Arkansas INBRE Research Conference

2022

Contents

October 21-22

Arkansas INBRE Research Conference

Arkansas IDeA Network of Biomedical Research Excellence

Schedule of Events

Friday, October 21, 2022

Graduate Hotel & Fayetteville Town Center

12:00 – 1:30 p.m.	Registration – Graduate Hotel Atrium, Second Floor Information Tables
1:30 – 1:45 p.m.	Opening Address: Krishan Arora, Ph.D., Branch Chief, Networks and Development Programs Branch, Division of Research Capacity Building, NIGMS
1:45 – 3:15 p.m.	Invited Faculty Platform Plenary Session – Graduate Hotel
3:45 – 5:15 p.m.	Invited Student Platform Sessions – physics, chemistry, biology – Graduate Hotel
5:15 p.m. - 6:15 pm	Student and Faculty Reception and Networking – Graduate Hotel
6:30 p.m.	Banquet – Fayetteville Town Center
7:15 p.m.	Keynote Seminar: "Mapping the Inner World of Cells" **Bo Huang**, Ph.D., University of California San Francisco – Fayetteville Town Center

Saturday, October 22, 2022

University of Arkansas Campus

7:30 a.m.	Breakfast – Hillside Auditorium
7:45 a.m.	Session A poster set up
8:00 a.m.	Poster Session A (posters come down at 9:00 a.m.) – Hillside Auditorium
9:00 a. m.	Session B poster set up
9:15 a.m.	Poster Session B (posters come down at 10:15 a.m.) - Hillside Auditorium
10:30 a.m.	Workshops– assigned locations
11:45 a.m.	Awards and closing session – Hillside Auditorium 202

Registration Information

The INBRE registration desk will be open:

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

Lodging will be at the Graduate Hotel, 70 N. East Avenue, Fayetteville, AR 72701 and at the Holiday Inn Express, 1251 N. Shiloh Drive, Fayetteville, AR 72704. The list of schools staying off-site will be rotated each year.

Parking:
Friday parking is complimentary in the Municipal Parking Garage, third level only (first level card access for registered guests of the Graduate Hotel). Saturday parking is free on the UA campus in designated yellow, green, and blue sign lots. Please note that lot sign designation takes precedence over map designation.

Arkansas INBRE

https://inbre.uams.edu/

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.

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

Ines Pinto and **Christian Tipsmark;** biological sciences
Jingyi Chen, Megan Parette, Feng Wang, and **Ying Yuan;** chemistry and biochemistry
Reeta Vyas; physics

INBRE Steering Committee

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Jerry Ware, Ph.D., UAMS, PC & DRP Program Director
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Jeffery Massey, Ph.D., Harding University
Newton Hilliard, Ph.D., Arkansas Tech University
Lance Gibson, Ph.D., Harding University
Samar Swaid, Ph.D., Philander Smith College
Mi-Seon Seong, Ph.D., Central Baptist College

Staff

Diane McKinstry, UAMS, Program Coordinator
Caroline Miller Robinson, UAMS, Business Manager
Megan Parette, UAF, Outreach Coordinator

Participating Institutions

Arkansas State University, Jonesboro
Arkansas Tech University, Russellville
Belmont University, Nashville
Central Baptist College, Conway
Harding University, Searcy
Henderson State University, Arkadelphia
Hendrix College, Conway
John Brown University, Siloam Springs
Lyon College, Batesville
McKendree University, Lebanon
Missouri State University, Springfield
Northeastern State University, Tahlequah
Northwest Arkansas Community College, Bentonville
Okayama University, Japan
Ouachita Baptist University, Arkadelphia
Pittsburg State University, Pittsburg
Rhodes College, Memphis
Southern Arkansas University, Magnolia
University of Alkhairaat, Indonesia
University of Arkansas, Fayetteville
University of Arkansas, Fort Smith
University of Arkansas, Little Rock
University of Arkansas, Monticello
UA Medical Sciences, Little Rock
University of Arkansas, Pine Bluff
University of Central Arkansas, Conway
University of the Ozarks, Clarksville

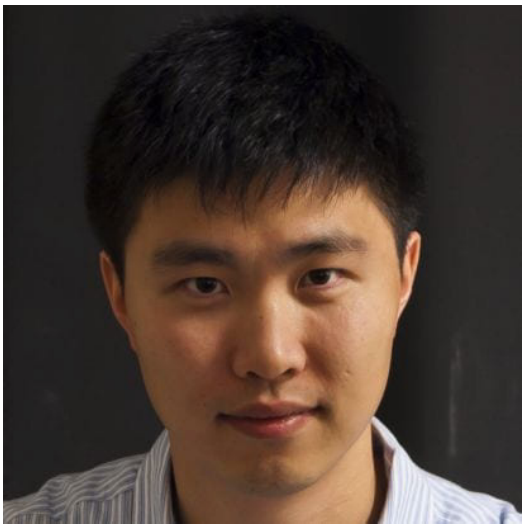
Featured Speaker

Friday, 7:15 p.m., Fayetteville Town Center

Yong Wang, PhD (Dept. of Physics, UAF)

Mapping the Inner World of Cells

Bo Huang, PhD



Department of Pharmaceutical Chemistry

Department of Biochemistry and Biophysics

University of California, San Francisco

Cellular processes are orchestrated by a large number of biomolecules in a spatially and temporally coordinated manner within a tiny volume. To uncover the underlying organizational principles and their functional relevance, we take microscopy visualization as the primary approach to systematically map their spatial localization, temporal dynamics and activity profiles. By combining small tags engineered from split fluorescence proteins and CRISPR/Cas9-mediated gene editing, we have enabled large-scale tagging of endogenous proteins in human cell lines for both microscopy visualization and biochemical analysis. Characterization of their live cell dynamics using epi-illumination light-sheet microscopy reveals intriguing phase condensation and decondensation behavior of many proteins during the cell cycle. We have further developed the deep-learning framework to connect cellular images of proteins to their amino acid sequences.

Faculty Plenary Talks

Friday, 1:45 p.m. – 3:15 p.m., Graduate Hotel

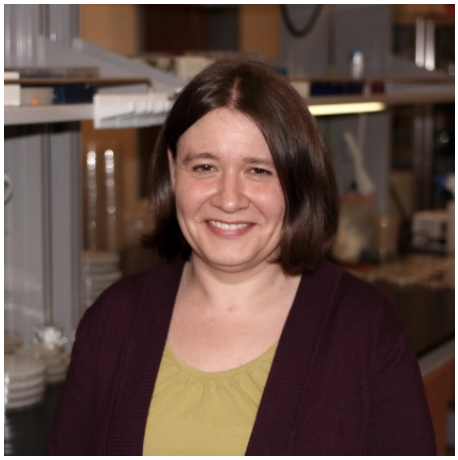
Hiro Nakamura, PhD (Dept. of Physics, UAF)

Biology

The social amoeba microbiome and bacterial symbiont dynamics

Tamara Haselkorn, PhD

University of Central Arkansas



Amoebae are natural predators of bacteria, feeding on them via phagocytosis. Bacteria that can resist this process are primed for intracellular adaptation, potentially becoming pathogens or symbionts in a variety of organisms. The social amoeba, *Dictyostelium discoideum* is a common model organism for studying bacterial-eukaryotic interactions, yet only recently has its natural microbiome begun to be described. I will discuss work my lab has done characterizing the microbiome of *D. discoideum* and other species of social amoebae. We have found that while there are many transient bacterial associates, the core of the microbiome is made up of bacterial symbionts in the genus Paraburkholderia and the phylum Chlamydiae. We are tracking these bacterial symbionts through natural populations of social amoebae in Arkansas. Parburkholderia are the most well-characterized symbionts and we have found that they infect primarily D. discoideum at high levels, dominating the microbiome, although their effects on their amoeba host are unclear. More common among other species of social amoeba are Chlamydiae bacteria. While Chlamydiae bacteria are well-known obligate intracellular parasites that have been characterized in several hosts, environmental DNA sequencing has recently uncovered a huge diversity of these bacteria prevalent in wide variety of environments, for most of which their hosts are unknown. We have discovered several novel lineages of Chlamydiae bacteria that are widespread among different social amoeba species. While their roles in host populations are also unclear, we are finding intriguing patterns of host specificity that suggest that this is a long-term co-evolved relationship that could serve as a useful model for characterizing host-bacterial interactions in this important phylum.

Chemistry

Tunable combination ionic nanomedicines: Synthesis, characterization, and biomedical application

Noureen Siraj, PhD

University of Arkansas at Little Rock

Ionic liquids (molten salts with melting points below 100 ºC) have been explored extensively in the last two decades due to their outstanding properties and wide scope of applications. Recently frozen ionic materials (solid at room temperature) are getting tremendous attention due to their ability to form stable nanoparticles. Ionic nanomaterials have been studied recently for multiple applications due to their tunable characteristics. One can easily achieve the desired characteristics by varying counterions and by tailoring the morphology of ionic nanomaterials. This presentation is mainly focused on the synthesis and characterization of frozen ionic materials and their nanomaterials for biomedical applications. By tuning the cation and anion, ionic materials with dual toxicity mechanism are synthesized. These ionic materials are converted into nanoparticles of tunable shape, size, and surface characteristics. Detailed photophysical characterization using absorption and fluorescence spectroscopy revealed their improved therapeutic potential. The cellular uptake, cytotoxicity and endocytosis mechanism of combination nanomedicines derived by ion pairing will be discussed. Examination of these results revealed that ionic nanomedicine exhibited better performance as compared to their respective parent compounds.

Physics

Exploring protein-DNA interactions using single molecule fluorescence resonance energy transfer (smFRET)

Julie Gunderson, PhD

Hendrix College

Protein-DNA interactions play central roles in many cellular processes that are important in the biogenesis of disease. To understand the functions and mechanisms of protein-DNA interactions, it is useful to study the conformational changes that occur when proteins interact with DNA substrates. Fluorescence resonance energy transfer (FRET) is a physical process that can be used to detect distance changes in biological macromolecules in the 20-80 Å range. On the ensemble level, FRET can be used to detect the presence of conformational changes, but distributions of individual conformers and short-lived conformers are lost in the ensemble average. In addition, it is difficult to obtain meaningful kinetic data via ensemble FRET due to non-synchronizable dynamics in heterogeneous populations. Single-molecule fluorescence resonance energy transfer (smFRET) measurements can readily determine the distribution of several conformations, not just the average of the conformations, making it possible to identify rarely visited and/or short-lived states. In addition, smFRET can be used to observe the conformational dynamics of individual protein-DNA interactions, and this data can be analyzed to obtain detailed information on the kinetics of the system without the need for synchronization. This presentation will include a discussion of the theory and design of smFRET experiments and will explore ways in which this technique has been used to study protein-DNA interactions.

Awards

Awards: Prizes will be awarded to the top oral and poster presentations by undergraduate students in each discipline. The awards will be presented Saturday at 11:45 a.m. in Hillside Auditorium Room 202.

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 talks and posters with undergraduate participation, and where a sole designated presenter is an undergraduate student, will qualify for awards.

Student Oral Presentations

Undergraduates will give 12-minute oral presentations followed by 3 minutes Q&A from 3:45 p.m. to 5:15 p.m. on Friday. All talks will take place at the Graduate 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

Brodie Payne Ballroom C-D
Xuan (Shaine) Zhuang, PhD, Chair

03:45 PM. Jax Gill

Henderson State University
Expression Levels of the Anti-Apoptotic BCL2 Family Explain why Primary Effusion Lymphoma Cell Lines Selectively Depend on MCL1 for Survival

04:00 PM. Nathan Rives

University of Arkansas at Fayetteville
Diverse Origin and Convergent Evolution of an Essential New Gene

04:15 PM. Harley Hines

Arkansas Tech University
Drosophila Adult Eye Development Depends on Tsh and CtBP Direct Interaction

04:30 PM. Madison Purifoy

University of Arkansas at Pine Bluff
Chymase Inhibitory and Free Radical Scavenging Properties of Sweet Potato

04:45 PM. Aspen Huseman

Henderson State University
Blue Goo and Petroleum Ponds: The Unique Microbial Ecology of Two Tennessee Cave Systems

05:00 PM. Dominic Dharwadker

University of Arkansas at Fayetteville
Deletion in the Promoter Element of Vacuolar H+ Translocating Pyrophosphatase (V-PPase) Impacts Germination and Seedling Growth in Rice by Inhibiting Sucrose Formation and Acidifying the Cytoplasm

Chemistry Oral Presentations

Brodie Payne Ballroom A
Bin Dong, PhD, Chair

03:45 PM. Scout Weatherford

Arkansas State University
Electrochemical study of Recombinant Mn Peroxidase from Corn on Disposable Screen Printed Biosensor to Detect Glucose

04:00 PM. Hope Murphy

Ouachita Baptist University
A New Synthesis for Modifying Alginate for Use in Biomedical Applications

04:15 PM. Emma G. Gruss

Rhodes College
Synthesis of Catechol Derivatives Substituted at the 6-Position

04:30 PM. Arisha Ishtiaq

University of Arkansas at Little Rock
Chemotherapy-Photo Thermal Therapy (Chemo-PTT) Combination Ionic Nanomedicines for Cancer Treatment

04:45 PM. Walker Hendricks

Harding University
A Novel Plate-Based Method for Proteomic Analysis of GeLC-12 Protein Samples

05:00 PM. Thomas J. Caldarera

Hendrix College
Agonists Stabilize Multiple Activated Cannabinoid CB1 Receptor Conformations During Molecular Dynamics Simulations

Physics Oral Presentations

Trammel Room
Woodrow Shew, PhD, Chair

03:45 PM. Jessica Fink

Missouri State University
The Effects of Magnetic Field on Bacterial Motility

04:00 PM. Arantxa Pardue

Belmont University
Flux Growth of hBN Single Crystals

04:15 PM. Jeremy Choh

Hendrix College
Optimization of Quantum Device Fabrication for the MonArk Quantum Foundry

04:30 PM. Skyler Gulati

University of Arkansas at Fayetteville
VUV-Light Generation Using Multiple Non-Linear Effects Through Hollow-Core Fiber

04:45 PM. Janae Tirado

Southern Arkansas University
The Role of 3D Printing in Biomedical Applications

05:00 PM. Ashley Allen

University of Arkansas at Pine Bluff
Using Liposomal Models to Study the Binding Kinetics of Cytosketal Proteins Inside of Bacteria

Poster Sessions

Poster set-up begins at 7:45 a.m. on Saturday
Hillside Auditorium

Session A – 8:00 to 9:00 a.m.
Session B – 9:15 to 10:15 a.m.

Presenters are expected to be present during the scheduled time. Business or business casual dress is encouraged. Please set up your poster 15 minutes before the start of each poster session.

Workshops

Saturday, October 22 10:30 am -11:30 am
Various locations on the U of A campus
Registration for Workshops will be at the Conference Registration Table

Workshop 1: The NIH R15 and SuRE R16 Mechanisms
***Jerry Ware, PhD**, Professor of Physiology and Biophysics, UAMS*
Location: Hillside 206

The NIH Academic Research Enhancement Award (AREA) program supports faculty research at campuses that have not received significant NIH funding in the past. This workshop highlights unique factors that distinguish the R15 mechanism from other RPG mechanisms, such as the RO1, where scientific merit and the investigators are major score driving criteria. New funding opportunities, the Support for Research Excellence (SuRE) Program and SuRE-First Program (R16s) have been released with the first-ever submission deadline of September 2021. Comparing the 2 FOAs and appropriateness for PUI faculty to apply for either will be discussed. Both the R15 and R16 have three main goals, ***1)*** to support meritorious science ***2)*** to strengthen the institution's research environment, and ***3)*** to expose students to research. Thus, special consideration for how/where to incorporate all three goals into the application will be discussed. The presenter has been part of recent NIH R15 Special Emphasis Panels and will share experiences with a goal of benefitting interested faculty and providing a perspective on how to write a competitive AREA application. Discussions will include what reviewers are "coached" to look for during peer review and some of the most common mistakes that can temper reviewer enthusiasm.

Workshop 2: Cryo-electron Microscopy
***Dylan Girodat, PhD**, Dept. of Chemistry and Biochemistry, UAF*
Location: GEAR 101
Participant capacity: 12

We are in the era of a resolution revolution in cryo-electron microscopy (cryo-EM) that started in the early 2010s through advancements made in electron microscopy technology. Cryo-EM allows for the near-atomic resolution determination of large macromolecular structures such as those of ribosomes, viruses, or splicesome. More recent advances have allowed for the resolution of molecular complexes to atomic resolution, where individual atoms can be directly visualized. One of the main utilities of cryo-EM is the ability to solve structures for molecules that are highly mobile (dynamic) or too large to be solved by other techniques such as X-ray crystallography or NMR. Furthermore, structures of complexes in heterogeneous mixtures can be solved through 3D classification techniques.

This workshop will go over the fundamental theory for how a 3D electron density can be generated from movies of particles. By the end an attendee will be able to have working knowledge of the workflow for single particle 3D reconstruction. As an example, the workshop will go through the single particle reconstruction of the large protein Apoferritin.

Workshop 3: Preparing for Graduate School
Colin Heyes, PhD, *Dept. of Chemistry and Biochemistry, UAF*
Location: CHEM 132

This workshop is targeted towards under-graduate students who are considering graduate school as a career. Topics to be discussed will include graduate school expectations and how to prepare for and select the right graduate school and program for you. A panel of faculty and graduate students will be available to share their tips, strategies, insights, and practical advice. We conclude with a Question and Answer session, with the possibility of breaking out into smaller groups based on specific interests.

Panelists:
Julie Stenken, Graduate student advisor, Dept. of Chemistry and Biochemistry, UAF
Kusum Naithani, Graduate coordinator, Dept. of Biological Sciences, UAF
Adnan Ali Khalaf Alrubaye, Associate Director of Graduate Program in Cell and Molecular Biology, UAF
David Ussery, Helen Adams & the Arkansas Research Alliance Chair in Biomedical Informatics, UAMS
Amanda Raley, Graduate student of Chemistry and Biochemistry, UAF
Cody Brazel, Graduate student of Chemistry and Biochemistry, UAF
Ayanna St. Rose, Graduate student of Biological Sciences, UAF
Rinalda Proko, Graduate student of Cell and Molecular Biology, UAF

Workshop 4: Molecular Modeling
Peter Pulay, PhD, *Dept. of Chemistry and Biochemistry, UAF*
Location: Union Computer Lab (Team Room)
Participant capacity: 8 active participants (more people can listen but there are no computer seats for them)

This workshop will demonstrate the use of small or personal computers to model molecules, calculate their geometry, infrared and Raman spectra, relative stability, NMR chemical shifts and other properties.

The software has two components:
(1) A Graphical User Interface allows the construction of molecules and, after the calculation, show the results, and display of molecular orbitals and electron density.
(2) A Quantum Mechanical program allows the determination of molecular geometries and other properties.

Several such programs are available but most have a fairly steep price. We will use the Parallel Quantum Solutions software developed in Dr. Pulay's group because a free version is available. Calculations will run on a cloud server at the workshop but the same programs can be installed free on Windows, Mac and Linux PCs from Dr. Feng Wang's website. Several examples have been prepared for the workshop but we will probably only be able to finish one. The following projects are available:

1. Singlet and triplet states of methylene, CH_2
2. A strange molecule: SF_4
3. The thermal ring opening of cyclobutene
4. Geometry and NMR chemical shifts of cyclohexene

Workshop 5: XRD New Capability for Art Restoration, Pharmaceutical Development, and Structure Determination of Pharmaceutical Targets Both Small and Large
***Josh Sakon, PhD**, Dept. of Chemistry and Biochemistry, UAF*
Location: CHEM 48
Participant capacity: 10

I strongly encourage you to bring powder samples (kidney stones, dyes, etc.), small molecules (sucrose, tartaric acid, etc.), or macromolecule crystals (lysozyme, cytochrome C, etc.).
The X-ray diffraction system, in the X-ray Core laboratory has played a role in the statewide research efforts in the structure determination of biomolecules. XRD replacement funded in 2021 by NIH will increase the functionality and usability of the system. The new generation of X-ray detector produces higher quality data than what can be done with the older X-ray detector and the software that now comes with the detector/goniometer. The instrument extends the capacity of the instrument from being a system dedicated to protein crystallography to one that is capable of also generating high-quality small molecule results, which can help the core facility to stay at the cutting edge of biomedical research, as well as provide needed service to additional research labs in the state. Let's solve the samples you have. The fundamental theory for XRD and small/macromolecule structure determination will also be discussed. Powder samples can also be analyzed by the instrument. Rigaku's near noiseless solid-state detector will enable the extraction of weak with better confidence from smaller samples than the systems currently used at Smithsonian and Getty Museums. The instrument gained ability to identify pigments from paintings or fresco particles.

