop production in the state of Arkansas as well as other areas of the United States. Pythium damping off and root rot has been shown to increase in high salt soils. Various crops as well as Pythium spp and nonpathogenic soil microbes were compared in a hydroponic setting at various ammonium salt concentrations to determine plant mortality and disease rates. Microbial reisolation rates were also calculated.

13B-U. Purification Of Cross-Linked Protein-Protein Complexes As A Means To Map Interactions in DNA Damage Response Pathways. James Brown, Sapna Das-Bradoo. *Natural Sciences, Northeastern State University, Tahlequah, OK 74464.*

Mcm10 is a highly conserved protein in eukaryotes that until recently was only suspected to play a part in DNA replication, specifically in activating the pre-replication complex and assisting in the elongation process. However, our group previously discovered that Mcm10 also interacts with mediator of replication checkpoint 1 (Mrc1) protein, which plays a vital role in the DNA damage response pathway. This finding lead us to suspect that Mcm10 may have many unexplored interactions within the cell and may be involved in many other cellular processes. Mcm10 mutations and changes in expression have been observed in many types of cancer. Our group's long term goal is to understand how these changes affect the progression and survival of cancerous cells. Towards this end, our long term goal is to optimize a method of identifying interacting proteins and cellular processes associated with wild-type Mcm10 and subsequently compare it to the binding partners associated with Mcm10 mutations found in cancerous cells. Our lab has been successful in creating Mcm10 cross-linked complexes in lysates produced via 1% formaldehyde treatment. Treatment of yeast cultures with formaldehyde cross-links interacting proteins, so that they remain bound in complexes throughout cell lysis and purification. Formaldehyde cross-linking worked efficiently for our yeast cells lysed under non-denaturing conditions using glass beads or under denaturing conditions using trichloroacetic acid. The protein-protein cross-linking was independent of the epitope tags - 6His and 18Myc. Our immediate goal moving forward is to purify Mcm10 using nickel column chromatography under denaturing conditions and then identify the bound proteins via mass spectrometry. This process is currently underway, and results will be discussed at this meeting.

14A-U. Sequencing of Plasmids Carrying an Ofloxacin Resistance Gene. Ashley Bonea, Kayla Schroeder, John de Banzie, Cindy Cisar. *Natural Sciences, Northeastern State University, Tahlequah, OK 74464*.

Antibiotic resistance in bacteria presents great challenges in the healthcare field. Understanding environmental sources of resistance genes and the mechanisms behind their spread is therefore important. We are interested in resistance to the antibiotic ofloxacin, which interferes with DNA gyrase function during DNA replication. Several ofloxacin resistance mechanisms are known, including efflux pumps that expel the antibiotic and mutations in a DNA gyrase subunit gene that render it insensitive to ofloxacin. We are interested in resistance due to a plasmid-carried gene, qnrS. This gene encodes a protein that causes destabilization of the gyrase–DNA–quinolone cleavage complex and prevents DNA damage. Ofloxacin-resistant aeromonads were collected from sediments downstream of a wastewater treatment plant between 2007 and 2010. Strains containing plasmids bearing qnrS genes were identified. We have sequenced plasmids from two of these strains using primer walking. Plasmid pT2Sofl-9 is 7973 base pairs long and plasmid pT2Sofl-122 is 7621 base pairs long. The two plasmids differ at only two positions: a short region upstream of qnrS and a one nucleotide indel. In addition to qnrS, both contain genes for plasmid replication and mobilization. We compare our plasmids to other qnrS-bearing plasmids obtained at different locations and dates. These data show global dissemination of qnrS-bearing plasmids over many years.

14B. Stabilizing Effects of Compatible Solutes on DNA. Melissa Menie, Anam Ashraf, Ratnaker Deole. *Natural Sciences, Northeastern State University, Tahlequah, OK 74464.*

Aquatic saline environments compose approximately 97% of water on earth and salt deposits may be found in over one fourth of the land. Organisms living in these hypersaline conditions are classified as Halophiles. Halophiles have adapted survival strategies that allow for growth, metabolism and reproduction in hypersaline conditions. One of these adaptations includes the accumulation of intracellular compatible solutes through de novo synthesis or through uptake from the environment. These compatible solutes, also known as osmolytes, balance the osmotic pressure inside the cell with the pressure surrounding the cell allowing the organism to maintain cell turgor and reduce osmotic stress. Furthermore, compatible solutes also play a role in protein stabilization, protecting against denaturation at high temperatures and in hypersaline conditions. Extensive research has been conducted to investigate the stabilizing mechanisms and effects of compatible solutes on proteins, however, limited research has been

conducted on the effects of compatible solutes on DNA. Halorhodospira halophila, an extreme halophile, accumulates ectoine and trehalose as compatible solutes. H. halophila was grown in media supplemented with NaCl ranging from 5 – 35%. DNA was extracted from the cells growing at each of the listed concentrations and was treated with 10mM, 500mM and 1M solutions of ectoine and trehalose. DNA melting curves were obtained using a UV/Visible Spectrophotometer, equipped with a Peltier temperature controller.

15A-U. Quantitative Analysis of Compatible Solutes in Halorhodospira halophila. Andrew Dodd, Melissa Menie, Ratnaker Deole. *Natural Sciences, Northeasern State University, Tahlequah, OK 74464.*

Aquatic saline environments compose approximately 97% of water on earth and salt deposits may be found in over one fourth of the land. Halophiles are organisms that thrive in environments such as these through the use of osmoadaptive mechanisms. The compatible-solute –strategy is a common osmoadaptive mechanism used among halophilic bacteria and eukaryotes. It involves de novo synthesis of compatible solutes or uptake of organic solutes from the environment. Compatible solutes adjust solute concentration inside the cell in response extracellular solute concentrations, allowing the organism to maintain cell turgor and reduce osmotic stress. Halorhodospira halophila, an extreme halophile, grows in a wide range of saline concentrations. Recently sequenced H. halophila genome shows that it has biosynthesis genes for ectoine, proline and trehalose and could possibly accumulate these as the compatible solutes. In this research, H. halophila was grown at salt (NaCl) concentrations ranging from 5-35%. Compatible solutes were extracted from H. halophila grown at each concentration. Each sample was then subjected to capillary electrophoresis along with proline, ectoine and trehalose standards (10mM – 1M). Ectoine and trehalose were both present in each sample and the quantity of each increased with increasing NaCl concentration. However, proline was not present is large enough quantities and did not show an increase due to NaCl concentration, therefore it is not considered to be used as a compatible solute in H. halophila.

15B-U. Regulation of UPR and Immune Response in Watermelon Crops from Tulsa County. Sara Cruz, Aktar Ali, Kyeorda L. Kemp. *Natural Sciences, Northeastern State University, Tahlequah, OK 74464.*

Introduction: Watermelon is important cash crop in the state of Oklahoma, generating roughly $3.5 million annually. Viral diseases contracted by the watermelon crops have been a major cause for decreased crop yield. Plants fight off pathogens via their immune response, and recent studies show a link between immune response in plants and the Unfolded Protein Response (UPR). The UPR is a conserved pathway that allows the Endoplasmic Reticulum, the main organelle responsible for protein folding, to resolve the accumulation of unfolded proteins. The UPR pathways play a role in plant induction and regulation of immune responses to abiotic and biotic stressors, such as viral infection, under laboratory conditions; however, this has not been investigated in watermelon growing in the field. The most widely spread viral diseases found in watermelon in Oklahoma are the Papaya ring spot virus (PRSV-W) and Watermelon mosaic virus (WMV). We seek to determine if the Unfolded Protein Response (UPR) associated genes and immune responses are differently regulated in watermelon infected with PRSV-W and WMV-2. Methods: Over the course of this past summer, multiple asymptomatic controls and symptomatic samples were collected from Tulsa watermelon fields. Each sample was tested through qRT-PCR to confirm both the health and infection of the two specified viruses. After confirmation, one non-infected sample, 2 samples infected with WMV and 2 samples infected with PRSV were randomly selected and sent off to the company Genewiz for analysis of mRNA whole genome expression by RNA sequencing. Results: We have recently received the lab results from the mRNA sequencing. Analysis has begun and will continue over the course of the next semester.

16A-U. Biofumigant effects based on age of leaf residues. William Black, Sean Potts, Laura Ortega, LaShall Bates, Gary Bates. *Biology Department, Northwest Arkansas Community College, Bentonville, AR 72712.*

Biofumigation is the process of using Brassica residues to release chemicals into a soil environment to reduce soil pathogens. Biofumigation has been shown to be effective in Arkansas utilizing canola and Indian mustards. Various cultivars of mustard, wheat, and peas were grown in a controlled setting and incorporated into saturated soil at different plant ages. The soil was inoculated with either pathogenic Pythium spp. or the non pathogenic environmental fungus Sordaria firmicula to determine the effect on microbial populations.

16B. Rapid transient expression of human tissue specific plasminogen activator (t-PA) in tobacco leaves. Yves Saint Damien Hall, Ashley Strain, Hannah Moreau, Kevin Wang. *Northeastern State University, Tahlequah, OK 74464.*

Current pharmaceutical production of t-PA utilizes mammalian cell cultures. In this study, we transiently expressed t-PA in tobacco leaves via the use of a

germinivirus-based single DNA replicon system. We employed codon optimization technology, and targeted the protein for sub-cellular localization in the apoplast with the LPH signal (plant codon-optimized leader peptide (LPH) derived from the heavy chain of the murine mAb24). All three t-PA versions (WT t-PA, Optimized t-PA and LPH-tPA) were introduced into germinivirus vector (pBYr2fp). This method of Vectors were transiently expressed in leaves 3 days after agroinfiltration. Bacterium-mediated transient expression utilizes a plant viral vector (pBYr2fp) transformed into agrobacterium, to imprint the gene of interest into the epidermal tissue of the tobacco leaf inducing an overexpression of the recombinant t-PA protein. Preliminary data indicates that two versions (optimized and LPH) caused necrosis in leaf tissue. The recombinant protein is isolated and purified using the His-tag binding method, and the protein presence is qualified using SDS-page. Purified recombinant t-PA proteins and can degrade fibrin. . In vector that can be introduced into tobacco leaves, through a proven transient expression technique, to over express the recombinant t-PA protein. This method of agrobacterium-mediated transient expression utilizes a plant viral vector (pBYr2fp) transformed into agrobacterium, to imprint the gene of interest into the epidermal tissue of the tobacco leaf, using syringe injection method, inducing an overexpression of the recombinant t-PA protein. The activity in leaf tissue at 3-5 days implies functional peak and the leaves are harvested. The recombinant protein is isolated and purified using the His-tag binding method, and the protein presence is qualified using SDS-page. The anti-thrombolytic properties are tested and qualified using a fibrin plate analysis. This approach through plant-based biotechnology offers a potential safer and more economically viable alternative fort-PA production.

17A-U. Bacterial Extracts Separated by Thin-Layer Chromatography Inhibit the Growth of Staphylococcus. Heidi Hughes, Ruth Plymale. *Natural Sciences, Ouachita Baptist University, Arkadelphia, AR 71998.*

Many bacteria have become resistant to commonly-used antibiotics. Therefore, new antibiotics are needed that will inhibit these resistant bacteria, possibly through a different mechanism. Bacteria found in soil are a likely source for these new antibiotics. We isolated soil bacteria and screened them for antimicrobial production against Staphylococcus epidermidis. Methanol extracts were made from entire agar plates of soil bacteria that inhibited the growth of S. epidermidis. These extracts were spotted on a lawn of Staphylococcus aureus; measuring growth inhibition to confirm that the extracts contained the antimicrobial compound. The confirmed inhibitory extracts were then separated by thin-layer chromatography using a chloroform-methanol mobile phase. The separated compounds were individually suspended in methanol and spotted onto S. epidermidis or S. aureus to assess inhibitory ability. Future research may characterize isolated compounds shown to have antimicrobial properties against Staphylococcus using high-performance liquid chromatography.

17B-U. Bioinformatic Analysis of Cluster T Phages. AlleaBelle Gongola, Alex Abbott, Meredith Bolin, Rachel Dilatush, Nolan Game, Buzz Hardin, Taylor Johnson, Nathan Malone, Hannah Pagan, Nathan Terry, Tyler White, Sam Wilson, Joseph Koon, Colby Smith, Ben Blankenship, Jace Bradshaw, Ruth Plymale, Nathan Reyna. *Natural Sciences, Ouachita Baptist University, Arkadelphia, AR 71998.*

For the last four years, students at Ouachita Baptist University have been isolating and characterizing mycobacteriophages that infect the common host Mycobacterium smegmatis mc2155. While genetic analysis usually focuses on an individual phage, analysis of groups (clusters) of genetically similar phages provides a more complete view of gene regulation and evolutionary development. Phage Cluster T was chosen for an in depth bioinformatic analysis. The three members of Cluster T were each isolated by different universities in the United States: Mendokysei (UC-Santa Cruz), Bernal13 (University of Florida), and RonRayGun (Ouachita Baptist University). The genomes were annotated using the program DNA Master and gene locations were predicted using Glimmer and GeneMark. As expected, most genes were conserved in all three genomes, including the tyrosine integrase enzyme and tapemeasure tail assembly protein. Analysis revealed nine unique genes or orphams, site-specific recombination attachment sites, transcription signals, and conserved repeated sequences. New insight on gene regulation was revealed by discovering the locations of hairpin terminators and SigA-like promoters in relation to their polycistronic gene cassettes. Bioinformatically identified promoters and terminators from this study were physically studied in the lab. Results provide insight into effective utilization of bioinformatic methods and comparative genomics in addition to the understanding of mycobacteriophages and associated organisms.

18A-U. Benthic Macroinvertebrates and Fish as Estimators of Water Quality in Four Clark County, Arkansas Streams. Morgan Cummins, Julie Nessler. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Water is a finite resource which should be protected. Regular monitoring of water quality is an important part of water resource management. One method of determining water quality is through sampling living

organisms that are tolerant or intolerant to changes in water quality. The use of living organisms to estimate water quality has been accepted by the EPA and the scientific community for many years. Studies show that the fish and benthic macroinvertebrate communities provide accurate and reasonable estimations of water quality. Fish and benthic macroinvertebrates are easily classified into indicator groups based on species. In this study we used rapid bioassessment protocols three (RBP III) and four (RBP IV) to estimate water quality in four Central Arkansas streams using the assessment of the benthic macroinvertebrate and fish communities. The fish and benthic macroinvertebrate communities from DeRoche Creek, Little DeGray Creek and Big Deceiper Creek were sampled and compared to that of the Caddo River community to determine if water quality declines were evident in these regional streams. Deviations from the reference stream were interpreted based on the accepted EPA models and knowledge of regional phenomenon.

19A-U. The Use of Fish as Biological Indicators of Water Quality in Three Central Arkansas Streams. Justin Rose, Jess Kelly. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Regular monitoring of water quality is an important part of water resource management. One method of determining water quality is through sampling living organisms that are tolerant or intolerant to changes in water quality. The use of living organisms to estimate water quality has been accepted by the EPA and the scientific community for many years. Studies show that fish communities provide accurate and reasonable estimations of water quality. Fish are easily classified into indicator groups based on species. In this study we estimated water quality in three Central Arkansas streams by assessing the fish communities. We analyzed DeRoche Creek and Big Deceiper Creek and compared them to that of the Caddo River community to determine if water quality declines were evident in these regional streams. Deviations from the reference stream were interpreted based on the accepted EPA models and knowledge of regional phenomenon.

19B-U. Otolith Aging of the Largemouth Bass, Micropterus salmoides. Julie Stanley, Jess Kelly. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Northfork Lake in Arkansas is a heavily fished lake. Most largemouth bass taken from the lake fall within the size of early reproductive individuals. Larger sizes in this species have not been recorded during several years of electrofishing sampling. It is unclear if the species is being overfished or if environmental factors such as crowding are causing stunted growth rates. In this study we removed the otoliths from from Largemouth bass, Micropterus salmoides and aged the bass. If the ages are advanced then it would support the conclusion of stunted growth however if the ages are observed to be consistently younger then we would need to look at lake management protocols to see if overfishing might be more likely.

20A-U. First Record and DNA Barcoding of the American Burying Beetle in Clark County Arkansas. Kyla Feather, Jess Kelly. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

The American Burying Beetle, Nicrophorus americanus, is a federally red-listed endangered species. We serendipitously recorded three records of this species during a forensic study during the summer of 2013. These specimens represent the first known records for Clark County, AR and the southeastern-most record in the State since the extirpation of the species from the region in the late 1800's to early 1900's. Two males and one female were collected, photographed, sexed and measured. One male specimen was deceased upon discovery but the other two were released. The U.S. Fish and Wildlife department was self-notified of the accidental catch and death of an endangered species as required and the specimen was awarded to Ouachita Baptist University where it is currently stored. We decided to use DNA barcoding to confirm our species identification in order to overcome any doubts of identification using short, standardized gene regions as identification tags. A discussion of this species, its rediscovery in Clark County and an update on future efforts will be discussed.

20B-U. Effect of Changing Light Wavelength on the Cultivation of Marine Microalgae. James Malatesta, Jack Hunley, Jim Taylor. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Space has always intrigued mankind. We have always dreamed of exploring new frontiers and determining what lies beyond Earth's reach. Only recently has technology permitted this dream to come true. However, due to the cost of space travel and the lack of available storage space for food and energy, missions to space must be of short duration. Utilizing marine microalgae can solve some of these issues. These algae can serve several purposes in space. These purposes include providing a steady, renewable source of food for astronauts, providing a source of biofuel to give energy to power the needed equipment, and filtering out carbon dioxide and producing oxygen. In order to make the algae possibility a reality, we have to determine how to grow the algae in the most cost efficient manner to save money and energy. This experiment focuses of finding the wavelength of light that produces the highest yield of algae growth. Using light chambers with LED bulbs to control the wavelength, algae cultures

were grown for a week at a time and then counted to estimate the amount of growth. Four chambers, each with a different wavelength of light were used. The chosen wavelengths were blue, red, green, and white (blue, red, and green combined). After three trials, results have been consistent on showing that algae grown under blue light grew best, with an average of 4.657 million cells/ml. White light showed the second best growth with 4.580 million cells/ml. Red light grew only 2.212 million cells/ml. Green light showed the least growth, giving 1.025 million cells/ml. Overall, it appears that blue light alone will suffice in growing the algae, which will save a decent sum of money, space, and energy.

21A-U. The Effect of Hypobaria and Increased Carbon Dioxide on Arabidopsis thaliana. Jack Hunley, Jim Taylor. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

NASA has announced plans for a trip to Mars sometime in the 2030s, and for the mission to be successful they believe plants will play a critical role. With plants' ability to convert carbon dioxide to oxygen, filter wastewater, and be a source of food, it is no surprise that they will be needed. In this study, Arabidopsis thaliana was tested in simulated outer space environments to test the effects of hypobaria on growth, as well as the impact that additional carbon dioxide (CO2) in the atmosphere will have on growth and development. A. thaliana was plated in an agar based media and grown in vacuum boxes where a vacuum pump worked to remove 50% of the atmosphere from the environment, either with or without carbon dioxide being added. Our results showed that the addition of carbon dioxide prior to germination prevented the seeds from germinating. However, when CO2 was added after the seeds were allowed to germinate for a week, the plants actually benefitted from it. This could be a promising finding when considering growing plants in a Martian atmosphere.

21B-U. The Effects of Cannabinoids on Tumor Vasculature in Ewing Sarcoma. Rebekah Davis, R.J. Quilao, Jessie Little, Lori Hensley, Robert Griffin, Jessica Webber. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Background: Ewing's sarcoma is the second most common pediatric bone cancer. With patients having a 5 year survival rate of 30%, alternative treatments must be developed. We studied the effects of various cannabinoids, particularly Ajulemic Acid (AJA) and Cannabidiol (CBD) on angiogenesis and tumor vasculature in models of Ewing's sarcoma. Methods: We performed tumor insterstitial fluid pressure (TIFP) studies in mouse xenograft ES tumors, looking at the effects of cannabinoids on IFP over the course of 30 minutes. After 24 hours, we then homogenized the tumors, and performed an angiogenic array looking for significant differences in protein expression. Results: The TIFP decreased significantly with CBD, showing a 41% decrease in tumor pressure. AJA also decreased TIFP by 27%, while the control did not affect the TIFP significantly. The tumor angiogenic array did not show substantial differences in the regulation of fifty-five angiogenic proteins. Conclusion: Our study showed that AJA and CBD both have potential as anti-tumor therapeutics through their effects on tumor vasculature. A decreased TIFP is largely correlated with a more positive prognosis in cancer patients. Our previous studies also show that cannabinoids can inhibit angiogenesis. However, the mechanism is still largely unknown. Because there was no substantial difference in angiogenic protein expression, we are doing a follow-up study to see if cannabinoids are inducing apoptosis in endothelial cells, which would cause an inhibition of angiogenesis. Acknowledgment: This work was funded by NCRR grant P20RR016460 and NIGMS grant P20 GM 103429 from the National Institutes of Health.

22A-U. Cannabinoids' Effect on the Vasculature of Ewing's Sarcoma Tumors. R.J. Quilao[1], Rebekah Davis[1], Sydney Heslep[1], Jessie Little[1], Jessica Webber[2], Klressa Barnes[1], Robert Griffin[3], ori Hensley[1]. [1]*Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.* [2]*Department of Pathology,* [3]*Department of Radiation Oncology, UAMS, Little Rock, AR 72205.*

Background: Ewing's Sarcoma (ES) is the second most common pediatric bone cancer. Ajulemic acid (AJA) and cannabidiol (CBD) are two cannabinoid compounds with no known psychotropic effects. In this study, we conducted two experiments to investigate AJA and CBD's effects on vasculature and angiogenic potential of ES cells/tumors. Methods: We conducted an angiogenic array assay on ES cell supernatants treated with 0μM, 5μM, and 10μM AJA. In a separate experiment, we measured the acute effects of AJA and CBD on tumor interstitial fluid pressure within xenograft ES tumors in nude mice. Change in TIFP was measured over thirty minutes using an SPR-671 Mikro-Tip catheter transducer. Results: Our angiogenic array potentially identified TIMP1 as differentially regulated by AJA. We are currently further investigating this finding via ELISA assays. TIFP's in nude mice displayed an average drop of 27% and 41% with AJA and CBD, respectively. Sole administration of the vehicle produced no statistically significant change. Conclusion: As elevated TIFP's are correlated with grim prognoses in cancer patients, AJA and CBD's drastic lowering of TIFP in vivo supports their validity as legitimate cancer treatments. With further studies, TIMP1's identification as a differentially regulated protein may help elucidate the mechanism by which cannabinoids affect ES tumor vasculature. Acknowledgement: This project was supported by the

Arkansas INBRE program, with grants from the National Center for Research Resources - NCRR (P20RR016460) and the National Institute of General Medical Sciences - NIGMS (P20 GM103429) from the National Institutes of Health.

22B-U. Isolation of Soil Bacteria Producing Broad-Spectrum Antimicrobial Compounds. John Givler, Ruth Plymale. *Biology Department, Ouachita Baptist University, Arkadelphia, AR 71998.*

Discovery of new antibiotics will be increasingly important as many commonplace bacteria are becoming resistant to current antibiotics. A possible source for novel antibiotics is environmental bacteria. Our goal in this project is to isolate soil bacteria that produce an antimicrobial agent effective against the majority of the following microbes: the bacteria Bacillus subtilis, Enterobacter aerogenes, Escherichia coli, Staphylococcus aureus, and Pseudomonas putida; and the fungi Candida albicans and Macrophomina phaseolina. Morphologically distinct soil bacteria were patched onto a lawn of one of the above "tester" microbes and antimicrobial production was determined by inhibition of tester microbe growth. Antimicrobial production was determined on brain-heart infusion agar, Luria-Bertani agar, potato dextrose agar, and tryptic soy agar. Soil bacteria grown on potato dextrose agar inhibited tester microbe growth better than the same soil bacteria grown on other media. Several soil bacteria were identified as being "broad-spectrum inhibitors", meaning that they inhibited the growth of at least one Gram-positive tester bacterium, at least one Gram-negative tester bacterium, and at least one fungus. Our next step is to select one of these broad-spectrum inhibitors for antimicrobial product isolation.

23A-U. Identification of Novel Variant of Cannabinoid Receptor CB1 in Cancer Cells. Lindsey Wood, Sebastian Pyrek, Anna Radominska-Pandya. *Biology Department, Southern Arkansas University, Magnolia, AR 71753.*

Cannabinoids receptors (CBRs) are G-protein coupled receptors (GPCRs) activated by the binding of a ligand. These ligands can be made in the body – endocannabinoids – or introduced into the body – exogenous cannabinoids. CBRs are active in many biological activities. The classical receptors are known as CB1 and CB2. CB1 is expressed in the brain and aids in psychoactive effects of cannabinoids. CB2 is mostly expressed in the spleen and aids in anti-pro-inflammatory effects. CB1 and CB2 are overexpressed in different cancers, but their role remains unknown. CB1 has six known splice variants. We hypothesize that cancer cell lines can express cancer-specific combinations of CB1 variants that are different from those found in normal brain cells. Our strategy is to design primers that can screen for CB1 variants, isolate mRNA from cancer cells, then reverse transcribe the mRNA into cDNA. This cDNA will be run in a semi-quantitative RTPCR in order to identify cancer-specific CB1 variants. The results will be compared to the control – non-cancerous brain cells. The semi-quantitative RTPCR of the housekeeping gene generated clear results; RTPCR of native CBs and variants are in progress. If the project is successful, then these splice variants can potentially be targets of anti-cancer drugs.