Workshop 6: Crystal Growth
***Jin Hu, PhD**, Dept. of Physics, UAF*
Location: PHYS 132 & PHYS Lab 131
Participant capacity: 10

Material science is closely related to our everyday life and the advancement of the modern technology. Synthesize materials is the very first step for fundamental scientific research and technology applications. This workshop will introduce the synthesis of bulk crystals of various important materials.

Workshop 7: Playing with Lasers
***Hiro Nakamura, PhD**, Dept. of Physics, UAF*
Location: NANO 105 & NANO Lab 222
Participant capacity: 15
The workshop will provide hands-on experiences on lasers. We first provide a brief introduction on the type of lasers we use in the lab, and some optical effects such as diffraction. Then participants will move to a physics lab and join a few short demo projects: 1) drilling a hole in a paper or card (feel free to bring one); 2) make a rainbow using grating; 3) attempt to "see" ultrafast laser pulses.

Workshop 8: Brain Science
***Woodrow Shew, PhD**, Dept. of Physics, UAF*
Location: PHYS 133
Participant capacity: 35

We will begin with a brief introduction to how large networks of neurons are responsible for our thoughts, perceptions and actions. Then we will have a fun brain trivia match and a "mind control" contest using the electrical signals of your own brain against your opponent's brain. Don't worry, it all will be quite safe.

Workshop 9: Physics REU and Graduate Application
Reeta Vyas, PhD, Dept. of Physics, UAF
Location: PHYS 134
Participant capacity: 15

In this workshop participants will learn about Physics REU at UA, career options for physics graduates, dos and don'ts of the application process for Physics Graduate Programs in the US – importance of and preparation for GRE, course work, recommendation letters, assistantships, etc.

Workshop 10: Bioinformatics Tools and Systems for Microbial Genomics
***Jeff Pummill**, AHPCC*
Douglas Rhoads, PhD, Cell and Molecular Biology Program, UAF
Location: SCEN 402

Coverage of tools and resources available to researchers on the web, at the Arkansas High Performance Computing Center, and beyond. Examples will be presented from assembly of genomes and phylogenomic analyses of bacterial pathogens. Topics to be covered include sequencing sources, user accounts, interactive desktops, software tools, web sites, and Linux resources.

Workshop 11: CRISPR-Cas9-mediated Targeted Mutagenesis
***Nagayasu Nakanishi, PhD**, Dept. of Biological Sciences, UAF*
Location: FERR 214, 323 and SCEN 122
Participant capacity: 5

CRISPR-Cas9 is a powerful genome editing tool whose applications are rapidly expanding across diverse fields from biomedicine to evolutionary biology. In this workshop, participants will learn how the CRISPR-Cas9 genome editing technology is used to investigate gene function in sea anemones. The hands-on session will involve microinjection of guide RNAs and Cas9 protein into zygotes of sea anemones to generate knockout mutations at a targeted locus.

Workshop 12: AIMRC – High Resolution Assessments of Cell Metabolism
***Timothy J. Muldoon, MD, PhD**, Dept. of Biomedical Engineering, Metabolic Imaging and Spectroscopy Core, Arkansas Integrative Metabolic Research Center, UAF*
***Narasimhan Rajaram, PhD,** Dept. of Biomedical Engineering, Metabolic Imaging and Spectroscopy Core, Arkansas Integrative Metabolic Research Center, UAF*
***Suresh Thallapuranam, PhD**, Dept. of Chemistry and Biochemistry, Arkansas Integrative Metabolic Research Center, UAF*
Location: CHEM 144

The Arkansas Integrative Metabolic Research Center is a NIH-funded COBRE that was established in March 2021 to study metabolism in cells and tissue. As part of the AIMRC, two research cores were established as fee-for-service resources – an imaging and spectroscopy core and a bioenergetics core. This workshop will present the technologies and capabilities available within these two cores for utilization by Universities and industry. The imaging and spectroscopy core currently houses state-of-the-art microscopes that allow high-resolution visualization of cell and tissue structure, function, and biomolecular composition. Two-photon microscopy enables quantification of cellular metabolism through endogenous fluorescence intensity and lifetime of the metabolic coenzymes, NADH and FAD. The bioenergetics core lodges cutting edge technologies to measure various aspects of cellular respiration and real-time metabolic analysis. The Oroboros O2k-FluoRespirometer provides a distinctive high-resolution approach to monitor cellular and mitochondrial respiratory function. In addition, the O2k-FluoRespirometer has the extraordinary capability to measure H2O2 flux, mt-membrane potential, ADP-ATP phosphorylation. Further, the Seahorse XFe8 /24 Analyzers, housed in the bioenergetics core, facilitate the measurement of key cellular functions such as mitochondrial respiration and glycolysis by measuring the oxygen consumption rate and the extracellular acidification rate of live cells. This workshop will present an overview of each technology currently available in the cores, potential applications, and details on how to access or get trained to use them.

Oral Abstracts

Biology Oral Presentations

03:45 PM. Expression Levels of the Anti-Apoptotic BCL2 Family Explain why Primary Effusion Lymphoma Cell Lines Selectively Depend on MCL1 for Survival

Jax Gill, Mark Manzano
Biology, Henderson State University

Kaposi's Sarcoma-associated Herpesvirus causes B-cell lymphoma and primary effusion lymphoma in HIV-AIDS patients. Our previous work showed that these tumor cells are highly addicted to the overexpression of several pro-survival oncogenes, particularly MCL1. MCL1 is a member of the BCL2 gene family, which functions to prevent intrinsic apoptosis and has been implicated in several cancers. Despite the overlapping functions of the BCL2 family, the tumor cells are only dependent on MCL1. Our initial hypothesis was that MCL1 performs non-canonical roles unrelated to apoptosis. However, here we present that this selective addiction is mainly dictated by the expression levels of the gene family. Reanalysis of published RNA-seq data indicates that BCL2 gene family expression is significantly skewed towards MCL1. We postulate that altering these ratios will cause the tumor cells to depend on a different BCL2 gene. We, therefore, individually overexpressed the BCL2 family members using lentiviral vectors in the PEL cell line, BC-1. We assessed how these cell lines resisted cell death triggered by a general apoptotic inducer, staurosporine (STS), and a highly specific inhibitor for MCL1 (S63845, MCL1i). Our results show that overexpression of other BCL2 family members can substantially buffer against the detrimental effects of both STS and MCL1i. BCL2 family members ultimately rescued cell viability and reduced apoptosis as measured by Caspase 3/7 activity. Together our data indicate that the expression levels of the BCL2 family likely explain why the PEL tumor cells are highly addicted to MCL1. More importantly, our results suggest that caution should be taken when considering MCL1i as a single treatment regimen for cancer, as resistance to this class of inhibitor can easily develop.

04:00 PM. Diverse Origin and Convergent Evolution of an Essential New Gene

Nathan Rives
Biological Sciences, University of Arkansas at Fayetteville

Over millions of years, new genes continuously form, leading to the fundamental question of how genetic novelty arises. To understand the process of gene birth and newly evolved traits, it is essential to investigate the evolutionary origins and mechanisms of new genes. The diverse fish antifreeze protein (AFP) provides a unique system for studying new gene and novel function formation, as they have reasonably recent origins, and their lifesaving function of preventing freezing is clearly defined and can be directly linked to natural selection. In this study, we investigate the genomic origin and evolutionary process of type I AFP (AFPI) genes in four distinct fish lineages. We have sequenced the complete genome of two AFPI-bearing species from two lineages and combining the available closely related AFPI-lacking outgroup species and other AFPI-endowed species from public database, we isolated the loci containing AFPI or homologous regions. In each lineage, the AFPI genes from AFPI-bearing species are annotated to show the gene structure, then used to compare against the genome of outgroup species and find the evolutionary precursor and homologous genomic regions. The AFPI genes in the four lineages show dissimilar sequence structure to each other and the loci do not share micro-synteny, suggesting AFPI independently evolved in each lineage. The AFPI genes in AFPI-bearing species have been linked to homologous regions in outgroup species that potentially contain the ancestor sequence. We identified different precursor genes in different lineages and will further deduce

the evolutionary process and molecular mechanism of the new gene birth. This study could provide an example of how novel function arises and advance our understanding of new gene formation.

04:15 PM. Drosophila Adult Eye Development Depends on Tsh and CtBP Direct Interaction

Harley Hines, Hannah Lomax, Mia Ratliff, Raven Newton, Surya Jyoti Banerjee
Biological Sciences, Arkansas Tech University

Organ development in metazoans depends on tight coordination between cell division and cell differentiation. These cellular responses are guided by differential gene expression in the precursor cells of an adult organ. Master transcription factor, with their different molecular partners alternatively expresses different target genes to regulate these cellular responses. For example, Drosophila ortholog of the human Pax6, called eyeless (ey), encodes a paired- & homeo-domain transcription factor associated with brain and eye development both in mammals and fruit flies. Ey regulates cell proliferation of the eye precursor cells, and later promotes retinal differentiation in a context specific manner within the larval eye tissue called the eye disc. During the third instar larval life, a morphogenetic furrow (MF) marks the boundary of between the anterior dividing cells, and posterior neuronal cells in the eye disc. Ey combines with different molecules, and targets specific genes to induce either cell division or retinal cell differentiation. Previous studies have shown that a specific molecular complex that includes Ey, and Teashirt (Tsh), a zinc finger transcription factor, promotes proliferation of the eye precursor cells anterior to the MF. Additionally, the C-terminal Binding Protein (CtBP), a conserved transcriptional co-repressor, is known to limit cell proliferation in the eye disc. Interestingly, CtBP has also been shown to interact with the Ey and Tsh in separate experiments during the eye development. However, experimental evidence is lacking to show if Ey and CtBP, or CtBP and Tsh bind directly with each other. It is predicted that Tsh is likely to bind directly with CtBP through its PxDLS motif. Thus, our hypothesis is- Tsh binds with CtBP by direct physical contact, and mediates the molecular association between CtBP with Ey. Our results indicate that Tsh directly binds with CtBP in vitro using GST pulldown assays, and both binds in the eye disc cells in vivo using co-immunoprecipitation. Furthermore, we have generated recombinant flies to assess the effect of Tsh and CtBP interaction in the cells of eye discs. For example, we have generated recombinant flies with hyper-expression of Tsh anterior to the MF and have found that these flies have no or very small adult eyes. For future study, we will use this recombinant fly to reduce or over-express CtBP, and record further change in the adult eye phenotype to assess the effect of their genetic interaction on eye formation. Further, we will be evaluating the role of such molecular and genetic interaction on the eye precursor cells using immunohistochemistry for molecular markers of cell division and retinal differentiation.

04:30 PM. Chymase Inhibitory and Free Radical Scavenging Properties of Sweet Potato

Madison Purifoy, Sankar Devarajan
Human Sciences, University of Arkansas at Pine Bluff

Hypertension affects 1 in 2 adults in the United States and is more common in non-Hispanic Black adults (54%) than in non-Hispanic white adults (46%). Because hypertension is a severe medical condition that can increase a person's risk of developing other chronic diseases and cause damage to vital organs, there is a national call to action to establish hypertension control. Chymase, a serine protease, upregulation in tissues is a detrimental factor in salt-induced hypertension. Its inhibition by a novel chymase inhibitor drug or foods with chymase inhibitory action reduced high blood pressure. Our study aims to screen the aqueous extracts of different sweet potato varieties, which include Burgundy, Covington, Beauregard, and Orleans, for chymase inhibitory action in vitro. We found that sweet potato Burgundy shows significant chymase inhibitory and free radical scavenging properties compared to other varieties. Findings from this study will have implications for in vivo chymase inhibition using salt-induced

hypertensive mice and may support the translation approaches in human chronic diseases, thus enhancing the quality of life of individuals with salt-sensitive hypertension.

04:45 PM. Blue Goo and Petroleum Ponds: The Unique Microbial Ecology of Two Tennessee Cave Systems

Aspen Huseman, Maya Robles, Mattison Fairchild, Kaitlyn Farr, James Engman, Michael Ray Taylor
Biology, Henderson State University

While most biological communities require solar energy, some relying on chemical energy have been discovered, including those found in deep-sea hydrothermal vents and hypogenic caves. Two of these, Secret Squirrel Cave (SSC) and Blue Lagoon Cave (BLC), are in Cannon County, Tennessee. SSC is a presumptive hypogenic-epigenic system, containing chemolithoautotrophic elements. Deep in the cave is the Petroleum Passage, named for its pervasive petroleum smell. Within it lies a pool containing crude oil-releasing "mini-vents," surrounded by colored bands of sediment. Metagenomic sequencing (16S rRNA) revealed unique microbial taxa, including thermophiles/hyperthermophiles, hydrocarbon degraders, and sulfur, methane, and ammonia oxidizers, similar to known chemolithoautotrophic systems. Observations of unusually high densities of salamanders and millipedes in the passage further support the hypothesis that chemolithoautotrophy is sourcing energy to multiple trophic levels. Stable isotope analysis (12C/13C), however, did not support this hypothesis. For 8 months, a time-lapse photography system captured daily images of pool activity. Assessment of the images and rainfall data from Cannon County could suggest a correlation between vent activity and rainfall. Additionally, a rimstone pool on a fallen boulder in nearby BLC sometimes contains taxa similar to SSC. It is lined with a viscous blue-black material surrounded by white, yellow, and brown jelly-like substances. The "Blue Goo" is suspected to be seasonal. Further genetic analysis in the ponds is proceeding, along with photo documentation in BLC and SSC. The microbes present and water chemistry in the two caves will be compared. Research and future surveys provide insight into microbial species in extreme environments on Earth and may offer a new example of systems previously suggested as potential models for life in subsurface environments on Mars.

05:00 PM. Deletion in the Promoter Element of Vacuolar H+ Translocating Pyrophosphatase (V-PPase) Impacts Germination and Seedling Growth in Rice by Inhibiting Sucrose Formation and Acidifying the Cytoplasm

Dominic Dharwadker, Peter James Gann, Chandan Maurya, Soumen Nandy, Shan Zhao, Vibha Srivastava
Biochemistry, University of Arkansas Fayetteville

Germination and seedling growth in rice relies on the breakdown of starch to generate sucrose in the endosperm. This process is inhibited by inorganic pyrophosphate (PPi). An enzyme, Vacuolar H+ translocating pyrophosphatase (V-PPase), hydrolyzes PPi into inorganic phosphate (Pi) as it translocates H+ from the cytoplasm into the vacuole. Although the enzymatic activity of V-PPase is known, its function in germination and seedling growth is poorly understood. We explored the role of V-PPase in early developmental stages through the regulation of its expression by heat and mutagenesis using CRISPR/Cas9 and investigated how its perturbation affected cytoplasmic pH and starch utilization in germination and growth. In mutagenesis by CRISPR/Cas9, the resulting lines harbored a mutation in one of the four predicted promoter elements, an ATC deletion in GATA. Interestingly, when six selected lines with homozygous ATC deletions were subjected to gene expression analysis, V-PPase was found to be downregulated. Additionally, these lines showed lower germination rates and slower seedling growth. Understanding that V-PPase downregulation can inhibit sucrose formation due to the potential build-up of PPi, the lines were tested for sucrose content to explain their poor germination and growth. All lines had a lower sucrose content, but external supply reverted their growth to normal. In downregulation by heat, calli

expressing the pH sensitive reporter, Green Fluorescent Protein (GFP), demonstrated a decrease in cytoplasmic pH which could disrupt and slow down enzymatic activities. Altogether, our findings provide insights into the impact of V-PPase on germination and growth and its underlying mechanisms.

Chemistry Oral Presentations

03:45 PM. Electrochemical Study of Recombinant MN Peroxidase from Corn on Disposable Screen Printed Biosensor to Detect Glucose

Scout Weatherford, Anahita Izadyar, Elizabeth E. Hood
Chemistry and Physics, Arkansas State University

we are studying the effect of co-immobilization of -gold nanoparticles (GNPs)- glucose oxidase (GOX)- plant-produced manganese peroxidase (PPMP) onto Screen printed electrodes by electropolymerization of polyaniline (PANI) using the electrochemical techniques to demonstrate a stable, sensitive, selective, low-cost, and flexible glucose biosensor.

04:00 PM. A New Synthesis for Modifying Alginate for Use in Biomedical Applications

Hope Murphy, Sharon K. Hamilton
Chemistry and Physics, Ouachita Baptist University

Wound healing is a complex biological process, with one of the most crucial phases being the remodeling of the tissues, which centers around the collagen present in the extracellular matrix (ECM). Degradable collagen mimics can be used to enhance and aid internal wound healing capabilities and to deliver therapeutics to local wound sites. Electrospinning natural and synthetic polymers has produced nanofibrous mats that mimic the architecture of the ECM for use in biomedical applications. Traditionally, the Hamilton lab has electrospun antimicrobial chitosan and poly(vinyl alcohol) (PVA) with novel, non-degradable collagen mimics to produce nanofiber scaffolds. Alginate, a natural polymer, can also be electrospun to produce materials for wound healing. The innate groups in alginate lend themselves towards modification to produce a biomimetic and degradable polymer that can be electrospun. Using a new concerted synthesis for the modification of alginate allows for the attachment of four functional groups via amide coupling and can be facilely conducted in an undergraduate research laboratory. This product can be oxidized to enhance alginate degradability. The modified alginate was co-spun with PVA to create nanofibrous scaffolding. The physical properties of these materials were characterized through scanning electron microscopy (SEM) and infrared (IR) spectroscopy. Cellular responses to these alginate-based fiber mats were examined including cell viability, proliferation, and migration. Ongoing nuclear magnetic resonance spectroscopy analysis will compare the efficiency of functional group attachments of this synthetic approach as compared to a traditional stepwise modification of this polymer. Future studies include analyzing antimicrobial properties and in vivo assays.

04:15 PM. Synthesis of Catechol Derivatives Substituted at the 6-Position

Emma G. Gruss, Jessica L. Steiner, Kameron Klugh, Trevor Squires, Ryan Marasco, Mark Betonio, Larryn W. Peterson
Chemistry, Rhodes College

Catecholic rings are structural components of plant woody tissue and the core of some neurotransmitters, such as dopamine. The breakdown process of these rings involves an essential protein catalyst, dioxygenase enzymes. In nature, the breakdown of the catecholic rings is used to make antibiotic and other bioactive materials. Substituted catechols are a toxic byproduct in oil mill production and contribute to smoke production due to involvement in cell wall generation; dioxygenases may be helpful in bioremediation. However, the bounds of application of this breakdown have not been completely explored due to a lack of catechol substrates. We report on the synthesis of multiple catecholic

compounds, including dihydroxyhydrocinnamic acid, L-3,4-dihydroxyphenylalanine, and dopamine, substituted a the 6-position to further continue the exploration of the ability and achievability to breakdown the rings.

04:30 PM. Chemotherapy-Photo Thermal Therapy (Chemo-PTT) Combination Ionic Nanomedicines for Cancer Treatment

Arisha Ishtiaq, Samantha Macchi, Nawab Ali, Robert Griffin, Noureen Siraj
Chemistry, University of Arkansas at Little Rock
Biology, University of Arkansas at Little Rock
Radiation Oncology / Winthrop P. Rockefeller Cancer Institute / Arkansas Nanomedicine Center, University of Arkansas for Medical Sciences

Cancer is still the second leading cause of death in the US only surpassed by heart disease. Nanotechnology has made great strides in improving treatment for the disease. Specifically, combination nanodrugs are gaining attention due to lessened side effects and tumor targeting ability of nanoparticles. In this work, we combined photothermal therapy (PTT) drugs with a chemotherapeutic drug to develop chemo-PTT combination drugs. Aqueous nanoparticles are derived from the therapeutic drugs using a simple reprecipitation method. The photophysical properties which influence the PTT performance and the light to heat conversion efficiencies are investigated in detail to determine the most promising combination for further in vitro studies.
Acknowledgement: Arkansas INBRE NS

04:45 PM. A Novel Plate-Based Method for Proteomic Analysis of GeLC-12 Protein Samples

Walker Hendricks, Dayoung Eom, Aaron Storey, Dennis Province
Chemistry and Biochemistry, Harding University

Proteomics is the large-scale study of the collection of proteins (called a proteome) expressed by the genome of a cell or other biological sample. The process of proteomics involves digesting proteins into peptides and analyzing those peptides on an LC-MS (liquid chromatography/mass spectrometry) instrument. Proteomics as a field must be high-throughput, cost efficient, and time efficient; as such, new procedures that better fit these criteria are being developed to replace old methods. One method of digesting proteins can be performed in a polyacrylamide gel. Traditionally, gel lanes were cut into smaller pieces and desalted, reduced, alkylated, and digested in separate Eppendorf tubes. In this study, the traditional method of digesting gels is compared with a more modern, instrument-aided plate-based gel digestion. Scaffold, a protein sample comparison software, was used to analyze the differences between the traditional and plate-based methods. It was determined that the plate-based method provided more consistency of types of proteins, less contamination, and equal or better amounts of protein compared to the traditional method. There is also evidence that the plate-based method greatly reduces the time required to get the proteins in digestion.

05:00 PM. Agonists Stabilize Multiple Activated Cannabinoid CB1 Receptor Conformations During Molecular Dynamics Simulations

Thomas J. Caldarera, Erin R. Borst, Emma Chavez, Mahmoud Moradi, Caitlin E. Scott
Chemistry, Hendrix College

The cannabinoid CB1 receptor is a G-protein coupled receptor (GPCR) in the central nervous system that can elicit a variety of responses, such as feelings of euphoria, hunger, or pain relief, when activated by an agonist. A range of substances, from chocolate to marijuana, contain agonists to generate

these sensations, but it is also believed that medications can be designed to activate this receptor and relieve pain. Although there are no FDA-approved pain medications that target this receptor, finding new activated conformations of CB1 can help drug designers create novel medications that will stabilize and activate the receptor to generate pain relief. We investigated the impact an agonist has on the CB1 receptor's activated conformations. We used AMBER software to perform 100 ns NPγT molecular dynamics simulations in triplicate on two systems: 1) the agonist-bound AM841-CB1 receptor complex and 2) apo-CB1, the receptor with the agonist removed. Principle Component Analysis (PCA), a statistical method used to identify significant changes in the protein structure over time, was used to analyze the three trajectories for each system. Principle Component 1 (PC1) indicates differences between the agonist-bound and the apo-CB1 cases. The agonist-bound CB1 samples PC1 from approximately 0.5 to 2.3 and apo-CB1 samples PC1 from -0.5 to 1.5. However, another agonist-bound CB1 structure samples PC1 from 0 to 1.5. Therefore, the agonist bound CB1 structure is able to take on multiple, distinct conformations. The measurements of the interhelical angles between helices 3 and 6, 3 and 5, and 5 and 6 also support this finding. In one of the three agonist-bound MD simulations, the helices are more parallel compared to the other two simulations. These data reveal that the agonist does not stabilize the structure of CB1 because the receptor is capable of sampling multiple conformations. Further studies can be conducted to identify if the agonist-bound conformations are similar to the Gi protein-bound case, or if this is a novel structure of CB1.

Physics Oral Presentations

03:45 PM. The Effects of Magnetic Field on Bacterial Motility

Jessica Fink, Diksha Shrestha, Yong Wang
Physics, Astronomy, Material Science, Missouri State University

Bacteria is a popular subject of research due to the influence bacteria has on the natural world. Bacteria are responsible for most notably infections and unsanitary water. Therefore, a great effort by researchers has been put forth to see what affects bacteria and why. One aspect of this research is to see how magnetic fields affect them. The application of magnetic fields to bacteria has been done by other research groups before. However, the previous research focused on bacterial growth and not the motility of the bacteria. This research project seeks to further the understanding of the role of magnetic fields applied to Escherichia coli. This ongoing project wants to test in a systematic way if magnetic strength, duration, type of field, etc. affect the motion of the E. coli. Preliminary data suggests that the bacteria do change in their ability to move after exposure. As of now, it appears that strong magnetic strength applied to the bacteria yields the result of decreasing velocity. Smaller strengths yielded little effect. Near the end of this project, a solenoid was created and tested on the bacteria. The results showed visually the bacteria acted abnormally. The data with the electromagnet has yet to be quantified. The conclusion of this project thus far is that bacteria do appear affected in their ability to move. Further research is necessary to understand why.

04:00 PM. Flux Growth of hBN Single Crystals

Arantxa Pardue, Jin Hu, Santosh Karki Chhetri
Chemistry and Physics, Belmont University

Hexagonal Boron Nitride (hBN) has recently attracted enormous interest as a 2D material structurally similar to graphene (Clubine, 2012, p2). As a thermally and chemically stable electric insulator, the synthesis of hBN is important for

dielectrics, which advances technology applications such as transistors (Wang et al., 2011, p1). The current hBN single crystals are mostly synthesized by a high-pressure growth method which requires expensive instruments not widely available. This REU project pursued the low-cost flux method to grow hBN single crystals using a high temperature tube furnace under a nitrogen atmosphere. The composition, structure, and quality of the obtained crystals were examined by energy-dispersive x-ray spectroscopy, then compared to existing high-quality hBN samples. This project aided in establishing a growth method with optimized parameters such as ratios of source materials, growth temperature, and temperature change rate, opening the possibility of testing other parameters in the future to reduce the cost of synthesis, and therefore semiconductor devices.

04:15 PM. Optimization of Quantum Device Fabrication for the MonArk Quantum Foundry

Jeremy Choh, Hugh Churchill, Peter Gea
Physics, Hendrix College

The MonArk Quantum Foundry is a collaborative project with a goal of machine learning integration to label hBN flake thicknesses from optical images. Currently, to find hBN flakes for quantum devices, there is a three step flake finding process. These steps are exfoliation, optical microscopy, and atomic force microscopy. While these steps may seem simple, it can take researchers from several hours up to several days to find suitable flakes for their quantum devices. The longest component of the flake finding process is the use of the AFM to ensure that the flake thickness is within the specifications of their device. The goal of the machine learning project is to completely eliminate the step of the AFM. A well-trained machine learning algorithm can be sensitive to small changes in color. When implemented, this algorithm will have a substantial effect on reducing the time spent during the flake finding process for hBN, thus allowing for the faster production of quantum devices. By the end of the summer, a model of the machine learning algorithm was created which identified flakes and labeled them within 10-12 nm of the flakes actual thickness.

04:30 PM. VUV-Light Generation Using Multiple Non-Linear Effects Through Hollow-Core Fiber

Skyler Gulati, Hiro Nakamura
Physics, University of Arkansas at Fayetteville

Vacuum-Ultraviolet (VUV) light has proven to be imperative to research regarding material and molecular physics. For example, this spectral region (6-120 eV in energy) is indispensable for photoelectron spectroscopy, which is increasingly recognized as the most powerful method of resolving electron states in solids. I've focused on utilizing nonlinear optical effects through negative-curvature hollow-core fibers, which is a relatively new method to generate these extremely short wavelengths. This approach relies on intense pulses from a primal mode-locked laser outputting in the near-IR wavelength range to drive multiple non-linear effects including high-harmonic generation (HHG) which can produce multiple harmonic orders throughout the VUV spectral region. We investigate the fundamental aspects that govern the nonlinear effects in a hollow core fiber such as the temporal pulse width after the beam propagation through it and the light-matter interaction when different gas species are introduced into the fiber. Besides shedding new insights into the nonlinear optics in fibers, the outcome of this project could help further develop photoelectron spectroscopy research as well as methods to pattern semiconductor wafers.

04:45 PM. The Role of 3D Printing in Biomedical Applications

Janae Tirado, Mahbub Ahmed, Austin Patricia, Md Islam
Engineering and Physics, Southern Arkansas University

The current project has two objectives; the first is to explore the role of 3D printing in anatomy education. Medical students rely on human cadavers to study anatomy. 3D Printing technology can aid

and enhance anatomy education in this regard. In some cultures, handling human cadavers and body parts can be an ethical issue. Even though they are permitted to be used legally in some countries, there may not be enough cadavers to meet the demand in anatomy education for medical students. Even in some countries, they could be costly for the students to afford. As part of this project, several anatomy models have been 3D printed using the PLA filament. The bone models have been 3D printed using white filament to represent the color of the bones. These CAD models, originally 3D scanned from human body parts, have been downloaded from open-source websites. The body's hard parts (models) were 3D printed with PLA plastics, and the softer parts were 3D printed with a special plastic filament to obtain similar properties. The project's second objective is to explore the feasibility of 3D printing bioceramic materials. Bioceramic materials are a subset of biocompatible ceramic materials. They can be used as implants or bone substitutes in the human body. To study the feasibility of 3D Printing bioceramic materials, an existing FDM-based 3D printer was modified to be capable of 3D printing clay and standard ceramic materials. The research will address the challenge of 3D printing ceramic materials and the standard procedures to test the 3D printed specimens to obtain mechanical properties. This research will provide insight and experience to take this research to the next level of 3D printing of bioceramics and testing. A detailed discussion about both objectives has been addressed in this presentation.

05:00 PM. Using Liposomal Models to Study the Binding Kinetics of Cytosketal Proteins Inside of Bacteria

Ashley Allen, Pradeep Kumar
Chemistry, University of Arkansas at Pine Bluff

All living cells require an enclosed structure that separates the internal part of the cell from the surrounding. Cells must maintain the stability and integrity of these structures while they are placed in extreme conditions. In nature, these enclosed structures are formed by lipids. Lipids form a mechanical bilayer that becomes the protective barrier of cells from being placed in aqueous solutions. Because of their amphipathic characteristics, they have a polar and nonpolar region which allows some molecules to enter and exit the cell. Vesicles compartments of the lipid bilayer that are separated from their extracellular environment. They are small spherical structures that are composed of liquid enclosed by a phospholipid bilayer. You can think of a vesicle as a cellular envelope that’s utilized to transport materials in and out of a cell, digest materials, and regulating the pressure in a cell. Methods used to construct vesicles include on the assembly of lipid bilayers that produce realistic properties of human vesicles. In our research, we have investigated the stability of artificial liposomes to study the phospholipid membrane under extreme conditions including high pressures and temperatures.

Poster Abstracts

Biology

1A. Cytokine Profiling in Pediatric Obesity

Kennedy Stringfellow, Shannon Rose, Kanan Vyas
Biology, Arkansas Children's Research Institute

Bioenergetics and Metabolism in Pediatric Population. Kennedy Stringfellow, Sponsored by Dr. Shannon Rose. University of Arkansas for Medical Sciences, Department of Pediatrics, Arkansas Children's Research Institute, Little Rock, AR. In a study of 5-9 year olds with a range of BMIs, there was a primary interest in whether PBMC bioenergetics differed among children based on obesity and insulin resistivity. Significant changes in biomarkers of metabolic health and inflammation were found in obese insulin resistant children. These markers have been proven to correlate with adult obesity and T2D, but there is little research testing this correlation in children with obesity or T2D. Objective: To determine whether physical activity levels of children with obesity differ among the age groups and discover a correlation between the activity levels and inflammatory markers, Study Design/Methods: Blood samples from children, ages 5-9, with a wide span of BMIs were collected over the course of the cross-sectional study. The subjects (and his/her parent[s]) were asked to complete a questionnaire that considered activity level over the course of a week. From the questionnaire, a score was calculated according to activity level, which was analyzed and organized by subject grade and range in score. Using the blood samples, the isolated PBMCs were analyzed through extracellular flux, using Seahorse technology. Assays were conducted to measure mitochondrial dysfunction and oxidative stress. Results: Compared to overweight insulin sensitive children, insulin resistant children's PBMCs use Oxidative Phosphorylation as a means to produce ATP over glycolysis. The assessments also showed that there is a positive correlation between PBMC bioenergetics and insulin, leptin, and the inflammatory cytokine MCP-1. The data from the score reports were compared using a one-way anova with Tukey's multiple comparisons tests and Pearson correlations, in which neither were found to be statistically significant. Conclusions: A study was conducted to explore the cellular bioenergetic correlation in obese children that had been seen in adults with obesity. Based on the data from the study, there is a correlation in children with obesity and insulin resistivity between their immune cell bioenergetics and metabolic dysfunction and inflammation in childhood obesity. In conclusion, with this particular questionnaire, we did not see significant differences in physical activity based on obesity or insulin sensitivity.

1B. Visualization of a Protein-Protein Interaction Between a F-Box Protein AT1G20790 and Arabidopsis SKP1-LIKE1

Abigail D. Barker, Mi-seon Seong
Math and Science, Central Baptist College

Protein degradation is an essential mechanism in plants for the development of photomorphogenesis and skotomorphogenesis in response to different light intensities. In eukaryotic cells, the ubiquitin-proteasome system is a key mechanism of selective protein degradation using polyubiquitin as a marker on a target protein. Transfer of ubiquitin from E2 ubiquitin-conjugating enzyme to substrate proteins is mediated by diverse E3 ubiquitin ligases that are specific for each target protein to be degraded. F-box proteins are the substrate-recognition subunits of Cullin-RING ubiquitin E3 ligase 1 (CRL1), also named SCF (SKP1-Cullin 1-F box protein). In this work, Bimolecular Fluorescence Complementation (BiFC) assay was used to study the protein-protein interaction of a putative F-box family protein At1g20790 and Arabidopsis-SKP1-like 1 (ASK 1) in protoplasts isolated from Arabidopsis leaves and cultured in NT-1 media. Fluorescence signals were observed in the protoplast cells transfected with a complementary set of expression vectors of

At1g20790-VYNE and ASK1-VYCE, indicating that AT1G20790 and ASK 1 form a complex and that AT1G20790 is involved in protein degradation as a subunit of CRL1.

2A. Is There a Sex-Biased Trade-off Between Growth and Immunocompetence in Eastern Bluebird Hatchlings?

Christopher Carter, William Kirkpatrick, Sarah DuRant
Biology, University of Arkansas at Pine Bluff

Previous research shows that sex plays an essential role in immune health differences. Females exhibit less pathology from infections than males because their immune system is more robust; however, this increase in immune function may come at a cost. Immunocompetence can be associated with slower growth rates in both sexes. However, male birds tend to grow faster than females in early development, which may contribute to the greater pathology they express during infection. Therefore, I predicted that female Eastern Bluebirds would have a higher level of immunity, signified by a higher white blood cell count, but males would grow faster at the cost of immune development. We monitored eggs until hatching and measured nestling beaks, tarsus, and mass on days 1, 5, 10, and 13 post hatch. Using blood collected from 10 day old nestlings, we made and analyzed blood smears to determine the relative abundance of lymphocytes, monocytes, heterophils, and eosinophils. There was no significant difference in white blood cell counts between sexes. However, male nestlings had distinguishably larger tarsus and beak sizes than the female nestlings. Based on these results, we plan to examine other aspects of nestling immunity to determine if a trade-off occurs that was not captured by white blood cell counts. Understanding how Eastern Bluebird immune systems differs between sexes can expand upon existing knowledge around immune development and growth.

2B. Effect of Maternal Disease Severity on Transfer of Antibodies to Offspring

Destiny Guillory, Sarah Durant, Erin Sauer, Madeline Sudnick
Biology, University of Arkansas at Pine Bluff

Individual variation in susceptibility to pathogens can be driven by many biotic and abiotic factors, including parental effects8. Parents provide the foundation for an individual's immune system through genetic inheritance and continue shaping offspring immunity during prenatal and postnatal development12. For example, the vertical transfer of maternal antibodies can differ due to many different nongenetic maternal factors, including environment, disease history, and behavior. Understanding the nongenetic ways parents contribute to offspring will allow us to better understand variation in disease susceptibility among individuals. Here we examine the effect of maternal infection severity on the concentration of vertically transmitted antibodies in the developmental environment (i.e., egg yolk). We collected unfertilized domestic canary eggs from 13 clutches of mothers with prior exposure to Mycoplasma gallisepticum (MG) and 13 naive mothers. Using the yolks from these eggs, we quantified total egg yolk antibodies with an enzyme-linked immunosorbent assay, or ELISA2. We found no significant effect of MG exposure, disease pathology, or MG-load on egg yolk antibody levels. Yolk antibody levels were also not affected by egg yolk mass. Further research is needed to determine whether MG-specific antibodies differed among treatments, whether other factors of maternal disease shape vertical transfer of antibodies, and how vertical transfer of antibodies varies with time post maternal infection.

3A. RNA-Seq Analysis of Arabidopsis Thaliana Seedlings Grown in Different Light Conditions and the Identification of At1g20790

Ashley Henderson, Mi-seon Seong
Math and Science, Central Baptist College

Photomorphogenesis is the light-regulated plant development where the growth patterns of organisms respond to different light signals. The discovery of light signaling pathway components has increased our understanding of proteasome-mediated protein degradation and the regulation of many important proteins in human health such as p53, the most mutated tumor suppressor protein in human cancers. In order to gain a deeper understanding of the regulation of hypocotyl elongation in different light conditions, RNA-seq analysis of Arabidopsis thaliana seedlings grown in high light, low light, and dark was performed. A putative F-box protein gene, At1g20790 was one of the genes that are differently expressed in dark and low light. To understand the function of At1g20790 in light signaling, a T-DNA insertional mutant of At1g20790, SALK133945 was grown in different light conditions and their hypocotyl length was measured. SALK133945 showed shorter hypocotyl length in low light than WT Columbia ecotype (Col-0), suggesting its negative regulation of photomorphogenesis in low light, which leads to hypocotyl elongation.

3B. Development of a Lysostaphin-Producing Strain of Lactobacillus Plantarum as a Biotherapeutic Treatment for the Prevention of Menstrual Toxic Shock Syndrome Caused by Staphylococcus Aureus

Abigail V. Weihe, Huanli Liu, Mark E. Hart
Math and Science, Central Baptist College

In the late 1970s, a dramatic increase in menstrual toxic shock syndrome (mTSS) cases was reported and upon further investigation, the increase was found to be primarily associated with a newly developed superabsorbent tampon being used primarily by young menstruating women and the presence of the gram-positive bacterium, Staphylococcus aureus and its ability to produce toxic shock syndrome toxin-1. Fortunately, the number of cases of mTSS decreased significantly when the highly absorbent tampon was voluntarily removed from the market by the manufacturer and a better awareness by the public and physician along with guidelines for the use of tampons. Despite the incidence rate for mTSS being rather low now (approximately 1 per 100,000 women between the ages of 13 – 54 years), the mortality rate is still as high as 10%. In most women, Lactobacillus species are the predominant microorganism found residing in the vaginal tract where their indirect use of glycogen results in a reduce pH in the vaginal tract which serves as an effective antimicrobial. However, during menstruation the influx of menstrual fluid causes the vaginal tract to go neutral and allows bacteria, such as S. aureus to proliferate and make toxin. We have taken a biotherapeutic approach in an effort to prevent mTSS by cloning the gene for lysostaphin into Lactobacillus plantarum and subsequently showing lysostaphin in vitro activity. Lysostaphin is a bacteriocidal endopeptidase that specifically cleaves the pentaglycine crosslink of the cell wall of S. aureus. The bioengineered, lysostaphin L. plantarum was lyophilized in commercially available tampons and used in an in vitro syringe model mimicking the vaginal tract containing S. aureus suspended in a modified genital tract secretion medium containing porcine blood. Unfortunately, no reduction in S. aureus cell viability was observed at 8 and 24 hours. The current study represents an attempt to determine why reduction of cell viability was not observed. While PCR demonstrated the presence of the lysostaphin gene in the chromosomal of L. plantarum, the lysostaphin protein was not observed by western analysis and activity was not detected in spend media isolated from L. plantarum. Preliminary investigations also demonstrated that porcine blood was not inhibitory for L. plantarum. Attempts now are to determine if the lysostaphin gene is being expressed by reverse transcript PCR.

4A. Paraburkholderia Symbiont Infections in Social Amoebas of Arkansas

Patricia Fiedorek, Mackenzie Hoogshagen, James DuBose, Tamara S. Haselkorn
Biology, University of Central Arkansas

Amoebae are a unique model for studying host-bacteria interactions, as they feed on bacteria in nature via phagocytosis and may drive the evolution of the bacterial intracellular symbiont lifestyle by providing a selective pressure for bacteria to evade or resist digestion. One well-characterized symbiotic relationship is between the social amoeba, Dictyostelium discoideum and their Paraburkholderia bacterial symbionts. While Paraburkholderia may confer nutrition supplementation or detoxification to their amoeba hosts in some environments, there is a fitness cost to infection and their function in natural populations is unknown. Only three species of Paraburkholderia are known to infect D. discoideum in nature, however, there are dozens of other social amoeba species found in Arkansas and their relationship with Paraburkholderia has not been characterized. We hypothesize that if Paraburkholderia is a host specific co-evolved mutualist then we will find high infection levels in other amoeba species of different species of Paraburkholderia that have similar evolutionary trajectories as their hosts. We have sampled eight additional social amoeba species from ten different locations across the different ecoregions of Arkansas using symbiont-specific PCR primers to assess infections. We are finding low infection levels of Paraburkholderia that vary across host species. Utilizing DNA sequencing and phylogenetic analyses we have identified a diversity of bacterial species from across the order Burkholderiales, suggesting a lack of host specificity. Future studies are needed to determine the effects of these symbionts in their amoeba hosts.