23B-U. Ordering Practices for Initial Out-Patient Echocardiograms by Pediatric Cardiologists. Don White, III, Elijah Bolin, R. Thomas Collins, Sean Lang. *Natural Sciences, UA Monticello, Monticello AR 71655.*

Echocardiography is the most commonly used imaging modality for evaluating cardiac structure and function in pediatric patients. For common indications, its routine use is neither highly diagnostic nor cost-effective. In 2014, the American College of Cardiology participated in a joint project with the American Society of Echocardiography, the Society of Pediatric Echocardiography and several other subspecialty societies and organizations to establish Appropriate Use Criteria (AUC) for the initial use of outpatient pediatric echocardiograms. This study sought to evaluate ordering practices for initial outpatient echocardiograms by pediatric cardiologists. Initial out-patient echocardiograms ordered by Arkansas Children's Hospital pediatric cardiologists from January 2014 to December 2014 were evaluated. Clinic letters were retrospectively reviewed to rate appropriateness from rarely appropriate (AUC score 1-3), moderately appropriate (AUC score 4-6), and appropriate (AUC score 7-9). Positive findings in echocardiograms were defined as any cardiac abnormality of structure or function, excluding patent foramen ovale. Of 450 initial out-patient studies available for classification, 346 (76.9%) were classified as appropriate, 37 (8.2%) were moderately appropriate, 47 (10.4%) were rarely appropriate, and 20 (4.4%) were not classifiable. The mean AUC score for ordered echocardiograms was 7.32. A total of 86 echocardiograms were positive (19.3%): 82 (95.3%) were appropriate, 3 (3.5%) were moderately appropriate, and 1 (1.2%) was rarely appropriate. Of the 346 appropriate echocardiograms, 82 (23.7%) were positive. Of the 37 moderately appropriate echocardiograms, 3 (8.1%) were positive. Of the 47 rarely appropriate echocardiograms, 1 (2.1%) was positive. The majority of pediatric cardiology echocardiograms ordered by pediatric cardiologists were appropriate, however approximately 10% of the cardiology-ordered echocardiograms were rated rarely appropriate studies. Rarely appropriate echocardiograms were understandably found to have an extremely low rate of positive findings. Our results provide a framework for improving quality and decreasing resource utilization in the pediatric population.

24A-U. **An automated pipeline for whole genome sequencing data analysis.** Chad Hayden, Mary Yang. *Bioinformatics, UA Little Rock, Little Rock, AR 72204.*

Background: Whole-genome sequencing data analysis is commonly used in revealing disease related SNPs, INDELs, and CNVs. Despite a number of software tools having been developed to process and analyze whole-sequencing data, presently no single variant identification tool can capture comprehensive genomic variations. We developed an automated pipeline for whole-genome sequencing data analysis, allowing easily adopting algorithms into the pipeline and consensus variant callings. Methods: The pipeline was built in python and is able to handle both paired-end and single-end reads. The pipeline includes quality control (QC), read alignment, variant calling and functional annotation. After QC, reads are aligned to the reference genome using BWA. Picard is used to mark and remove PCR duplicate reads. Read re-alignment and re-calibration, as well as variant calling, are performed using GATK. FreeBayes and Platypus variant callers are used along with GATK to provide consensus results. The ANNOVAR package is used for functional annotation of the genetic variants. Results: We used datasets from the 1000 Genome Project to test and validate out pipeline. Our results can be compared with the variant calling results provided by the 1000 Genome Project. Hence we are able to adjust software components and parameters of the pipeline based on benchmark results. Furthermore, MuTect program is used to call somatic mutations in the analysis of sequencing data form paired cancer and health samples. Conclusion: Our automated pipeline can facilitate whole-genome sequencing data analysis and foster biomedical research collaboration. The pipeline serves as a flexible tool to allow users with minimal programming knowledge to easily run NGS data analysis. Acknowledgment: This work was supported by grants from NCRR (P20RR016460), NIGMS (P20GM103429), 1R15GM114739 and Arkansas Science and Technology Authority (ASTA).

24B. Performance evaluation for gene set analysis approaches for RNA-seq data. Yasir Rahmatallah, Galina Glazko. *Biomedical Informatics, UAMS, Little Rock, AR 72205.*

Transcriptome sequencing (RNA-seq) is steadily replacing microarrays for high-throughput studies of gene expression. Gaining insights into the biological processes underlying phenotypic differences is the major challenge in analyzing the expression of thousands of genes. For this purpose, gene set analysis (GSA) emerged as the method of choice, in particular because it incorporates pre-existing biological knowledge in the form of functionally related gene sets into the analyses. We consider several statistically different GSA approaches (competitive and self-contained) that were adapted from microarrays practice or specifically designed for RNA-seq data. We perform a comprehensive evaluation of their performance in terms of Type I error rate, power, robustness to the sample size and heterogeneity, as well as the sensitivity to different types of selection biases on simulated and real RNA-seq data. We show that the performance of various methods depends on the statistical hypothesis they interrogate and not on the platform type for which they were designed for. We found that competitive methods have lower power as well as robustness to the samples heterogeneity than self-contained methods, leading to poor results reproducibility. Moreover, we found that the power of unsupervised competitive methods is highly affected by the balance between up- and down-regulated genes between two phenotypes in the tested gene sets. Our evaluation provides a concise guideline for selecting proper GSA approaches, and warns against using others in their current form.

25A-U. Stimulation of Bone Mass by Sclerostin Antibody Treatment in Down Syndrome (Ts65Dn) Mice. Jami Schmidt, Larry Suva, Dana Gaddy. *Orthopedic Research, Lyon College, Batesville, AR 72503.*

Down Syndrome (DS) is the most common genetic abnormality in humans and is caused by trisomy of human chromosome 21 (Hsa21). As life expectancy of people with Down Syndrome has increased, a higher risk of bone fracture has been observed. Our lab has previously studied a murine model of Down Syndrome (Ts65Dn) and reported low bone turnover and a low bone mineral density (BMD) phenotype; however, the details of this characteristically low bone BMD phenotype are currently lacking. Sclerostin, a cytokine secreted by native bone cells, is a known inhibitor of the Wnt signaling pathway which, when uninhibited, leads to osteoblast differentiation and ultimately, new bone formation. We hypothesis that the administration of sclerostin antibody (Scl-Ab) will inhibit sclerostin thus leading to more osteoblast differentiation and more bone formation. This study shows, after three weeks of antibody injections, Ts65Dn mice demonstrated a significant increase in BMD, bone volume/tissue volume ratio, as well as an increase in the number of mesenchymal stem cells recruited into the osteoblast lineage, thus resulting in new bone formation.

25B-U. Effect of Nigella sativa extracts on oral cancer cells. Destiny Jones, Selma Dagtas. *Biology Department, UA Pine Bluff, Pine Bluff, AR 71601.*

Effect of Nigella sativa extracts on oral cancer cells Oral cancer treatment is far from satisfactory despite the advances in surgical techniques. Usually, following the successful removal of the initial lesion, secondary

lesions develop elsewhere in the mouth under the influence of the very same predisposing factors that gave rise to the initial lesion at the first place. Therefore, a preventive chemotherapeutic method is required for the effective and comprehensive treatment of oral cancer. Natural compounds present a nontoxic, inexpensive alternative to conventional chemotherapeutics that cannot be justified for prevention due to their toxicity. Thymoquinone, a major constituent in the Nigella sativa seeds have been promising as a potent and selective natural anti-cancer agent against a number of cancer types in vitro and in vivo. Nigella sativa is an herb that is used to decorate bakeries. It is safe to consume and it has been used traditionally against a number of illnesses. In this study, we have tested Nigella sativa whole seed extracts on mouse squamous cell carcinoma (SCC) VII cells and showed their effect in a dose dependent way. Chewing Nigella sativa seeds may prove to be a safe and inexpensive solution for the prevention of oral cancer.

26A-U. Analysis of a Ribosomal Protein Gene in Tumor Development. Seth St. John, Devon Wray, Helen Beneš, Mary Stewart. *Mathematical and Natural Sciences, UA Monticello, Monticello, AR 71655.*

In humans, mutation of genes involved in ribosome production, including ribosomal protein genes, is known to cause a set of pathologies called ribosomopathies. Clinical symptoms of ribosomopathies include anemia, craniofacial abnormalities and abnormal blood cell production, all of which may be associated with decreased rates of protein synthesis. In some cases, ribosomopathy patients have a predisposition to solid tumor or hematological tumor formation. Similarly, mutations in ribosomal protein genes in Drosophila melanogaster (fruit fly) causes phenotypes consistent with reduced protein synthesis such as delayed development and short, thin bristles in adult flies .In addition, mutation of some D. melanogaster ribosomal protein genes, such as the ribosomal protein S6 gene (RpS6), can cause tumors in developing animals. The RpS6 gene is a "dual gene" because this gene contains information for the RpS6 protein as well as a small non-coding RNA thought to function as a snoRNA. Our current work involves genetic and molecular approaches to understanding what phenotypes of RpS6 mutant flies are caused by reduced expression of RpS6 versus effects that may be caused by altered expression of the snoRNA.

26B-U. E-cadherin expression in prostate cancer cells growing in suspension. John A. Martindale, Calin O. Marian. *Biology Department, University of Central Arkansas, Conway, AR 72035.*

E-cadherin expression in prostate cancer cells growing in suspension John A. Martindale and Calin O. Marian

E-cadherin is a transmembrane glycoprotein that plays an important role in cell-to-cell adhesion and its role in the process of epithelial to mesenchymal transition was well documented for several cancer types. In prostate cancer, there is a significant correlation between decreased E-cadherin expression and the loss of tumor differentiation. Three of the most common prostate cancer cell lines used in research (LNCaP, DU145 and PC3) are maintained in various types of media as monolayers or suspensions. The culture conditions can influence dramatically the expression of E-cadherin in these cells. For this study, all three cell lines were cultured in the same media and the E-cadherin protein expression was analyzed to identify changes that occur in response to the lack of attachment to the substrate.

27A. The ferredoxin-like domain and [4Fe-4S] clusters of subunit D play important roles in RNA polymerase assembly and activity in Methanosarcina acetivorans. Matthew E. Jennings, F.H. Lessner, E.A. Karr, D.J. Lessner. *Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Iron-sulfur (Fe-S) clusters are prosthetic groups that serve a variety of functions in many different proteins. The D subunit of RNAP from numerous archaea and the homologous subunits of RNAP from several eukaryal species (Rpb3/AC40) contain a ferredoxin-like domain (FLD) predicted to bind one or two [4Fe-4S] clusters. A FLD is absent from the RNAP of all sequenced bacteria. The function(s) of the FLD and the bound [4Fe-4S] cluster(s) is unknown. We hypothesize the FLD provides a mechanism to correlate information processing (i.e. transcription) with energy conserving metabolism. Subunit D forms a heterodimer with subunit L, the first step in the assembly of multi-subunit RNAP. Loss of the [4Fe-4S] cluster(s) in response to cellular signals (such as oxygen or Fe/S levels) may affect formation or stability of the D/L heterodimer and therefore serve to regulate assembly of RNAP. We have previously demonstrated that the methanogen Methanosarcina acetivorans possesses a subunit D that binds two oxygen-labile [4Fe-4S] clusters [1]. Using M. acetivorans we have probed the in vivo role of the clusters and provide evidence that the [4Fe-4S] clusters and FLD of subunit D are important, but not essential, for assembly of RNAP downstream of the formation of the D/L heterodimer. Loss of [4Fe-4S] cluster one had a greater impact on RNAP assembly compared to cluster two, consistent with cluster one being more conserved in RNAP subunits from numerous archaea and eukaryotes. Gene replacement experiments confirmed that the [4Fe-4S] clusters and the FLD are not essential for functional RNAP in M. acetivorans but are required for optimal growth. Biochemical and molecular experiments showed that the loss of FLD and cluster(s) has a negative impact on RNAP assembly and transcription activity. A more severe impact was also observed when cluster one

was absent compared to cluster two. Overall, these results support the hypothesis that the presence of the [4Fe-4S] clusters and FLD are required for optimal assembly of RNAP and for the stability of holo-RNAP in M. acetivorans. This mode of regulation may be conserved in other archaea and eukaryotes which also possess the FLD and [4Fe-4S] cluster(s).

27B. The functional analysis of Robo2 in axon guidance. LaFreda J. Howard, Timothy A. Evans. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Roundabout (Robo) family proteins regulate many axon guidance decisions in the Drosophila embryonic central nervous system. Robo1 and Robo2 facilitate midline repulsion in response to Slit, while Robo2 and Robo3 define the lateral position of longitudinal axon pathways. In addition to these shared roles, Robo2 can also promote midline crossing of axons, an activity that is not shared by the other Drosophila Robos. Previous gain of function and genetic rescue studies suggest that the different roles of Robo2 are specified by individual immunoglobulin-like (Ig) domains within the receptor. Ig2 is required for Robo2's pro-crossing function, while Ig1 and Ig3 are thought to regulate lateral positioning. It has been assumed (but not directly demonstrated) that Robo2 acts as a canonical cell-autonomous Slit receptor to signal midline repulsion; if so, this activity would likely require the Slit-binding Ig1 domain of Robo2. We are using a CRISPR/Cas9-based gene replacement approach to investigate which domains of Robo2 (Ig & Fn) are required for each of its axon guidance activities. By replacing the robo2 coding region with epitope-tagged cDNAs in which individual domains have been deleted, we can examine the contributions of each domain to receptor localization, regulation, and Robo2-dependent axon guidance outcomes. Our results promise to increase our understanding of how individual receptors can contribute to multiple axon guidance outcomes during developmental wiring of the nervous system.

28A-U. Occurrence of the Northern Saw-whet Owl in Late Fall in Northwestern Arkansas. Mitchell Pruitt, Kimberly G. Smith. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

The elusive Northern Saw-whet Owl (Aegolius acadicus), which breeds in the northern boreal forests, is now believed to be much more widespread during fall and winter in the United States than previously thought. Of the few places in the southern United States conducting research on this species, all have been successful. Research to determine their occurrence in northwest Arkansas began last fall. The methods involve setting up four mist nets along a trail in woodland that is mostly pine and cedar with some deciduous trees and fairly dense undergrowth. A speaker was set up in the center of this arrangement and broadcast the owls' call, acting as an audio lure to bring the birds into the nets. The nets were checked every 45 minutes. Once captured, an owl is extracted from the net, weighed, measured, sexed, aged, banded, and released. During our first field season (November 2014-January 2015), we captured two adult female saw-whet owls in Madison County in late November and early December; thus, establishing their presence in northwestern Arkansas. Prior to this there had been only 13 records of this owl in Arkansas in the last 55 years. This species is known to be more migratory in certain years than in others, and fall/winter of 2014-2015 was not a good "flight year". This study will continue this coming October 2015-January 2016.

28B-U. In vivo analysis of Slit binding-deficient Drosophila Robo1. Haley Brown, Marie Reichert, Tim Evans. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

The repellant ligand Slit and its Roundabout (Robo) family receptors regulate many aspects of axon guidance in bilaterians, including midline crossing of axons during development of the embryonic CNS. Slit proteins are produced by midline cells and signal through Robo receptors expressed on the surface of axonal growth cones to repel axons from the midline. Disruption of Slit-Robo signaling causes ectopic midline crossing phenotypes in the CNS of a broad range of animals, including insects and vertebrates. Although the genetic relationship between Drosophila slit and robo1 has been well characterized in vivo, and the biochemical nature of Slit-Robo interaction has been studied intensively in vitro, a disconnect still remains between these in vitro interaction studies and in vivo functional studies. For example, whether Robo1's in vivo role in midline repulsion depends on its ability to bind Slit has not been directly investigated, and it is unknown whether Robo1 expression or in vivo regulation (for example, its clearance from commissural axon segments) depend on interactions with Slit. Here, we bridge this gap by replacing Drosophila Robo1 in the embryonic CNS with a Robo1 variant that is unable to bind Slit (Robo1DIg1). Using a genomic rescue construct based on endogenous robo1 regulatory regions, we restore expression of Robo1DIg1 in embryonic neurons in robo1 mutants. We find that deleting the Slit-binding Ig1 domain of Robo1 does not affect its expression, axonal localization, or subcellular regulation in vivo, but completely removes its ability to prevent axons from crossing the CNS midline. Our results deliniate Slit-dependent versus Slit-independent aspects of Robo1's function and regulation during embryonic axon guidance, and demonstrate that Slit binding via Ig1 is absolutely required for Robo1's midline repulsive role in an endogenous expression context in intact animals.

29A-U. Exploiting Natural Genetic Variation to Understand MKT1 Function. Emma Cox, Rebecca Sides, Jeffrey Lewis. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

A major goal in genetics is to understand how individuals with a different genetic makeup respond to their environment. Understanding these "gene-environment interactions" is important for the development of personalized medicine. For example, gene-environment interactions can explain why some people are more sensitive to certain drugs or are more likely to get certain cancers. Understanding the rules that govern gene-environment interactions in humans is a challenge, so we turned to brewer's yeast as a model. In particular, we wanted to explore the genetic basis of natural variation in the global gene expression response to acute ethanol stress. We were interested in gene expression variation because it is widespread in nature, and is thought to play a major role in shaping the differences we see between individuals. To understand differences between yeast strains responding to acute ethanol stress, we employed linkage mapping in two yeast crosses. Our genetic mapping identified many "hotspots" that control the expression of many genes, as well as a surprising amount of genetic interactions between hotspot loci, that we call "epi-hotspots." Exploring these hotspots and epi-hotspots gives us new insight into how different individuals respond to acute environmental change.

29B. Titanium dioxide nanofiber based biosensor for low level detection of CEA target cells. Anishkumar Manoharan, Jared Hopkins, Ryan Tian, Simon S. Ang. *Electrical Engineering, University of Arkansas, Fayetteville, AR 72701.*

A highly sensitive titanium dioxide (TiO2) nanofiber based biosensor device for detection of colon cancer was fabricated using a bottom up approach on commercially available titanium sheets. The TiO2 nanofibers were synthesized by a hydrothermal process using 1M sodium hydroxide aqueous solution. The solution was heated in a 100 ml teflon lined auto clave vessel at 240oC for 4 hours, containing a chemically cleaned titanium sheet. The resulting nanofibers had a mean diameter of around 100 nm with a few micrometers in length. These nanofibers were then used as a biosensor for the detection of low-level carcinoembryonic antigen (CEA), a type of glycoproteins involved in cell adhesion. CEA is normally produced in gastrointestinal tissue during fetal development, but the production stops before birth. Therefore, in adults, an abnormal level of CEA may be a sign of cancer. A detection limit of up to 1ng/ml of CEA was demonstrated in these TiO2 nanofiber sensors.

30A. Examining Archaeal Iron-sulfur Cluster Biogenesis. Syed Raza Mahmood, Jeffrey Lewis. *Cell and Molecular Biology, University of Arkansas, Fayetteville, AR 72701.*

Posttranslational modifications (PTMs) of proteins are involved in regulating a wide variety of cellular processes in eukaryotes, ranging from growth and development to signal transduction and adaptation. PTMs include but are not limited to acetylation, phosphorylation and methylation of proteins and allow the cell to dynamically regulate and diversify protein structure and function. Since PTMs provide the cell with one of the fastest means to respond to environmental stimuli, they likely play a critical role in regulating the response of the budding yeast Saccharomyces cerevisiae to various environmental stresses. Our focus has been on protein acetylation, where we have found that protein deacetylase activity is necessary for the acquisition of thermotolerance in the absence of protein synthesis. In this study, we are leveraging natural variation in wild yeast isolates to identify novel connections between protein acetylation and stress defense. We have found that acquired thermotolerance in the absence of protein synthesis only occurs in our commonly used lab strain and not any of the wild strains we have tested. This phenotype correlates with differences in the protein acetylation profile of the strains as assessed by western blot analysis. Our future goals are to perform quantitative acetyl-proteomics to identify which proteins are differentially acetylated across wild and lab strains, and to identify the genomic regions responsible for the acquired thermotolerance differences observed between the lab strain and wild strains. The results from these studies will provide novel insight into the mechanisms that underlie natural variation in stress tolerance.

30B. Examining Archaeal Iron-sulfur Cluster Biogenesis. Thomas Deere, Faith Lessner, Evert Duin, Daniel Lessner. *Cell and Molecular Biology, University of Arkansas, Fayetteville, AR 72701.*

Iron-sulfur clusters are important prosthetic groups used to catalyze diverse reactions essential to life, particularly in methanogenic archaea. These clusters must first be assembled by iron-sulfur cluster biogenesis systems. Despite these facts, no such system has been fully characterized for any archaeon. We are investigating the Isc cluster biogenesis system in the methanogenic archaeon Methanosarcina acetivorans. We have cloned genes of putative homologs of the core Isc proteins, IscU (iron-sulfur cluster scaffold protein) and IscS (cysteine desulfurase), into Escherichia coli expression strains, purified the translation products, and confirmed that these proteins can carry out their predicted functions.

31A. Ecology of Microorganisms Applied to Management and Conservation of Natural Resources in the Brazilian Amazon Forest. Isadora L. Coelho, Beatriz R. Lisboa, Stephenson L. Stephenson. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Biodiversity loss is a silent crisis, and if not stopped, will lead to biotic homogenization of the planet. The decline of biological populations, species extinction threat, the loss of genetic diversity among species, degradation of ecosystems, and extensive habitat loss are the evidence of this crisis. The Brazilian Amazon Forest is one of the most biological diverse and threatened biome of the planet. Until now, there are still relatively few studies about its microbiota, especially when regarding myxomycetes, dictyostelids and protostelids distribution, ecology and their role in the ecosystems' balance. myxomycetes, also called slime molds, dictyostelids and protostelids are cosmopolitan groups of protists found in humid places where there is presence of abundant decaying organic matter, developing more rarely on living plants. The different phases of their life cycle (e.g., amoebae, flagellates, plasmodia) include a wide variety of organisms as their food source, and usually occur in microhabitats with large populations of bacteria. As predators of bacteria and fungi, they participate in the balance of microorganisms that are involved in the decomposition of organic matter of plant origin. Presumably, important in nutrient cycling and, as such, would have a major influence on forest conservation. Aiming to increase the knowledge about the Amazon microbiota, collections were performed on different substrates in a fragment of Amazon forest located in the Viruá National Park in the municipality of Caracaraí, state of Roraima, Brazil. The 1,855 samples obtained from moist chambers and field collections were analyzed, identified, and deposited in the UARK herbarium. A total of 122 species of myxomycetes, six species of dictyostelids and two species of protostelids were recorded so far. Even though there is no reliable information relating to the conservation status of any species belonging to these groups, some species appear to be extremely rare. Being the first time that some of these species were found in Latin America. This project yielded a considerable body of new information on the distribution, ecology and species diversity of microorganisms in tropical rainforests. In an effort to protect and preserve examples of existing ecosystems in the Amazonia biome, this knowledge was used as the first step to better manage and expand the original area of the Viruá National Park, thereby ensuring the preservation of its natural resources, and providing opportunities for controlled public use, education and scientific research. Tropical forests are currently listed as biodiversity hotspots with a high priority for conservation. Although most studies have placed primary emphasis on certain groups of organisms (i.e., vascular plants, larger animals), it is essential that research also be directed towards microorganisms, such as fungi, lichens, myxomycetes, and other protists, all of which are crucial for the conservation planning of the remaining areas of tropical forest in Brazil.