4B. Effects of Seasonal Variation on Desert Microbes and Their Biological Activity

Jason Sanders, Vinay Raj, Ashley Allen
Chemistry, University of Arkansas at Pine Bluff

Effects of seasonal variation on desert microbes and their biological activity Jason Sanders, Ashley Allen and Vinay Raj Organisms that reside in the desert environments have limited availability to critical resources such as water, nutrients, and are also exposed to high heat from the sun. The organisms in these arid regions are affected by variations in temperatures, pH, saline conditions, and precipitation. Microbial communities are an important component in the structure and function of desert ecosystems. Microbes in these regions play a pivotal role in the biological life of plants as well as improving agricultural productivity. The microbial diversity in the Atacama Desert, the driest place on earth, for example facilitates the adaptations to plants to extreme environmental conditions. Seasonal variations such as changes in temperature and an unusual amount of precipitation affect the microbial dynamics in these desert ecosystems. The variations alter the established adaptations of plants with extensive microbial associations In this study, we primarily characterize the microbes such as the bacterial communities such as Proteobacteria, Actinobacteria, Acidobacteria, Cyanobacteria and other microbes in these arid regions. We then examine the role of seasonal variations on the microbial dynamics in these desert ecosystems. Our study contributes insights into the importance of aridity and the dynamic network with microbes in these environments

5A. Investigation of the Interactions Between REV1 and DHX36 During Replication of G-Quadruplex DNA

Mary Katherine McKenzie, Bethany Paxton, Amit Ketkar, Robert Eoff
Biology, Henderson State University

G-quadruplexes (G4s) are secondary DNA structures that provide physical barriers to DNA replication and transcription. Unresolved G4s can result in stalling of the replication fork, causing double-strand breaks, chromosomal fragmentation, and subsequent cell death. Certain translesion synthesis polymerases, such as Rev1, are necessary for efficient DNA replication without loss of vital genetic information. Rev1 has the unique ability to unfold G4s and recruit other proteins to further assist in G4 bypass. Previous research has shown the importance of Rev1 in preventing the accumulation of single-stranded DNA in response to G4-induced replication stress, but the protein-protein interactions that govern this process are poorly defined. Proteomics results led to the discovery that the DEAH-box helicase 36 (DHX36) was depleted near replication forks in the absence of Rev1. DHX36 assists with G4 replication by creating a loading zone for the replicative helicase downstream of the quadruplex structures. While Rev1 and DHX36 have been independently implicated in G4 bypass, no previous research has established a physical or functional relationship between them. To investigate the relationship between Rev1 and DHX36, we performed chromatin fractionation experiments to determine if the presence of Rev1 influences the relative abundance of DHX36 on chromatin. Completion of the proposed studies could provide new mechanistic insights into G4 replication and maintenance.

5B. Investigating the Role for DNA Polymerase Kappa as a Sensor of Redox Imbalance in Glioblastoma

Isabel Ritter, Julie Gunderson, Reham Sewilam
Chemistry, Hendrix College

DNA that has been affected by oxidative stress or otherwise damaged must be replicated by translesion DNA synthesis (TLS) polymerases, such as those in the Y-family. Polymerase k (pol k) is a widely conserved y-family polymerase capable of replicating DNA with oxidative lesions. Human pol k is upregulated in gliomas including glioblastoma (GBM), an aggressive tumor with a poor prognosis and mostly palliative therapies available. Development of GBM increases with oxidative stress. Among the most common oxidative lesions is the guanine derivative 7,8-dihydro-8-oxo-2'-deoxyguanosine (8-oxo-dG), which pol k often copies incorrectly by preferentially inserting 2'-deoxyadenosine monophosphate (dAMP). When 8-oxo-dG is paired with dAMP, the MutYH DNA glycosylase (MUTYH) removes the adenine and base excision repair (BER) adds back cytosine, which allows 8-oxoguanine DNA glycosylase (OGG1) to remove the 8-oxo-dG lesion. Both pol k and MUTYH have been linked with activation of the ATR kinase-mediated replication stress response but a mechanism relating the two enzymes has not been found. The present study tested the hypothesis that pol k-catalyzed insertion of dAMP opposite 8-oxo-dG increases recruitment of MUTYH to chromatin in GBM cells and that this activates the replication stress response. We have isolated chromatin from GBM-derived T98G cells and performed Western blotting to determine if WT and POLKKO cells have different amounts of chromatin-bound MUTYH. This study will help us better understand how a redox sensing DNA replication mechanism helps GBM cells tolerate conditions threatening genomic integrity.

6A. High-Power Rocket Workshop

Katherine Hunter, David J. Thomas, Braden Glenn, Taylor Mitchell
Science Division, Lyon College

The National Association of Rocketry designates High-power rockets as including a single motor with impulse of more than 160 Newton-seconds, multiple motors which all together exceed 320 Newton-seconds, a motor with more than 80 Newtons average thrust, more than 125 grams of propellant, a total mass of more than 1500 grams, a hybrid motor, or any airframe parts of ductile metal. These guidelines distinguish High-Power Rocketry from Model Rocketry. Since the spring semester of 2022, our research group has focused on Model Rocketry. We have built dozens of Model Rockets which use motors ranging from A to E. Model Rockets do not need to be able to withstand the same forces as do High-power, so they are made with lighter materials such as cardboard, balsa wood, paper, and wood glue. In High-power, materials must be durable. However, care must be taken not to make the rocket so heavy that it cannot reach a sufficient altitude. Component materials of High-power rockets can include plywood, fiberglass, aluminum, and epoxy resin. High-power rockets are generally much larger than model rockets. High-power rocketry can be used for scientific testing. They often include a payload section in which scientific tools and other cargo can be stored. One typical payload is an altimeter device, which is used to measure the altitude the rocket reached. Samples or live-specimens can also be placed in the payload section to test their reaction to changes in altitude and G-forces. Cameras are also common, though they are typically mounted externally, not in the payload section. Cameras record the rocket's flight looking down at the ground across the aft end of the rocket. At the High Powered Rocket Workshop held at Southern Arkansas University in Magnolia, our research team learned about High-power rocketry and what it takes to successfully launch and become certified to purchase High-power engines. We also gained experience in using 3D modeling software to create our own parts. We built our rocket, The Highlander, from scratch under the direction of the workshop instructors. The launch was successful, but recovery was delayed for several weeks after The Highlander became lodged in a tree on its descent. After recovery, we were able to examine the on-board technology and determine the altitude of the launch was 2705 feet, over 200 feet higher than the projected altitude.

6B. Biological Rocketry

Katherine Hunter, David J. Thomas, Braden Glenn, Taylor Mitchell
Biology, Lyon College

Model and High-power rocketry can be used to conduct scientific experiments. These experiments often make use of the payload section of the rocket, which can hold relevant technology or specimens. Our research team has used rocketry to conduct biological research. During the summer of 2022, we made progress in our research with the LADCAP (Launchable Automatic Device for Collecting Airborne Particles). The LADCAP is made up of a vacuum pump which draws air through a hole in the side of the rocket and then through a filter. The filter catches airborne microbes that can later be cultured and identified. The vacuum is instructed by an onboard flight computer to begin collecting samples after a particular amount of time from launch. This system could potentially be used with a wide range of craft, but our air-testing this summer was conducted with the custom-built mid-power rocket G-Lifter. During our most recent flight, the G-Lifter sustained considerable damage, so we plan to conduct future LADCAP experiments with our scratch-built High-power rocket The Highlander. LADCAP collects high-altitude microorganisms which can withstand extremes including temperature, low pressure, desiccation, and increased UV flux. The particles are thusly considered extremophiles. The data collected about extremophiles on earth can potentially be extrapolated to extremophiles in other locations, including those elsewhere in the solar system. Biological research with the LADCAP system and rocketry is contained within the designation of "aeromicrobiology." This summer, we began

planning our research on the effects of G-forces on brown planaria. Brown planaria are flatworms which detect light through two eye spots located on their triangular heads and consume meat and detritus through a tubular pharynx which is located medially on the underside of the body. Due to the presence of stem cells called neoblasts, planaria have the ability to regenerate when cut. When a worm is cut in half, two worm clones will grow from the pieces. Past research done aboard the International Space Station has been conducted to measure the effects of low-gravity on planaria regeneration. Our research team intends to test the effects of G-forces. We will use both rocketry and the centrifuge to conduct these tests. Our brown planaria have been sourced locally from the Batesville area. This research is supported with grants from the Arkansas Space Grant Consortium.

7A. The Map Kinase Effectors, TAOK1, TAOK2, and TAOK3, Are Differentially Expressed During Early Embryogenesis

Amy Tran, Alexis Vann, Kamryn, Humphrey, Mick Yoder
Biology, University of Central Arkansas

Embryonic development requires an intricate symphony of coordinated cell-cell signaling in order to properly execute the morphogenetic program. Errors in any one of these critical signal pathways can lead to a number of birth defects, such as neural tube closure defects and limb abnormalities. One of the critical signaling pathways is the Mitogen Activated Protein Kinase (MAPK) pathway. The MAPK pathway employs a cascade of proteins, starting with MAP kinase kinase kinases (Map3K), leading to phosphorylation of MAP kinases and subsequent activation of downstream targets. Thousand and One Amino Acids Kinases (TaoK) are a family of Map3ks, with three paralogs: TaoK1, TaoK2, and TaoK3. Using Xenopus laevis as a model organism, our goal is to characterize the spatiotemporal expression of the Tao kinases and elucidate their embryonic function through a combination of qPCR, in situ hybridization, and embryology. Our data show that the Tao kinases all exhibit a similar, yet slightly different, spatiotemporal pattern of expression. Taok1 and Taok3 share overlapping expression in the early blastula and gastrula stage embryos, where Taok2 is undetectable. Conversely, all three Tao kinases have a strong overlapping presence in the nervous tissues in later stage embryos. Future studies will be aimed at understanding how the Tao kinases contribute to the normal developmental program and the expression profile shown here provides a means to probe their functions in a tissue specific manner.

7B. The Role of Tao Kinase 3, a map3K, During Early Embryonic Development in Xenopus Laevis

Kirsten LeCompte, Jordan Cormier, Amy Tran, Mick Yoder
Biology, University of Central Arkansas

Embryogenesis is a complex process that requires constant feedback between the extracellular and intracellular environments to provide positional cues relative to the dorsal-ventral (D-V), anterior-posterior (A-P), and left-right (L-R) axes. Many of these positional cues result from morphogen gradients emanating from signaling centers throughout the embryo, which provide instructions for both differentiation and cell migration. The Map kinase pathway is a known regulator of embryogenesis and responds to extracellular ligands through an intracellular cascade of kinases leading to ERK, p38, and JNK phosphorylation and activation. We recently demonstrated that the Map3K, Thousand and One Amino Acid Kinase 3 (Taok3), is specifically expressed in the dorsal mesodermal tissue of the X. laevis embryo and hypothesized that this expression is required for notochord morphogenesis. In order to investigate Taok3 function, we have created a series of wild-type and mutant constructs for use in both cell culture and embryo-based experiments. In cell culture, all Taok3 plasmids are expressed and detectable through western blotting and immunofluorescence, providing a critical tool for further exploring Taok3's ability in the Map kinase pathway. Similarly, mRNA injection into X. laevis embryos results in protein expression of the tagged Taok3 constructs. Interestingly, both over-

expression of wild-type and mutant Taok3 lead to gastrulation defects in the embryo, as evidenced by delayed blastopore closure. Current efforts are focused on which downstream member(s) of the Map kinase pathway Taok3 is activating, through analysis of phosphorylated levels of p38 and JNK, and how this activation specifically affects development, through gene expression analysis and evaluation of mutant phenotypes. This project was supported by the Arkansas INBRE program, with a grant from the National Institute of General Medical Sciences, (NIGMS), P20 GM103429 from the National Institutes of Health.

8A. Fluorescently Tagging Proteins to Study Polymerase Epsilon Complex

Julia Green, Lydia Ostmo, Sapna Das-Bradoo
Cellular and Molecular Biology, Northeastern State University

DNA polymerase epsilon is an essential enzyme responsible for synthesis of the leading strand during DNA replication. It is composed of four subunits, POLE1, POLE2, POLE3, and POLE4. Two of the subunits (POLE1 and POLE2) are essential components. Deficiencies and mutations in DNA polymerase epsilon catalytic subunit (POLE1) cause severe developmental abnormalities and cancers. Our laboratory is interested in understanding if mutations in POLE1 affect the interaction between the different polymerase epsilon subunits and thus the functionality of the complex. To this end, we decided to fluorescently tag the individual subunits and study protein-protein interactions through co-immunoprecipitation. Using restriction enzyme digestion, ligation, transformation, and sequence analysis, we have confirmed the successful construction of the GFP-tagged POLE3 vector. Western blot results further confirmed the expression of the tagged proteins. Next, we will complete tagging the POLE2 subunit and then study the interactions among the epsilon subunits in normal and mutant cell lines.

8B. Bactrim's Helpful Use in Controlling Uropathogenic Bacteria

Jonathan Crosse, Janaki Iyer
Science and Health Professions, Northeastern State University

Of the bacterial infections plaguing the human body, one of the most prevalent ones are urinary tract infections (UTIs). People from different age groups and sexes contract UTIs but the group most susceptible are women. The causative agents for these infections are most commonly uropathogenic Escherichia coli (E. coli) followed by Klebsiella pneumoniae (K. pneumoniae). With increasing resistance to antibiotics happening, it is important to both find out how effective common antibiotics are against these strains and come up with other ways to stop infections. The objective of this research was to find out the efficacy of trimethoprim and sulfamethoxazole (TS), the components of Bactrim, on K. pneumoniae and E. coli. We investigated the effects of a combination of TS on uropathogens as well as human bladder cells. The findings of this study show that TS did not harm human bladder cells but had varying effects on the growth of E. coli and K. pneumoniae. E. coli growth was inhibited at a 1X concentration of TS, but higher concentrations of TS were needed for K. pneumoniae, demonstrating the variable effectiveness of TS on uropathogens. These findings will lay the groundwork for novel ways to counter these UTIs.

9A. The Effects of DJ-1 Protein Mutants on Mitochondrial Dynamics in Dictyostelium Discoideum

Hyoju Kim, Kari Naylor
Biology, University of Central Arkansas

Mitochondrial dysfunction plays a role in the progression of Parkinson's Disease (PD), thus understanding mitochondrial dysfunction is one of the important keys to finding PD treatment. The study of the relationship between the cytoskeleton and fission and fusion in our model, Dictyostelium discoideum suggests that insufficient fission can

cause a tangle of interconnected mitochondria and insufficient fusion can cause mitochondrial aggregates that lead to a decrease in mitochondrial motility and potentially damaged organelles. To continue to understand the relationship between mitochondrial dynamics and PD, we are determining the rates of fission, fusion, and motility when overexpressing and under-expressing DJ-1 in D. discoideum. DJ-1 is a protein linked to PD and mitochondria, yet its function is poorly understood. Our results will help clarify its function and the relationship between DJ-1, dynamics, and mitochondrial dysfunction. We have analyzed 7 DJ-1 mutants to identify fission and fusion events and calculated the average number of events/min/cell in 30 cells. Our preliminary data suggest that overexpression of DJ-1 has little effect on the rates of fission and fusion compared to wild-type cells (AX2), while loss of DJ-1 increases fission. These results suggest that DJ-1 is an inhibitor of fission with little effect on fusion. Our future work includes an analysis of mitochondrial motility and the cytoskeletal structure in these cells which plays a role in mitochondrial dynamics. Ultimately, this work will contribute to a better understanding of the DJ-1 function and pathogenesis of PD.

9B. Determining Parameters of Host-Specificity Between Social Amoeba Species and Paraburkholderia

Jordan Bowen, Terry Uhm, Tamara S. Haselkorn
Biology, University of Central Arkansas

Amoebas are a promising model for understanding endosymbiosis as they are thought to function as evolutionary training grounds for bacteria, potentially promoting the evolution of bacterial pathogenesis for infectious diseases in animals and humans. One amoeba that has been used to study these endosymbiotic interactions is social amoeba Dictyostelium discoideum. Three bacterial species within genus Paraburkholderia have a symbiotic relationship with D. discoideum: P. agricolaris, P. hayleyella, and P. bonniea. Currently, this endosymbiotic interaction has only been studied within D. discoideum, despite the existence of hundreds of distinct species of social amoebas. We hypothesized that a host species' ability to initiate, maintain, and support an endosymbiotic relationship with Paraburkholderia is directly correlated to its evolutionary distance from the original host, Dictyostelium discoideum. Six species across the phylogeny of social amoebas, ranging from closely related (sister species D. citrinum) and others in the same genus (D. giganteum and D. purpureum) to species in other families Polysphondylium violaceum and Cavenderia aureostipes), were artificially infected with the three symbiont species of Paraburkholderia. Initially-infected species were subjected to bacterial colony counting to measure the ability of the endosymbiont to infect. One week after the initial infection, amoeba species were generationally passaged 2 times to determine persistence. Before each passage and after one week of growth, amoeba species were tested to identify symbiont infection status and effect. If the endosymbiotic relationship of D. discoideum with Paraburkholderia is host-specific, we predict a decrease in its ability to infect, maintain infection, and decreased physiological benefit for amoeba species that are more distantly related to D. discoideum. Preliminary results with P. bonniea and P. hayleyella suggest that Paraburkholderia can persist through generational passaging with negligible variation between amoeba species. There may, however, be a difference in bacterial infection levels, although not consistent with our hypothesis of host specificity. By testing the impact of harboring these Paraburkholderia species in varyingly related species of social amoeba, we can begin to piece together parameters of Paraburkholderia host-specificity and begin devising a general model for endosymbiotic evolutionary development and propagation.

10A Acetylated H4 and H3K27me3 Antibodies and Their Role in Early and Late RNA Transcription of Transfected SV40 Chromatin

John Schaller, Barry Milavetz
Biochemistry and Molecular Biology, Hendrix College

Using Simian Virus 40 (SV40) as a model, epigenetic regulation can be further investigated. Specifically, histone modifications to histone proteins 3 and 4 give insight into the way SV40 regulates transcription. This study tested the role of these proteins in the transcription process. The modifications include acetylation of histone H4 and tri-methylation of histone H3 (H3k27me3). SV40 virus was modified with these histone modifications and antibodies attached to these histone proteins for removal. African green monkey cells were then used for transfections of these modified SV40. Virus chromatin was extracted from these cells and further analyzed for early and late transcription using real-time qPCR and gel electrophoresis techniques. Results shown on the gels suggest the antibody to acetyl H4 blocks both early and late transcription of SV40 RNA. The antibody to tri-methylated histone H3 appears to have no effect on either stage of SV40 RNA transcription. These results suggest a necessary role of acetyl histone H4 in SV40 transcription while methylated H3 plays a lesser role in the process.

10B. HLTF-Mediated Fork Reversal of G-Quadruplexes

Kathryn Diekman, Bethany Paxton, Mary Katherine McKenzie, Julie Gunderson, Amit Ketkar, Robert Eoff
Biochemistry, Hendrix College

G4 quadruplexes (G4s) are four-stranded nucleic acid structures that can form in guanine rich regions. Putative G4 forming sequences are found frequently in portions of the genome with important regulatory functions. Folding of G4 structures can cause replication stress by preventing access to the genetic information within the quadruplex. Rev1, a Y-family polymerase, helps the cell combat G4-related replicative stress through a multi-faceted mechanism of action. The Eoff lab recently used a mass spectrometry-based approach to study Rev1-dependent interactions in the G4 replisome. They discovered that loss of Rev1 leads to the accumulation of proteins involved in fork reversal and recombination-mediated fork restart in cells treated with the G4 stabilizing compound pyridostatin (PDS). One of the proteins enriched at sites of DNA synthesis in PDS-treated REV1KO cells was the Rad5 homolog Helicase-Like Transcription Factor (HLTF), a key enzyme involved in fork reversal. The goal of my summer project was to validate the proteomics results using a chromatin fractionation assay to determine if HLTF is indeed more abundant in REV1KO cells experiencing G4 stress. A long-term goal of this project is to determine if fork reversal compensates for defective translesion synthesis past G4 motifs and whether this response adequately maintains the genetic and epigenetic features necessary for the biological functions of these non-B-form DNA structures.

11A. Purification of Mutant ColG Collagenase

Moe Saiga, Josh Sakon, Osamu Matsushita, Eria Saito
Medicine, Okayama University

The objective of this collaborative research is to show how bacterial collagenases bind to and hydrolyze collagen. Bacterial collagenases belong to the Zn-metalloprotease family. Glu residue in their consensus motif, His-Glu-X-X-His, binds to a substrate water molecule, essential for hydrolytic activity. We replaced the Glu with a Gln of a bacterial collagenase ColG, resulting that it can bind to collagen but not hydrolyze them. We expect it forms a stable complex with triple-helical substrate mimics. We will continue the structural study at Dr. Sakon's lab.

11B. Purification of WT ColG Collagenase

Eria Saito, Joshua Sakon, Osamu Matsushita, Moe Saiga
Medicine, Okayama University

Clostridium histolyticum, a causative agent for gas gangrene, is known to produce two classes of collagenases to destroy collagen fibrils. Class I collagenase, ColG, has a multi-domain structure composed of a Catalytic Module, CM; a Polycystic Kidney Disease domain, PKD; and two collagen-binding domains, CBDs. It is not well understood how the PKD and CBD jointly supply CM with a tropocollagen molecule, nor how CM unfolds the triple helix. We have tried to produce full-length ColG using an E. coli signal peptide, but it was not secreted. We fused His-tag at the N-terminus of ColG, but this protein did not bind to Ni-affinity beads. We inspected the CBD structure (PDB 4HPK) to find that the C-terminal carboxyl group is freely available. We fused His-tag at the C-terminus of ColG to purify the protein in a sufficient yield. We just started structural analysis in Dr. Sakon's lab.