31B. Understanding the role of iron-sulfur clusters in RNA polymerase. Stephen C. Granderson, F.H. Lessner, D.J. Lessner. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

DNA-directed RNA polymerase (RNAP) is a multi-subunit enzyme which synthesizes RNA from a DNA template, and is essential to all organisms. Archaeal RNAP consists of 12-13 subunits and is similar to eukaryotic RNAP II, which contains 12 subunits, but not bacterial RNAP, which contains only five. Subunit D of RNAP from many species of archaea contains a ferredoxin-like domain which is predicted to bind one or two [4Fe-4S] clusters. The homologous Rpb3/AC40 subunits of RNAP from several eukaryotes also contain this domain, consistent with archaeal and eukaryotic RNAP having a common ancestor. The function of the domain and clusters is not yet known. We hypothesize the ferredoxin-like domain was acquired to coordinate RNAP assembly and activity (i.e. transcription) with the metabolic state of the cell. Subunit D forms a heterodimer with subunit L, which is the first step in the assembly of RNAP. Interestingly, only RNAP from strictly anaerobic archaea is predicted to bind two [4Fe-4S] clusters, including the majority of methanogenic archaea (methanogens), whereas RNAP from other archaea and eukaryotes are predicted to bind a single [4Fe-4S] cluster or lack clusters entirely. We have previously demonstrated that subunit D of RNAP from Methanosarcina acetivorans, a member of the Methanosarcinales, contains two oxygen-labile [4Fe-4S] clusters, which impact the stability of the D-L heterodimer [1]. However, not all methanogens contain a subunit D predicted to bind two [4Fe-4S] clusters. For example, RNAP from Methanobrevibacter smithii contains a subunit D predicted to bind only one [4Fe-4S] cluster. M. smithii is the dominant methanogen found in the human gut, and plays an important role in the efficiency of polysaccharide digestion. The goal of this project is to purify the D-L heterodimer from M. smithii and determine the number, type, and properties of the Fe-S clusters, as well as the impact of the clusters on the stability of the D-L heterodimer. A plasmid-based system was developed to co-express recombinant subunit D and subunit L in Escherichia coli. Preliminary data revealed that co-expression of D and L in E. coli results in the formation of a D-L complex, whereas expression of D alone results in inclusion bodies. Purification of the M. smithii D-L complex, reconstitution with iron and sulfide, and analysis of the color and UV-visible absorbance of the protein produced results consistent with the presence of a [4Fe-

4S] cluster. Further results are expected to extend our understanding of the role of the [4Fe-4S] clusters in RNAP assembly and activity both in archaea and in eukaryotes, due to the similarities and common evolutionary origin of archaeal and eukaryotic RNAP.

32A. Nanofiber Bioscaffold sensor for cancer cell detection. Hanan Alismail[1,2], Yuchun Du[1,3], Jianhong Zhou[3], Anishkumar Manoharan[4], Z. Ryan Tian[1,2]. *[1]Cell and Molecular Biology, [2]Institute of Nanoscience/Engineering, [3]Biological Sciences, [4]Electrical Engineering, University of Arkansas, Fayetteville, AR 72701.*

A simple, sensitive, and reliable method that can distinguish cancer cells from normal cells is critical for cancer screening and treatment, in which little has been reported in literature on turning a bioscaffold into an electrochemical sensor. Here we present some preliminary results from the development of a label-free electrochemical biosensor on a bioscaffold for direct detection of cancer cells in, hopefully, both qualitative and quantitative manners. In the present work, a sensory nanobioscaffold was incubated with two types of human cancer cells and one type of corresponding normal human cells, respectively. These three types of cells showed significant differences on the bioscaffold-sensors, suggesting that these cells upon bounding on the scaffold have altered the surface charge-density on the nanobioscaffolds. This new method can be potentially used in various important applications in cancer screening and monitoring, which are doable in vivo at ultralow-cost and in real-time.

32B-U. Using Environmental and Natural History Traits to Predict On-Going Global Amphibian Die-offs. Kristina Frogoso, Scott Connelly, Jim Winter. *Ecology, UA Little Rock, Little Rock, AR 72204.*

Global losses in biodiversity are occurring at unprecedented rates. Declines in amphibian diversity play a large role in these losses. Many of the dramatic and on-going declines in amphibian populations are due to infectious diseases. One pathogen in particular that has been associated with widespread amphibian losses is the fungus Batrachochytrium dendrobatidis (Bd), which causes chytridiomycosis, an often fatal amphibian disease. A number of environmental factors may play a role in the prevalence and pathogenicity of Bd, and not all amphibian species are affected equally after exposure to the pathogen. Our study asks: Can we use environmental and amphibian natural history traits to help predict and prevent the decline of amphibians due to chytridiomycosis? A multiple linear regression model was created on RStudio to simulate the relationship between twelve environmental variables and the threat status of global amphibian species. Then, ten amphibian natural history traits were added in the explanatory variable to more fully characterize threat status. We made predictions of their threat status and compared the predicted to the actual threat status. Threat status was correctly predicted for 1799 species out of 2333, showing 77% accuracy. We applied the same methods to predict the threat status for species with unknown conservation status. The logistic regression analysis quantifying the relationship between natural history traits and predicted threat status showed that breeding site type (permanent or ephemeral) was the strongest predictor of threat status, with species using more permanent breeding sites tending to be more threatened ($p < 0.05$). This analysis showed that future research should focus on understanding of both environmental factors and an organism's specific natural history characteristics to best predict the threat status for each species.

33A-U. Targeting Psoriasis with Topically-applied TNF-α Antisense Nanoconjugates. Taylor Washington, Jim Winter. *Biology Department, UA Little Rock, Little Rock, AR 72204.*

Psoriasis is a common inflammatory skin disease that affects approximately 2% of the population. The cause of this disorder is currently unknown, but studies suggest that tumor necrosis factor alpha (TNF-α) is important for inflammatory cell activation and recruitment of infiltrate to psoriatic plaques. TNF inhibitors given by subcutaneous injection are one of the current effective treatments for this disease and have been shown to cause irritation and adverse side effects. Recently, researchers have discovered a potentially effective nucleic acid-based therapy using liposomal (L) and self-assembling (SA) spherical nucleic acid (SNAs) conjugates. SNAs have been shown to penetrate biological barriers, enter cells easily, resist nuclease degradation, and control targeted gene expression without observed toxicity, immune activation, or off target effects. Our study investigated the effectiveness of the topical application of L- and SA SNAs to suppress TNF-α expression in a mouse psoriasis model with an expectation of preventing abnormal immune response and inhibiting the development of a psoriatic phenotype. Treated mouse skin was cut in 4-µm sections for H & E staining and examined under a light microscope to identify significant skin thickening and infiltrate presence. Although preliminary studies from our lab have shown promising effects of topical therapy targeting TNF-α with L- and SA SNAs, results from my study showed that neither L- nor SA SNAs were able to completely prevent the development of a psoriatic-like phenotype. Further investigation is needed to develop a more effective and consistent way of applying these treatments in a mouse psoriasis model to properly test the effectiveness of targeting TNF-α topically using these SNAs.

33B-U. Cyanobacteria Responses to Stress Induced by Copper Contamination and Light Intensity. Jacob Ellis, Qingfang He, Soumana Daddy, Morgan Gillum, Jim Winter. *Biology Department, UA Little Rock, Little Rock, AR 72204.*

Cyanobacteria are novel organisms for the study of photosynthesis, biomass production, and biotechnological applications, as they successfully combine effective metabolic pathways in a single compartment and can undergo nitrogen fixation. However, cyanobacteria have to cope with fluctuating environmental conditions, including variable light intensities and heavy metal concentrations, which induce stress and affect the efficiency of photosynthesis. Copper is both an essential cofactor and a toxic element, so photosynthetic organisms have developed mechanisms to regulate its homeostasis relative to the environmental copper concentration. There is evidence to suggest that carotenoids play an essential role in both the photo-protective mechanisms of cyanobacteria and resistance to copper toxicity by protecting the photosynthetic apparatus. The physiological and biochemical responses of Synechocystis sp PCC 6803 cells under excess copper concentrations and elevated light intensity were examined in this study. Cells of wild type Synechocystis sp PCC 6803 and slr1573Δ strain, a mutant lacking the gene coding for the laccase protein, were exposed to different copper concentrations (1.5 µM and 3 µM) and light conditions (50 µmol of photon m2s-1 and 300 µmol of photon m2s-1) for up to five days. The results indicate that copper toxicity begins at 1.5 µM concentration and is more prominent under high light conditions. There is minimal difference between wild type and mutant stress responses under normal light conditions but significant under high light conditions. The laccase mutant appears to have a higher tolerance to the combined high light and copper conditions than the Synechocystis sp PCC 6803 wild type.

34A-U. AAV Delivery of an Anti-Methamphetamine scFv: in vitro & in vivo functional analysis. Sinthia Jahan[1], Laura Ewing[2], Chris Bolden[2], Charles Hay[2], Emily Reichard[2], Eric C. Peterson[2]. [1]*Biology Department, UA Little Rock, Little Rock, AR 72204;* [2]*Department of Pharmacology and Toxicology, College of Medicine, UAMS, Little Rock, AR 72205.*

Methamphetamine (METH), a central nervous system (CNS) stimulant, is one of the most abused drugs in the USA and worldwide. Currently, there are no FDA-approved pharmacological treatments for METH abuse. In response to this, our lab has developed two different single-chain antibody fragments (scFv6H4 and scFv7F9) as potential therapeutics to target METH in the blood. We used adeno-associated virus (AAV) to induce mice to constantly express these scFvs over a 2-month period. Our first goal was to examine whether AAV-scFv expressed in mice and scFv expressed in vitro will exhibit the same binding affinity for METH. We conducted titration binding assays to determine the scFv concentration at which 20% binding of 3H-METH occurred. We used competition binding assays to measure the IC50 of each scFv for METH using the scFv concentration derived from the titration assays. The IC50 values of AAV-scFv6H4 and scFv6H4 did not differ significantly, suggesting that AAV-delivered scFv6H4 and scFv6H4 produced in vitro display similar binding affinities for METH. In contrast, AAV-scFv7F9 showed a 2-fold stronger affinity for METH than scFv7FF9 produced in vitro. Our second goal was to determine if AAV-scFvs can alter brain and blood METH concentrations in mice after a subcutaneous METH injection. Mice received intravenous administration of AAV-scFv7F9, AAV-scFv6H4, and saline (n=8 per group). Fifty-six days following AAV administration, mice received a 0.56 mg/kg 3H-METH, subcutaneously. At 10 and 30 minutes after METH injection, mice were sacrificed by decapitation under anesthesia, and trunk blood and whole brain samples were collected. Serum and brain 3H-METH concentrations were determined by liquid scintillation counting. METH concentrations of the saline and both AAV-scFv treated groups, for both brain and blood samples, did not differ significantly. We think this result could be due to experimental set-up and execution, as inconsistencies were observed within groups. These studies will be repeated. Future studies will also include clinical trials of the ability of the virus delivered antibody fragments to treat METH addiction. These studies were supported by the American Society for Pharmacology and Experimental Therapeutics Summer Undergraduate Research Fellowship (ASPET SURF), and NIDA Grant R01 DA036600.

34B-U. **Sediment as a Source of Contamination Tri-State Mining District.** Amber Hil, Laura Ruhl, Jim Winter. *Geosciences Department, UA Little Rock, Little Rock, AR 72204.*

Mining of lead and zinc from 1850s to 1960s in the Tri-State Mining District has led to severe environmental degradation in SW Missouri, SE Kansas, and NE Oklahoma. Piles of mining waste remain where contaminants wash into streams and poison humans, birds, and aquatic biota. The town of Picher, OK was evacuated when children had blood lead levels >10 µg/dl. The purpose of our study was to explore the effects of mining on sediment in waterways near Picher. Additionally, we determined how far contamination in sediment extended downstream from the mining region and the chemical behavior of contaminants in sediment. We conducted experiments where sediment from the mining district was mixed with leaching solutions to simulate various environmental conditions (using rainwater and deionized water). In the first experiment,

deionized water was mixed with sediment from the streams in the mining region at a 10:1 liquid to solid ratio and reacted for 24 hrs. In the second experiment, sediment was mixed with synthetic rainwater (very dilute nitric and sulfuric acid water) at a 20:1 liquid to solid ratio and reacted for 20 hrs. Trace metal analysis of the leachate was conducted with an Inductively Coupled Plasma Mass Spectrometer (ICPMS) and an ion chromatograph (IC) for cations and anions. Samples leached in deionized water had higher concentrations of Na, K, Mg, and Ca. Cations leached off sediments were at higher concentrations at the mining site and decreased in the sediment downstream. Sulfate concentration in the leachate drastically increased at the mining site likely from oxidation of sulfide minerals mined at the site. A high concentration of nitrate was leached from the sediment at one site and may be due to farmland runoff. Elevated concentrations of Ca, Mg, and SO4 were present in the sediment closest to the mining region from the host rock of mined minerals. Metals (Cd, Zn, Pb, Ni) leached from sediment were elevated in the mining region and decreased downstream. Metals in sediment result from mining waste and could dissolve in water and be ingested by wildlife and humans. The decrease in concentrations downstream is due to dilution by sediment inputs from the Neosho and Spring Rivers. Our data will reveal the extent of contamination from mining activities and identify areas that need remediation. In the future, I would like to perform different leaching experiments and to analyze the sediment at more downstream sites.

35A-U. Fragment Based Drug Discovery of Allosteric FAK Inhibitors. Osvaldo Cossio[1], Ramon Campos-Olivas[2], Clara Santiveri[2], Daniel Lietha[2], Marta Acebron[2]. *[1]Biology Department, UA Little Rock, Little Rock, AR 72204; [2]Spanish National Cancer Research Centre, Madrid Spain.*

The Focal Adhesion Kinase (FAK) is a cytoplasmic tyrosine kinase that plays a key role in cell matrix adhesion signals. Here, signaling is essential for cell migration and proliferation. In several advanced-stage solid cancers, FAK is overexpressed and helps to promote tumor invasion and metastasis. This discovery has led to much research on developing small molecule FAK inhibitors that target the FAK Kinase Domain ATP binding site. However, due to the similarity of ATP binding sites between different kinases this raises concern on the undesired toxicities that could result. Therefore, our research focuses on finding allosteric small molecule FAK inhibitors that target the kinase function but not the active ATP-binding site. To find novel allosteric small molecule FAK inhibitors, we employed the fragment-based drug discovery approach. A collection of about 500 fluorinated small molecules was screened against the FAK protein target with 1D 19F Nuclear Magnetic Resonance (NMR). To identify the binding between small molecules and FAK protein targets, the increase in the small molecules' 19F NMR signal linewidth was used. The hits identified in our research represent potential fragments that can be used to further develop them into lead compounds possessing drug-like properties against this protein overexpressed in cancer. Our future studies will involve further characterizing the hits with WaterLOGSY (WL) and saturation transfer difference (STD) NMR experiments, SPR analysis, and crystallography.

35B-U. Dye Degradation using PNDCs. C'Asia James, Brian Berry. *Biology, UA Little Rock, Little Rock, AR 72204.*

This research focuses on the use of phosphorus nitrogen co-doped carbons (PNDCs) for the photocatalytic degradation of organic dyes for wastewater remediation and water purification. PNDCs are synthesized from spent coffee grounds and found to exhibit photocatalytic properties under visible light. Results from the photocatalytic degradation of methylene blue dye demonstrated PNDCs degraded methylene blue significantly more than control and was shown to be reusable. PNDCs adsorption of methylene blue dye was also observed in the dark and potentially coupled with dye degradation.

36A. Imaging Data Storage and Software Tools. Joshua Strong, Venessa Overton, Tiffany Howell, Karl Walker. *Computer Science, UA Pine Bluff, Pine Bluff, AR 71601.*

Imaging devices are used for capturing changes in phenotypes in plant and animal species. In this work, we created a database schema for storing various types of imaging data (CT, PET, Radiotracer imaging, etc.) and a workflow pipeline for analyzing images using multiple software packages. We also developed imaging software tools using the iPlant API.

36B-U. Transcriptional regulation of robo2 in the Drosophila embryonic nervous system. Gina Hauptman, Tim Evans. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

During nervous system development, neuronal axons are guided to their synaptic targets by receptors expressed on the surface of the axon. The Drosophila Robo2 axon guidance receptor is a member of the evolutionarily conserved Roundabout (Robo) protein family, and controls a number of axon guidance decisions during embryonic development. For example, Robo2 regulates midline crossing of axons in response to the repellent ligand Slit, and specifies the medial-lateral position of longitudinal axon pathways in the ventral nerve cord. The different roles of Robo2 depend on its expression in various subsets of cells within the central nervous system (CNS). Thus, precise regulation

of Robo2 expression is an important aspect of nervous system development in Drosophila. To investigate the genetic regulation of Robo2 expression, we looked for regulatory elements in and around the robo2 gene. Using a transgenic approach, we screened fragments of genomic DNA to find those that reproduced aspects of robo2's expression pattern in the CNS. Our observations indicate that different aspects of Robo2 expression are conferred by distinct regulatory elements in the robo2 gene. We are now working towards determining the relationship between transcriptional regulation of robo2 and its various functional roles in axon guidance.

37A. Characterization of the thioredoxin system in Methanosarcina acetivorans reveals complexity of the system in methanogens. Addison C. McCarver, Faith H. Lessner, Daniel J. Lessner. *Cell and Molecular Biology, University of Arkansas, Fayetteville, AR 72701.*

The thioredoxin system is composed of a thioredoxin reductase (TrxR) that utilizes electrons from NADPH to reduce thioredoxin (Trx). Trx is an electron donor to biosynthetic enzymes, and serves a key role in protecting cells from oxidative stress by reducing protein disulfides. However, there is a limited understanding of how the thioredoxin system works in methane-producing archaea (methanogens). The genome of model methanogen Methanosarcina acetivorans encodes seven Trx homologs (MaTrx1-7) and a homolog of TrxR (MaTrxR). Biochemical studies revealed MaTrx2, MaTrx6, and MaTrx7 are disulfide reductases, but MaTrx1, 3, 4, and 5 are not disulfide reductases and may have alternative functions. Moreover, M. acetivorans contains a complete thioredoxin system composed of MaTrxR and MaTrx7. Interestingly, NADPH serves as the electron donor for MaTrxR, despite F420H2 and reduced ferredoxin being the primary electron donors in methanogens. Biochemical studies demonstrate that F420H2:NADP oxidoreductase (Fno) can supply NADPH to the M. acetivorans MaTrxR-MaTrx7 system; thus, linking the system to the physiology of methanogens. Overall, these results support that M. acetivorans, and likely most methanogens, contain a functional NADPH-dependent thioredoxin system.

37B. Netrin-Frazzled/DCC signaling in the insects Drosophila melanogaster and Tribolium castaneum. Logan Terry, Tim Evans. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Proper nervous system development during embryogenesis in organisms with a bilateral bauplan is dependent upon proper commissural crossing of axons. Chemoattractive Netrin ligands and their DCC family receptors promote midline crossing of commissural axons in a broad range of animal taxa. Netrins are produced and secreted at the midline of the embryonic central nervous system (CNS) and signal through DCC family receptors to attract axons towards and across the CNS midline. Mechanisms regulating axon pathway development have undergone evolutionary change in a number of animal groups. To directly investigate the conservation and diversification of axon guidance mechanisms during embryonic CNS development, we have begun a comparative analysis of Netrin-Frazzled/DCC signaling in the insects Drosophila melanogaster (fruit fly) and Tribolium castaneum (red flour beetle). In Drosophila, two Netrin genes (NetA and NetB) act redundantly to signal midline attraction through the single Drosophila DCC ortholog, Frazzled (Fra). We have cloned and sequenced cDNAs encoding the single Tribolium Netrin (TcNet) and Fra (TcFra) orthologs. Both TcNet and TcFra exhibit a high degree of similarity to their Drosophila orthologs in terms of domain structure and sequence identity. In gain of function experiments, we have found that TcFra can signal midline attraction when expressed in Drosophila neurons. Using GAL4/UAS-based rescue experiments, we are investigating whether TcFra can substitute for Drosophila Fra to promote midline crossing in commissural neurons in the Drosophila embryonic CNS. This project will provide broader insight into the role of Netrin-Frazzled signaling in midline crossing in insects, and will contribute to our understanding of the conservation and diversification of axon guidance mechanisms during evolution.

38A-U. An Analysis of the Effects of Trichlorethylene on the Development of Autoimmune Disease. Harrison Daniel, Dusty Barnette, Rachel Lee, Kathleen Gilbert. *Microbiology and Immunology, Ouachita Baptist University, Arkadelphia, AR 71998.*

The etiologies of autoimmune diseases continue to be a mystery and the subject of intensive study. However, evidence based on mouse models suggests that exposure to environmental toxins can trigger these classes of disease. Adult exposure to trichloroethylene (TCE), an organic solvent commonly used commercially as a degreaser, has been shown in previous research to trigger an onset of autoimmunity. Our study attempted to ascertain whether gestational exposure in autoimmune prone mice (both the mother and her pups) compromises immune health and the triggers the onset of a variety of autoimmune disorders. In order to better understand the data collected, a new way of analyzing the data had to be developed. Analysis of the various data points collected showed very few significant differences in the means of the groups. As a result, the use of correlation coefficients was incorporated into the analyses of these data. When using the correlation coefficients within the groups rather than the means to compare the groups, the data produced many more points of interest. The way in

which this was done was by studying the correlations within the different groups and how the correlations changed with respect to the amount of TCE they were given. Numerous points of interest for further research in the effects of TCE on the onset of autoimmunity have been uncovered using the aforementioned method of analysis.

38B. CRISPR/Cas9-based gene modification to study axon guidance genes in Drosophila. Marie Reichert, Timothy Evans. *Biological Sciences, University of Arkanss, Fayetteville, AR 72701.*

Axon guidance in the central nervous system of Drosophila involves a complicated series of events mediated by the precise temporal and spacial expression of axon guidance receptors and their ligands that serve to direct developing axons to their correct targets. The analysis of the functional roles of these axon guidance molecules is vital to promote the greater mechanistic understanding into how the nervous system is properly wired during development. With a mere fraction of Drosophila's greater than 15,000 annotated genes having been studied, and even less functionally characterized, several gene-manipulating approaches including transposable element insertion and forms of homologous recombination-based gene targeting, have been successfully utilized for unbiased and targeted mutagenesis. However, these approaches are often very time-consuming, labor-intensive, and limited in application. Recently the CRISPR/Cas 9 system has emerged, enabling direct and specific changes in the genome to be made in a relatively easy, versatile, and efficient manner. Precise targeted double-stranded breaks in the genome are generated with ease with the injection of plasmids encoding a guide RNA that targets a specific site in the genome into transgenic fly embryos expressing the Cas9 enzyme. These same double-stranded breaks may be repaired by providing a donor plasmid with the desired modified changes to be made in the genome. Here we demonstrate that the CRISPR/Cas9 system can successfully mediate targeted genome modification in genes playing important roles in axon guidance in the model organism Drosophila. Replacement of endogenous axon guidance genes with tagged, modified versions allows for the visualization of the knock-in protein that can be functionally characterized for its ability to rescue knockouts and/or introduce new phenotypes. This is a powerful and promising technique that can potentially lead to the dissection not only of the precise roles of individual domains of axon guidance proteins in Drosophila, but to the diverse functional roles of axon guidance molecules that have contributed to the evolution and diversity of nervous systems across different species.

39A-U. Mechanisms of Ion Retention and Uptake in Rainbow trout exposed to Ion Poor Water. Joseph Gasser, Rebecca J. Bollinger, Maryline C. Bossus, Christian K. Tipsmark. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Mechanisms of Ion Retention and Uptake in Rainbow trout exposed to Ion Poor Water Joseph M Gasser, Rebecca J Bollinger, Maryline C Bossus, Christian K Tipsmark. University of Arkansas, Fayetteville In order to maintain stable internal plasma ion concentrations fishes living in freshwater have to limit the loss of ions that occurs across the gill epithelium. Meanwhile they maintain compensatory salt uptake by the action of gill Na,K-ATPase. Some species, including rainbow trout have the ability to survive in very ion poor water with sodium concentration < 50 micro molar. The present study examined gill expression of determinants of passive permeability (tight junction proteins of the claudin family) and active transport (Na,K-ATPase catalytic α1a and regulatory fxyd11 subunit) during acclimation of trout from regular freshwater to ion poor water. Control fish were maintained in dechlorinated tap water (Fayetteville, AR) and compared to fish transferred to tap water diluted 10x with deionized water. Sampling was performed over a 7 day time-course. Muscle water content was elevated in fish exposed to ion poor water after 6 hours, mirrored by a decrease in plasma osmolality. This osmoregulatory imbalance was corrected after 24 hours. Analysis of gill mRNA showed elevated expression of claudin-27a in ion poor water, suggesting that this tight junction protein may help retain plasma ions by decreasing gill permeability. No change in transcript abundance of Na,K-ATPase catalytic α1a were observed while the regulatory fxyd11 subunit were stimulated. Thus part of the acclimation process to ion poor water may rely on modulation of Na,K-ATPase activity without altering the abundance of existing pumps. Ongoing protein analysis via western blot and enzyme assay will provide more evidence to support this hypothesis. Keywords: Rainbow trout Claudin NKA α1a Fxyd11 Osmolality.

39B. Dissecting the killing mechanism of a novel antifungal peptide. Cody Bullock, David S. McNabb, Ineś Pinto. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

Candida species represent the predominant cause of fungal infections in humans, ranking as the fourth most common hospital-acquired infection. New antifungal therapies are needed as current treatments of Candida infections are not effective against all species. Moreover, the mortality rate from systemic Candida infections ranges from 35-40%. Antimicrobial peptides are known to kill both bacterial and fungal pathogens. Humans produce a number of peptides as part of their innate immune response. The Histatins are a family of

naturally-occurring peptides secreted into the oral cavity and display significant antimicrobial activity. Histatin 5 is a twenty-four amino acid peptide that displays strong antifungal activity. Studies from our laboratory have identified two small histatin-derived peptides, designated KM23 and KM29, which yield fungicidal activity 10-fold greater than Histatin 5 against a number of Candida species. To understand the molecular mechanisms by which these peptides kill yeast, we are using Saccharomyces cerevisiae as a genetically tractable model to identify mutations that confer increased resistance or sensitivity to the peptides. We will present data on the various genetic pathways that influence peptide-sensitivity and the development of a strategy to perform a whole genome screen for increased sensitivity or resistance to KM29.

40A-U. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. Elizabeth McDaniel, Tara N. Stuecker, Isaac Elkon, Audrey Gasch, Jeffrey Lewis. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

All organisms must recognize and respond to various environmental stresses throughout their lifetime. Salt stress is commonly encountered in natural environments, and cells have developed strategic mechanisms to maintain low intracellular sodium levels during salt exposure in an attempt to survive. The budding yeast Saccharomyces cerevisiae has long been a model for understanding eukaryotic salt tolerance. In yeast, induction of the Ena1p sodium efflux pump reduces intracellular sodium levels when cells face life-threatening salt concentrations. The regulation of ENA1 is surprisingly complex, coordinating multiple signal transduction cascades, transcription factors, and environmental cues. However, our understanding of ENA1 regulation has been largely limited to commonly used laboratory strains. While investigating natural variation in the yeast ethanol response, we made a remarkable discovery – we found that transcription of ENA1 was activated by ethanol in a wild vineyard isolate, but not in the laboratory strain. This connection between ethanol stress and salt stress then led to the identification of a new role for ENA1 in salt cross-protection by ethanol, which is absent in the lab strain as well. To understand the genetic basis of these newfound regulations of ENA1, we are analyzing by swapping promoters to construct strains of the lab strain and the wild vineyard isolate that differ only by whether they contain the respective or reciprocal ENA1 promoter region, and subsequently evaluate by quantitative real-time PCR (Q-PCR) and growth analysis. This design will allow us to test whether the expression differences between the lab and wild alleles of ENA1 are due to local effects (e.g. promoter mutation) or distant effects (e.g. transcription factor mutation). By exploiting the natural variation between wild and laboratory yeast, we are providing new insights into the regulation of the well-studied Ena1p sodium pump system, and the molecular mechanisms that underlie gene expression variation.

40B-U. Evolutionary conservation of axon guidance: regulation of midline crossing by Robo receptors. Trent Daiber, Tim Evans. *Biological Sciences, University of Arkansas, Fayetteville, AR 72701.*

In animals with bilateral symmetry, coordination between the two sides of the body depends on proper connections being formed across the midline of the central nervous system (CNS). To achieve this, developing axons must choose whether or not to cross the midline. An evolutionarily conserved family of proteins known as the Roundabout (Robo) family regulate this decision in a broad range of animals including vertebrates, insects, and nematode worms. Robo receptors are expressed on axons and prevent them from crossing the midline in response to the repellant ligand Slit. Although Robo family members are present in each of these species, it is not known that their mechanisms function the same way. To directly compare the midline repulsive activity of Robo receptors from different animals, we are introducing Robo receptor genes from other species into Drosophila and determining whether they can substitute for Drosophila robo1 to regulate midline crossing of axons in the fly embryonic CNS. We are focusing on Robo genes from the nematode Caenorhabditis elegans (which has a single Robo receptor known as SAX-3) and the mouse Mus musculus (which has three Robo receptors known as mRobo1, mRobo2, and mRobo3). We have successfully transformed the C. elegans sax-3 gene into Drosophila embryos, and we find that SAX-3 can be properly expressed in fly neurons and localized to axons in the CNS. Preliminary data suggest that SAX-3 can partially substitute for Drosophila robo1 to regulate midline crossing of axons, supporting the idea that Robo receptors in flies and worms may function through a conserved mechanism.

41A-U. Effects of 2 gray of radiation on rat aorta. Quinton Kaufman, Brent Hill. *Biology, University of Central Arkansas, Conway, AR 72035.*

In today's era, one of the leading causes of death is cardiovascular disease. Studies have also shown that radiation can lead to an increased risk for heart disease through increased blood pressure. I hypothesize that this is caused by the radiation effecting calcium transporters. In order to determine this, I took rats that had been exposed to 2 gray of radiation and dissected out the aortas after sacrifice and I plan to do western blots to determine western blots.

41B. In Vivo Regulation of β1, 2, 3, & 4 Subunits of CaL Channels in Response to Ovariectomy. Krystal Pham, Brent Hill. *Biology, University of Central Arkansas, Conway, AR 72035.*

17β-estradiol (E2), the primary female sex hormone, functions as a vasodilator and plays a significant role in maintaining vascular tone via voltage-gated L-type calcium channel (CaL) regulation. The intracellular component of CaL, the beta subunit (Cavβ) is essential in maintaining the gating properties of these calcium channels through regulation of various cell signaling molecules (G proteins, kinases, GTPases, etc.). In postmenopausal women, E2 levels decline and susceptibility to cardiovascular disease (CVD) increases. Furthermore, recent studies demonstrate various detrimental effects in Cavβ knockout models towards cardiovascular health in postmenopausal women. Therefore, the purpose of our study is to understand the mechanisms of CaL, specifically the beta-subunit isoforms 1-4, in maintaining healthy arterial blood pressure. Mice will be menopause-induced via ovariectomy, sacrificed 4-weeks post-surgery, and aortas will be excised and analyzed. This study intends to measure protein level and mRNA expression of each beta subunit in mice aortas after ovariectomy via western blot and qRT-PCR analysis, respectively.

42A. Improving human health by improving plant health. Jackie Thomas, Ryan Hiltenbrand, Hannah McCarthy, Alex Howell, David Zimulinda, Arijit Mukherjee. *Biology, University of Central Arkansas, Conway, AR 72035.*

Major advances in the Human Microbiome Project have shown the significance of the microbial community in our gut. Interestingly, the microbial community in the ground is as important as the one in our guts. Soil microbes especially fungi and bacteria cycle nutrients and water to plants, to our crops, the source of our food, and ultimately our health. Unfortunately, the soil microbiota is under constant threat due to overuse of fertilizers, fungicides, pesticides, and heavy tillage to boost crop productivity. Nutrient pollution (too much nitrogen and phosphorus) in water is one of America's most widespread, costly and challenging environmental problems, which can have diverse and far-reaching impacts on public health, the environment, and the economy (U.S. Environmental Protection Agency). For instance, excess nitrogen from fertilizer run-offs in drinking water can cause serious health problems like rashes, stomach or liver illness, respiratory problems, neurological affects, reproductive and developmental risks, and even cancer (National Institutes of Health). Clearly we need alternatives to these harmful fertilizers for improving crop productivity. Biological Nitrogen Fixation (BNF) is increasingly being viewed as a viable alternative for supplying N to plants and improving yield and overall plant health. Several reports have shown that in rice the BNF comes from species of Azospirillum, Herbaspirillum, and Azorhizobium etc. The replacement of fertilizers with N-fixing plant growth-promoting bacteria could save billions of dollars per harvest. Therefore, the use and improvement of such a promising agricultural tool could provide enormous health, economic, and environmental benefits. Unfortunately, our understanding of how plants respond to rhizospheric endophytic bacteria is very poor. We clearly need specific studies that will identify host plant genes during interactions with rhizospheric bacteria that can fix N for the plant. Our specific objective for this project is to identify differential gene expression in rice roots during colonization by N fixing bacteria, Azorhizobium, Azospirillum and Herbaspirillum. This will identify candidate plant genes involved during symbioses with these beneficial bacteria. Towards these goals, we have already set up an experimental system to study these host-microbe interactions. Recently, we performed an RNA Sequencing (HiSeq2500 PE 2x100 bp) experiment in rice roots upon colonization with Azorhizobium caulinodans ORS571. Once the data is analyzed, we will proceed with data mining, validating RNA Seq results, and functional genomics. We aim to identify genes in the host plant that regulate this interaction and characterize the genetic pathway. We have also initiated similar studies between rice-Azospirillum brasilense and rice-Herbaspirillum seropedicae. In the long term, these studies will help us better understand how the host plant recruits its genes during interactions with these beneficial bacteria and improve its own health and contribute to our health.

42B. OCT4 and NANOG Expression Levels in Human Fibroblasts with Short Telomeres. Ethan M. Clement, Calin O. Marian. *Biology, University of Central Arkansas, Conway, AR 72035.*

Cellular senescence denotes the biological aging of the cell due in part to the shortening of telomeres. In somatic cells, during normal chromosomal replication, the lagging DNA strand is not continuously replicated like the leading strand. This phenomenon, known as the end replication problem, leads to gradual telomere shortening after each cell division. Our ultimate goal is to investigate the impact of short telomeres on cell functions, specifically on self-renewal pathways mediated by the OCT4 and NANOG transcription factors. BJ human fibroblasts were propagated in vitro for several population doublings in order to induce telomere shortening. Samples were collected at different time points and the expression levels of OCT4 and NANOG were examined in these cells.

Chemistry and Biochemistry

Friday Oral Platform Session

ORAL – 3:20. **DFT Study of the Selectivity of DOPA-decarboxyalse.** Abby Ritter, Emily C. Harrison, Larryn W. Peterson, Mauricio Cafiero. *Chemistry Department, Rhodes College, Memphis, TN 38112.*

L-DOPA is commonly used as a xenobiotic for patients with conditions such as Parkinson's disease. Clinically administered L-DOPA is transformed into dopamine by DOPA-decarboxylase. In order to be pharmacologically effective, L-DOPA must not be metabolized before it crosses the blood brain barrier. In order to prevent premature metabolism, DOPA-decarboxylase may be inhibited in the periphery. By selectively designing an inhibitor for the DOPA-decarboxylase enzyme, the effectiveness of the L-DOPA can be extended. A suite of dopaminergic derivatives have been developed as potential inhibitors of the DOPA-decarboxylase enzyme. The inhibitory effectiveness of these dopaminergic derivatives has been measured via in silico models in which the strength of interaction between each substrate and the enzymatic active site was analyzed. A crystal-structure of the DOPA-decarboxylase active site, docked with a known DOPA-decarboxylase inhibitor, Carbidopa, was isolated from the Protein Data Bank (PDB ID: 1JS3). The positions of novel dopaminergic derivatives were optimized in the active site using M062X/6-31G with implicit solvation and with flexible amino acid side-chains. Interaction energies between the ligands and the protein were calculated using M062X and MP2 with the 6- 311+G* basis set. At present, 6-cyanodopamine appears to be an effective competitive inhibitor of the DOPA-decarboxylase enzyme.

ORAL – 3:35. Design of Tautomerically Ambiguous Cytosine-Based Nucleosides as Potential Anti-HIV Agents. Duy Ha, Vincent K. Dunlap. *Chemistry Department, Henderson State University, Arkadelphia, AR 71999.*

Antiretroviral therapy for treatment of human immunodeficiency virus (HIV) has developed with great success over the last few decades. While the current therapies are successful, patients often meet with severe side effects and the mutagenic nature of the HIV virus leads to a constant need for new drug development. One such method of development involves incorporation of bases with ambiguous hydrogen bonding faces. We have synthesized a set of nucleosides with such characteristics, which, when incorporated into the viral DNA, will destabilize the DNA. When combined with the high error rate of the RNA polymerase enzymes of the HIV virus, such incorporation may lead to an error catastrophe. Presented here are the results of the synthesis and initial work on the thermal denaturation of DNA duplexes containing the described nucleosides.

ORAL – 3:50. Towards the synthesis of 1-arylethyl-4-arylmethanesulfonyl-piperazines as potential serotonin 2A/2C receptor antagonists. Nick Niggemann, James Donelson. *Chemical & Physical Sciences, Missouri Southern State University, Joplin, MO 64801.*

Autism is a broad spectrum disorder encompassing a wide range of signature core symptoms of which no single medication or combination of medications effectively treats. Of the medications classified as atypical-antipsychotics which show capability in the management of some core symptoms, aripiprazole and risperidone are the only two FDA approved for the latter and are also among the few that are approved for use in children. These two drugs are used to combat a set of particular core symptoms: irritability, aggression, and behaviors resulting in self-injury. However, both drugs can wield side-effects which range from undesirable nuisances to irreversible chronic physiological damage such as Tardive dyskinesia and. Apripiprazole acts mechanistically as an antipsychotic as an agonist for the D2 receptor, a partial agonist of the 5-HT1A receptor, and an antagonist of the 5-HT2A receptor. However, it also displays a high affinity to other 5-HT receptors outside of the targeted domain for treatment, along with a moderate amount of affinity toward a-adrenergic receptors, D4 receptors, histamine receptors, and serotonin transporters. Additionally, it is unlike other atypical-antipsychotics in that binding is not preferential at any localized region of the brain. Risperidone acts mechanistically as an antipsychotic antagonistically at 5-HT2A receptors, a1-adrenergic receptors, and histamine receptors. Risperidone is believed to show affinity for more than twenty receptors, the vast majority being outside of the targeted domain for treatment, including the dopamine receptors D1, D2, D3, D4, and D5. The aim of this study is to design a novel and selective antagonist of the serotonin 2A and 2C receptors. To accomplish this, a large number of known compounds with activities at the various structures were analyzed for their structural properties and their binding data. Based on our observations, a novel series of 1-arylethyl-4-arylmethanesulfonyl-piperazines have been targeted for synthesis.

ORAL – 4:05. Iron Heteroscorpionate Complexes. Katherine Demaree, Patrick Desrochers. *Chemistry Department, University of Central Arkansas, Conway, AR 72035.*

Scorpionates are aggressive tridentate chelates with broad applications encompassing nearly every metal ion on the periodic table. Heteroscorpionates (where one of the three nitrogen donor groups is varied) introduce interesting asymmetry in the complexes prepared. The heteroscorpionate Tp' was developed in our lab following a simple pyrazole-for-triazole substitution strategy. Tp' represents the scorpionate chelate hydrobenzotriazolyl-bis(3,5-dimethylpyrazolyl)borate, a monoanion. For the present work, new iron complexes, (Tp')2Fen+, will be described. The iron(II) form (n=0) and iron(III) form (n=1, as its BF4- salt) of the ligand were synthesized, both of which have been characterized by paramagnetic 11B NMR as well as through infrared and electronic spectroscopies. The two oxidation forms are readily interconnected using simple oxidants and reductants. Interestingly—one of the two isomeric forms of Fe(Tp')2n+ is chiral, suggesting the potential for targeted redox controlled biological activity. These reactions demonstrate the utility of this scorpionate with earlier transition metals; presently only late metals have been employed (nickel and copper) with Tp'. Iron and still earlier metal ions introduce interesting redox and magnetic properties that may be exploited on resin-supported analogs and further applications in the medical and technology fields such as magnetic contrast agents and potential cell phone speaker replacements, respectively.

ORAL – 4:20. Synthesis of Various Dopaminergic Compounds for Analysis in SULT1A3. C. Skyler Cochrane, Jennifer C. Rote, Gabrielle E. Bailey, Diana J. Bigler, Mauricio Caifiero, Larryn W. Peterson. *Organic Chemistry Department, Rhodes College, Memphis, TN 38112.*

Sulfation is a very important metabolic process in the human body due to it being the predominant pathway through which endogenous catecholamine and xenobiotic substances are inactivated and/or removed from the body. One family of enzymes that implement this sulfation are the sulfotransferases (SULTs), which catalyze the transfer of a sulfuryl group (-SO3-) from 3´-phosphoadenosine-5´-phosphosulfate (PAPS) to various substrate molecules. Of particular interest is SULT1A3 because, while it shares 93% amino acid sequence identity with SULT1A1, the two sulfotransferases demonstrate very unique substrate selectivity with SULT1A1 preferentially sulfating simple phenols and SULT1A3 preferentially sulfating catecholamines, such as dopamine. This study will focus on the synthesis of several dopaminergic compounds, which each having a different substituent at the 6-position. The presence of an electron donating or withdrawing substituent will modulate the deprotonation of the phenolic hydroxyl groups, as well as provide potential points of interaction with the enzyme. Computational results have shown that 6-bromodopamine, 6-carboxydopamine, 6-ethenyldopamine, and 6-cyanodopamine all display very interesting binding characteristics, and their syntheses will be discussed.

ORAL – 4:35. The Effect of Retinoid Receptor Agonists on K562 Cellular Adhesion, Proliferation, and α5β1 Integrin Cell Surface Expression. Raynin Phomakay, Madison Lee, Melissa Kelley. *Chemistry Department, University of Central Arkansas, Conway, AR 72035.*

Establishment and maintenance of proper immunity requires a precise balance between cellular adhesion and proliferation. A disruption in either event culminates in a variety of pathologies encompassing immunosuppression, auto immunity, and cancer. Retinoids, profoundly affect immune function by mediating cellular adhesion and proliferation in certain leukocytes. Retinoids, by binding to retinoid receptors (RARs or RXRs), modify the expression of a variety of signaling proteins involved in immune cell proliferation and adhesion including, integrins. Integrins are a family of transmembrane heterodimeric receptors consisting of non-covalently linked α and β subunits that are considered to be the principle receptors involved in attachment to the extracellular matrix and provide adhesive interactions that control cellular proliferation. Currently, the contributions by retinoids in immune cell adhesion and proliferation have been independently examined; however, in retinoid responsive immune cell lines there appears to be a potential synergism between cellular adhesion and proliferation, which may be mediated through integrins, specifically the α5β1 subset. In this study, the effect of all-trans-retinoic acid agonists on K562 cellular adhesion, proliferation, and α5β1 integrin cell surface expression was investigated. RARgamma agonist exposure increased K562 cellular adhesion to RGD containing extracellular matrix proteins fibronectin and FN-120 in a time dependent manner. Additionally, cell surface expression of the β1 integrin subunit was increased in the presence of a RARgamma agonist. Interestingly, K562 cellular proliferation levels were decreased in a time-dependent manner when cells were treated with the RARgamma agonist. In the presence of the RARalpha or RARbeta agonists, K562 cellular adhesion, proliferation, and α5β1 integrin cell surface expression was comparable to the vehicle control. Our study is the first to demonstrate that specific RAR agonists alter cellular adhesion, proliferation, and intergrin cell surface expression.

Chemistry/Biochemistry

A – Saturday 8:00 – 9:00 Posters

B – Saturday 9:15 – 10:15 Posters

(Posters designated "U" will be judged.)

101A. Cloning and characterization of the dinuclear 4Fe-4S ferredoxin from halothiobacillus neapolitanus. William Fletcher, Newton Hilliard. *Physical Sciences, Arkansas Tech University, Russellville, AR 72804.*

Cloning and characterization of the dinuclear 4Fe-4S ferredoxin from halothiobacillus neapolitanus Halothiobacillus neopolitanus is an autotrophic purple sulfur bacteria (PSB) often associated with marine thermal vents. Unlike other PSB it is an aerobic, non-photosynthetic carbon dioxide fixing "mesophile". Genomic DNA sequence analysis indicates the presence of a gene for a dinuclear 4Fe-4S ferredoxin, homologous to that found in photosynthetic electron transfer pathways. In order to investigate the potential role of this ferredoxin in transferring electrons from sulfur oxidation reactions to carbon dioxide fixation mechanism, PCR amplification of genomic DNA was performed using primers matching the ferredoxin gene locus (Hneap_1558) followed by cloning into the pF1k expression vector. Successful clones were identified by colony PCR and sequencing. Protein expression studies were carried out after transformation into E. Coli strain BL21DE. IPTG was added to overnight cultures to a final concentration of 0.5 MM in order to induce protein synthesis. Sodium dodecyl sulfate-PAGE shows two fold increase in a low molecular weight band with apparent mass consistent with the known mass of ferredoxin. Maximum induction occurred between 2 and 4 hours. Further investigated studies are currently underway..

101B. A novel fused gene thiosulfate dehydrogenase. Newton Hilliard. *Physical Sciences, Arkansas Tech University, Rssellville, AR 72804.*

Halothiobacillus neapolitanus is an obligate chemolithoautotroph capable of utilizing the extracytoplasmic oxidation of inorganic sulfur compounds as its sole source of metabolic energy. Physiological measurements show loose coupling between substrate oxidation and oxygen reduction with e:O ratios ranging from 1:1.16 to 1:1.6 depending on substrate. ADP depletion is not detected during O2 consumption measurements again implying loose coupling between substrate oxidation and ATP generation. Recent genomics data has shown the presence of a gene for a potential heterodimeric thiosulfate dehydrogenase (tsdAB). The putative tsdAB gene, loci Hneap_1476 and Hneap_1477, contains the ATGA coexpression motif indicating a potential expression stoichiometry of 1:1. In order to verify the tsdAB stoichiometry, PCR was used to amplify the entire Hneap_1476/1477 gene coding region including the region surrounding the gene fusion site. PCR amplicon was then subcloned into the pF1K expression vector and successful transformants identified by colony PCR and plasmid sequencing. Overnight cultures of E. coli BL21DE transformed with pF1K/tsdAB were subcultured into fresh media and gene expression induced by addition of IPTG. SDS-PAGE results clearly show increased relative concentrations of two bands at apparent molecular masses of 32kDa and 24kDa respectively. Quantitation of the ratio of the two bands was accomplished via coomassie blue staining and analysis using Quantity One software. Results were consistent with a 1:1 expression stoichiometry.

102A-U. Characterization of Intermediates from the Purification Process of Tc24, a Chagas Disease Vaccine Antigen Component. Kevin Naceanceno, Jo Goy. *Biochemistry and Molecular Biology, Harding University, Searcy, AR 72143.*

There is a comparable advantage for the development of a vaccine for Chagas disease, a leading cause of heart disease in Latin America. Tc24, a Ca2+ binding protein in Trypanosoma cruzi parasite is expressed as a recombinant protein in an Escherichia coli system. Downstream process development involves antigen purification by anion exchange and size-exclusion chromatography. After the capture step by anion-exchange chromatography, one-dimensional denaturing polyacrylamide gel electrophoresis (SDS-PAGE) showed higher molecular weight impurities co-eluting with Tc24, reducing the yield of the target protein. The goal of this project was to a) identify the higher molecular weight proteins co-eluting with Tc24, and b) determine whether there were any proteins co-migrating with Tc24. The information obtained in these investigations provided data to optimize downstream processing, thus potentially increasing the yield of the vaccine antigen component.

102B-U. **The implications of the presence of Lycotoxin in the venom of the wolf spider Rabidosa rabida (Areanae Lycosidae).** Sara Wilmsen, Ryan Stork, Dennis Province. *Biology Department, Harding University, Searcy, AR 72143.*

Background: Rabidosa rabida is a large, lycosid spider that is common across much of the eastern half of North America. Because of its large size and availability, this spider is a good candidate for venom and digestive fluid collection. Both venom and digestive fluid are protein-rich substances that have not been studied in this spider before. However, two antimicrobial proteins have been described in a spider of the same family as rabida. These are known as lycotoxin I and lycotoxin II. Methods: We performed reverse-phase high performance liquid chromatography (RP-HPLC) and

mass spectroscopy (MS) analysis on Rabidosa rabida's venom and digestive fluid looking for lycotoxin I and II; and also similarities between the two substances. We also plan to send samples of venom and digestive fluid to UAMS to have them analyzed by matrix assisted laser desorption ionization - time of flight mass spectrometry (MALDI-TOF MS). We then hope to be able to isolate different proteins in these two substances. Results: Lycotoxin I seems to be present in both the venom and digestive fluid. Other than the toxin, these two substances do not seem to be very similar. Conclusion: Lycotoxin I has been shown to have antimicrobial properties associated with them. Having found this toxin in both digestive fluid and venom in Rabidosa rabida we may find others with similar properties. .

103A-U. **Titan Atmospheric Chemistry.** Stephanie J. Inabnet, Edmond W. Wilson, Jr. *Chemistry, Harding University, Searcy, AR 72143.*

Saturn's Moon Titan is the second largest moon in the Solar System. It is bigger than Earth's Moon and is unusual because of its significant atmosphere, primarily composed of nitrogen. It is the only moon with a dense atmosphere and is interesting because Titan's atmosphere is thought to be similar to Earth's early atmosphere although colder. We examined some of the interesting molecules believed to be present in Titan's atmosphere. This was done using spectrographs that operated in the ultraviolet, visible and the near infrared portions of the electromagnetic spectrum. Spectra were recorded over a range of pressures, temperatures and concentrations appropriate for Titan.