12A. Vitro Bacteriophage Treatment for a Staphylococcus Aureus and Pseudomonas Aeruginosa Co-culture

Alexis Perry, Waqas Chaudhry, Nathan Reyna, Ruth Plymale
Biology, Ouachita Baptist University

Recent studies show that up 27-36% of all infections are polymicrobial, involving more than one bacteria species. In all categories, polymicrobial infections are often more virulent and harmful to the patient. Since different types of bacteria can communicate with each other through quorum-sensing when in the presence of each other, they can display different genomic characteristics. Further research into polymicrobial infections needs to be done because these changing characteristics can prevent treatment from working, such as antibiotics or bacteriophage therapy. This experiment focused on the co-culture between the two bacteria, Pseudomonas aeruginosa and Staphylococcus aureus, which can be found co-existing in Cystic fibrosis patients. With an HRQT assay, the two experiments were conducted: comparing phage's capability when a bacterium was put in another bacteria's filtrate and a phage cocktail's ability when put into a co-culture of Pseudomonas and Staphylococcus. The results in the first experiment showed a significant influence of a bacteria's filtrate on both the growth of other bacteria and the ability of phage to lyse. In the second experiment, the phage cocktail was still able to kill the bacteria for 6 more hours than the control. When comparing the phage capability between the two experiments, the results emphasize the importance of quorum-sensing between bacteria.

12B. Predicting Prophage Clusters Using Phylogenetic Trees

Luke Lawson, Ruth Plymale
Biology, Ouachita Baptist University

In this experiment we are proposing to identify the phylogenetic cluster for putative prophage detected in Gordonia genomes using a SplitsTree diagram. The results of this experiment will tentatively identify the cluster of prophages, allowing better interpretation of interactions between lysogens and different phage. The initial database of phage genomes were chosen at random from the fifteen most populated Gordonia phage clusters on phagesDB and these genomes were used to create the base SplitsTree diagram. We then attempted to validate the predictive ability of the diagram by mapping ten phage from known but blinded clusters (the "known unknown" phage). Subsequently, Gordonia genomes were chosen at random from the list of complete Gordonia genomes on NCBI and run through PHASTER in order to identify putative prophages. These putative prophage genomes were then added to the base SplitsTree diagram and their cluster was predicted. The results of this analysis will be presented.

13A. Prevalence and Characterization of Antibiotic Resistant Strains of Enterococcus spp. And Acinetobacter spp. In Community Household Environment

Madison Reese, Niamh Dixon, Monika Jirak, Alex Tush, Anuradha Ghosh
Biology, Pittsburg State University

With increasing prevalence of antibiotic resistance threats, there is an upsurge in the occurrence of community-acquired infections. The purpose of this study is to assess the ecology and prevalence of Enterococcus spp. and Acinetobacter spp. (that are well-known antibiotic resistant nosocomial pathogens) in the household environment. Each household sampling kit contained 5 swabs for each of shoe bottom, restroom, cleaning supply, kitchen top, and door step/handle as well as a demographic data sheet to be filled up. A total of 30 such kits (n=150) have been processed. The swabs were subjected to enrichment using selective media for test bacterial species. A panel of antibiotics were selected for testing using disc-diffusion method. Twenty-two out of 30 (73%) and 28/30 (93%) kits were positive for growth of Enterococcus spp. and Acinetobacter spp., respectively. Door steps, cleaning supplies, and shoe soles (13-20%) were less frequently contaminated with enterococci compared to that of kitchen tops (16/30, 53%) and restrooms (12/30, 40%). Although majority of the locations swabbed were contaminated with suspected Acinetobacter spp., door step/handles were free of any selected microbe. Overall, 102/150 (68%) of the swabbed surfaces were contaminated with Acinetobacter spp. in contrast to 43/150 (28%) with enterococci. Biochemical tests confirmed identity of 34% (140 out of 408) Acinetobacter and 71% (123/172) Enterococcus isolates at the genus level. Susceptibility testing revealed 41 of each of Acinetobacter and enterococcal isolates were resistant to 3-6 antibiotics. Multi-drug resistant isolates are being tested for their capability of forming biofilms in 96-well microtiter plates along with their amylase and protease production using agar-media based assays. The antibiotic-resistant isolates will be genotyped and compared to their relative nosocomial strains. The community will be outreached with recommended cleaning protocol and stewardship in antibiotic consumption and resistance. The outcome of this study may help facilitate effective and appropriate antibiotic treatment against community-acquired infections.

13B. Characterization of Culturable Bacterial Isolates Obtained from Guano of Gray Bats in Southeast Kansas

Bobbi Monroe, Haley Price, Alexis Paynter, Andrew George, Anuradha Ghosh
Biology, Pittsburg State University

Humans have historically had an ambivalent relationship with bats. On one hand, bats perform an important service to humans by reducing populations of insect pests. On the other hand, they can act as reservoirs of diseases, as highlighted by the recent Coronavirus pandemic. In the U.S., many bat populations have been threatened by white nose syndrome, caused by the fungus Pseudogymnoascus destructans. This study aims to characterize the bacterial and fungal diversity associated with the Gray Bat (Myotis grisescens) in southeast Kansas. Guano samples were collected from bats roosting in the sewer system and a total of 32 bacterial isolates with different colony morphology were recovered on tryptic soy agar media after enrichment. The majority (21/32, 65%) of isolates was Gram positive. All isolates were tested for their growth on various selective and differential media. Sugar fermentation profiles generated using glucose, maltose, lactose, and sucrose showed that 78% (25 of all isolates) fermented all four sugars, 9% (3/32) fermented three sugars, another 9% (3/32) fermented two sugars, and one isolate (3%) fermented only one sugar. Notably, urea was hydrolyzed by seven (21%) isolates while one isolate (3%) was positive for indole production. Experiments are underway to isolate fungal isolates as well as to determine sensitivity to antibiotics. Identification of both known and novel bacteria/fungi in bats is important for prevention of disease spread and in the long-term preservation of bat populations.

14A. Developing an Angelman Syndrome Model in Drosophila Melanogaster Using Tissue-Specific Crispr to Knockout Dube3a

Katherine Cruse, Benjamin Geier, Walter Kreuger Lawrence T. Reiter
Neurology, Rhodes College

Angelman Syndrome (AS) is a neurological disorder occurring in ~1/15,000 births and is characterized by cognitive disability, ataxia, seizures, speech impairment, and a happy disposition with sporadic bursts of laughter. AS is caused by a loss-of-function or deletion mutations in the maternal allele of UBE3A, a gene that encodes an E3 ubiquitin ligase. Drosophila UBE3A, or Dube3a, is 77% identical to the human protein, making Drosophila melanogaster a powerful genetic model for AS studies. Although there is an AS model which was developed in Drosophila, Wu et al 2008, the two alleles from this original study, specifically Dube3a-15b, have genetically drifted and are no longer homozygous viable. In addition, AS is caused by a complete loss of UBE3A function, but the Dube3a-15b allele may still make some product hindering the potency of AS specific experimentation. Our goal was to use new tools available in Drosophila to produce an improved AS model via a complete excision of the Dube3a locus using a tissue-specific CRISPR-Cas9 system. Moreover, using this system, we will make Dube3a loss of function excisions in somatic tissues (neurons and glial cells) to observe which tissue-specific deletions lead to ataxia, a key phenotype of AS. We have not yet achieved a successful Dube3a knockout in the germline, but we continue to perform the crossing scheme to capture the moment when the Cas9-gRNA system successfully creates Dube3a deletions in fly gametes. We have observed significantly slower climbing ability of flies with a ubiquitous deletion (actin-Cas9) and a glial cell (repo-Cas9) specific deletions of Dube3a compared to control flies, but we are still collecting data for climbing rates of flies with neuronal-specific deletions (elav-Cas9).

14B. Elucidating the Potential Role of Candidate dube3a Substrates in the Pathogenesis of dup15q Syndrome

Anna Sherwood, Benjamin Geier, Lawrence T. Reiter
Neurology, Rhodes College
Biomedical Sciences / Neurology / Anatomy and Neurobiology / Pediatrics, University of Tennessee Health Science Center

Duplication 15q syndrome (Dup15q) is a genetic disorder with a prevalence of ~1 in 50,000 children. Characteristics include intellectual disability, hypotonia, epilepsy, and a high incidence of Autism Spectrum Disorder. Dup15q is caused by the presence of at least one additional copy of the Prader-Willi/Angelman critical region (PWACR) in the chromosome 15q11.2-q.13.1 region. Within the PWACR is the paternally imprinted gene UBE3A (maternally expressed). This gene encodes a ubiquitin ligase E3A (UBE3A), a HECT ligase whose primary role is targeting proteins for proteasomal degradation. Excess UBE3A from the duplicated locus may cause the unwanted degradation of substrates, resulting in complex phenotypes presented by children suffering from Dup15q. To investigate the molecular etiology of Dup15q syndrome we are using the powerful genetic model Drosophila melanogaster. Drosophila UBE3A (Dube3a) shares high homology (~77%) to human UBE3A, making Drosophila an excellent model to study Dup15q. Previous proteomics work in our lab revealed a list of potential Dube3a substrate candidates that may be involved in Dup15q pathogenesis. Our goal here is to examine if cell-specific knockdowns (KDs) of these proteins of interest (POIs) can recapitulate the disease phenotypes of Dup15q. For these studies we used available UAS-TRiP/RNAi (gene silencer) lines to KD our POIs. Flies from the UAS-RNAi lines were crossed with flies from cell-specific Gal4 drivers, including actin-Gal4 (global), elav-Gal4 (neuron-specific), and repo-Gal4 (glial). The progeny of these crosses were tested using a Bang Sensitivity Assay for seizure susceptibility and observed for both seizure activity and other behavioral abnormalities, like motor deficits. Of the UAS-

RNAi lines tested thus far RPN10 and ArgK displayed the strongest seizure phenotype when compared to TRiP control lines. Additionally, while the KD of AnxB10 did not result in a seizure phenotype, a high percentage displayed motor deficits that will require further investigation. These studies will reveal Dube3a substrates that may be involved in motor and seizure defects found in Dup15q syndrome.

15A. Computational Analysis of Potential SARS-CoV-2 Main Protease Resistant Mutants against Paxlovid

Emma Chavez, Christine Zardecki, Sagar D. Khare, Stephen K. Burley, Brian P. Hudson, Zhoufan Shen, Joseph H. Lubin, Jordania Urquizo, Margeaux Meyers
Biochemistry and Molecular Biology, Hendrix College

The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) pandemic has led to an urgent need for antiviral medication. The US Food and Drug Adminstration (FDA) has approved the emergency use of Paxlovid for the treatment of mild-to-moderate SARS-CoV-2. Paxlovid combines ritonavir and nirmatrelvir to inhibit the main protease 3CLpro (also known as Mpro) of SARS-CoV-2 and prevent its replication. Mpro, a cysteine protease, cleaves a polypeptide into non-structural proteins that are crucial for the replication of the virus (Jochamns et al. 2022). Previous studies have shown that Mpro is highly conserved and resistant to mutations in the active site, making it an attractive target for drug design (Lubin et al. 2022). However, as SARS-CoV-2 evolves, mutations in Mpro can lead to Paxlovid resistant strains. Pfizer's release of nirmatrelvir has led to the development of various potential inhibitors that will function against future resistant strains of SARS-CoV-2. In this research, we use computational modeling and analysis of experimental SARS-CoV-2 structures archived in the Protein Data Bank (PDB) to identify potential escape mutations that might limit the effectiveness of inhibitors against SARS-CoV-2. To identify potential escape mutations, we curated a dataset of potential inhibitors using Mol* to visualize various Mpro-ligand complexes deposited in the PDB. Rosetta software is used to generate structural models of Mpro mutants to identify mutations that preserve Mpro function but are energetically unfavorable for inhibitor binding. Identification of potential escape mutations and inhibitors for SARS-CoV-2 may potentially mitigate future coronavirus pandemics, should another coronavirus jump the species barrier to humans. This research is funded by the NSF REU and RCSB PDB under grant DBI-1832184, US Department of Energy (DE-SC0019749), National Cancer Institute, National Institute of Allergy and Infectious Diseases, and National Institute of General Medical Sciences of the National Institutes of Health under grant R01GM133198.

15B. Quantifying Musashi in The Pituitary of Mice When the Neonatal Leptin Surge is Altered by a Mild Maternal Undernutrition

Victoria Ortega, Tiffany K. Miles, Alexandra N. Lagasse, Angela K. Odle
Biochemistry and Molecular Biology, Hendrix College

Maternal nutrition is known to affect offspring metabolic function in adulthood, but the mechanisms behind how offspring are programed for metabolic dysfunction due to maternal nutrition needs to be elucidated. Leptin is a hormone secreted by adipose tissue and regulates appetite. A surge in leptin was characterized in mice during the first postnatal week, peaking at PND10, and occurs independent of adipose mass. Current work in the Childs lab supports published data showing that the postnatal leptin surge in mice can be blunted or shifted depending on the severity of the maternal undernutrition. Musashi (MSI), a translational regulator, was reported by the Childs/MacNicol group to increase in mice lacking leptin receptors in somatotropes. The focus of this study is to determine the effect of an altered neonatal leptin surge, due to maternal undernutrition, on Msi mRNA expression in the pituitary. The hypothesis is that a 30% maternal caloric restriction mice model will decrease serum leptin at PND10 and cause an increase in Msi gene expression in the

pituitary. In this study, we characterized in the offspring of ad libitum (control) fed and 30% calorically restricted dams (CR30) both neonatal serum leptin and pituitary Msi mRNA expression. To initially determine the impact of low leptin on Msi expression, we measured serum leptin and Msi targets (extracted by immunoprecipitation) at postnatal-day (PND) 4, 5, and 15, when leptin expression is expected to be low. Interestingly, mRNA was not detected at PND4 and 5 but was detected at PND15. Pituitaries and trunk serum of offspring from underfed (CR30) and fed dams was collected at PND10, the expected peak of the neonatal leptin surge. Serum leptin in CR30 offspring was lower compared to fed offspring. Pituitary Msi1 expression was unchanged in the CR30 offspring. Msi2 expression decreased by over 50%. Pou1f1 expression decreased by over 80% in the CR30 offspring. This data completed the characterization of an altered neonatal leptin curve, showing that the CR30 diet blunted the neonatal leptin surge in offspring. Msi regulation needs to be further quantified to provide insight into maternal nutritional programing on pituitary development.

16A. Characterization of Snake Immunity for a Novel Animal Model

Alana Hedden, Jeremy Chamberlain, Lorin Neuman-Lee, Daniel McDermott
Biology, Southern Arkansas University

A challenge with human immune and disease research is the use of genetically inbred animal models maintained in highly controlled environments that do not represent inherent variability in human populations. One way to address this issue is comparatively examining wild, non-traditional vertebrate populations. Additionally, most research has focused on organisms with robust adaptive immune responses, obscuring observation of innate response. Natricines snakes exhibit robust and primarily innate immune responses. Therefore, these common reptiles are a promising vertebrate model for answering questions about variability and diversity in innate immune responses. However, reptilian models are poorly understood in immune research. In order to establish these animals as a model in immune and disease research, we quantified different leukocyte subsets of three species of watersnake (Nerodia fasciata, N. rhombifer, N. erythrogaster) from southern Arkansas. We assessed functional immune responses using flow cytometry to determine the make-up of specific immune cell populations in the blood, including lymphocytes, heterophils and azurophils. We quantified baseline cell population frequencies to assess levels of variability between several parameters, including sex and inter-species. Additionally, we examined individual responses to stress. This research allows us to assess differences in innate immune cell populations and variability in immunocompetence in heterogeneous wild populations. By establishing snakes as a model system to examine the innate immune system, we are able to better parse this critical immune system which hopefully can be translated to human systems.

16B. Aligned Type I Collagen Scaffolds for Peripheral Nerve Repair

Danielle Cagna, Mackenzie Lewis, Gabriel David, Young Hye Song
Biomedical Engineering, University of Arkansas at Fayetteville

Peripheral nerve injury affects about 13-23 out of every 100,000 people worldwide each year. Nerve grafts are commonly used to repair damaged nerves; however, they are limited in their construction and customization. Type I collagen scaffolds have grown in interest as an alternative for testing and implantation. Studies have found that manipulating axonal direction has an advantageous effect in the treatment of peripheral nerve repair. Furthermore, collagen scaffolds embedded with adipose-derived stem cells (ASCs) have been found to secrete proangiogenic and neurotrophic factors, as well as create degradation pores which allow the invasion of other cell types. This study aims to create an aligned collagen I scaffold with embedded ASCs that promotes aligned neurite outgrowth and an increase in neurotrophic and proangiogenic signaling. The collagen concentration and ASC density were optimized to create scaffolds which

provide support while also allowing cell growth. The ASCs were shown to align and remain viable in the aligned collagen scaffolds. These ASCs were also found to secrete neurotrophins and deposit aligned ECM. Further testing may involve implantation of these scaffolds to observe the response of the ASCs in vivo.

17A. Testing of Potential Small Molecule Therapeutics for Antibacterial Properties Using Bacteria and Dictyostelium – Microbe Model System

Sydney Du, Jeff Shaver, Sandhya Baviskar, Roger Lightner
Biological Sciences, University of Arkansas at Fort Smith

Multidrug-resistant (MDR) bacteria are a notorious threat to global public health, earning their reputation for killing at least 1.27 million people worldwide. Antibiotic-resistant bacterial infections threaten our ability to control and treat infectious diseases, thus making novel antibacterial scaffolds for the treatment of such infections a high and urgent demand. A majority of these infections are caused by the ESKAPE panel of MDR bacteria, which includes Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acetinobacter baumanii, Pseudomonas aeruginosa, and Enterobacteriaceae species. Penicillin-binding protein 2x co-crystal structure (PBP-2X) from Streptococcus pneumoniae (PDB: 2ZC3) and dihydrofolate reductase co-crystal structure (DHFR) from Staphylococcus aureus S1 (PDB: 2W9S) were employed to identify small molecules with potential inhibitory activity. Based on the results from a collaborative molecular modeling-based screening study against both receptors, a group of small molecules from the MolPort library were shown to possibly have inhibitory activity. MolPort-002-251-854 (receptor: PBP-2X), MolPort-019-887-571 (receptor: PBP-2X), and MolPort-027-859-042 (receptor: DHFR) were 3 of the multiple small molecules that presented strong binding affinities for their respective receptors. For our current study, using these 3 antibacterial candidates, we utilize traditional disk diffusion assay and minimum inhibitory concentration (MIC) determination tests to determine the antimicrobial properties of each drug candidate against safe standard (Staphylococcus epidermidis and Escherichia coli) bacteria. Future studies may also include Pseudomonas aeruginosa and pathogenic bacteria (e.g., Methicillin-resistant S. aureus (MRSA) and P. aeruginosa). Since a high percentage of antimicrobial agents fail when tested in cell-based assays or in vivo conditions, these potential agents will also be further screened using Dictyostelium discoideum as a host-pathogen model.

17B. Identifying Sources of Eurasian Hemp Borer Resistance in Hemp (C. sativa)

Mataya Duncan, Shelby Ellison
Biology, University of Arkansas at Little Rock

The biggest insect pest to hemp (C. sativa) in the midwest United States is Eurasian Hemp Borer (EHB). Currently, there are no synthetic insecticide options legally available for use in the crop. Feralized hemp has grown throughout the Midwest during the past 7 decades despite Cannabis becoming illegal at the same time. This material may be a source of genetic resistance for EHB as it has thrived in the presence of the pest during this time. In this study, feral and cultivated hemp accessions were screened for EHB in leaf, stem, and floral tissue as well as other phenotypic traits, plant height and stem diameter, to identify potential sources of genetic resistance or tolerance to EHB. We found no significant differences in EHB prevalence between feral and cultivated hemp accessions.