103B-U. Methodology for Measuring Pentane in Human Breath. Jacob Hatvany, Edmond V. Wilson, Jr. *Chemistry, Harding University, Searcy, AR 72143.*

Throughout history, breath has been used as an indicator of certain illnesses. This began by noticing certain patients has tell-tale breath odors related to their illness. Diagnoses was done by simply smelling the breath of a patient. More recently, with the advent of mass spectrometers, diode lasers and other sophisticated research grade instruments, analysis of human breath has become a possibility and attractive because of its non-invasive nature compared with blood and urine samples. The amounts of indicator molecules in breath is very low in the ppm and ppb range in most cases. By using a universal method for concentrating the samples and removing the major components of breath: nitrogen, oxygen, water and carbon dioxide, it may be possible to use instruments of lower sensitivity making the method less expensive and simpler to perform. The results of our methodology using pentane as a target marker for medical diagnosis is outlined and reported.

104A-U. Lead in Chocolate: The Dangers of Heating Foil Wrapped Chocolate. Alexis Fuller, Dennis Province. *Chemistry, Harding University, Searcy, AR 72143.*

Children are marked as one of the most vulnerable age groups to heavy metal contamination in food, and chocolate is a favorite food item. Children ages 2-6 years old can absorb 30-75% of ingested lead into the digestive tract. Lead is removed from the body very slowly, thus consumption over time can lead to permanent neurological damage, including the child's ability to learn and retain information. Short term symptoms include constipation, vomiting, weight loss, abdominal pain, or digestive problems. My question was whether Hershey's Kisses foil contained lead, and if it did, could the lead in the foil possibly leach into the chocolate with the application of heat past the FDA's recommended maximum of 0.1 ppm. The focus is to analyze the amount of lead in Hershey's chocolate kisses and foil by using atomic absorption and anodic stripping voltammetry. For our experiment, there were two different batches of chocolate: one that was subjected to heat to simulate being left in a hot car, and chocolate left on the benchtop to serve as a control and find the baseline of lead in Hershey kisses. My initial research findings indicate that with the application of heat, the lead content increases past the FDA's safe limit. When analyzing using atomic absorption, the chocolate increased from 0.083 µg Pb/g sample (control) to 0.166 µg Pb/g (oven) sample. The results from anodic stripping voltammetry also showed a similar trend: the samples of chocolate were found to be 0.0698 µg Pb/g sample (control) and 0.4803 µg Pb/g (oven) sample. According to this study, both analysis methods recommend to not consume chocolate left in a hot car, since both results (0.166 µg Pb/g and 0.4803 µg Pb/g) are well above the FDA's maximum recommended limit.

104B-U. Synthesis & Characterization of a Novel Cyclodiphosph(III)azane tungsten complex. Brian Cole, Ingo Schranz. *Chemistry, Henderson State University, Arkadelpia, AR 71999.*

The purpose of this study is to attempt to synthesize a new heterocyclic catalyst by treating $W(O)(CHCMe_3Cl_2PMe_2Ph)_2$ with Bis(tert-butylamido)cyclodiphosph(III)azane (CPT) and to characterize the results by using x-ray crystallography in addition to ^{1}H-MNR. The multistep synthesis and characterization of all intermediates will be reported.

105A. Mitochondrial CYP2E1 overexpression increases mitochondrial mass in HepG2 cells. Andres Caro, Grover Miller. *Hendrix College, Conway, AR 72032.*

Oxidative stress in mammalian cells induces mitochondrial biogenesis. An active source of cellular reactive oxygen species (ROS) that causes oxidative stress is the mitochondrial isoform of the enzyme cytochrome P450 2E1 (CYP2E1), which is induced in the liver by ethanol. In the current study, we evaluated the possibility that mitochondrial CYP2E1-generated ROS produce an activation of mitochondrial biogenesis in hepatocytes. Mitochondrial CYP2E1 overexpressing HepG2 cells (mE10 cells) showed a two-fold increase in mitochondrial DNA content compared to parental P450-negative HepG2 cells (C34 cells), as measured by real-time PCR. The increase in mtDNA content was associated with increased mitochondrial ROS levels evaluated by MitoSOX Red fluorescence, and mitochondrial mass evaluated by MitoTracker Green fluorescence. Mitochondrial CYP2E1 overexpression increased mRNA and protein levels of PGC1alpha (the master regulator of mitochondrial biogenesis), and increased the activity of the enzyme citrate synthase in cell homogenates (which usually correlates with mitochondrial mass). These results show that mitochondrial CYP2E1 overexpression in hepatocytes causes an increase in mitochondrial mass possibly associated with activation of mitochondrial biogenesis by ROS.

105B-U. Method Development to Study Atmospheric Aerosols. Jake S. Higgins, Dagen Hughes, Courtney D. Hatch. *Chemistry, Hendrix College, Conway, AR 72032.*

Atmospheric aerosols are small solid or liquid particles suspended in ambient air. They are emitted by natural sources, like desert dust and volcanic ash, and anthropogenic sources, such as factories and automobiles. Aerosols' effect on atmospheric phenomena is widespread. Particulate matter influences atmospheric chemistry and visibility, global cooling, and human and animal health. It is therefore important to increase our knowledgeability of the composition and concentration of atmospheric particles. Recent field studies have shown that the aerosol mass fraction is most dense in the southeast United States and is dominated by Organic Aerosol (OA), which is largely due to fossil fuel emissions and the oxidation of biogenic volatile organic compounds (VOCs). The purpose of this project is to develop a method to study the organic component of PM10 aerosols using a high volume PM10 sampler followed by extraction and analysis of the organic aerosol fraction using common analytical instrumentation, such as Gas Chromatography/Mass Spectrometry (GC/MS) and Ion Chromatography (IC). Our ultimate intent is pedagogical: We hope to integrate these methods into the undergraduate chemistry curriculum at Hendrix College. Current PM10 concentrations calculated by the high volume sampler fall below the National Ambient Air Quality Standards (NAAQS) of 150 µg/m3 and are statistically similar to weekly concentrations in the region from 2005 to 2014. Extraction and quantification methods for OA analysis have been compared, and particulate organic components have been identified upon comparison to the NIST GC/MS library. Future work involves developing a specific day-to-day protocol to implement this analysis into a chemistry laboratory section.

106A-U. Towards the Synthesis of 3-S-Alkyl-Indoles as Potential Inhibitors of Isoprenylcysteine Carboxyl Methyltransferase. Kurt Housh, James Donelson. *Chemical and Physical Sciences, Missouri Southern State University, Joplin, MO 64801.*

Isoprenylcysteine carboxyl methyl transferase (ICMT) catalyzes the methylation of the carboxyl terminus of over 100 cellular proteins, including the oncoprotein Ras. Ras is believed to be responsible for between 15 to 20% of all human cancers. Prior to methylation, Ras proteins must first be lipidated with a 15-carbon farnesyl group. This farnesyl group serves to help anchor the Ras proteins to the cell membrane. Studies have shown that blocking the methylation of Ras by ICMT leads to mislocalization of the Ras protein, followed by inhibition of tumor cell growth and apoptosis. A synthesis has been developed utilizing a 1-methyl-2-carboxy-3-thioindole as a scaffold to build potential inhibitors of ICMT. Some key steps in the synthesis include: carboxylation of 1-methylindole, thiocyanation of 2-carboxyindole, followed by the reductive removal of the cyano group and finally S-alkylation of the resulting free thiol group. This simple, four-step synthesis will allow for the facile synthesis of a large number of S-lipidated carboxy indoles to fully probe the lipid-binding domain of ICMT and lead to further development of potent inhibitors of this enzyme.

106B-U. Towards the synthesis of methyl-aryl-[4-(4-arylmethanesulfonyl-piperazin-1-yl)-cyclohexyl]-amines as potential antagonists of serotonin 2A/2C receptors. Huyen Tran, James Donelson. *Chemical and Physical Sciences, Missouri Southern State University, Joplin, MO 64801.*

According to the CDC, about 1 in 68 children are diagnosed with autism spectrum disorder (ASD) in 2014, a 30% increase from 1 in 88 children back in 2012. Symptoms of ASD include social impairment, communication difficulties, and repetitive behavior (stereotypy). Signs and symptoms usually occur between the ages 2 and 3 though there are very early indicators of the disorder. The most common feature of ASD is lack of social interaction; kids with ASD typically appear unresponsive to their name, don't make eye

contact, lack empathy, and withdraw themselves from social engagement. Repetitive behaviors and resistance to changes in their usual daily activities also commonly occur in children with ASD. Though there is no cure for ASD, there are drugs approved to treat some of the symptoms of ASD in children. Some atypical antipsychotics have been shown to alleviate irritability, hyperactivity and stereotypy. The beneficial effects of the atypical antipsychotics is largely attributed to their ability to antagonize the serotonin 2A and 2C receptors. Unfortunately, atypical antipsychotics also exhibit several highly undesirable side effects, the most severe being tardive dyskinesia. Many of these negative effects are associated with antagonism of many of the dopamine receptors. The focus of this project is to develop a novel class of selective serotonin 2A/2C receptor antagonists.

107A-U. A novel synthetic strategy towards the aryl-[4-(4-arylmethanesulfonyl-piperazin-1-yl)-cyclohexyl]-amines as potential antagonists of serotonin 2A/2C receptors. Kristina Niggemann, James Donelson. *Chemical and Physical Sciences, Missouri Southern State University, Joplin, MO 64801.*

Autism spectrum disorder (ASD) is a range of complex neurodevelopmental disorders including social impairments, communication difficulties, and restricted, repetitive, and stereotypical patterns of behavior. Autism affects broad age ranges and is equally prevalent across ethnicities. The FDA has approved two drugs for treating irritability associated with the autism spectrum disorder in children (risperidone and aripiprazole). Although the drugs do not fully treat the three core symptoms, these drugs ease some of the core symptoms, relieving irritability, and improving sociability, reducing tantrums, aggressive outbursts and self-injurious behaviors. Risperidone is an atypical antipsychotic drug that functions as an antagonist of dopamine receptors and serotonin type 2 (5HT2) receptors. Aripiprazole is a quinolone derivate and an atypical antipsychotic agent which has partial agonistic activity at several dopamine receptors and serotonin 5HT1A receptor and potent antagonistic effects on serotonin 5HT2A receptors. This project seeks to develop a novel, selective chemical scaffold based loosely on the structures of risperidone and aripiprazole that will maintain the antagonistic effects on 5HT2A and 5HT2C receptors while eliminating the former compounds affinity for the dopamine receptors.

108A-U. Antimicrobial light-curable polymeric composites of Silver(I) cyanoximates for indwelling medical devices. Snow Popis, M. Patrauchan, M. Whited, N. Gerasimchuk. *Chemistry, Missouri State University, Springfield, MO 65897.*

Of the 40 known cyanoximes, only 12 form light-stable silver (I) complexes and shown in Figure 1. Synthesized cyanoxime silver (I) compounds demonstrate stability towards visible light and UV-radiation in addition to poor water solubility, and high thermal stability up to 150 °C and have shown pronounced antimicrobial activity in solid state studies to gram positive and gram negative microorganisms makes this molecule ideal for indwelling medical devices to combat biofilm formation. The chemical and biological aspects of application Ag(I) cyanoximes-based coordination polymers are discussed.

108B. Comparison of 2,4-Dienoyl-CoA Reductase Isozymes in Rat Liver. Zachary Randall, Addie Padgett, Dean Cuebas. *Chemistry, Missouri State University, Springfield, MO 65897.*

Fatty acids are a major energy source and are degraded via a β-oxidative process in both mitochondria and peroxisomes. Unsaturated fatty acids with double bonds extending from even-numbered carbons require in addition to the four β-oxidation enzyme necessary for saturated fatty acid degradation, two auxillary enzymes, 2,4-dienoyl-CoA reductase and 3,2-enoyl-CoA isomerase. The reductase (DECR) catalyzes the hydrogenation of 2,4-dienoyl-CoAs to 3-enoyl-CoAs and utilizes exclusively NADPH as the reductant. In animals, DECR has been found associated with both mitochondria (DECR1) and peroxisomes (DECR2). These two isoforms display high sequence homology and the crystal structure of the mitochondrial isoform is known. Using hydroxyapatite chromatography, our group has clearly demonstrated the existence of at least one additional isoform of 2,4-dienoyl-CoA reductase in rat liver. A phosphate gradient allows for the separation of early eluting (DECR2), middle (new isoform), and later eluting (DECR1) isoforms. The previously characterized mitochondrial (DECR1) and peroxisomal (DECR2) isoforms were identified by Western blotting using polyclonal antibodies raised against the corresponding recombinant proteins. Various 2,4-dienoic acids and their Coenzyme A derivatives were synthesized and used to probe the substrate specificities of the three isoforms of 2,4-dienoyl-CoA reductase. The uncharacterized isoform displays a substrate specificity that is very different from either DECR1 or DECR2 and supports the conclusion that this activity represents a new enzyme whose purpose remains to be discovered.

109A-U. Computational Investigations of Enantiospecificity of Mutated CYP2C9. Logan Bond[1], Grover P. Miller[2], Martin D. Perry, Jr.[1]. *[1]Ouachita Baptist University, Arkadelphia, AR 71998, [2]UAMS, Little Rock, AR 72205.*

Background: In previous research conducted in our lab, the enantiospecificity of CYP2C9, the most enantiospecific member of a family of enzymes known

as cytochrome P450's, was examined. The data obtained from these studies revealed that there were significant residues within CYP2C9 that contributed to the overall enantiospecificity of CYP2C9. In the current study, we mutated these significant residues and followed the same procedures as the previous research in order to compare our results to those previously obtained. The differences were then analyzed and graphed. Methods: We used a molecular modeling suite, Sybyl-X, in order to simulate oxidative reactions between a crystalized structure of CYP2C9 and six NSAIDs. After simulation, we used a written program to analyze the topography data output of Sybyl-X. We then graphed the total energy per residue by calculating the energies using the Van der Waals and hydrogen bonding energy equations. Results: Final analysis of the energies by residue revealed that a mutated CYP2C9 can have entirely different enantiospecificity after mutation of a single, significant residue. This suggests that in the un-mutated version of CYP2C9, these significant residues play an important role in CYP2C9's expressed enantiospecificity. Conclusion: The results reveal that critical residues within CYP2C9 contribute to CYP2C9's expressed enantiospecificity in a significant way. In certain cases where CYP2C9 preferred one enantiomer over the other, one mutation caused CYP2C9 to change its preference toward the other enantiomer of the ligand. Also, this study shows that mutations of CYP2C9 cause no consistent pattern of change from ligand to ligand in terms of CYP2C9's preference for one form or another. Acknowledgment: This project was supported by the Arkansas INBRE program, with grants from the National Center for Research Resources - NCRR (P20RR016460) and the National Institute of General Medical Sciences - NIGMS (P20 GM103429) from the National Institutes of Health.

109B-U. Analysis of PARP1 Interactions with Cannabinoids. Sydney Heslep, Lori L. Hensley, Martin D. Perry, Jr. *Chemistry, Ouachita Baptist University, Arkadelphia, AR 71998.*

Background: Cannabinoids show promising results for the treatment of Ewing's Sarcoma (ES), a pediatric bone cancer with a low survival rate. Cannabinoids would be ideal drugs because they have been shown to relieve pain and inflammation, and induce apoptosis in ES cell lines without the controversial psychoactive effects. While there is a lot of promise with cannabinoids, the biochemical pathway is still widely unknown. PARP1, a protein expressed in ES cells that functions in DNA repair, is a promising target for the drug. Methods: In order to test the interactions between the drugs and PARP1, a computational docking suite within SYBYL-X-2.1.1, is used to dock cannabinoids to the ligand-binding domain of PARP1. The results show binding between the protein and the drug. An ELISA is used to investigate the presence of cleaved PARP1 in cannabinoid-treated ES cells in order to elucidate the potential mechanism of cannabinoids for apoptosis. Results: Surflex Docking shows similar hydrogen binding of PARP1 inhibitors and the glycine 202 residue of PARP1. ELISA methods show cleavage of ES cells with cannabidiol, hemp oil, and possibly ajulemic acid. Conclusion: Cannabinoids have great potential for ES treatment because they have the ability to bind and cleave PARP1. When combined with chemotherapy, a drug that cleaves PARP1 would be a great candidate for Ewing's Sarcoma treatment to eliminate the ES cells and prevent their return. Acknowledgment: This project was supported by the Arkansas INBRE program, with grants from the National Center for Research Resources - NCRR (P20RR016460) and the National Institute of General Medical Sciences - NIGMS (P20 GM103429) from the National Institutes of Health.

110A-U. The Effects of Residue Mutations on the Enantiospecificity of CYP2C9. Trevor Meece[1], Grover P. Miller[2], Martin D. Perry, Jr.[1]. *[1]Ouachita Baptist University, Arkadelphia, AR 71998, [2]UAMS, Little Rock, AR 72205.*

Background: CYP2C9 is an enzyme that helps to detoxify many foreign molecules primarily in the liver. Previous research with CYP2C9 has shown that it has significant enantiospecificity in some of its residues, notably Leu366, Phe100, and Phe476. Understanding how important these residues are to the overall enantiospecificity of the enzyme and what properties that they have make them so important, will lead to a greater understanding of how the enzyme functions. Methods: In order to obtain data on the residues in CYP2C9 cheaply and efficiently, we use a computer program called Sybyl-X. The data obtained from the program is theoretical and can be used to direct later studies in a biochemical lab. To determine the importance of the residues, we mutated them to amino acids with different properties and performed dynamics runs with NSAIDs similar to what was done in previous research in our lab. Results: The residues that were deemed important to the enantiospecificity of CYP2C9 caused significant changes in the enantiospecificity of other residues after mutation. The mutated residues always showed differences from the non-mutated residues. In many cases, the mutation had such a significant effect that the enantiospecificity of the enzyme was changed. Conclusion: The fact that the enantiospecificity of the residues were so greatly changed by the mutation of certain residues means that those residues are of particular importance to the overall enantiospecificity of CYP2C9. Mutations of certain residues show very specific effects. This data can be used to determine if these effects can be used synergistically with other mutations to create a desired effect on the enantiospecificity of CYP2C9 or even other properties. Acknowledgment: This project was

supported by the Arkansas INBRE program, with grants from the National Center for Research Resources - NCRR (P20RR016460) and the National Institute of General Medical Sciences - NIGMS (P20 GM103429) from the National Institutes of Health.

110B-U. Simultaneous Determination of Bisphenol A and Bisphenol S in Methanol:Water Samples. Jean Eudes Benecyo, Sara E. Hubbard. *Chemistry, Ouachita Baptist University, Arkadelphia, AR 71998.*

Bisphenol A (BPA) has been one of the most used plasticizers with more than 4.8 million tons produced in 2012. BPA is also an endocrine disruptor that has been linked to adverse health effects such as cancer, obesity, behavioral and mood changes, lowered fertility, developmental changes and more in humans and other animals. The evidence of the toxicity of BPA, even at very low levels, has caused many countries to limit its use, especially in baby bottles and other baby-related hard plastic items. In these items, BPA has been replaced with other bisphenols, such as Bisphenol S (BPS). However, BPS is also an endocrine disruptor and can behave like BPA in cellular activities. It has been linked to adverse health effects similar to BPA. Also, studies have shown more dermal penetration of BPS than BPA. In this research, methods were developed to simultaneously determine concentrations of BPA and BPS in samples using UV-VIS Absorption Spectrophotometry and High Pressure Liquid Chromatography (HPLC) and analytical figures of merit were determined for these methods (LODBPS = 0.13µg/mL and LODBPA = 1.18µg/mL). The effectiveness of the UV-VIS Absorption Spectrophotometry in determining concentrations of BPA and BPS in samples was compared to HPLC using statistical analysis. These methods were applied to methanol:water (1:1) samples exposed to different kinds of plastics, food cans and thermal receipt paper to test for leaching of BPA and/or BPS. The concentrations of BPA and/or BPS determined ranged from undetectable to concentrations above the Total Daily Intake approved by the FDA or the European Food Safety Authority (TDIBPA = 5 µg/mL/kg body weight). The methods used suggested that other chemicals may leach out in addition to BPA and BPS. Conditions of time (0 hours–10 days) and temperature (22-70°C) were varied to simulate everyday use of these products.

111A-U. Synthesis, Characterization, and Cytotoxicity of a Series of Novel Water-Soluble Porphyrins. Allie Hegi, Joesph E. Bradshaw. *Chemistry, Ouachita Baptist University, Arkadelphia, AR 71998.*

Porphyrins are large aromatic compounds composed of four conjugated pyrrole rings. Derivatives can be formed by adding different side-chains to the periphery of the porphyrin structure. Porphyrins and their derivatives have shown to be successful in photodynamic therapy. This project entails the addition of a series of hydroxy-amines to the porphyrin core, H2TPPC. The characterization of these novel water-soluble porphyrins using UV-vis, infrared (IR), and nuclear magnetic resonance (NMR) spectroscopies has been carried out. Additionally, the purity of the compounds was ensured via high performance liquid chromatography (HPLC). Finally, the cytotoxicity of these novel porphyrins on TC-71 Ewing's Sarcoma cells under both light and dark conditions was determined using MTT assay.

111B-U. Kinetics of Proton Transfer for Ligands in the SULT1A1 Active Site. Danielle Wilson, Amelie Weems, Larryn Peterson, Mauricio Cafiero. *Chemistry, Rhodes College, Memphis, TN 38112.*

We have studied the substrate selectivity of the sulfotransferase enzyme (SULT1A1) by identifying important protein-ligand interactions in the active-site through electronic structure calculations. The sulfotransferase enzymes (SULTs) catalyze the addition of a sulfate group to a variety of small molecules, including neurotransmitters and xenobiotics. This reaction can activate or deactivate bio-active molecules or change their pharmacokinetic behavior. A set of dopamine analogs with substituents in the 6 position were chosen for study. In previous work, we have studied the interaction energies between the ligands and the amino-acids of the active-site using MP2 and M062X with 6-311+g*; these energies were used to determine the thermodynamic stability of the ligand in the active site. The addition of the sulfuryl group to the ligand depends on deprotonation of a phenol group on the ligand. Thus, the activation energies for proton extraction from the ligand to the histidine residue were calculated for all ligands using M062x/6-31++g**. Our results show a strong dependence of the activation energy of the proton transfer of the substituent on the 6 position.

112A-U. **DFT analysis of water clusters, dopaminergic derivatives, and their desolvation energies.** Mallory Morris, Katie Hatstat, Larryn Peterson, Mauricio Cafiero. *Chemistry, Rhodes College, Memphis, TN 38112.*

The catechol-O-methyltransferase enzyme is responsible for the metabolism of the neurotransmitter dopamine, a catecholamine involved in the degenerative disorder known as Parkinson's Disease. One treatment for Parkinson's disease is L-DOPA therapy, where this dopamine precursor is transformed into dopamine by DOPA decarboxylase. The dopamine derived from L-DOPA is degraded by COMT; therefore, inhibiting COMT would be ideal to prolong the effectiveness of L-DOPA and to increase pharmacological efficiency by preventing the premature

metabolism of the medication. Computational models of dopaminergic analogs were used to examine the substrates' binding in the enzymatic active site. The binding of a ligand to an enzyme not only involves the interaction between the ligand and the enzyme but also the energy lost or gained by desolvation of the ligand. Desolvation of dopaminergic derivatives was examined using a series of hydration shells that increase in size. The desolvation energies were calculated using M062X with the aug-cc-pvdz, cc-pvdz, and cc-pvtz basis sets. Ligands with the carboxylic acid and nitro substituents exhibited the least favorable energies, whereas the nitrile substituents exhibited the most favorable desolvation energies in each of the explicit water models. The implicit Polarizable Continuum Model was also used together with explicit solvation to calculate desolvation energies of dopaminergic ligands. The use of implicit and explicit models was compared. This information will be combined with prior research done on ligand/enzyme interaction in order to get a more comprehensive understanding of ligand binding in this system.

112B-U. DFT design of inhibitors of the LPXC enzyme. Carolyn Dishuck, Allison J.L. Dewar, Larryn Peterson, Mauricio Cafiero. *Chemistry, Rhodes College, Memphis, TN 38112.*

In recent years bacterial infections have become more resistant to treatments, posing a challenge for both researchers and health professionals. It has become imperative that novel, effective therapies against these resistant bacterial infections be discovered. Gram-negative bacteria present an additional challenge due to the presence of a selectively permeable outer membrane. Among the components of the outer membrane is Lipid A, which is responsible for the growth and pathogenicity of Gram-negative bacteria. The enzyme LpxC is responsible for catalyzing the first committed step in the biosynthetic pathway of Lipid A. The inhibition of LpxC would therefore, prevent the production of Lipid A, and hence result in a corrupted outer membrane. Starting from a LpxC crystal structure with a natural substrate bound in the active site, we have docked several novel ligands in the active site. The structure for these ligand-protein complexes were optimized using m06l and the 6-31G basis set (and lanl2dz for zinc) both in vacuo and in solution phase. Interaction energies for the ligand and protein complex were calculated using m06l and mp2 with the 6-311+G* basis set (and lanl2dz for zinc). Suitability studies have also been performed to confirm that our model chemistry described the zinc binding in the protein appropriately. Finally, desolvation energy calculations have been performed to account for desolvation of the ligand and the zinc ion.

113A-U. DFT analysis of the selectivity of known bioactive ligands in the sulfotransferase and catechol-o-methyltransferase enzymes. Calli Pinckney, Larryn Peterson, Mauricio Cafiero. *Chemistry, Rhodes College, Memphis, TN 38112.*

We have studied the substrate selectivity of a number of known bioactive ligands in sulfotransferase enzyme (SULT1A3) and catechol-o-methyltransferase (COMT) by identifying important protein-ligand interactions in the active-sites through electronic structure calculations. SULT1A3 is responsible for activating and improving the solubility of catecholamines while COMT deactivates catecholamines. Understand how ligands behave in both of these enzymes leads to a greater understand of the fate of dopaminergic molecules in the body. The SULT1A3 and COMT enzymes catalyze the addition of a sulfate group and a methyl group, respectively, to a variety of small molecules, including catecholaminergic molecules. Crystal structures of the SULT1A3 (PBD ID 2A3R) and COMT (PDB ID 2CL5) enzyme active sites were isolated from the Protein Data Bank. A suite of molecules with known activity in COMT were chosen from PubChem and their positions in each active site were optimized using M062X/6-31G including implicit solvation and using flexible amino acid residues. Interaction energies between the ligands and the proteins were calculated using M062X with the 6-311+G* basis set. Calculations have shown that molecules active in COMT also show a promise of strong activity in SULT1A3.

113B-U. Inhibiting Lipid A biosynthesis in Gram-negative bacteria: The design, synthesis, and zinc binding analysis of natural substrate analogues of LpxC. Kayla A. Wilson, Gene G. Lamanilao, Sarah N. Malkowski, Mauricio Cafiero, Larryn W. Peterson. *Chemistry, Rhodes College, Memphis, TN 38112.*

Bacterial infections, including those that lead to septicemia, the 10th leading cause of death in the United States, have become an increasingly serious problem. The emphasis of this study is the development of novel antibacterial compounds which combat Gram-negative bacterial infections via the inhibition of LpxC. LpxC, a zinc-dependent deacetylase, is involved in the biosynthesis of Lipid A, an important part of lipopolysaccharide, which makes up the outer cell membrane of Gram-negative bacteria. When LpxC is inhibited, the production of Lipid A is halted and the virulence of the bacteria is significantly reduced. Using key information provided by the crystal structure of LpxC and the work done by our computational collaborators, this study focuses on molecules that mimic the enzyme's natural substrate and act as inhibitors. The design and synthesis of these molecules and progress towards zinc binding affinity testing will be discussed.

114A-U. Investigating the Active Site of LpxC in Gram-negative Bacteria through Interactions with Synthesized Natural Substrate Analogues. Gene G. Lamanilao, Kayla A. Wilson, Sarah N. Malkowski, Mauricio Cafiero, Larryn W. Peterson. *Chemistry, Rhodes College, Memphis, TN 38112.*

Lipopolysaccharide (LPS), an intrinsic component of Gram-negative bacterial cell walls, is a prerequisite for cell viability, and its structure includes a hydrophobic moiety, lipid A, that contributes to the virulence of LPS. The first committed step in the biosynthesis of lipid A is catalyzed by LpxC, which possesses an active site with characteristic structural regions: a polar region, a zinc ion, and a hydrophobic passage. As a result, analogues have been designed to model the natural substrate, all of which feature a general structure containing a nucleoside coupled to a hydroxamic acid moiety and a hydrophobic group via a triazole linker. Thus, the focus of this research is to synthesize and characterize different natural substrate analogues, each varying in hydrophobicity by altering the hydrophobic group, in order to investigate the structural moieties necessary for optimal binding and inhibition of LpxC.

114B-U. **Molecular Dynamic Investigation of Ice Nucleation and Growth in Supercooled Water in the Presence of an Electric Field.** Autumn Webb, Kai Leong, Feng Wang. *Natural Sciences, UA Monticello, Monticello, AR 71655; Chemistry, University of Arkansas, Fayetteville, AR 72701.*

Formation of ice from supercooled water plays an important role in many biological and atmospheric problems. This study clarifies the difference between ice nucleation and growth to help to understand how the competition between nucleation and growth is influenced by an electric field. In an experimental study conducted by the Lumonirsky group, it is demonstrated that the melting temperature of supercooled water is affected by an electric field. The objective of the investigation is to elucidate these effects from the electric field. The Water potential from Adaptive force matching for Ice and Liquid (WAIL) will be used to accomplish this simulation. The model was selected because it accurately captures specific properties of supercooled water that are needed for this investigation. The melting temperature of the WAIL model was confirmed to be 270 K in this study. Future direction of the research is discussed at the end.

115A-U. Determination of Fatty Acid Content in Native Algae. Don White, T. Snider, Andrew Williams. *Natural Sciences, UA Monticello, Monticello, AR 71655.*

Characterization of algae for their fatty acid content is one of a variety of tests done to determine the applicability of the algae. Applications include use as nutrients for aquaculture, in human consumption, or potential ability as biofuels. A number of freshwater eustigmatophyceae have been tested to determine if there are any differences in fatty acid concentration between species. While there are a number of algaes that have been described in this same manner, we want to compare a native species to these others. In order to do so, modification of previous sample preparation methods have been required, and will be described. Fatty acid content was then determined through GC-MS analysis. Current results show that the fatty acids analyzed compromise 0.7239-1.2217% of the total mass of the dry algae, with additional samples to be analyzed.

115B-U. **Cabbage Inhibits Nitrate Reduction in Celery during Storage.** Cynthia Robinson, Autumn Webb, Jinming Huang. *Natural Sciences, UA Monticello, Monticello, AR 71655.*

Nitrate (NO_3-) in spinach, lettuce, and celery can be reduced to nitrite (NO2-) during storage as we reported previously. However, nitrate in cabbage can not be reduced to nitrite during storage. More interestingly, we discovered that cabbage can inhibit nitrate reduction in celery during storage. Nitrate concentration was determined by the electrochemical method with a nitrate ion selective electrode, while nitrite concentration was determined by a Griess assay. Our results showed that cabbage juice inhibits 100% in nitrate reduction in celery juice (50%/50%, V/V) during eight days storage in refrigerator at 4oC. If cabbage juice boiled 5 minutes prior mixing with celery juice then no inhibition effect on nitrate reduction observed. If cabbage juice treated with 1mM EDTA prior mixing with celery juice also no inhibition effect on nitrate reduction observed. These interesting results strongly suggest that inhibition of nitrate reduction in celery is metal ion dependent when metal ion is removed by EDTA, a well-known chelator, no inhibition effect observed. Boiling experiment on cabbage also suggest that the inhibition of cabbage on nitrate reduction in celery involving some enzymes. When this enzyme was inactivated by boiling 5 minutes, then no inhibition effect observed. Principal Investigator, Ph: 870-460-1866, Fax: 870-460-1316, Email: huang@uamont.edu, Acknowledgements: this project is supported by grants from Arkansas Space Grant Consortium (NASA-ASGC, UAM 24019-24020).

116A-U. Characterization of a novel phosphorylation site in yeast helicase Pif1. Oktawia Clem, Zachary Waldrip, Alan Tackett. *Biochemistry, Henderson State University, Arkadelphia, AR 71999; UAMS, Little Rock, AR 72205.*

Virtually all aspects of nucleic acid metabolism require helicase activity. This activity is vital for maintaining genomic integrity. For example, a human genetic

disease xeroderma pigmentosum is caused by a mutation in the helicase XPD. This results in an ineffective nucleotide excision repair that leads to excessive DNA damage. Individuals with this defect rarely survive beyond the age of 20, suffering from various forms of malignant melanoma and squamous cell carcinoma. The Pif1 helicase family is ubiquitous and highly conserved in all eukaryotes. In healthy cells, the Pif1 helicase serves many roles that help to maintain genomic stability. It is known to bind and unwind G-quadruplex DNA, promote DNA synthesis during break-induced replication, play an important role in Okazaki fragment maturation and negatively influence telomerase activity. In mitochondria, Pif1 may be involved in mtDNA recombination and replication, possibly as a part of the mitochondrial replisome. In this research, we use the model organism Saccharomyces cerevisiae to study posttranslational modification of Pif1 helicase. Modifications such as serine phosphorylation are known to rapidly change protein activity, and the helicase Pif1 has seven known phosphorylation sites. Under normal growth conditions Pif1 is phosphorylated only at a basal level, with additional phosphorylation occurring in response to DNA damage. This is consistent with our hypothesis that additional phosphorylation activates a DNA damage response function of the Pif1 protein. The goal of our research is to characterize the function activated by phosphorylation of posttranslational modification site serine 170 in the yeast helicase Pif1. Understanding regulation of helicase activity can contribute to our understanding of cellular replication disorders, including genetic diseases and cancer.

116B-U. Structure-based mechanistic sutdies of bacterial collagenases and the expression system in Vibrio alginolyticus. Takahiro Honda, Ryan Bauer, Perry Caviness, Joshua Sakon, Takehiko Mima, Osamu Matsushita. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

Bacterial collagenases secreted by Vibrio alginolyticus and Clostridium histolyticum cause serious wound infections in immunocompromised people. Vibrio alginolyticus collagenase production is controlled by a two-component system, which consists of a sensor kinase, VarS and a response regulator, VarA. VarS consists of two transmembrane domains connected by a periplasmic linker, histidine kinase A (HisKA), signal receiver (REC), and histidine phosphotransfer (HPT) domains. It has been shown that phosphate is transferred from His 300 to Asp 718 and then to His 874 in VarS. However, the mechanism of phosphotransfer is not well understood. To elucidate this mechanism, I over-expressed and purified REC and HPT domains. Cysteine residues were alkylated to prevent unwanted aggregation during in-house crystallization screening. Meanwhile, clostridial collagenases are composed at a collagenase module and varying numbers of polycystic-kidney disease-like and collagen-binding domains. The enzymes are believed to be activated by Ca2+-triggered domain reorientation. To study the role of Ca2+ in domain reorientation, I analyzed the shape of these domains in the presence of a Ca2+ gradient using SAXS. I also used SAXS to analyze the shape of the complexes of the domains with collagenases peptide.Analysis of VarS will provide new insight into our understanding of the phosphorylation mechanism as well as assist in the development of new antibiotics. Analysis of collagenase domains will provide new insights into the Ca2+ activation mechanism and will assist in the development of collagenase domains as drug delivery agents.

117A-U. Morphology-dependent water wettable properties of aluminum oxide nanotubes grown by anodic oxidization. Portia Stone, Ganesh Kannarpady. *Center for Integrative Nanotechnology Sciences, UA Little Rock, Little Rock, AR 72204.*

Currently, there is no commercially viable technique to prevent ice accumulation on structural surfaces such as automobile bodies, power transmission lines, and airplane wings. Ice accumulation on such surfaces during severe winter weather conditions can impede day-to-day activities or even render them dangerous. Here, we discuss the fabrication of nano-textured coatings using anodic growth of aluminum oxide nanotubes tailored to repel water and thereby prevent ice accumulation. Aluminum oxide nanotubes with various sizes and morphologies were prepared using various anodization parameters and electrochemical solution concentrations. The surface energy of aluminum oxide nanotubes was reduced by depositing a thin layer of Teflon using pulsed laser deposition. The water wettable properties of the fabricated surfaces were studied using the contact angle measurement system. Depending on the morphology of the surface, the contact angle of water varied from 30° to 155°. Since the water droplets bounced off the surfaces at contact angles of 150 and above, these surfaces could potentially be used as anti-icing coatings in a variety of applications.

117B-U. Responses of Arginine-Containing Transmembrane Peptides to Cholesterol. Jordana Thibado, Roger E. Koeppe II. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

An essential component of animal cells, cholesterol exerts significant influence on the physical properties of the membrane and in turn, its constituents. One such constituent, the membrane protein, often contains polar amino acids. Although sparse, polar residues are highly conserved and play vital roles in determining specific structural and functional properties. To gain a greater understanding of the membrane, and more

broadly, cellular function, a model peptide framework termed "GWALP23" (acetyl-GGALWLALALALALALALWLAGA-amide) can provide useful information. The limited dynamic averaging of NMR observables such as the deuterium quadrupolar splittings of labeled alanine residues makes GWALP23 favorable for single residue replacements. Previously, GWALP23 family peptides were characterized with single Leu to Arg mutations at positions 12 and 14 in single-lipid membranes [J. Am. Chem. Soc., 132, 5803-5811, 2010]. GWALP23-R14 adopts a single tilted orientation in DOPC bilayers, whereas GWALP23-R12 displays multi-state behavior. The goal of this research is to further characterize these peptides in cholesterol-containing bilayers. Specific deuterium-labeled alanine residues were incorporated into the R12 and R14 sequences to identify transmembrane peptide orientation by means of solid-state deuterium NMR. Both peptides were incorporated into phospholipid bilayers with varying cholesterol content (0%, 10%, or 20%). Our findings suggest that 10% or 20% cholesterol content has minimal impact on the dynamics and orientation of GWALP23-R14 peptide. Conversely, cholesterol appears to reduce the multi-state behavior of GWALP23-R12, favoring a single transmembrane state for the helix. With 10% or 20% cholesterol content, the spectra exhibit defined quadrupolar splittings, suggesting that GWALP23-R12 adopts a predominant, tilted orientation in the presence of cholesterol. These results convey a conditional sensitivity of a complex multi-state peptide helix to the presence of cholesterol.

118A. Total synthesis and biological evaluation of the C-11 epimer of ipomoeassin F. Eric Barber, Guanghui Zong, Hazim Aljewari, Wei Shi. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

Ipomoeassin F, a resin glycoside isolated from the leaves of Ipomoea squamosa, has been shown to have a cytotoxicity in the low nanomolar range for a number of cell lines. Despite its high bioactivity, little is known about its mode of action. The macrolide ipomoeassin F consists of a disaccharide moiety linked through an intramolecular esterification to a 16-carbon fatty-acid derived aglycon. The aglycon contains a sole chiral center at C11 in the S configuration. In an effort to gain insight into the activity of this natural product, we synthesized an epimer with a change in configuration at this sole chiral center to explore the effect of the stereochemistry on the activity. This epimer of ipomoeassin F was then subjected to a few biological assays in human cells and compared to the previously synthesized natural product. The results showed a decrease in activity for the epimer by greater than 30 fold for all cell lines indicating the importance of the stereochemistry of the compound.

118B-U. Synthesis of Microgel Polymers as Catalysts. Hannah Miller, Susanne Striegler. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

New developments in organic synthesis show promise in achieving the best catalytic properties for the hydrolysis of glycosidic bonds through microgel polymers and transition metal complexes. A monomer mix of ethylene glycol dimethacrylate, butyl acrylate, and styrene form miniemulsion polymers after sonication and exposure to UV light. Gravimetrical analysis is used to determine the most suitable polymerization conditions by performing experiments at varying pH values, temperatures, dilutions of polymer mixtures, cross-linking amounts, initiator amounts, and stirring speeds. The studies form the basis for improved polymers that will eventually serve as macromolecular catalysts. Preliminary results will be presented and discussed.

119A-U. The 3D structure of bacterial collagenase. Momoka Goda, Joshua Sakon, Ryan Baue, Osamu Matsushita, Takehiko Mima. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

Collagen is the most abundant molecule in the extracellular matrix. It is difficult to dismantle collagen fibers. Flesh-eating bacteria produce a variety of collagenases to hydrolyze these fibers to rapidly expand infectious foci. So the function of collagenase is the key for their pathogenesis. How such complicated collagen fibers can be hydrolyzed very rapidly? Bacterial collagenases are composed of three different types of domains; catalytic domain S1, PKD domain S2, and collagen-binding domain S3. I purified S2bS3a, S3aS3b and S3aS3bS997C from E. coli. The goal of my project is to determine some of the structures of the collagenase by using X-ray crystallography, which needs the crystal of the protein. To crystallize them, first I conducted Pre-crystallization test to determine the suitable protein concentration. Second, I carried out a high-throughput screening using 96-well trays. Finally, I tried to crystallize the protein by using hanging drop vapor diffusion technique to optimize conditions. To reveal the protein envelope by using small angle X-ray scattering (SAXS), I sent the samples to Lawrence Berkley National Laboratory. The SAXS data are analyzed by software ATSAS 2.4. SAXS technique is used to reveal the physiological shape solution.

119B-U. Biomimetic Synthesis of Nano-Structured "Exoskeletons." Savannah Thornburgh, Parker Cole, Bailey Burnett, Z. Ryan Tian. *Chemistry and Biomedical Engineering, University of Arkansas, Fayetteville, AR 72701.*

The course of evolution on life yields complex organisms capable of producing hierarchical structures from organic-inorganic hybrid materials under the help of

templating by biomolecules in the process of biomineralization. The longstanding challenge in mimicking the biomineralization process is to harness Mother Nature's methods for materials scientists to develop and mass-produce innovative and complex architectures out of novel nanomaterials at low-cost for large-scale industrial applications. Titanium dioxide, TiO_2, has many important applications in areas such as photocatalysis and environmental purification, gas sensing, high effect solar cell, Li-batteries, and electrochromic display. Nano-structured TiO_2 can be more interesting due to the large surface-to-volume ratio. Thus, if the nanomaterial can be ordered into architecturally exotic shapes, their multifaceted properties can be exploited further in addition to their cosmetic appeal. Here we are reporting the biomimetic synthesis of the nanostructured "exoskeletons" out of the TiO_2-based nanofibers for the first time. Our product has been characterized using scanning electron microscopy (SEM) and X-Ray diffraction (XRD). These new structures showed the potential to perform typical TiO_2-nanostructure's functionality while adding an aesthetic component for commercial appeal. Furthermore, our methods will highly compliment the recent advances in 3D-printing technology, which will give us more versatility in designing more sophisticated architectures from many other TiO_2-nantsructures.

120A-U. Evaluating substrate specificity of several galactonoamidines toward the inhibition of β-galactosidase from Aspergillus oryzae. Logan Mills, Susanne Striegler. *Chemistry, University of Arkansas, Fayetteville, AR 72701.*

Previous experiments have demonstrated the potential of several synthesized galactonoamidines to function as inhibitors of β-galactosidase from Aspergillus oryzae. These compounds resemble the structure of the complex formed by a glycoside and a glycosidase during the transition state of the substrate hydrolysis and may therefore classify as transition state analogues (TSAs). In order to verify this hypothesis and provide deeper insights into the mechanism of the selected enzyme, fast-screening assays based on UV-Vis spectroscopy are used. Current insights are summarized and will be discussed.

120B-U. Novel Phosphorus and Nitrogen Co-Doped Carbon for Utilization in Supercapacitors. Zachary Hicks, Sunil Kumar Ramasahayam, Saad Azam, Tito Viswanathan. *Chemistry, UA Little Rock, Little Rock, AR 72204.*

Traditional capacitors have long been used as a means of storing energy for electronic devices. Supercapacitors, otherwise known as ultracapacitors, are an emerging solution to efficiently store greater amounts of energy. Supercapacitors exhibit both the characteristics of batteries (high energy density) as well as capacitors (high power density). They are unique in that they utilize a porous carbon material and thinner dielectric, in order to greatly increase their overall capacitance. Novel phosphorus and nitrogen doped carbon materials (PNDC) prepared in our lab have been used to fabricate supercapacitors and evaluated for their energy storage characteristics. The PNDC-containing supercapacitors have shown to out-perform non-doped carbon supercapacitors. Our PNDC material is important to green energy research, because it is made from the readily abundant, renewable resources of tannin and used coffee grounds. This represents environmentally friendly alternate energy storage devices.

121A-U. Unique Pharmacodynamic Properties of AB-Pinaca; a New Synthetic Cannabinoid Found in K2/Spice. Rachel D. Hutchison[1], Benjamin M. Ford[2], Paul L. Prather[2]. *[1]Department of Chemistry, UA Little Rock, Little Rock, AR 72204, [2]Department of Pharmacology and Toxicology, College of Medicine, UAMS, Little Rock, AR 72205.*

Introduction: Synthetic cannabinoids (SCBs) are found in illicit street products known as K2 or Spice, often referred to as "legal cannabis". However, in contrast to use of marijuana that primarily produces euphoria, recreational abuse of SCBs can additionally result in anxiety, psychosis, chest pain, seizures and death. To potentially explain higher toxicity associated with SCB use, we hypothesized that AB-Pinaca, a SCB commonly found in K2/Spice, and its phase one metabolites exhibit higher affinity and activity at the CB1 cannabinoid receptors (CB1Rs) relative to Δ9-tetrahydrocannabinol (THC), the principal psychoactive cannabinoid present in marijuana. Methods: The affinity of all drugs for CB1Rs was determined by radioligand competition receptor binding in Chinese Hamster Ovary cells stably expressing CB1Rs (CHO-hCB1 cells). Two assays were employed to quantify the activity of drugs acting at CB1Rs, the ability of SCBs to activate G-proteins in membrane preparations, and to inhibit activity of the intracellular effector adenylyl cyclase in intact CHO-hCB1 cells. Results: AB-Pinaca exhibited higher affinity, potency and efficacy at CB1Rs relative to THC. Furthermore, phase one metabolites of AB-Pinaca retained affinity and full agonist activity at CB1Rs. Co-incubation of THC with AB-Pinaca, or a major metabolite of AB-Pinaca, resulted in a reduction in both the potency and efficacy of CB1R-mediated activation of G-proteins by THC (e.g., antagonism). Finally, chronic treatment of cells with AB-Pinaca produced greater desensitization of CB1Rs (e.g., tolerance) than similar exposure to THC. Conclusions: The higher affinity and activity of AB-Pinaca at CB1Rs relative to THC might be expected to produce enhanced psychotropic and adverse effects, contributing to the reported abuse and marked toxicity of this novel SCB.

121B-U. The Effects Of Chronic Oral Nicotine Exposure On Nicotine Metabolism In Female Rats. Nathanael D. Hall[1], Jessica H. Hartman[2], Amy R. Pearce[3], Grover P. Miller[2]. *[1]Chemistry, Ouachita Baptist University, Arkadelphia, AR 71998, [2]Department of Biochemistry and Molecular Biology, UAMS, Little Rock, AR 72205, [3]Department of Psychology and Counseling, Arkansas State University, Jonesboro, AR 72401.*

Smoking is one of the most pressing global health issues of our time with 1 out of 5 deaths attributed to cigarettes. Cigarette smoke contains over 7,000 chemicals, 69 of which are known to cause cancer. The addictiveness of nicotine has caused the continuing use of tobacco products. In attempt to remove the addictive component, nicotine, from the cacogenic chemicals in cigarettes, cessation aids have been made available such as nicotine gum (oral nicotine). However, the long-term health effects of chronic oral nicotine exposure are still unknown. Previous studies have shown that chronic oral nicotine exposure leads to a decrease in sera and urine levels of cotinine. However, further studies have shown that CYP2B1 activity does not decrease despite the drop in cotinine levels, which CYP2B1 is the cytochrome P450 involved in nicotine oxidation. Therefore, we investigated alternate oxidative and conjugative metabolic pathways for nicotine to explain the observed decrease in cotinine levels. Specifically, we assessed changes in (1) oxidation of cotinine by P450s, (2) glucuronidation of cotinine, and (3) glucuronidation of nicotine as a function of chronic oral nicotine exposure. These specific reactions were analyzed by HPLC conditions developed in Dr. Miller's lab and made use of previously prepared rat liver microsomes. The completion of these studies would provide a foundation for future studies to determine the reaction kinetics and enzymes responsible for the respective metabolic pathways.

122A-U. Analysis of Two Base-Ring Ware II Juglets from the Late Bronze Age for Opioid Derivatives via GCMS. Jackson R. Petty. *Department of Chemistry, Harding University, Searcy, AR 72143.*

It has been suggested that Base-ring juglets from the Late Bronze Era (circa 1650 BC) were used to transport opium. The debate between archaeologists stems from the appearance of these characteristic juglets coinciding with the emergence of the opium trade and the aesthetic properties of the vessels closely resembling an inverted opium pod in size, shape and detail. Specifically, two separate Base-Ring II juglets from the Late Bronze Age were analyzed to determine if the major components of opium latex (most likely from the Papaver Somniferum L. poppy) could be detected and quantified. The primary components of the latex (from the narcotic cultivar C048-6-14-64) are the alkaloids morphine, thebaine, and codeine. Gas Chromatography with a Quadrupole Mass Spectrometer detector (GCMS) was used to detect for these compounds by matching the mass spectrum of the components found in the juglet extraction to known standards of these alkaloids. In addition, Single Ion Monitoring (SIM) was implemented to analyze ions specific to the opiates of interest. The detection was further validated by matching the retention time of components to that of the eluted standards. Samples were prepared for GCMS analysis by extraction with a 5:1 mixture of chloroform and isopropanol, derivatized with bis(trimethylsilyl)acetemide, and then analyzed with a final solvent of dichloromethane. Preliminary tests suggest the presence of morphine in one of the two juglets with a retention time of 11.632 min. In the same juglet there is a promising codeine SIM peak at 10.895 min. Further research will focus on concentrating samples for higher detection levels, establishing a Limit of Detection (LOD), detecting thebaine, and extracting ionic salts of opiates.