18A. Identification of the Causative Agent of Cucurbit Leaf Spot Disease in Oklahoma

Hannah Taber, Jenna Teyrien, Dulanjani Wijayasekara
Biology, Northeastern State University

Bacterial leaf spot disease is known to cause by Xanthomonas campestris pv. cucurbitae, a gram-negative bacterium. Bacterial leaf spot disease is one of the most important diseases of cucurbits

which was first reported in Hubbard squash in New York in 1926. Symptoms of bacterial leaf spot disease appear small and dark lesions with a yellow margin on leaves and later coalesce to form larger necrotic areas. Squash and pumpkin leaf samples with symptoms including severe dark small, and round necrotic spots with yellow margins were collected from Oklahoma. The causative agent of the disease was isolated by surface sterilizing lesions, planting them on nutrient agar plates, and incubating at 25°C for 48 hours. A total of eighteen bacterial isolates were obtained from squash samples and eleven isolates from pumpkins. All these bacterial isolates were subjected to Gram staining, simple stanning, several biochemical tests (Oxidase, Catalase, KOH, and Kovac's), and differential media (Simmons citrate, Triple sugar Ion, Motality, and MacConkey) to confirm the identity of the bacteria. All 18 isolates from squash and eleven from pumpkin were Gram-positive bacillus. None of the bacterial isolates from squash and pumpkin could grow colonies on MacConkey agar. Nine out of eighteen bacterial isolates from squash were non-motile, while the rest showed turbidity in the motility test. All eighteen isolates from squash were catalase positive. Further, ten isolates were Kovac's positive. All eighteen squash isolates were inoculated to two-week-old squash seedlings, and only one isolate was able to produce symptoms. Our study showed that one bacterial isolate from squash could have symptoms on seedlings, and this isolate will be sent to be sequenced to confirm identity further.

18B. Investigating Polymerase Epsilon's Role in Replication Initiation and Elongation by the Analysis of Pol 2 Mutants

Victoria Fairchild, Carlos Cuza, Sapna Das-Bradoo
Natural Sciences, Northeastern State University

DNA Polymerase Epsilon (Pol ε) is essential for replication of a cell's genome. It plays an important role in the synthesis of the leading strand of DNA. Malfunctions of Pol ε are associated with cancers and other diseases. Replication of DNA is a very important process and thus prompts the investigation into the structure, function and associations of Pol ε. There is still more to understand about the structure of Pol ε, but it is known that it is made of four subunits each with their own unique roles. In yeast, the subunits are referred to as Pol2, dpb2, dbp3, and dpb4. In our laboratory, we are interested in investigating if mutations in the essential C-terminus of Pol2 disrupt origin activation and the replication elongation process. For this purpose, we studied two Pol2 mutants, pol2-GE1425,1428AA, which disrupts interaction with Mcm10 and pol2-W1272A, which interferes with a stable Pol ε complex formation. DNA sequences bound to Pol2 were pulled down by Chromatin immunoprecipitation and purified. Then PCR was performed to test for the presence of early, late origins and non-origins to assess if there was a loss of functionality in replication within the mutant yeast cells. Our findings exhibit that pol2-GE1425,1428AA mutants show a delay in binding to early and late origins (late S phase) while the pol2-W1272A mutants exhibit an unstable association with both early and late origins. These results are in contrast to the wild-type Pol2 cells that associate with early and late origins in early S phase. Similarly, wild-type Pol2 proceeds with elongation, but the mutants showed significantly delayed progress. We plan to repeat our experiments with the mutants and perform quantitative PCR to further investigate this replication delay in the mutant cells.

19A. Investigation of Cell Sorting During Notochordal Morphogenesis in Xenopus Laevis

Alexis Vann, Emily Fronek, Alexis Altamirano, Mick Yoder
Biology, University of Central Arkansas

Embryonic development is a highly complex process leading to the formation of a fully formed organism from a single fertilized egg. Aberrations in this process can lead to numerous types of congenital birth defects including heart and muscle malformations and spina bifida. Morphogenesis of embryonic tissues is facilitated by changes in cell-cell adhesion, allowing for the formation of these

complex structures. Cells can regulate the amounts or types of adhesion molecules in their membranes, making them distinct from their neighbors, leading to differential cell adhesion. In most instances, the cadherin superfamily of proteins plays a central role in this process and their effect can be fine-tuned through the co-expression of specific regulatory proteins. In the frog model, Xenopus laevis, a classical cadherin called C-cadherin is the only cadherin protein expressed throughout early development, so early morphogenetic events require tissue-specific regulation of C-cadherin-based adhesion. This can be observed in mesodermal tissue, as it sorts into two distinct sub-populations: axial mesoderm and paraxial mesoderm, giving rise to the notochord and somites, respectively. A sub-group of the cadherin superfamily, called protocadherins, are known regulators of cadherin-based adhesion, where protocadherin8 (pchd8) can down-regulate C-cadherin adhesion and cause cells to sort to the paraxial mesoderm. Conversely, cells that express a related protein, pcdh1, specifically sort into the axial mesoderm and later into the developing notochord. Previous work shows that pcdh1 does not directly influence C-cadherin adhesion, but is required for notochord formation, so this project is designed to understand the functional mechanism of pcdh1-based cell sorting, using explanted X. laevis tissues and live-cell imaging.

19B. Optimization of Plate Based SP4 (Solvent Precipitation, Single-pot, Solid-Phase Sample Preparation) Protein Digestion Method with Using Positive Pressure Manifold

Dayoung Eom, Walker Hendricks, Aaron Storey, Dennis Province
Biology, University of Central Arkansas

Proteomics is the study of the proteome, which is the entire set of proteins expressed by a genome, cell, tissue, or organism at a specific time under defined conditions. The IDeA National Resource for Quantitative Proteomics performs ‘bottom-up’ proteomics, using nano-LC coupled to Orbitrap mass spectrometers to obtain quantitative information on peptides that are digested from the proteins. It is significant to conduct complete, reproducible, high throughput protein digestion from the starting level of the sample because, due to the dynamic range of the proteome, it always has a ‘dark corner’ of the proteome where MS has difficulty detecting. Single-pot, solid-phase sample preparation (SP3) has been a remarkable protein digestion method in which organic solvent and magnetic beads denature and capture proteins while removing contaminants. However, SP3 potentially loses peptides during wash steps, and small carboxylated coated magnetic bead particles can clog the LC system and MS instruments. On the other hand, a modified version of the SP3 method (SP4) omits magnetic beads, and instead, it uses a high organic solvent and spherical glass beads to capture protein from cell lysates, promoting elevated protein recovery. We designed a plate-based SP4 protocol using a TECAN A200 machine, a positive pressure manifold with an automated liquid dispenser, to pursue a high throughput protein digestion method. First, we compared the number of protein and peptide IDs detected from the plate-based SP4, SP3, and chloroform-methanol extraction (CME), the most common traditional protein digestion method, to evaluate the efficiency of the plate-based SP4. Plate-based SP4 showed a comparable result of protein ID detected compared to CME and SP3 but with 40% less work time. Also, the plate-based SP4 method was further optimized by examining the range of the organic solvent, Acetonitrile (ACN), different sample sizes, and different detergent amounts of Sodium Dodecyl Sulfate (SDS) and Radio Immunoprecipitation Assay buffer (RIPA).

20A. Application and Refinement of The Protein Landscape

Cole Dwyer, Dina L. Newman, Kate Wright
Biology, University of Arkansas at Little Rock

Proteins are important biomolecules that are not directly observable to learners, and are depicted with a wide variety of representations. A protein's form or shape often indicates its function, but figures may not accurately depict this relationship. To investigate the landscape of protein illustrations,

we analyzed protein-containing figures from 8 undergraduate textbooks (n=4364) and 8 scientific journals (n=1236). We refined and implemented a new framework known as The Protein Landscape, which classifies illustrations of proteins based on their scale and degree of realism. Biochemistry textbooks showcase more aspects of proteins, with more emphasis on realistic shapes than both biology textbooks and journals. Textbook figures skew towards abstract representations of protein-protein interactions, while figures in journals have a more diverse spread. Furthermore, transport proteins have the least abstraction in textbooks. The Protein Landscape is a useful tool for educators and researchers to improve biology education.

20B. Parental Influence on Programming of Adipose Tissue in Offspring

Ahad Nadeem, Henry A. Paz, Ying Zhong, Umesh D. Wankhade
Biology, University of Arkansas at Little Rock

Background: Obesity, a disease characterized by excessive fat accumulation, is widely prevalent in the United States. Amongst several well-studied causes such as genetics, reduced physical activity, and poor diet, parental role in programming of obesity has been overlooked. Parental dietary habits and behavioral patterns prior to and during pregnancy have been shown to play a role in inducing obesity in early childhood and adulthood. Furthermore, environmental temperature has a direct impact on metabolism, especially cold temperature which is a known activator of brown adipose tissue, the main site of non-shivering thermogenesis. Objective: In this study, we are seeking to discover how ambient temperature modification prior to and during pregnancy impacts offspring metabolism. We hypothesize that ambient temperature manipulations in both parents prior to conception and during pregnancy lead to altered programming of adipose tissue and influences metabolism and disease risk in offspring. Methods: For 1 week prior to conception, both male and female mice were kept at 22°C (room temperature), 8°C (cold exposure), or 30°C (thermoneutral). Female mice, after conception, continued at their respective ambient temperatures for 2.5 weeks. The offspring born to the different temperature treated parents were challenged with either control diet (Con, 17% Kcal from fat) or high fat diets (HFD, 45% Kcal from fat). Metabolic phenotyping (weight, food intake, body composition, indirect calorimetry, etc.) was performed on the offspring during the dietary intervention. Upon euthanization, all adipose tissue depots were collected for histology, transcript and protein assays. Results: Ucp1 expression was not affected by parental temperature or diet in females, but a significant interaction (parental temp and offspring diet) ($P = 0.001$) was observed in males. For male mice fed the Con diet, ucp1 expression was greater at 8°C, whereas for male mice fed the HFD, Ucp1 expression was greater at 30°C. Dio2 expression was affected by diet ($P = 0.003$) only in male mice where dio2 expression was greater in mice fed HFD compared to control. Parental temperature did not affect Dio2 expression in female or male mice. Conclusions: Parental temperature and diet impacted expression of gene markers of BAT thermogenesis in a sexually dimorphic manner. Further analyses are planned in order to contextualize these results. Future directions for research include uncovering novel gene/protein targets and signaling pathways influenced by parental treatment. Funding: This research was supported, in part, by the Arkansas Children's Research Institute, the Arkansas Biosciences Institute, and the Center for Childhood Obesity Prevention funded under the National Institutes of Health (P20GM109096).

21A. KRAS Mutation Cell Metastasis

Mackenzie Rodgers, Djamali Muhoza
Biochemistry, University of Arkansas at Monticello

This presentation is over the marvels of the capability of small molecule binding to protein pockets in hopes of finding a drug for KRAS to put an end to the metastasis of cancer cells. Kras is a proto-oncogene responsible for making the Kristen RAt Sarcoma virus. This gene is the main reason for cell growth and development serving as your bodies' own personal light switch. When switched

on it tells cells to grow and then once guanosine triphosphate (GTP) converts into guanosine diphosphate (GDP) the switch gets turned off. The mutation causes the switch to stay on and never converting into GDP thus resulting in the metastasis of cancer cells. Our goal is to use simulation docking and find small molecules with high binding affinities capable of attaching to the mutation and continuing the process of GTP to GDP conversion thus stopping the metastasis of cancer cells from the KRAS mutation. Then use the best molecules to convert into a drugs and test on live cells.

21B. Ticks and Tick-Borne Pathogens in Feral Hogs in Southeast Arkansas

Mark Hairston, Keith Blount, Ty Say
Mathematical and Natural Sciences, University of Arkansas at Monticello

Feral Hogs (Sus scrofa) are an invasive species to the United States living throughout Arkansas. They damage agriculture, timber land, and harm other animal populations by outcompeting for food sources. Ticks and their associated pathogens are carried by the hogs and the widespread home range of hogs creates the potential for spread of these diseases. In this study from June 2021-August 2022, feral hogs were killed in traps set by USDA APHIS Wildlife Services and ticks were collected to be sampled for pathogens. 186 out of 253 hogs sampled were infested with several species of ticks. Four species of ticks observed include: the Lone Star tick (Amblyomma americanum), American Dog Tick (Dermacentor variabilis), Black Legged Tick (Ixodes Scapularis), and the Gulf Coast tick (Amblyomma maculatum). As of 2021, 66 feral hogs and 351 ticks were examined, A. americanum (n=224), D. variabilis (n=41), and A. maculatum (n=33) coming to a mean of 5 ticks per hog. These ticks were divided into pools of their sex, lifestage, and host sampled from. There were also 3 unidentified nymphs present. Pathogens observed were Rickettsia amblyommatis, Borrelia burgdorferi, Ehrlichia ewingii, Ehrlichia chaffeensis, Rickettsia rickettsii, Rickettsia parkeri, and the novel agent Rickettsia buchneri. Sex and age of the hogs seemed to have an effect on infection rates of certain species were prevalent. This study is done in conjunction with an ongoing survey through the University of Arkansas-Monticello dealing with off host ticks. Additional ticks have been sampled but are not yet recognized in this study's results.

22A. Evaluation of Antibacterial Activity of Native Plants, Aesculus Pavia and Celtis laevigata

Katie Huffman, Raven Turner, Suparna Chatterjee, Suresh Subedi
Biological Sciences, Arkansas Tech University

Aesculus pavia (red buckeye) and Celtis laevigata (Sugarberry) are native plants of Arkansas. Natural products from native plants have been found previously to have antibacterial properties. In this study, the antibacterial properties of A. pavia and C. laevigata are investigated against three gram positive (Bacillus cereus, Bacillus subtilis, and Staphylococcus epidermidis) and three negative bacteria (Alcaligenes faecalis, Escherichia coli, and Serratia marcescens). The disc diffusion assay method is employed to identify any potential antibacterial properties of both plants. For this experiment, 6.41 g of dehydrated plant material (leaves for both species) was combined with 50 mL of 75% ethanol creating their respective tinctures which were processed to remove alcohol and make power samples. The antibacterial activity of the powders in sterile Milli-Q water was tested against 75% ethanol and hydrogen peroxide controls. After 24 and 48 hours of incubation at 37°C the zones of inhibition were measured for each bacteria/plant sample combination. Both species of plant samples were tested for inhibition for the six bacteria. We used a polynomial regression analysis to examine the effect of different concentrations of each plant sample on the zone of inhibition. Preliminary investigations showed antibacterial properties in both species. Current data indicates that the native plant species in this study can have potential medicinal properties.

22B. Investigating Antibacterial Activity of Extracts From American Beautyberry, Devil's Walking Stick, and Winged Sumac

Kayla Medina, Harley Hines, Andurin Rivero, Suresh Subedi, Suparna Chatterjee
Biological Sciences, Arkansas Tech University

Many native plants are used for the treatment of various diseases. Mainly those species in high chemical compound plant families can have antimicrobial properties. We selected three native plants in Arkansas, American beautyberry (Callicarpa Americana), Devil's walking stick (Aralia spinosa), and Winged sumac (Rhus copallinum), and tested them for antibacterial properties. We used three gram-positive bacteria (Bacillus cereus, Bacillus subtilis, and Staphylococcus epidermidis) and three gram-negative bacteria (Alcaligenes faecalis, Escherichia coli, and Serratia marcescens). The disc diffusion method is employed to identify any potential antibacterial properties for the three plant species. For this experiment, 6.50 g of dehydrated plant material (leaves of each plant species) was combined with 50 mL of 75% ethanol creating their respective tinctures which were processed to remove alcohol and make power samples. The antibacterial activity of the powders in sterile Milli-Q water was tested against 75% ethanol and hydrogen peroxide controls. After 24 and 48 hours of incubation at 37°C, the zones of inhibition were measured for each bacteria/plant sample combination. The plant samples were tested for inhibition of each bacterial species. We used nested ANOVA (analysis of variance) to examine the effect of different concentrations of plant samples and two different incubation times (24h and 48h) of each plant species on zones of inhibition for six different bacteria. Preliminary investigations showed antibacterial properties in the samples. This indicates that native plant species can have potential medicinal properties.

23A. Genome-Wide Association Study of Agronomic Traits in Potato (Solanum tuberosum L.)

Re'Nyah Vincent, Laura Shannon, Xiaoxi Meng
Biology, University of Arkansas at Pine Bluff

Potato is the world's fourth most important crop following rice, wheat, and maize. According to USDA statistics, Minnesota potato production in 2020 totaled 17.9 million cwt, ranked 6th nationally in potato production. Uncovering the genetic basis of agronomic traits in potatoes (Solanum tuberosum L.) is crucial for potato breeding. Genome-Wide Association Study (GWAS) is a research method used to identify genomic variants associated with a particular trait. To discover genetic architecture governing key agronomic traits in potatoes, yield and yield components, hollow heart presence, specific gravity, chip frying color, skin color, skinning, skin lightness, tuber roundness, and tuber length width ratio were evaluated for 133 potato varieties from the year 2021 at the University of Minnesota Sand Plains Research Farm in Becker, MN. The panel of varieties was genotyped using the Potato V4 Infinium single-nucleotide polymorphism (SNP) marker array. 19,481 high-quality SNPs were used to identify loci associated with agronomic traits using GWAS. Additive, 1-dominant, and 2-dominant models were tested for each trait with the R package GWASpoly. QQplot was used to evaluate the performance of each model. Loci significantly associated with tuber weight, specific gravity, skinning, length-width ratio, and hollow heart were identified.

23B. Regulation of Castration-Resistant Prostate Cancer by Canagliflozin and Enzalutamide

Genesis Jackson, Kristian Davis, Tunde Smith, LaMonica Stewart
Biology, University of Arkansas at Pine Bluff

Prostate cancer is the most prevalent cancer in men in the United States of America. One protein associated with the progression of prostate cancer is the androgen receptor (AR). AR is a type of nuclear receptor stimulated by binding to androgens such as

testosterone and dihydrotestosterone. Consequently, androgen deprivation therapy (ADT) is the initial therapy used to treat men with metastatic prostate cancer. ADT, which lowers androgen levels in the bloodstream, initially reduces the function of AR and suppresses tumor growth. However, the tumors ultimately advance to a stage where they stop responding to ADT and become castration-resistant. Castration-resistant prostate cancer has been treated successfully with enzalutamide, an AR antagonist drug also known as MDV3100. However, resistance against enzalutamide gradually develops and the drug ceases to be effective. Therefore, there is a need for better therapeutic strategies for drug-resistant forms of prostate cancer as well as drugs that can increase sensitivity to enzalutamide. Canagliflozin is an inhibitor of the sodium-glucose cotransporter 2 (SGLT2) that is used clinically to reduce serum glucose levels in patients with type 2 diabetes. Previous results from our laboratory demonstrated that the antidiabetic medication canagliflozin reduces proliferation in multiple types of prostate cancer cells. The extent to which canagliflozin alters the growth of AR-positive castration-resistant prostate cancer cells is not known. It is also unclear if drug combinations involving canagliflozin could serve as effective treatments for prostate cancer. In the current study, we explored whether canagliflozin combined with AR antagonist enzalutamide would regulate proliferation and the AR pathways in C4-2B cells. C4-2B cells were used because they are a castration-resistant human prostate cancer cell line contains AR. Presto Blue viability assays were performed to determine the effect of the drug combination on cell proliferation, while quantitative reverse transcription-polymerase chain reaction was used to examine the impact of these drugs on the expression of AR and its target genes. Enzalutamide alone (10 uM) slightly reduced C4-2B cell proliferation. However, canagliflozin alone dramatically decreased the proliferation of C4-2B cells. A significant decrease in C4-2B cell proliferation also occurred following exposure to the combination of canagliflozin and enzalutamide. Canagliflozin alone and the canagliflozin-enzalutamide combination also reduced the amount of AR mRNA and the levels of two AR target genes, prostate-specific antigen (PSA) and Nkx3.1. Together, these data suggest that, when compared to enzalutamide, canagliflozin is a better regulator of AR signaling and proliferation of C4-2B cells and possibly other castration-resistant prostate cancer cells.

24A. Ferristatin Alleviates Inflammation-Associated Oxidative Stress in Activated Cultured Mouse Microglial Cells

Alyssa Scott, David Donley
Chemistry and Biochemistry, Harding University

Cellular signaling relies on free radicals to drive oxidation/reduction (redox) reactions. Oxidative stress is caused by the buildup of free radicals, which damage cells. Microglial cells are Central Nervous System resident immune cells that are particularly sensitive to oxidative stress. Inflammation results from oxidative stress and the microglial response to disease-associated stimuli such as amyloid beta (Aβ). In microglia, the enzymes inducible nitric oxide synthase (iNOS) and Arginase are determinants of pro- and anti-inflammatory responses of microglia, respectively. Microglial dysfunction, resulting from oxidative stress, has been implicated in the potentiation of neurodegenerative diseases such as Alzheimer's Disease (AD) and is associated with elevated iron. However, the relationship between redox-active iron, oxidative stress, and microglial inflammation is unclear. Therefore, we used immortalized murine microglia to study this relationship. We treated cells with ferristatin, a transferrin receptor inhibitor and putative radical scavenger, with and without Aβ stimulation. We determined that ferristatin decreases ROS generation in cultured microglia. We then measured iNOS and Arginase enzyme activity to study the effect of ferristatin on the activation state of microglia. Cells stimulated with Aβ and treated with ferristatin had decreased iNOS and increased Arginase activity compared to Aβ-stimulated cells. This indicates that ferristatin pushes microglia away from a pro-inflammatory state and towards an anti-inflammatory state. These data point to a pro-inflammatory role for free radicals generated by iron, but the complete

mechanism of how iron interacts with Aβ and contributes to disease-associated inflammation in microglia is unknown. However, our results indicate that dysregulation of redox-active iron promotes oxidative stress that promotes inflammation and modulates microglial responses to extrinsic stimuli.