122B-U. Effects of Glucoraphanin and Phenethyl Isothiocyanate on Non-Small Cell Lung Cancer Proliferation and Cancer Cell Metabolism. Enock Rwamuza, Daniel Sappington, Sharda Singh, Gunnar Boysen. *Chemistry, University of Central Arkansas, Conway, AR 72035.*

Lung cancer is the leading cause of cancer-related deaths in the US and worldwide. Non-small cell lung cancer (NSCLC) accounts for 80% of all lung cancers. Phytochemicals found in cruciferous vegetables have been shown to be chemopreventative and demonstrate chemotherapeutic potential. Two cruciferous-derived phytochemicals, glucoraphanin and phenethyl isothiocyanate (PEITC) have demonstrated anti-proliferative effects on cancer through altering the glutathione pathway. The applications of these compounds to NSCLC have not been fully explored. Therefore, two NSCLC cell lines (H460 and A549) were grown under standard growth conditions and treated with phytochemicals; Glucoraphanin and PEITC. Glucoraphanin (0.1 to 50 μM) and PEITC (0.01 to 40 μM) were used to disrupt carcinogenesis in NSCLC cell lines and the effects were measured using cell proliferation and colony formation assays. Additionally, extracellular media aliquots were sampled over time to monitor changes in glutathione pathway metabolites. The metabolites were extracted from the media and analyzed using a tandem LC/MS/MS (Agilent HPLC-QqQ mass spectrometer). Both glucoraphanin and PEITC reduced NSCLC cell proliferation (ED50: 28.2± 8.8 and 3.7±0.2 μM in H460; 28.5±9.4 and 18.7±15.5 μM in A549, respectively) and colonies formed in dose-dependent manners (ED50: 16.9±5.3 and 2.1±0.2 μM in H460; 14.1±1.1 and 5.5±3.4 μM in A549, respectively). The cell lines demonstrated ≈3-fold increased sensitivity

to PEITC compared to glucoraphanin. Glucoraphanin altered the glutathione pathway by potentially inhibiting the γ-glutamyl cycle with a marked accumulation of extracellular glutathione and γ-glutamyl-substrates in dose-dependent manners. Additionally, an altered glutathione pathway was also observed with PEITC, and is most likely due to a change in the metabolism of the glutathione precursor, glutamine. These results demonstrate the NSCLC therapeutic potential of glucoraphanin and PEITC. Further investigation into the mechanisms of glucoraphanin and PEITC are warranted..

Physics

Friday Oral Platform Session

ORAL – 3:20. Techniques to enhance endothelial cells attachment to microcarrier beads, achieving microgravity treatment. Darryl Webb, Rupak Pathak, Abdel Bachri, Sanchita P. Ghosh, Igor Koturbash, Marjan Boerma, Martin Hauer-Jensen. *Engineering and Physics, Southern Arkansas University, Magnolia, AR 71753.*

In order to study whether the exposure to space radiation and near zero gravity contribute to an increased risk for cardiovascular disease, we irradiate Human Umbilical Vein Endothelial Cells (HUVECs), and subject them to ground-based simulated microgravity. HUVECs are used because cardiovascular diseases have been linked to genomic instability in endothelial cells. We use the High Aspect Ratio Vessel (HARV) bioreactor to seed the cells onto Cytodex-3 microcarrier beads and cause them to undergo free suspension, a condition similar to near zero gravity in the outer space. A key component for this experiment is to standardize the microcarrier bead concentration, cells attachment and the HARV rotation speed to achieve free suspension. This standardization is required in order to prevent damage to the cells during the long microgravity treatment and optimize cell recovery. There are three main possible damage mechanisms; (1) collisions among the microcarrier beads, (2) strong turbulent fluid currents and forces due to unnecessarily high rotation, and (2) shear stress due to bubble inside the vessel chamber. All of these mechanism are considered during the process of standardizing techniques to improve cell attachment and microgravity treatment. We discuss all of the above in this work.

ORAL – 3:35. Molecular Dynamics Simulations of the Mechanical and Hydrothermal Properties of Mesoporous Silica and Aluminosilica. James K. Thomas, R. Sakidja, H. Osman, R.A. Mayanovic. *Physics, Missouri State University, Springfield, MO 65897.*

Mesoporous silica and aluminosilica constitute wide bandgap semiconductor with catalytic properties of use in industrial and energy harvesting applications. Our investigations are focused on the hydrothermal and mechanical stability properties of mesoporous silica and aluminosilica using atomistic modeling. For this purpose, LAMMPS molecular dynamics software is used on the Stampede supercomputer cluster. The nano-sized pores created in the simulation cells are arranged to represent the meso-porous structures and to assess the mechanical strength. By evaluating the average pressures and pore volumes, the effect of porosity on the bulk modulus has been quantified as a function of pressure and porosity level.

ORAL – 3:50. Optical Characterization of CdSe Collodial Quantum Dots. Gabrielle Abraham, Pooja Bajawa, Colin Heyes, Joseph B. Herzog. *Physics, University of Arkansas, Fayetteville, AR 72701.*

This work investigated the photoluminescent properties of colloidal, semiconductor Cadmium Selenide (CdSe) quantum dots (QDs) with optical spectroscopy measurements. Images, videos, and spectra of samples were collected to study the effects of polarization, sample density, uniformity, and QD aging with time. A custom-built microscope was used to detect single to a few molecules, shown by fluorescent intermittency, or QD blinking. Differences in the spectrum were noted as related to the age of samples, the density of the quantum dots, polarization of excitation light as compared to emission light, and the concentration of samples. Further experiments include studying other nanoscale semiconductor materials, such as monolayer MoS2, and combining the photoluminescent materials with gold nanoparticles or nanostructures which exhibit the potential for plasmonic enhancement.

ORAL – 4:05. Aluminide Diffusion Coatings. Zach Leuty, Ridwan Sakidja. *Physics and Materials Science, Missouri State University, Springfield, MO 65897.*

To increase the efficiency of steam power plants, operating temperatures must be raised above 700C. Steel corrodes very rapidly under these conditions. Aluminum diffusion coated steel is extremely corrosion resistant under these high-temp, water vapor conditions. The aluminizing process is typically performed at 900-1000C, which inevitably degrades the mechanical integrity of the steels structure. Recent advances in pack-cementation show that a low temperature (650-700C) aluminizing is feasible using certain halide salt activators. In this study, we examine how the growth kinetics are affected by selecting a different steel substrate (18-8 stainless steel vs. no-chromium alloy steel), halide salt activator (ammonium chloride, ammonium fluoride), growth time, and

furnace temperature. We have found that chromium in the steel can inhibit the growth process, therefore coatings on stainless steel are thinner. A higher iron content in the steel creates a thicker coating. Chloride based activators create a thicker coating than fluoride based activators. There is also a positive direct correlation with the temperature/time and the thickness of the diffusion coating.

ORAL – 4:20. Gamma Ray Burst 150518a. Elizabeth Apala, Alicia Soderberg. *Physics, East Central University, Ada, OK 74820.*

Gamma Ray Burst (GRB's), extremely energetic flashes of Gamma Rays, are caused by either deaths of massive unstable stars or colliding binary neutron stars. A unique burst, GRB 150518a, had two recorded bursts fifteen minutes apart which is very rare and is considered to be ultra-long, lasting around thirty minutes total and is associated with a Supernova explosion. GBR 150518a is also extremely close compared to the average burst being measured to have a redshift of .2, this is important to note because GRB's measuring less than a redshift of .3 only are seen every ten years. Gamma rays are emitted by supernovae, neutron stars, black holes, and quasars and by studying GRB's it allows us to see more deeply into how these objects function. The first few days of GRB 150518as' detected afterglow was plotted in different wavelengths, including optical, x-ray, radio, and infrared, in flux verses time. Data is continuously being added as time goes on. This research is funded by the NSF, grant number 1358990.

ORAL – 4:35. Graphene-Biointerface for Biosensor Applications. Dan Jones, Kartik Ghosh. *Physics, Astronomy, and Materials Science, Missouri State University, Springfield, MO 65897.*

The use of graphene in biosensor applications has been the focus of much research in the past decade due to its high conductivity, biocompatibility, and ease of functionalization towards specific biomolecules. In this study the nano-bio interaction of the graphene-biomolecule interface is examined in different pH environments. This examination is performed by the analysis of specific binding patterns between drop casted samples containing aqueous solutions of graphene and an amino acid, tyrosine. This study shows that the binding occurs more successfully when graphene and tyrosine are combined in a low pH solution. It is also shown that decreasing the pH of the solution functionalizes graphene to bind with the amino acid. The binding structure between these molecules is investigated from Raman spectra by analysis of the D, G, and 2D peaks of graphene compared to the respective peaks observed from the graphene-Tyrosine solutions. SEM imaging is also used to visualize the bonding pattern exhibited by the solutions. Future studies will include binding studies and functionalization of graphene with other amino acids. Understanding the nano-bio interface between graphene and biomolecules can lead to improved biosensing technology with wide ranging applications.

Physics

A and B – Saturday 8:00 – 10:15 Posters

(Posters designated "U" will be judged.)

201A. Comparison of Vanadium Oxide Thin Films Prepared Using Femtosecond and Nanosecond Pulsed Laser Deposition. Ying Deng, A. Pelton, R.A. Mayanovic. *Physics, Astronomy, and Materials Science, Missouri State University, Springfield, MO 65897.*

Pulsed laser deposition (PLD) is a thin film deposition technique whereby a high-energy pulsed laser is focused onto a target in a vacuum chamber. The target material is vaporised by the high laser intensities and forms a plasma plume that travels towards the substrate, which is subsequently condensed on the substrate to form a thin film of the target material. My project is to investigate the properties of materials prepared using two variations of the pulsed laser deposition (PLD) technique. The first technique is femtosecond PLD, whereby the laser used to ablate the target has a significantly higher peak intensity and shorter pulse duration as compared to excimer-based nanosecond PLD. Experiments have been conducted on the growth thin films prepared from V2O5 targets on Si wafer or glass substrates. The film properties are studied systematically as a function of the deposition parameters of laser fluence, spot-size, oxygen pressure, target-to-substrate distance and temperature. The surface morphology, structural and vibrational properties of the films are studied using XRD, SEM, Raman Spectroscopy, and XPS characterization techniques.

201B-U. Tools for automating crop and soil analysis using consumer technology. Christian Hale, Jacob Malone, Edmond Wilson. *Department of Engineering and Physics, Harding University, Searcy, AR 72143.*

Over the years America's approach to farming has changed from small farms to large scale intensive farming, the goal being to maximize output while minimizing labor and space. Automation achieves this goal and is used in large scale industrial farms. We have the opportunity to democratize this technology and bring autonomy to farms of all sizes, reducing labor or rerouting it to more productive tasks and allowing for

sustainable intensive farming while maintaining high yield and profit. Using custom software we can turn consumer electronics into a specialized industrial machine. In this case we are using a raspberry pi, inexpensive digital cameras, and an android device acting as the user interface. Our goal in proving these technologies is to culminate our efforts into a small maneuverable rover capable of autonomy and 360 degree real time photo analysis of plant health with a suite of instruments for soil and environmental analysis.

202A-U. A Robotic Instrument Suite for Diagnosing and Remediating Agricultural Crops. Shelby V. Sorrells, Edmond Wilson. *Department of Engineering and Physics, Harding University, Searcy, AR 72143.*

The long-term goal of this project is to place a robotic vehicle into Arkansas fields that will inspect plants individually for a variety of parameters such as insect damage, low nutrients, moisture availability, weeds and then treat the plants needing remediation by injecting, pesticides, herbicides, moisture, fertilizer as needed. A first attempt produced a robotic arm equipped with a camera and spectrographs to be used to produce a protocol for measuring plant health. Microprocessor control of the cameras and spectrographs was expedited by the use of Android devices to quickly carry out the measurements and which allowed the system to function without large computers and displays. An advantage of this approach allows for remote control of the robotic devices from anywhere that cell phone coverage is available.

202B-U. Additive Manufacturing of Hybrid Rocket Fuels. Rachel Beeman, Edmond Wilson. *Department of Engineering and Physics, Harding University, Searcy, AR 72143.*

Rockets launched by the civilian space industry are powered almost exclusively by hybrid rocket motors using hydroxyterminated polybutadiene, HTPB, as the fuel and liquid nitrous oxide, N2O as the oxidizer. These motors are inherently safer to build, store and operate because the fuel and oxidizer only come into contact at the point of combustion. They are also simpler than liquid rockets but have the advantage that they can be throttled, stopped and restarted during flight. Hybrid rocket motors have approximately greater specific impulse than solid rocket motors and about the same as liquid hydrocarbon liquid rocket motors. Our studies investigate the use of a different fuel for hybrid rocket motors, ABS plastic (acrylonitrile-butadiene-styrene polymer), formed using additive manufacturing processes. Additive manufacturing allows the use of different fuel grain geometries, porosities and novel enhancing additive materials, such as aluminum. We report on the design of our hybrid rocket test facility and the results of our study.

203A-U. Optical Communications Between NanoSats. Maurisa G. Orona, Edmond Wilson. *Department of Engineering and Physics, Harding University, Searcy, AR 72143.*

Our goal of placing a constellation of nano satellites (NanoSats) around Saturn's Moon Titan to investigate the atmosphere and liquid hydrocarbon lakes of the Solar System's second largest Moon requires communications amongst the constellation members to maintain the desired flight formation and share in the data collection. Formation flight of satellites is a new concept and it seemed appropriate to design our communications system to operate by transmission of electromagnetic radiation in the form of light signals rather than radio or microwave signals. Much initial development is required for a successful space mission. Our first objective is determining the range, sensitivity and resolution of cooperating NanoSats in the constellation. These studies are hampered by the long distances between satellites and the light pollution here on Earth. On Earth, light waves are attenuated by mists, fog, rain and aerosols unlike space which does not have these limitations. Reported here is the results from using different types of light sources and receivers, including video devices to reach our initial objective.

203B. Nano-Bio Interactions of Zinc Oxide and Adenosine Triphosphate. Daniel Soden, Austin Shearin, Ridwan Sakidja, Kartik Ghosh. *Physics, Astronomy, and Materials Science, Missouri State University, Springfield, MO 65897.*

Medical research into the marriage of biological and inorganic materials has been a scientific focus for many years, yet even after all this time the precise interactions at the nano-bio interface still remain shrouded in mystery. In this investigation, pulsed laser deposited Zinc Oxide (ZnO) nanorods are brought into proximity with the energy exchange biomolecule Adenosine Triphosphate (ATP) in an effort to map their short and long term interactions via characterization methods such as scanning electron microscopy, raman spectroscopy, and x-ray diffraction. In parallel with this investigation, quantum espresso dft calculations are run to verify the optimum energy configuration between the two materials, giving a more complete picture of their interaction via simulation. Raman spectra of the two species are also computationally predicted to corroborate research values and spectral graphs. With this knowledge in hand, a ground floor understanding of the nano-bio interface can be formulated, and even more advanced cases can be studied. Progress in this area is especially important; as it has the potential to ultimately lead to a plethora of applications like advanced drug delivery and biocompatible organ and limb replacement, giving patients an ever greater

capacity for both treatability of disease and injury as well as post-treatment quality of life.

204A. In Situ SAXS Investigations of SBA-15 and Al-SBA-15 Mesoporous Materials under High Pressure and Hydrothermal Environments. Dayton G. Kizzire, S. Dy, S.T. Anderson, Z. Wang, M. Mandal, K. Landskron, R.A. Mayanovic. *Physics, Astronomy, and Materials Science, Missouri State University, Springfield, MO 65897.*

Periodic mesoporous SBA-15 silica and Al-SBA-15 aluminosilica possess high surface to volume ratio and nano-scale pores making them potential candidates for heterogeneous catalysis, ion exchange, gas sensing and other applications 1-3. The objective of this study is to investigate the mechanical and hydrothermal stability properties of periodic mesoporous SBA-15 silica and SBA-15 type aluminosilica (Al-SBA-15). Both SBA-15 and Al-SBA-15 possess amorphous pore walls and have similar pore size distribution (pore size ~ 13-14 nm). Small angle x-ray scattering (SAXS) measurements were made at the B1 beamline, at the Cornel High Energy Synchrotron Source (CHESS) on both materials. The mesoporous SBA-15 silica and Al-SBA-15 aluminosilica samples were loaded in a diamond anvil cell (DAC) for pressure measurements, and, separately, with water in the DAC for hydrothermal measurements to high P-T conditions (to 280 °C and ~ 200 MPa). Analyses of the pressure-dependent SAXS data show that the mesoporous Al-SBA-15 aluminosilica has a bulk modulus $\kappa = 34.7 \pm 6.5$ GPa whereas mesoporous SBA-15 silica has a $\kappa = 12.0 \pm 3.0$ GPa. The hydrothermal SAXS data reflects small net expansions of the pores at elevated P-T conditions, with dissolution of water into the pore walls. At high temperatures the pressure effect takes over in Al-SBA-15 and dehydrates the mesoporous framework. Our results show that Al-SBA-15 is more hydrothermally stable than the SBA-15 silica. These results will lead to a better understanding of amorphous framework stability under extreme conditions and advances in technology utilizing mesoporous silica or aluminosilica for heterogeneous catalysis. [1] A. Corma, Chem. Rev. 97 (1997) 2373-2419. [2] G. J. de A.A. Soller-Illia, C. Sanchez, B. Lebeau, J. Patarin, Chem. Rev. 102 (2002) 4093-4138. [3] R.A. Mayanovic, H. Yan, A.D. Brandt, Z. Wang, M. Mandal, K. Landskron, W.A. Bassett, Micorporous Mesoporous Mater. 195 (2014) 161-166.

204B. A Comparative Study of MoO3 Films Grown Using Femtosecond and Nanosecond Pulsed Laser Deposition. Krishna Harsha Puppala, Anthony Pelton, R.A. Mayanovic. *Physics, Astronomy, and Materials Science, Missouri State University, Springfield, MO 65897.*

Pulsed Laser Deposition is a promising, inexpensive method for the preparation of nanostructured thin films that may be suitable for heterogeneous catalysis. During the course of this study we have prepared MoO3 thin films by using two types of Pulsed Laser Deposition (PLD). The first method is carried out at US Photonics, Springfield, MO, using a femtosecond laser while the second method uses an excimer (nanosecond) laser located at Missouri State University. The PLD films were deposited on glass and silicon substrates. The thin films were annealed to 450 °C for up to 20 hours in air using a Linkam stage. Characterization of the films' structure and morphology was made using SEM, XRD, and Raman spectroscopy, both before and after annealing. Prior to annealing, the films made using femtosecond PLD are rougher and more textured whereas the ones fabricated using the nanosecond PLD are smoother. The femtosecond PLD (F-PLD) films have combined 3-D nano-crystalline and amorphous structures, whereas the nanosecond-PLD fabricated thin films have predominantly amorphous structure before annealing. In addition to the characterization described above, our results from X-Ray Photoelectron Spectroscopy made of the thin films will be discussed.

205A-U. Ultra-High Vacuum PLD for WTe2 Thin Films. Trey Grimes, Dan Soden, Kartik Ghosh. *Physics, Astronomy and Materials Science, Missouri State University, Springfield, MO 65897.*

The study of two dimensional thin films has yielded a variety of fascinating materials that posses extreme characteristics which may make these materials useful in future industry and technology. One such compound, Tungsten Telluride (WTe2) though not well studied, may have a very high magnetoresistance value, making it useful in magnetic sensors, memories, hard drives and miniaturized circuitry. After having synthesized the WTe2 and built a vacuum chamber specific for this purpose, our group plans to grow and study Tungsten Telluride thin films under ultra-high vacuum conditions via pulsed laser deposition techniques. We seek to find optimal conditions for deposition and then examine various properties of the compound using X-ray diffraction, Ramann spectroscopy, and ETS.

205B. Tuning the structural and electrical properties in reduced graphene oxide thin film. Md. Abdullah-Al Mamun, Kartik Ghosh. *Physics, Astronomy and Materials Science, Missouri State University, Springfield, MO 65897.*

Graphene, consisting of 2D layer of sp2 hybridized carbon atoms, is a promising material for future electronics due to its unique optical, electrical and mechanical properties. It's a highly stable thin sheet of carbon atoms with high charge carrier mobility but the incorporation of its valance band and conduction band at Fermi level make it a zero-gap semiconductor. Also, recent graphene devices showed some Schottky barriers

raising further investigations for changing the band gap. People followed different ways to decorate its basal plane with different oxygen containing functional groups such as epoxy (C-O-C), carbonyl(C=O), carboxyl (COOH), hydroxyl(C-OH) etc. that affect the structure. We synthesized thin films of reduced graphene oxide (RGO) by Pulsed Laser Deposition (PLD) technique. The electrical properties of RGO depend on the amount of sp2 and sp3 hybridized carbon atoms of the structure. The structural properties of the films vary due to different deposition parameters. The parameters are deposition temperature, pressure, no. of laser shots, annealing temperature, annealing time, gases used for annealing and even the graphene transfer method. These parameters were varied through deposition and then the optimal growth parameters were tuned to find the expected properties from the film. Electrical properties were measured by Hall-measurement that confirmed p-type characteristics of the thin films. The measured maximum mobility was 686 $cm^2 v^{(-1)} s^{(-1)}$ in the optimum sample. The structural properties, analyzed by micro Raman spectroscopy and X-ray Diffraction (XRD), were average size of sp2 clusters, degree of reduction, defect density, crystallite size, no. of layers and interlayer distances.

206A. Nanowire Thermoelectronic Properties. Neva Agarwala. *Physics, Astronomy and Materials Science, Missouri State University, Springfield, MO 65897, Imperial College of London.*

The project presents the comprehensive explanation to thermoelectronics and is intended to provide the details overview of all the techniques that are used throughout this research as well as the change in behaviors of the samples due to their doping levels and nanowire lengths. As examples of practical realization of the measurement principles, this experimental setup is for current and resistance measurements at voltage sweeps from -2.5 to 2.5 Volts for the temperature difference between the two surfaces of the samples. The comparisons among the measurements of each setup are done in order to understand and observe the electrical contacts and transport behaviors of the samples. Throughout the investigation, an interesting result has been found that is, the control sample without any grown nanowire gives very different results from the rest of them and the current – voltage curves seem to be more ohmic with the grown nanowires samples.

206B. Magnetic Properties of Transition Metal (Co, Ni, Mn, Fe) Incorporated Core Shell MxCr2-xO3-Cr2O3 Nanoparticles. M.D. Hossain, S. Dy, M. Benamara, R.A. Mayanovic. *Department of Physics, Astronomy & Materials Science, Missouri State University, Springfield, MO 65897.*

Magnetic core shell nanoparticles have great application potential in magnetic random access memory, spintronic devices and drug delivery systems. Our investigations are focused on the synthesis and the characterization of the structural and magnetic properties of inverted core shell nanoparticles. By using the hydrothermal epitaxy technique, we are able to incorporate the transition metal elements (Co, Ni, Mn, Fe) with Cr and O, resulting in the formation of MxCr2-xO3-Cr2O3 core shell nanoparticles. In some cases, this results in the formation of a metastable ferromagnetic/ferrimagnetic MxCr2-xO3 shell and antiferromagnetic Cr2O3 core structure. High resolution TEM (HR-TEM) results provide direct evidence for the formation of core-shell nanostructure with the M transition metal being predominant in the shell region. The combined use of HR-TEM and XRD characterization confirm the corundum phase being present in both the shell and core regions. XPS analysis has been made to determine the oxidation state of all the constituent elements. Magnetic measurements show well developed hysteresis loops: Field cooled magnetization measurements manifest horizontal shifts in the applied field axis and vertical shifts in the magnetization axis compared to the zero-field cooled hysteresis loop. This substantiates the exchange bias effect between the antiferromagnetic Cr2O3 core and the ferromagnetic/ferrimagnetic MxCr2-xO3 shell.