24B. Myeloperoxidase Is a Mediator of Inflammation in Cultured Mouse Microglial Cells in Response to Amyloid-Beta 42

Tayler B. Appleton, Savannah Ewing, David W. Donley
Biology, Harding University

Free radical signaling and oxidation-reduction (redox) pathways are important inflammatory signaling mechanisms. Microglia are the primary immune cells of the Central Nervous System (CNS) that mediation inflammatory processes in the brain. Dysregulation of redox pathways promotes disease-associated oxidative stress and CNS degeneration. Recently, the pro-oxidant enzyme, myeloperoxidase (MPO) has been associated with Alzheimer's disease progression but little is known about its role in neuroinflammation. The goal of this study was to characterize the role of MPO on inflammatory responses of microglia to disease-relevant stimuli. In Alzheimer's disease, amyloid-beta-42 (Aβ-42) and elevated iron are both associated with elevated brain inflammation. We found that MPO activity is increased in cultured microglia after Aβ-42and iron stimulation. To address the role of MPO, we treated immortalized microglial cells with the MPO inhibitor (MPOi) in the presence and absence of activating stimuli. We found that the MPO decreases glycolic activity in both Aβ-42-stimulated and unstimulated cells. Since metabolic activity is a determinant of activation state, we measured the effect of MPO inhibition on production of pro-inflammatory cytokines. We found that MPO inhibition decreased cytokine production, suggesting that MPO contributes to inflammatory processes. Interestingly, we found that MPO inhibition had little effect on production of reactive oxygen species after iron and Aβ-42 stimulation These results indicate that MPO may be an indirect mediator of inflammation in microglia. Further research is needed to determine the interplay between MPO and disease-relevant stimuli and how MPO shapes the redox state of the cell. Further research is needed to determine the interplay between MPO and disease-relevant stimuli and how MPO shapes the redox state of the cell. This work will impact our understanding of the role of MPO as a biomarker for disease and mediator of inflammation.

25B. Investigation of Epoxide Adducts Using Mass Spectrometry And Nanopore Sequencing

Ethan Talley, Intawat Nookaew, Taylor Wadley
Biology, University of Arkansas at Fayetteville

Chemical mutagens can induce DNA adduct formation, which can lead to mutations and cancer. Nanopore sequencing technology can be used to identify the positions of adducts within a DNA sequence. The goal of this study was to use the Oxford Nanopore Technology (ONT) sequencing platform and the publicly available ELIGOS analysis software to detect, identify, and locate DNA adducts induced by the epoxide mutagens ethylene oxide and styrene oxide. Samples of the shuttle vector pTGFP-T7-Hha10T were treated with ethylene oxide and styrene oxide and tested for the presence of adducts using liquid chromatography-mass spectrometry. Based on the results of this analysis, samples exposed to each mutagen were chosen for nanopore sequencing, and an Ames test was performed to assess mutagenicity. Analysis of sequencing data did not clearly identify adducts, likely due to low adduct quantity. More sensitive analytical techniques or higher adduct concentrations are needed for nanopore sequencing to be practical in this application.

26A. Investigating the Molecular Mechanisms Regulating Growth Promotion and Salt Tolerance During Interactions Between Rice and Plant Growth-Promoting Bacteria, Azospirillum Brasilense

Seth Dixon, Samuel Hoggard, Zach Degon, Mary Galloway, Sophia Gulutzo, Hunter Price, Arijit Mukherjee
Biology, University of Central Arkansas

Abiotic factors (e.g., salt stress, heat and drought stress, nutrient deficiency) are major concerns for crop productivity. For instance, most food crops, such as rice and maize, display severe yield losses (50-80%) under moderate to extreme salinity. Problems associated with soil salinity are anticipated to worsen because of adverse climatic conditions. For improving crop performance under saline conditions, it is necessary to implement sustainable agricultural strategies. One option is to take advantage of beneficial plant-microbe associations. Plants can form associations with different beneficial microbes including, arbuscular mycorrhiza, rhizobia bacteria, plant growth-promoting bacteria (PGPB). Several studies have suggested that PGPB improve plant growth via multiple mechanisms, including nitrogen fixation, hormone synthesis, protection against biotic and abiotic stresses, etc. Azospirillum brasilense is one of the most studied PGPB to mitigate salinity stress in different crops such as maize and wheat. However, not much is known about the molecular mechanisms by which A. brasilense mitigates salt stress. Recently, we optimized an experimental system where rice growth was improved in A. brasilense-inoculated plants compared to the uninoculated plants when these were grown under high salt concentration. We hypothesize that A. brasilense inoculation would improve salt tolerance in rice via regulation of specific host genetic pathways previously reported to be involved in this association. Currently, we are initiating experiments to perform an RNA-seq study to identify the transcriptomic responses in rice plants during A. brasilense-mediated salt stress tolerance. Overall, our findings will provide a novel understanding of gene expression changes in A. brasilense-inoculated rice during salt stress.

26B. Uncovering the Diversity of Chlamydiae Symbionts in Social Amoebas

Donovan Clark, Mackenzie Hoogshagen, Gabe DuBose, Hailee Gerner, Bailey Skinner, Tamara S. Haselkorn
Biology, University of Central Arkansas

Bacteria in the phylum Chlamydiae have been found to be symbionts in certain amoeba species and have been found most recently in the social amoeba Dictyostelium discoideum. While Chlamydiae bacteria are mostly considered pathogens, the role of Chlamydiae in amoebae is currently unknown, and mutualistic interactions have been observed in some species. The D. discoideum Chlamydiae endosymbionts are novel bacterial lineages, and while they do not seem to have any fitness costs in the lab, their function in natural populations is unknown. Recently, Chlamydiae bacteria have also been found in natural populations of other species of social amoeba, although the prevalence, diversity, and host-specificity of these symbionts are unclear.We PCR-screened 8 different social amoeba species collected from 12 different populations across Arkansas to determine the infection prevalence and genetic diversity of Chlamydiae in different social amoeba species. For select species we sequenced the full Chlamydiae 16SrRNA gene to reconstruct a phylogeny to explore the evolutionary relationships of these symbionts and look for patterns of co-evolution and host specificity. We found high, but variable Chlamydiae infection prevalence across the different locations and among the different social amoeba host species. The highest prevalence (60%) was found in the amoeba species D. giganteum. With our PCR screen sequencing we found 41 novel Chlamydiae haplotypes in our social amoeba species. Our full-length 16SrRNA phylogenetic reconstruction shows patterns of host specificity coevolution for some of the Chlamydiae infecting our species. Social amoeba species are common hosts of diverse Chlamydiae lineages, which unlocks the potential to gain insight into the

evolution of these important parasites. Patterns of co-evolution and host specificity indicates that this is a long-term relationship. Furthermore, the high Chlamydiae prevalence in D. giganteum suggests that this may be a mutualist relationship, at least in this species, although their function remains to be determined.

27A. Genomic Characterization of Staphylococcus cohnii from Lame Broilers

Louisa C. House, Amer Hasan, Andi Asnayanti, Khawla Alharbi, Adnan Alrubaye, Douglas Rhoads
Biology, John Brown University

Our project is to characterize the genome of Staphylococcus cohnii isolates from chickens with Bacterial Chondronecrosis with Osteomyelitis (BCO). BCO has a significant impact on the welfare of chickens in the broiler industry. Samples from BCO lesions from our challenge experiments at the UA poultry research farm present a poly-microbial infection, including S. cohnii which represents a significant percentage of the isolates. Although there are bovine and human isolates of S. cohnii in the NCBI genome database, there are none from chicken isolates. Our laboratory has published that specific mobile elements are associated with other bacterial species switching to infect chickens. We are sequencing 18 distinct chicken isolates to determine if there is a mobile element present in these genomes to compare to the 81 human and cattle isolates in the database. To begin this experiment, 35 isolates of S. cohnii from the farm isolates were grown on chromogenic streak plates, and there were 6 different color patterns. Each isolate was then analyzed by qPCR with S. cohnii specific primers to confirm the species identification. Genomic DNA was purified for 18 isolates representing all 6 color patterns, and submitted for Illumina paired end (2x151) next generation sequencing. Sequence data was quality trimmed and assembled at patricbrc.org. Phylogenomic trees were constructed using poppunk to analyze core genome shared SNPs. Representative genomes from human, cattle and chicken hosts were then compared through genomic segmental BLASTs using Proksee server.

27B. Improving Sleep Medicine Referral Patterns in Children with Spina Bifida

Grace Bornemeier, Laura Hobart-Porter, Supriya Jambhekar
Biology, Ouachita Baptist University

Etiologies relate to sleep disordered breathing (central or obstructive), primary insomnia, and behavioral factors in varied degrees in myelomeningocele patients. If these sleep-related breathing disorders are left untreated, a sleep deficit can result in behavioral, cognitive, and motor impairments in an already vulnerable population. Early diagnosis, intervention, and management are key to maximizing outcome. This project is for Quality Improvement purposes and seeks to further address the connection between myelomeningocele patients and sleep related disorders. We created sleep questionnaires that include various age ranges from 0-21 years of age. The questionnaires are based on a Likert-type scale of 0 (I don't know),1 (Never), 2 (1-2 times per week), 3 (3-4 times per week), 4 (5-6 times per week), and 5 (7 or more times per week). There are two sets of questions on the questionnaires with the first set focusing on past medical/surgical history that specifically pertain to myelomeningocele patients and the second set of questions focusing on the patient's sleep habits and problems. There are three versions of the sleep questionnaires: Newborn to Early Preschool Children (Birth-4 years old), Preschool and Elementary School Children (5-12 years old), and Junior High to High School Students (13-18 years old). These three questionnaires, human determination protocol, and survey study telephone consent form were submitted for human determination approval and are currently awaiting approval. Following approval, we will obtain existing patient health and contact information through a protected medical records database at Arkansas Children's Hospital. We will contact 250 myelomeningocele patients and their families over the telephone and conduct the questionnaires with their consent. All responses and management will be stored in REDCap, a protected medical records database, and further analyzed for improved quality of treatment in the spinal cord disorders clinic and

referrals for a sleep study or sleep disorders clinic visit at Arkansas Children's Hospital.

28A. Comparative Microbiome Analysis of Cactophilic Drosophila Species

Thomas B. Crook, Gabe Dubose, Luciano Matzkin, Tamara S. Haselkorn
Natural Sciences and Mathematics, University of Central Arkansas

Microbiomes can play key roles in their host's health, ecology, and evolution. The microbiome composition has been extensively studied in the model organism Drosophila melanogaster, a generalist fruit fly species that feeds on yeasts and bacteria in a wide variety of fruits. Other species of Drosophila are cactophilic and depend entirely on different species of cactus for shelter and nutrition, although these cactus rots have toxins. It is suspected the microbiome plays a role in enabling Drosophilids to exploit the cactus as a primary food source. While the microbiota has been characterized for one species of cactophilic Drosophila, D. nigrospiracula, how the microbiota composition varies across other species of cactophilic Drosophila, and how it compares to D. melanogaster in the same location is unclear. We are conducting a microbiome analysis on individuals from four species of cactophilic flies collected from natural populations in Arizona: D. arizonae, D. mettleri, D. mojavensis, and D. nigrospiracula, as well as D. melanogaster from the same location. We have extracted DNA from 35 flies and sent samples for 16S rRNA amplicon sequencing. We are currently analyzing our sequences using the QIIME2 pipeline with the goal of comparing the microbiota composition across these different species. We expect that our cactophilic flies will have a similar microbiota composition as previously identified in D. nigrospiracula, which was dominated by Orbales, Dysgonomonas, and Serpens microbes, although there may be patterns of host specificity and compositional differences between the specialist and generalist species. This microbiome analysis of cactophilic Drosophila will lend insight into the effects of the microbiome on its host, as well as the roles of genetics and environment on microbiota composition. Once the bacterial species which constitute the microbiome have been identified, genomic databases can be used to determine the possible metabolic contributions symbionts provide their host.

28B. Macrophage Markers CD206 and CD204 Expression and Role as Prognostic Indicators

Ashley Allen, Vinay Raj
Biology, University of Arkansas at Pine Bluff

Macrophages are an important part of the immune system affecting the development and prognosis of chronic and fatal diseases. The M1 and M2 macrophage polarization and role in the cellular microenvironment contributes to their metabolic processes and the progression or suppression of the disease. CD 206 and CD 204 cell surface receptors have been extensively used as macrophage markers with their expression especially in tumor-associated- associated macrophages associated with worst prognosis in some forms of cancer but contradicting results have also been seen in some other forms of cancer. The differential expression is also a characteristic feature in other inflammatory diseases affecting the liver, lung etc. Macrophages like the Tumor Associated Macrophages (TAMs), pulmonary macrophages etc. could influence the proliferation of malignancies and other diseases. The expression of macrophage markers is becoming more significant in understanding the role of the macrophages in the different diseases. In this research, we characterized the CD206 and CD204 macrophage markers. We then studied the literature for the expression of these macrophage markers in different diseases to gain insights into the role of the macrophage polarization and also elucidate the role of these macrophage markers as prognostic indicators. Our findings suggest that an increased expression of the CD 206 and CD 204 markers has a significant impact on the outcome of patients' survival especially in solid cancers. The potential for these macrophage markers to be used as prognostic indicators has to be evaluated further extensively.

29A. Effects of Elderberry Extracts on Glioblastoma Development

Noah Solomon, Will Dockery, Kaili Ralston, MJ Exner, Gary Bates
Biology, Northwest Arkansas Community College

Glioblastoma (GBM) is an aggressive brain cancer that occurs in specialized support cells for nerve cells and is almost always lethal. Polyphenol and phytoestrogen extracts from elderberry (Sambucus nigra) have shown reduced tumor cell proliferation in breast cancer and colon cancer. Further research comparing whole berry or flower extracts to different cancers demonstrated positive reductions in proliferation as well. Experiments were conducted comparing behavior of U87 malignant cells to differing amounts of elderberry extracts. Elderberry concentrations demonstrated extreme morphological differences and elevated rates of apoptosis compared to the control cells.

29B. Effects of Curzerene Phytoalexin Extracts on Glioblastoma Proliferation

Will Dockery, Kaili Ralston, Brandon Prado, LaShall Bates
Biology, Northwest Arkansas Community College

Glioblastoma, or GBM, is a fast and aggressive malignant brain cancer. While it is one of the rarer forms of cancer, the survivability rate after five years is an extremely low five percent. Curzerene is a volatile aromatic terpenoid phytoalexin found in many plants. These plants include those in Curcuma and Commiphora. Curzerene has been shown to have promising effects in lung, liver, and colon cancer, and possibly GBM. Experiments were conducted comparing different amounts of turmeric (Curcuma longa) and myrrh (Commiphora myrrha) extracts to U87 malignant brain cells. While all concentrations of Myrrh extracts had lethal effects on GBM cells, cells grown in conjunction with turmeric had a positive effect in limiting GBM cells ability to rapidly grow and differentiate in vitro.

30A. Assessing the Relationship Between Native Arkansas Plants and Arbuscular Mycorrhizal Fungi

Amiles Ramos-Etienne, Qingfang He
Biology, University of Arkansas at Little Rock

Abiotic stresses such as drought and extreme temperatures hampers plant productivity. It is imperative to develop environment-friendly management techniques for enhancing crop productivity. One promising technique is to fertilize plants with Arbuscular mycorrhizal fungi (AMF). AMF are symbiotic fungi that allow plants to draw more nutrients and enhance their tolerance through various abiotic stresses. Nearly 90% of plant species can develop symbiotic or interdependent relations with AMF, which form vesicles, arbuscules, and hyphae in roots to significantly enhance the access of roots to a large soil surface area, improving nutrient and water absorption. The objectives of this study are: 1) to determine the composition and structure of AMF associated with native plants in Arkansas, 2) to understand the impact of human cultivation practices on AMF community structure and diversity and 3) to determine other influencing factors that might protect and increase plant productivity. Our study site will be UA Little Rock Campus garden. Soil samples will be collected, air-dried, ground and sieved to achieve desired sizes before they are used for physicochemical property determination and enzyme metabolic analysis. We will quantify available P, total N, and organic carbon following standard protocols. To assess AMF colonization and isolate AMF spores, fine roots of plants will be collected, cut, cleared, rinsed on a fine sieve, acidified and stained. AMF structures of root segments will be assessed using a light microscope. AMF colonization (%) will scored and calculated and the total number of spores will be determined using a dissecting microscope. DNA will be extracted from both samples and amplified by PCR before subjected to high throughput sequencing to analyze and identify AMF associated with native Arkansas plants. These studies will pave the foundation for their future application in conservation efforts.

30B. The Study of the Effect of Bacillus Expressing Plant Elicitor Peptides on Germination and Growth Parameters in Soybean Plants

Joseph Chrisman, Fiona Goggin, Payal Sanadhya, Abeer Alnasrawi
Biology, University of the Ozarks

Soybean is the second most widely-grown crop in the US, but it suffers significant yield losses to plant-parasitic nematodes and other pathogens. Plant elicitor peptides (Peps) are produced by plants in response to pathogens and other stresses, and they activate the plant's immune response to fight off infection. Artificially delivering "extra" doses of a plant's own Peps can provide extra protection against pathogens. Several Peps including GmPep1, GmPep2, and GmPep3 have been identified in soybean. When they are synthesized in vitro and applied to soybean seeds, they can reduce subsequent nematode infections on soybean seedlings. However, there is a need for other methods to deliver Peps throughout the plant's life cycle rather than just at the seed stage. One possible delivery method would be to use plant growth-promoting rhizobacteria (PGPR) such as Bacillus subtilis, which grow in close association with plant roots. A recent study in potato has shown that B. subtilis can be used to express and excrete Peps, and the Goggin laboratory has also developed a B. subtilis strain expressing GmPEP3 for pest management on soybean. However, it is important to test whether this Pep delivery strategy might have any beneficial or negative side-effects on plant growth. PGPRs typically promote root growth whereas some but not all studies report that Pep applications can inhibit root elongation. The objectives of my study are to measure the effects of B. subtilis expressing GmPEP3 on plant growth, and to compare these effects to those of B. subtilis or GmPep3 treatments alone. To assess plant growth, I am using image-based phenotyping to measure root morphology in addition to assessing germination rates, above- and below-ground biomass, and other measures of plant vigor. This study will help understand the effects of Pep application and develop environmentally-friendly pest management alternatives to boost plant productivity.

31A. Pathological Cross-talk Between Osteocytes and Cancer Cells in Bone Metastatic Breast Cancer

BreeAnna Scott, Manish Adhikari, Olivia Reyes-Torres, Aric Anloague, Sharmin Khan, Maria Almeida, Jesus Delgado-Calle
Mechanical Engineering, University of Arkansas at Fayetteville

Bone tissue provides a hospitable environment for breast cancer (BCa) cell proliferation and is the most common site of BCa metastasis. Previous in vitro studies in the Delgado-Calle lab using cell lines indicate that BCa cells induce senescence in osteocytes, the most abundant cells of bone tissue. In turn, factors released by osteocytes increase proliferation, migration, and invasion capacity of BCa cells. The molecular mechanisms and functional consequences of interactions between osteocytes and BCa bone metastasis remain understudied. Through ex vivo calvarial bone organ culture, we found that BCa conditioned medium (CM) upregulated the expression of senescence markers (p16, p21) and senescence-associated secretory phenotype (Mmp13, Mmp9, Vcam-1) in primary osteocytes. Additionally, using the in situ hybridization technique RNAscope, we revealed an increase in senescence-associated p-16 gene expression in primary osteocytes incubated in 50% BCa-CM. Together, these findings confirmed that BCa cells genetically reprogram osteocytes to express senescence. Next, we investigated the effect of factors released by senescent osteocytes on BCa proliferation. We used BCa-CM to produce senescent osteocyte experimental groups and applied senolytics to selectively kill senescent osteocytes for the formation of senescence-free groups. BCa cells were then incubated in CM from the various osteocyte groups, and proliferation was monitored. Selective elimination of senescent cells did not block cancer proliferation, indicating that some factors other than senescence-associated factors from osteocytes previously exposed to BCa-CM are responsible for increases in BCa proliferation.