207A-U. The Effect of Ionizing Radiation and Microgravity on Human Endothelial Cells, GT3 Radioprotection. Ricardo Romo, Rupak Pathak, Abdel Bachri, Sanchita P. Ghosh, Igor Koturbash, Marjan Boerma, Martin Hauer-Jensen. *Engineering and Physics, Southern Arkansas University, Magnolia, AR 71753.*

Chromosome aberrations arise from plethoric occurrences of biological damages. Such damages include radiation interactions with the atoms of the DNA molecule, or some other cellular component critical to the survival of the cell. Since the cells are mainly composed of water, radiation has a higher probability of interacting in an indirect effect with the ions of the water. When high or low Linear Energy Transfer (LET) gamma radiation interacts with a cell, the physical interaction between radiation and matter lead to break the water molecules down into hydrogen (H) and Hydroxide (OH). These remnants may recombine or interact with other fragments or ions to form toxic substances, such as hydrogen peroxide (H_2O_2), which can be destructive to the cell. If enough atoms are affected DNA double strand breaks occur and my rejoin improperly, leading to genomic instability; which is the hallmark of cancer. The effect of outer space radiation exposure and near-zero space gravity environment on DNA damage is not well documented, and is a primary concern to NASA in furthering its goal for deep space exploration. Thus, finding a new way to reduce

chromosomes instability due to radiation and microgravity is key. An enriched vitamin-E known as Gamma Tocotrienol (GT3) has been tested to be a strong antioxidant, was selected to test with radiosensitive cells and was shown to be effective. Bone marrow cells from female mice are categorized as highly radio sensitivity cells, and therefore were first experimented with 5 Gy of Cesium (137) gamma radiation. We run an equivalent test on Human Umbilical Vein Endothelial Cells (HUVECs) and had a similar positive outcome. Chromosome aberrations were characterized with Fluorescence in Situ Hybridization (FISH) and Spectral Karyotyping (SKY). Both (FISH) and (SKY) produced reliable karyotypes that confirm GT3's potential to reduce chromosomes aberrations in human endothelial cells.

207B-U. Electrical Transport and Atomic Force Microscopy. Kahlil Wade, Jak Chakhalian, Paul Somers. *Engineering and Physics, Southern Arkansas University, Magnolia, AR 71753.*

We investigate the behavior of materials at varying temperatures with explanations underlying in the understandings of quantum physics. In temperatures near absolute zero, the behavior of electron movement cannot be understood accurately by simply using classical mechanics alone. By using a cryostat with the ability to cool samples between 78K and 300K, observations will be made between various types of metals and their conductivity as it relates to varying temperature and behaviors that occur when particular metals are cooled to very low temperatures. The idea of materials electrical resistance being altered by change of temperature is tested with running a current through a metal while the metal is being cooled inside a cryostat, and measuring the resistance of the material as the temperature decreases. This paper will also discuss atomic force microscopy (AFM) in regards to the operations and techniques used to measure various roughness properties of materials.

208A-U. Decision-Making in Noisy Brain Circuits. Kylie McClanahan, Woodrow Shew. *Physics, University of Arkansas, Fayetteville, AR 72701.*

How the brain processes input from the senses depends crucially the collective interactions among large networks of neurons in the cerebral cortex. One important property of how neural networks respond to input is dynamic range, which quantifies the range of input intensities that lead to distinguishable responses. Recent studies suggest that dynamic range is maximized when the interactions among neurons in the network are tuned to a special regime, called criticality. However, these studies have averaged over many repetitions to allow for easier calculation of dynamic range. This is unrealistic, as the trial-to-trial variability is high at criticality and the brain does not have the luxury of averaging over thousands of repetitions. This begs the question: is criticality still optimal if variability is accounted for? Using Signal Detection Theory, I am researching this question using a computational model. We find that criticality does not allow for optimal distinguishing between two stimuli. Instead, we find that a slightly subcritical state is best.

208B-U. Changes in Elasticity of Rat Bones Exposed to Simulated Microgravity and Radiation. Lawrence M. Benzmiller, Hayley N. Heacox, Rahul Mehta, Azida Walker. *Department of Physics and Astronomy, University of Central Arkansas, Conway, AR 72035,* M. Dobretsov, *Department of Anesthesiology, UAMS, Little Rock, AR 72205,* P. Chowdhury, *Department of Biophysics and Physiology, UAMS, Little Rock, AR 72205.*

This research aims to study the changes in elasticity of rat bones, studied under space-like conditions of simulated microgravity and cosmic radiation. Specifically, the leg bones (tibia and femur) were bent with an applied force, and the corresponding strain was measured. The bones were then cross-sectioned. Microgravity was simulated through hind-limb suspension (HLS) of the animals for two weeks before they were sacrificed. Cosmic radiation was simulated via x-ray radiation. A 2.50 GY dose was administered at five-day intervals, 0.50 GY per dose, over 30 days. The non-radiated and/or the unsuspended animals provided the control data. A LASER-based bending setup (Cantilever) enabled measurements of the elasticity of the leg bones. A three-point bending technique with a force sensor to measure applied forces and a stepping mechanism with precise increments allows for an additional measurement of the elasticity. In both methods, analysis of a graph of stress versus strain was used to determine the elastics modulus of the bones. Assuming that the leg bones can be treated as a cylindrical shell, Euler-Bernoulli beam theory can be applied to estimate the Young's modulus for the leg bones. Analysis of results clearly point to a less elastic nature of leg bones exposed to HLS compared to leg bones that were not suspended. In addition, the trend of the stress versus strain graph (beyond the linear range) indicates a substantially lower breaking point for HLS leg bones. Similar results from the cantilever and three-point bending methods support this conclusion. The elastic modulus indicated a weakening of the bones under space-like conditions of microgravity. The changes were even greater when radiation effects are taken into account. †Supported by a grant from Arkansas Space Grant Consortium.

209A. A Hierarchical Task Analysis of Virtual Arthroscopic Tear Diagnosis and Evaluation Platform (VATDEP). Alexander Yu, Doga Demirel, Tansel Halic, Sinan Kockara, Jake Farmer, Matthew Martens, Ahmadi

Shayyar, Larry J. Suva. *Computer Science, University of Central Arkansas, Conway, AR 72035.*

Arthroscopy is a minimally invasive procedure for diagnosis and surgical treatment of a joint disorders[1]. Training for such a procedure is challenging due to limited field of view, constrained instrument motions and unintuitive hand-eye coordination [2]. Conventional methods of training for these surgeries such as cadavers, mannequins, apprenticeship model have several deficiencies as high cost and limited in use, not-realistic or very risky approach. In contrast, Virtual Reality (VR) based surgical simulators could offer a low-cost, realistic risk-free training and assessment platform where the trainees can repeatedly perform tasks and receive quantitative feedback on their performance. These qualities allow for improved operating room (OR) performances and reduce the learning curve [3]. In our ongoing study, we are developing a virtual arthroscopic rotator cuff repair surgery simulator. One of the most critical steps of developing such a VR simulator is the derivation of a Hierarchical Task Analysis (HTA). We developed HTA for the rotator cuff surgery that breaks down the procedure into a hierarchy of tasks and subtasks to describe each step. We expanded HTA with examining each step and defined a performance metrics specific to the rotator cuff. In this work, we present a detailed HTA with surgery metrics and common pitfalls/errors that will be the basis for the validation studies of VR simulator for quantitative evaluation of the surgery performance. References [1] R. Treuting, "Minimally Invasive Orthopedic Surgery: Arthroscopy," Ochsner J., vol. 2, no. 3, pp. 158–163, Jul. 2000. [2] S.-R. Lyu, Y.-K. Lin, S.-T. Huang, and H.-T. Yau, "Experience-based virtual training system for knee arthroscopic inspection," Biomed. Eng. OnLine, vol. 12, p. 63, Jul. 2013. [3] M. P. Fried, R. Satava, S. Weghorst, A. Gallagher, C. Sasaki, D. Ross, M. Sinanan, H. Cuellar, J. I. Uribe, M. Zeltsan, and H. Arora, "The Use of Surgical Simulators to Reduce Errors," in Advances in Patient Safety: From Research to Implementation (Volume 4: Programs, Tools, and Products), K. Henriksen, J. B. Battles, E. S. Marks, and D. I. Lewin, Eds. Rockville (MD): Agency for Healthcare Research and Quality (US), 2005.

209B-U. Homopolar Motor. Shaohui Qiu, Azida Walker. *Physics and Astronomy, University of Central Arkansas, Conway, AR 72035.*

When a current carrying wire is placed in a dipole magnetic field, there will be electromagnetic force acting on it. Fixing the rotation axis, the torque should change with the change of the shape of the wire. To produce the extreme angular acceleration, moment of the inertia of the wire must be considered as well. This research project calculated the torque for a randomly shaped wire, and proved the torque is constant when two ends are fixed using the method of Calculus of Variation. The extreme moment of inertia is also approached in this project. The test of theoretical outcomes is preformed with building the system using Solidworks, and 3D printer. The main materials that are used are copper wire and copper disk, cylindrical magnetic, and batteries. The final result will give the shapes with different length limits wire that will produce the maximum and minimum angular accelerations.

210A-U. Experimental Measurements of Chaotic Circuits. Douglas Roisen, Paul Niyonkuru, Stephen Addison. *Physics and Astronomy, University of Central Arkansas, Conway, AR 72035.*

Precision measurements were made on electric circuits that are equivalent to differential equations of increasing complexity. Component values were varied to produce chaotic oscillations in these circuits. Component values that produced period doubling bifurcations were recorded and the chaotic regions were mapped. The methodology for making these measurements will be described. Ongoing efforts to investigate a family of third order chaotic differential equations will be described.

210B-U. Potential Differences in Problem Solving When Using Different Textbooks. Charles Bertram, Andrew Mason. *Physics and Astronomy, University of Central Arkansas, Conway, AR 72035.*

In the spring 2015 semester the College Physics series of courses switched to "College Physics" by Etkina, Gentile, and Van Heuvelen which is a textbook that takes a specific focus in developing problem solving skills. With this project we hope to show that there is a difference in problem solving when the course uses "College Physics" instead of the textbook used prior to Spring 2015, "Physics: 9th Edition," by Cutnell and Johnson. Audio-visual data and written artifacts have been collected that demonstrate group-problem solving during a pre-lab context rich problem. This data is being analyzed for trends in the frequency of problem solving strategies that were used to solve a similar problem during the spring 2014 (with "Physics: 9th Edition") and spring 2015 (with "College Physics") semesters. If the frequencies of epistemic games across the two semesters are determined to be significantly different from each other then we can say that there is a difference in trends in problem solving when using different textbooks.

211A-U. Gaining Educational Perspective on Inquiry Based Learning from Math and Science Teachers in Central Arkansas. Cassandra Lange, Andrew Mason. *Physics and Astronomy, University of Central Arkansas, Conway, AR 72035.*

STEMteach at The University of Central Arkansas is a program that was made available to students starting the fall of 2012 and is designed to allow students pursuing a STEM (Science, Technology, Engineering, and Mathematics) major to receive a minor in education. As a replication from the Uteach program at The University of Texas at Austin, STEMteach focuses on the creation and implementation of inquiry based math and science lessons. A study is being conducted to gather and analyze information on the educational views regarding inquiry based teaching from mentor teachers who allow STEMteach students to do fieldwork in their classroom. Understanding the perspective of mentor teachers on inquiry based lessons will help the STEMteach program at UCA grow and improve. Key questions about inquiry in the classroom are being answered in an online survey by math and science teachers around the Central Arkansas region. When all the data is collected, the participants will be able to better understand how the mentor teachers support, discuss, and practice inquiry based teaching within their classroom. If the data shows a lack of support for inquiry in math and science lessons, then the program will be able to make efforts to help current teachers understand and implement inquiry lessons by creating professional development workshops for mentor teachers.

211B-U. Measuring The Elasticity of Rat Bones. Fawzi Alzahrani, Rahul Mehta, Azida Walker. *Physics and Astronomy, University of Central Arkansas, Conway, AR 72035.*

Bones like any material in the nature as they have resistance when they are been subjected to external forces that deform their shape and change their volume. Bone material has an elastic modulus that resist change of length and shape and when stress removed, the bone get back to original shape. My research is to use rat bones and subject them to varying forces and measure their bending parameter. We changed the bone orientation relative to cross section of the bone and use the forces again to measure the elastic modulus. This was done using different bones. The actual bending set up (Cantilever) used mirrors and laser beam. Statistical inference of the data can be analyzed and mathematical model can be built to find a relationship between the elasticity modulus of the bones and the forces applied with other variables (the cross section, the weight, the orientation of the force and the length). Supported by Arkansas Space Grant Consortium.

212A. Optical Characterization of Si-based Ge1-xSnx Alloys with Sn Compositions up to 12%. Eleni-James Becton, Wei Du, Mansour Mortazavi, Sattar Al-Kabi, Sayed Amir Ghetmiri, Hameed A. Naseem, Shui-Qing Yu. *Physics, UA Pine Bluff, Pine Bluff, AR 71601.*

Silicon (Si) photonics is one of the interesting topics in the infrared device applications. Fabrication of cost effective and high-efficient Si-based emitters that can cover the short wave and mid- infrared range of spectrum is desired for Si photonics and optoelectronic industry. That range of spectrum is important for some opto-communication, and also military applications. Currently, emitters from group III-V compounds, such as GaAs and InGaAs are widely used for that range of spectrum; however, their high cost and also incompatibility with Si complementary metal- oxide semiconductor (CMOS) process is still a challenge to deliver a cost effective device to the market. Ge is considered as a pseudo-direct bandgap material, because the difference between the direct and indirect bandgap of Ge is only 0.140 meV. Another method that has been analyzed and studied is providing GeSn alloy by adding Sn to Ge. In this technique, increasing Sn composition results in bandgap shrinkage to GeSn alloy ultimately it provides a direct bandgap GeSn material. In this research, we plan to study the bandgap of GeSn materials with different Sn compositions using temperature-dependent photoluminescence (PL) measurement, along with Raman Spectroscopy. GeSn samples with Sn composition of $x > 10\%$ will be inspected under these optical measurements.

212B. Temperature dependence of nGaAs quantum dots. Luis Delgado, Bamidele Odalayo Olaleye, Mansour Mortazavi, Vasyl P. Kunets, Vitaly Dorogan, Gregory Salamo. *Physics, UA Pine Bluff, Pine Bluff, AR 71601.*

The field of Nano-Science has made a lot of progress in recent years. Now it has dominated many fields of science such as physics, biology, chemistry, and many more. However, there is still no reliable theoretical method to guide the experimental outcome. So, most of the current results depend on the trial and error; and testing of the outcome. In this research, we are focusing on the temperature dependency InGaAs quantum dots. The indium quantum dots are grown on GaAs substrate in a molecular Beam Epitaxy (MBE) by self-assembly method, and characterized by photoluminescence (PL) means with the collaboration of Nano-Science Institute of the University of Arkansas. PL is a non-destructive optical method used to characterize the materials which can be with many variable factors such as density of the dots, temperature, layers of the growth, etc. However, here, we are concentrating on the temperature dependency which shows the change of the bandwidth of photon emissions due to the noise in higher temperatures. We expected that throughout these experiments, it is possible to develop more energy efficient, faster semiconductor devices to be used in electronics, lasers, and in medicine in the future.

Alphabetical Index of Presenters

Presenter Name	Session	#
Abdullah-Al Mamun, Md.	B	205
Abraham, Gabrielle	Oral Physics	3:50
Agarwala, Neva	A	0:00
Alismail, Hanan	A	32
Alzahrani, Fawzi	B	211
Anderson, Quinton	Oral Biology	4:20
Apala, Elizabeth	Oral Physics	4:20
Ascone, Anthony	A	11
Banh, Bryan	B	8
Barber, Eric	A	118
Becton, Eleni-James	A	212
Beeman, Rachel	B	202
Benecyo, Jean Eudes	B	110
Bertram, Charles	B	210
Black, William	A	16
Blank, Marshal	B	12
Boakye, Jeffrey	B	3
Bond, Logan	A	109
Bonea, Ashley	A	14
Bradshaw, Jace	Oral Biology	3:20
Brown, Haley	B	28
Brown, James	B	13
Brown, Joel	B	7
Brown, Susie	B	4
Bullock, Cody	B	39
Caro, Andres	A	105
Chen, Jing	A	1
Clem, Oktawia	A	116
Clement, Ethan M.	B	42
Cochrane, C. Skyler	Oral Chemistry	4:20
Coelho, Isadora L.	A	31
Cole, Brian	B	104
Cossio, Osvaldo	A	35
Cox, Emma	A	29
Cruz, Sarah	B	15
Cummins, Morgan	A	18
Daiber, Trent	B	40
Daniel, Harrison	A	38
Davis, Rebekah	B	21
Deere, Thomas	B	30
Delgado, Luis	B	212
Demaree, Katherine	Oral Chemistry	4:05
Deng, Ying	A	201
Dishuck, Carolyn	B	112
Dodd, Andrew	A	15
Ebijoyeldhas, Miracline	B	5
Eichhorn, Angela	B	2
Eledge, Michael	A	2
Ellis, Jacob	B	33
Feather, Kyla	A	20
Fletcher, William	A	101
Fredrickson, Samantha	A	12
Frogoso, Kristina	B	32
Fuller, Alexis	A	104
Gadila, Shiva	B	9
Gasser, Joseph	A	39
Givler, John	B	22
Goda, Momoka	A	119
Gongola, AlleaBelle	B	17
Granderson, Stephen C.	B	31
Gregory, Bryana	A	3
Grimes, Trey	A	205
Ha, Duy	Oral Chemistry	3:35
Hale, Christian	B	201
Hall, Corbett	B	1
Hall, Nathanael	B	121
Hall, Yves Saint Damien	B	16
Hatvany, Jacob	B	103
Hauptman, Gina	B	36
Hayden, Chad	A	24

Heacox, Hayley	B	208
Hegi, Allie	A	111
Hernandez, Jose	A	13
Heslep, Sydney	B	109
Hicks, Zachary	B	120
Higgins, Jake	B	105
Hill, Amber	B	34
Hilliard, Newton	B	101
Honda, Takahiro	B	116
Hossain, M.D.	B	206
Housh, Kurt	A	106
Howard, LaFreda	B	27
Hughes, Heidi	A	17
Hunley, Jack	A	21
Hutchison, Rachel	A	121
Inabnet, Stephanie J	A	103
Jahan, Sinthia	A	34
James, C'Asia	B	35
Jennings, Matthew	A	27
Jones, Dan	Oral Physics	4:35
Jones, Destiny	B	25
Kaufman, Quinton	A	41
Kinney, Ryan	A	8
Kizzire, Dayton	A	204
Lamanilao, Gene	A	114
Lange, Cassandra	A	211
Lee, Taylor	A	4
Leuty, Zach	Oral Physics	4:05
Mahmood, Syed Raza	A	30
Makaraci, Pelin	B	11
Malatesta, James	B	20
Manoharan, Anishkumar	B	29
Martindale, John	B	26
May, Jeffery	B	6
McCarver, Addison	A	37
McClanahan, Kylie	A	208
McDaniel, Elizabeth	A	40
McReynolds, Jeanita	A	7
Meece, Trevor	A	110

Menie, Melissa	B	14
Miller, Hannah	B	118
Mills, Logan	A	120
Mohite, Shilpa	A	10
Morris, Mallory	A	112
Naceanceno, Kevin	A	102
Niggemann, Kristina	A	107
Niggemann, Nick	Oral Chemistry	3:50
Olawoyin, Olamide	Oral Biology	3:50
Orona, Maurisa	A	203
Padgett, Addie	B	108
Petty, Jackson	A	122
Pham, Krystal	B	41
Phomakay, Raynin	Oral Chemistry	4:35
Pinckney, Calli	A	113
Popis, Snow	A	108
Pruitt, Mitchell	A	28
Puppala, Krishna	B	204
Qiu, Shaohui	B	209
Quilao, R.J.	A	22
Rahmatallah, Yasir	B	24
Reichert, Marie C.	B	38
Ritter, Abby	Oral Chemistry	3:20
Robinson, Cynthia	B	115
Roisen, Douglas	A	210
Romo, Ricardo	A	207
Rose, Justin	A	19
Rwamuza, Enock	B	122
Saimani, Uma	B	10
Schmidt , Jami	A	25
Shaffer, Cullen	Oral Biology	3:35
Soden, Daniel	B	203
Sorrells, Shelby	A	202
St. John, Seth	A	26
Stanley, Julie	B	19
Stone, Portia	A	117
Strong, Joshua	A	36
Terry, Logan	B	37

Thibado, Jordana	B	117
Thomas, Jackie	A	42
Thomas, James	Oral Physics	3:35
Thornburgh, Savannah	B	119
Tran, Huyen	B	106
Tripod, Morgan	Oral Biology	4:05
Umfress, Alan	A	5
Wade, Kahlil	B	207
Wann, Jarrett	A	6
Washington, Taylor	A	33
Webb, Autumn	B	114
Webb, Darryl	Oral Physics	3:20
White, Don	B	23
White, Don	A	115
Whitlock, Sara	Oral Biology	4:35
Wilmsen, Sara	B	102
Wilson, Danielle	B	111
Wilson, Kayla	B	113
Wood, Lindsey	A	23
Woodman, Sara	A	9
Yu, Alexander	A	209

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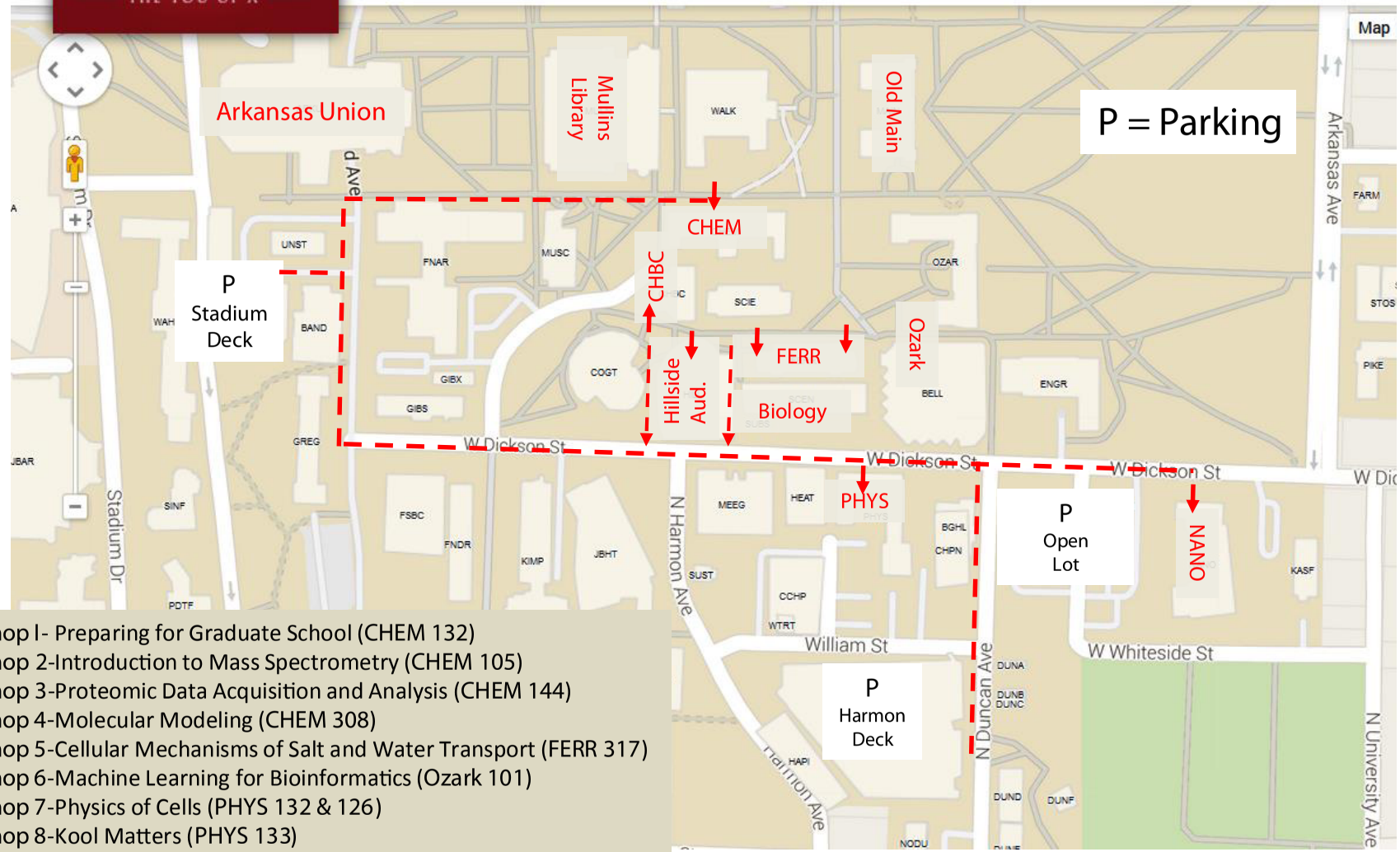
INBRE Workshops: 10:30 -11:45



Workshop I- Preparing for Graduate School (CHEM 132)
Workshop 2-Introduction to Mass Spectrometry (CHEM 105)
Workshop 3-Proteomic Data Acquisition and Analysis (CHEM 144)
Workshop 4-Molecular Modeling (CHEM 308)
Workshop 5-Cellular Mechanisms of Salt and Water Transport (FERR 317)
Workshop 6-Machine Learning for Bioinformatics (Ozark 101)
Workshop 7-Physics of Cells (PHYS 132 & 126)
Workshop 8-Kool Matters (PHYS 133)
Workshop 9-Nano Building Tours (NANO 105)
Workshop 10-Physics Lab Tours (PHYS 129, 245, 124, 128/130, 111)

– <u>Notes</u> –