Chemistry

101A. Synthesis and Antimelanoma Properties of Fused Thiazolo-diosgenin

Abbey Stillwell, Subrata Roy, Mohammad A. Alam
Chemistry and Physics, Arkansas State University

Diosgenin is a pharmacologically potential steroidal sapogenin found in tubers of Dioscorea villosa, wild yam. This active natural phytochemical has been used for the treatment of different diseases including cancer. Melanoma is the fifth and seventh most common cancer among men and women respectively in the United States. In this work, a library of novel thiazolo-diosgenin compounds was synthesized by using a three-step reaction process. In the first step, diosgenin was converted into diosginone using the Meerweein-Ponndorf-Verley reaction reacting with cyclohexanone and Al-isopropoxide. In the 2nd step, α,β-unsaturated ketone of diosginone is transformed into α,β-epoxyketone by using an epoxidation reaction with sodium hydroxide and hydrogen peroxide. In the 3rd step, successive nucleophilic attacks of sulfur and nitrogen of thiourea to the α,β-epoxyketone of diosgenin form a fused-thiazole ring. Two molecules of elimination of water will complete the formation of a thiazole ring with a vinylic bond near it. A total of 30 new thiazolo-diosgenin molecules were synthesized and a 400 MHz NMR spectroscopy was used to confirm the purity of the compounds. These compounds have been tested against four melanoma cell lines and several of these compounds are found to be potent growth inhibitors at micromolar concentration.

101B. Chemical and Biological Investigation of Sambucus Canadensis Anthocyanins

Elizabeth T. Martin, Harley L. Hines, Amber M. Parnell, Chiraz Soumia M. Amrine
Physical Sciences, Arkansas Tech University

New treatments for cancer and bacterial infections are needed, especially because most patients acquire resistance to conventional first-line treatments. Many natural product metabolites exhibit potent activity. Sambucus sp., or elderberry, is a well-known shrub for its therapeutic benefits. This study aims to analyze how anthocyanins are extracted from the native American Elderberry, Sambucus canadensis. It also aims to investigate the process of vinegar baking of the Elderberries to enhance the chemical space and increase the biological properties. Frozen elderberries baked in vinegar and non-vinegar baked elderberries were utilized to test this theory. A Soxhlet extractor was used to extract anthocyanins. For many liquid-liquid extraction steps, a rotary evaporator and a separatory funnel were required. The samples are subjected to normal phase chromatography, then to High-performance liquid chromatography coupled to a mass spectroscopy HPLC-MS in the hope of identifying new secondary metabolites. Our preliminary results show an improvement in the antibacterial activity with the elderberries baked in vinegar extract compared to the raw organic extract.

102A. Development of UCP1 Function Assay in Brown Adipose Tissue Mitochondria

Mary Barre, Craig Porter
Chemistry, University of Central Arkansas
Pediatrics, University of Arkansas for Medical Sciences / Arkansas Children's Research Institute

Brown adipose tissue (BAT) mitochondria contain uncoupling protein one (UCP1), which plays an important role in mammalian thermoregulation. UCP1 activity is regulated in vivo by free fatty acid concentrations as well as purine nucleotides such as ATP, ADP and GDP. One current approach to measure UCP1 function involves quantifying UCP1-dependent respiration in the presence of saturating (mM) GDP concentrations, which does not allow for the analysis of UCP1 sensitivity to GDP. Here, we describe a method to assess UCP1 sensitivity to GDP in isolated BAT mitochondria using high-resolution respirometry. Methods: BAT was harvested from the interscapular region of young male rats. Mitochondria were isolated from BAT by differential centrifugation, and protein content was determined using a bicinchoninic acid

assay. BAT mitochondrial respiratory function was measured using high-resolution respirometry via an Oroboros O2k FluorRespirometer. Respiratory substrate (10mM G3P) was added into the O2k chamber before sequential titration of GDP (over 10 injections) up to 5120 µM. The effects of GDP titration on mitochondrial respiration were used to determine the sensitivity of UCP1 to GDP by analyzing the half-maximal inhibitory concentration (IC 50) values. Results: BAT mitochondrial protein content was 6.5 mg/mL. Previous mitochondrial protein titrations revealed that 0.1 mg of protein per chamber was optimal for respirometric analysis. The measurement of IC 50 is normally indiscernible with millimolar additions of GDP. However, with micromolar additions, we determined that the IC 50 of BAT mitochondria to GDP was 319.8 µM., with a coefficient of variance of 9% (n=4 technical replicates). Conclusion: UCP1 sensitivity to GDP can be determined using micromolar titrations of GDP with high-resolution respirometry. Further experiments should establish potential diversity in UCP1 GDP sensitivity based on animal strain, tissue type, and housing conditions to determine the broader utility of this assay.

102B. Investigating the Calcium Ion Induced Changes in the Calmodulin-binding Protein PEP-19

Madeline Davidson, Mattalyn Gordon, Tori B. Dunlap
Chemistry, University of Central Arkansas

PEP-19 is a small, intrinsically disordered protein (IDP) that regulates the binding response of Calmodulin (CaM) to calcium. Calmodulin is a central translator to the calcium ion signal. It affects up to more than 300 target proteins when in the presence of calcium. PEP-19's involvement with the calcium signaling process is to bind to CaM and increase the rate of calcium ion C-terminal lobe of CaM. PEP-19 has shown decreased levels in the brain in Parkinson's disease and there is an increase of PEP-19 in the brain area spared in Alzheimer's disease. The presence of PEP-19 appears to help protect against calcium overload. Our preliminary studies have suggested that PEP-19's conformation when bound to Ca2+-CaM shows more helix, and is more compact, than when PEP-19 is bound to apo-CaM. Because the C-terminal half of PEP-19 is helical when bound to either apo- or Ca2+ CaM, we hypothesized that the extra helix seen in Ca2+ -CaM bound PEP-19 is in the N-terminal half of PEP-19. For investigation, we used circular dichroism spectropolarimetry of PEP- 19, CaM, with and without calcium to determine where the extra helix is located in PEP-19.

103A. Investigation of Photothermal Properties of Gold Nanocages for Their Potential Use in Photothermal Therapy

Kñeisha McDonald, Deborah Okyere, Jingyi Chen
Natural Sciences and Mathematics, University of the Ozarks
Chemistry and Biochemistry, University of Arkansas at Fayetteville

There has been a growing need to develop new ways to combat antibiotic-resistant pathogens. Metal nanoparticles such as gold and silver have been the subject of many antimicrobial studies. Such studies have established that, synergistically, photothermal treatment and antibiotic delivery can be used to treat bacterial infections. More will be understood by building on this foundation using gold nanocages to support their use in photothermal therapy in clinical settings. This study aims to investigate the photothermal effects of gold nanocages in water. The samples are irradiated with a diode laser centered at 808 nm and their temperature profiles are measured when the laser is on and off. Moreover, the variables for each experiment such as laser intensity and frequency are studied in detail. In water, it is found that the concentration of the samples affects the amount of energy absorbed and the rate constant of heat dissipation. The higher the concentration of the sample, the more energy is absorbed. By contrast, samples with lower concentrations have a larger rate constant of heat dissipation. The energy absorbed and dissipated are analyzed quantitatively at varying irradiation conditions.

103B. Development of Cadmium Detecting PADs for the Use of Human Milk

Kennedy White, Suzanne M. Neidhart, Robert M. Breece
Chemistry, Henderson State University

Breast milk is an infant's first line of defense from infections and viruses. Still, breast milk cannot correctly contribute to the infant's microbiome if contaminated with heavy metals such as cadmium. Our group is developing a paper analytical device (PAD) for the detection of cadmium using a G-quadruplex. Cadmium forms a complex with DNA strands to form a G-quadruplex which is detectable via fluorescents. This work is the proof of principle that we can form these G-quadruplexes in the presence of cadmium in a biological sample.

104A. Synthesis and Characterization of Copper Complexes Supported by A Binucleating Amide Ligand

Dillon Rea, Nathan Taylor, Lei Yang
Chemistry and Biochemistry, University of Central Arkansas

The goal of our work is to develop new copper complexes with potential application on carbon dioxide conversion. A binucleating amide ligand was employed in order to construct binuclear copper complexes with side-open topology. A group of Cu(II) complexes have been synthesized and characterized by X-ray crystallography, UV-vis and FT–IR. The diverse structural features of these complexes clearly demonstrated the flexibility of the ligand platform. Further characterizations of these complexes are currently in progress.

104B. Novel N-Heterocyclic Carbene Phosphonite Ligands for the Amination of Aryl Ethers

Katherine Peters, Kerry Barnett
Chemistry and Biochemistry, University of Central Arkansas

Aryl amination reactions are central to the production of bioactive organic molecules including pharmaceutical treatments for disease. The Hartwig-Buchwald Amination (HBA) reaction is the palladium catalyzed aryl amination of aryl halides and a variety of amines. However, palladium catalysts are high in cost due to the limited natural abundance of the metal ion. In addition, palladium catalysts have a limited electrophile scope for amination reactions. The use of nickel, also a Group 10 metal, in amination reactions proposes a solution to this drawback. The two main advantages to using nickel are cost effectiveness and it can oxidatively add to a wider range of electrophiles. Few studies aim to design ancillary ligands specific to nickel for the purpose of amination. It is understood that oxidative addition of Ni(0) complexes can be assisted by sigma donating ligands that create an electron rich metal center. The rate determining step is reductive elimination involving Ni(II). Studies have shown that the presence of an electron accepting ligand assists the reductive elimination step. To overcome this, our group has proposed a specific nickel designed ligand that includes both an electron donating (N-heterocyclic carbene) and an electron withdrawing (phosphonite) bond to the nickel atom. This advancement in nickel catalysis can contribute significantly to the production of pharmaceuticals and bioactive natural products.

105A. Tableau Public as a Tool to Display Air Emissions Data

Maggie Greer, Cindy White
Chemistry, Harding University
Biology, Harding University

The Arkansas Department of Energy and Environment hosts five different divisions. One of these divisions is the Division of Environmental

Quality. The Office of Air Quality is one of the offices within the division. The four sections within Air Quality include Permits, Compliance, Policy and Planning, Asbestos, and Enforcement. The Policy and Planning Branch develops plans to ensure accordance with the Clean Air Act and state laws. I completed a summer internship and research project with this branch. Air quality conditions and emissions information are gathered and evaluated by this branch in order to provide technical expertise to other branches and to the public. Part of Policy and Planning is to continuously expand on the outreach and information available to the public. Every facility in Arkansas that has an air permit is included in one dataset. This information can be entered and manipulated in Tableau to create interactive infographics. Tableau Public is a free data visualization software that can be used for many purposes. The goal of this project is to assess Tableau Public's ability to create visualizations that portray air emissions in Arkansas.

105B. Conjugating Modified DNA to Thiolated Silica Nanoparticles Towards Nanoparticle Self-Assembly

Rachel Galfo, Nathan Green
Science and Health Professions, Northeastern State University

Silica nanoparticles (SiNPs) exhibit high stability, low toxicity, and a large surface area to volume ratio, making them viable biocompatible carriers and biomarkers with significant potential for surface functionalization. Modifying functionalized SiNPs with custom ssDNA oligos allows for a system of self-assembly that effectuates controlled nanostructure formation via base pairing. This "bottom-up" approach enables greater spatial control in tuning the size and shape of nanostructures — a feature important for cellular-targeting in drug delivery systems — compared with "top-down" approaches of shaping materials from bulk. A modified Stöber method was used to prepare 30-60 nm monodisperse SiNPs which were dye-doped and regrown to encapsulate fluorophore molecules, confirmed by transmission electron microscopy (TEM). SiNPs were thiolated and subsequently conjugated with DNA via thiol-maleimide crosslinker. Gel electrophoresis was used to visualize DNA attachment by comparing movement of conjugated SiNPs against unconjugated controls. The results suggested successful formation of cross-linked DNA with unsuccessful conjugation to the thiolated silica surface. While the DNA-linker reaction is promising, further research should be conducted in running thiol-maleimide reactions to optimize conditions for SiNP DNA attachment. Successful conjugation will allow for future experiments to proceed in testing DNA-based nanostructures for properties of cell specificity and localization with applications of targeted drug delivery and biosensing.

106A. Monitoring BPA Leaching from Feminine Hygiene Products using Fluorescence Spectrophotometry

Madison Easley, Sara Hubbard
Chemistry, Ouachita Baptist University

Bisphenol-A (BPA) is a compound commonly used as a stabilizer in plastic products, including food storage containers and thermal paper receipts. Because BPA is able to bind to and activate estrogen receptors, it is linked to reduced fertility, altered development, and hormone-related cancers. A recent study at NYU Medical School confirmed the presence of BPA in pantiliners, pads, tampons, feminine washes and deodorants. This is concerning due to the high absorption capacity of the vulvar skin. For the research performed in our lab this summer, the goal was to determine if fluorescence spectrophotometry could be used to determine the presence of BPA in feminine hygiene products by monitoring the release of BPA over time into a solution of 50% methanol/water. Fluorescence is a sensitive, selective and affordable method of analysis, and BPA is a fluorescent compound that absorbs energy at 278 nm and emits at 304 nm. First, a calibration curve was obtained and analytical figures of merit were determined: linear range, limit of detection and limit of quantitation. Due to the complex sample matrix and the small concentrations of BPA in these products, the

standard addition method was employed for analysis. Pantyliners, tampons and tampon applicators were tested for the presence of BPA. The top/outside layer of the feminine hygiene product which comes into direct contact with skin was removed and cut into small pieces. In the case of applicators, the entire applicator was utilized. Samples were then placed into beakers containing 100 mL of 50% methanol/water solution, one per time point to be tested from 0 minutes to 6 hours. At each time point, aliquots of sample solution were removed and transferred to 25-mL volumetric flasks containing various concentrations of BPA stock solution. Fluorescence emission intensities at 304 nm were obtained in quadruplicate, and standard addition graphs were utilized to determine the concentration of BPA that had leached from the sample at each time point. These values were graphed to give a visual of BPA leaching from the sample over time.

106B. Albuterol Delivery Via Heated High Flow Cannula System

Joshua Spiva, Ariel Berlinski
Chemistry and Physics, Ouachita Baptist University

Heated high flow nasal cannula (HFNC) is a treatment modality widely used to provide respiratory support in pediatric patients. Delivery of aerosols through HFNC offers advantages for pediatric patients for whom removing the HFNC to administer medication may result in worsening of the respiratory condition. Aerosol delivery through HFNC may be better accepted than a mask, especially when patients require frequent administration of drugs with shorter half-lives. A recent survey showed that 75% of practitioners delivered aerosol while pediatric patients were receiving HFNC support. Aerosol size characteristics may vary as the aerosol travels through the HFNC delivery system. This is important because particle size is one of the determinants of lung deposition.Aerosol characteristics of nebulizer significantly changed when connected to HFNC system. Cannula size affected drug delivery. The reported changes in aerosol characteristics could potentially alter lung deposition.

107A. Utilizing Drug Repositioning in Order to Develop Effective Treatments for Schistosomiasis

Kassity Pace, Gregory Naumiec
Chemistry, University of Central Arkansas

Parasitic diseases have enormous health, social and economic impact and are an increasing problem in developing regions of the world. Diseases caused by protozoa and helminths, such as malaria and schistosomiasis, are the cause of most parasite-related morbidity and mortality, with an estimated 1.1 million combined deaths annually. The global burden of these diseases is exacerbated by the lack of funding for research and a lack of interest from the global healthcare industry. Unfortunately, when drugs are available, their usefulness is being increasingly threatened by parasite drug resistance. The need for new drugs drives antiparasitic drug discovery research globally and requires a range of innovative strategies to ensure a sustainable pipeline of lead compounds. For the research proposed I will be utilizing one of these approaches, drug repurposing or repositioning, with a focus on Schistosomiasis treatment.

107B. Divalent Mg2+ Ion Interactions with a Functionalized Surface and DNA

Imeril Johnson, Makenzie Long
Chemistry, University of Central Arkansas

Divalent cations such as Mg2+ can bind to DNA, then causing that DNA to bind to nanoscale structures, but the specific mechanism for this process is unknown. This research could improve the development of future DNA-based nanoscale devices, such as fluorescence signaling and biotracking. In this study molecular dynamics simulations provide information about interactions among Mg2+ ions, DNA, and MUA (11-Mercaptoundecanoic Acid). There are also Na+ and Cl- ions in the simulation to create a neutral charge. All of this is solvated by a TIP3P water box with a

vacuum above it to ensure that the MUA does not interact with itself through periodic boundary conditions. Analysis of time-based data shows that Mg2+ likes to bind through direct and indirect contacts to MUA, but primarily indirect contacts to the phosphate backbone of DNA. Na+ ions also contribute to DNA binding through direct contacts to both DNA and MUA. With the better understanding of Mg2+ ions interactions with DNA and a functionalized surface, nanoscale devices and future research can be better optimized for utilization of Mg2+.

108A. Using Recyclable PIB-bound Amines to Separate Acids from Polar Organic Solvents

Ramy Z. Yousef, Sopida Thavornpradit, David E. Bergbreiter
Chemistry, Hendrix College

Synthetic chemists must separate compounds from one another to purify them. Extraction is one technique used in the purification of organic compounds. This technique works quite well with organic acids and bases. Nevertheless, the reagents and solvents used in acid/base extractions are not always recyclable, and extraction does not work with miscible pairs of organic solvents. The purpose of this project was to synthesize a recyclable base that could be used to extract acids from polar organic solvents. We synthesized a polyisobutylene (PIB)-bound amine and used 1H NMR spectroscopy to examine the basicity of this amine in heptane relative to a similar amine in acetonitrile (MeCN). We then used this alkane-soluble PIB-bound amine to extract various organic acids from MeCN. We found that the PIB-bound amine could be used as a recyclable extracting agent and removed >90 % of benzoic acid, camphorsulfonic acid, ibuprofen, and p-toluenesulfonic acid from MeCN. The PIB-bound amine removed >70 % of acetic acid and propionic acid from MeCN. Future studies can investigate whether or not the PIB-bound amine can extract organic acids from other polar organic solvents.

108B. Kinetics of NO Reduction by the Repair of Iron-Center Enzyme, YtfE

Cierra Daniels, William A. Gunderson
Chemistry, Hendrix College

To protect against bacterial infections, mammalian cells produce high concentrations of reactive oxygen species (ROS) and reactive nitrogen species (RNS). ROS and RNS neutralize pathogens by damaging proteins, lipids, and DNA. Proteins that contain iron-sulfur (FeS) clusters are particularly susceptible to damage by nitric oxide (NO), a common RNS. FeS clusters are found ubiquitously in nature and have a wide range of functions that underlie essential biological processes including transcriptional and translational regulation, DNA replication genome maintenance, and metabolism. Disruption of FeS activity leads to inactivation of proteins and eventually cell death. One essential bacterial response system utilizes non-heme diiron enzymes that facilitate the direct repair of FeS centers following exposure to oxidative or nitrosative stress. Genes from this repair of iron cluster (RIC) class of metalloproteins have been identified in several pathogenic bacteria and are upregulated upon exposure to NO and hydrogen peroxide. Of this class of proteins, the E. coli RIC-protein YtfE is the best characterized. YtfE has been shown to reduce NO to N2O, protecting the bacteria from nitrosative stress. Here, we measured kinetic rates of NO reduction by YtfE using UV-visible spectroscopy. Catalytic turnover rates suggest that YtfE is not an efficient NO reducer, suggesting that this is not the primary function of YtfE.

109A. Substituent Effects on Solvatochromism of Group 6 Metals

Emma Dove, William T. Eckenhoff
Chemistry, Rhodes College

Solvatochromism is the property of a compound that causes it to change color in the presence of solvents with varying polarity. This phenomenon is most strikingly evidenced by a compound's variable appearances in solvents of different polarities.

Previous success in synthesizing the solvatochromic complex, [Mo(bpy)Cl4]- (bpy= 2,2'-bipyridine), which shifts over 100 nm in various solvents, lead to interest in the theoretically solvatochromic [Mo(bpy)Br4]-, [W(bpy)Br4]-, and [W(bpy)Cl4]-. However, synthesis of the bromide Mo complex, and tungsten analogs, have produced various challenges: low yields, rapid deterioration, imperfections, and extra bromide ions in the received crystal structure. Investigation into these challenges has prevented successful solvatochromism testing but given us the opportunity to synthesize the complex in multiple unique ways. Future experiments will hopefully confirm or deny [Mo(bpy)Br4]-'s and tungsten analogs' nature as solvatochromic complexes.

109B. Investigation of Ni(EtImPDI)2+ as a Catalyst for Light-driven Hydrogen Production

Robert Musicante, Liam Rhodes, Will Eckenhoff
Chemistry, Rhodes College

With an ever-increasing global population, the need for avant-garde sources of energy continues to advance as well. An alternative source of energy can be found via the implementation of artificial photosynthesis to produce hydrogen gas. Therefore, the development of more active and robust catalysts is necessary in order to make artificial photosynthesis a viable method of hydrogen generation. Recent studies have shown that metal complexes with redox non-innocent ligands and pendant base groups are highly active for proton reduction. EtPyPDI has shown to be a promising catalyst by producing hydrogen gas using Ru(bpy)32+and ascorbic acid generating turnover numbers of 1400. Because the activity of this catalyst is in part due to both the pKa and hemi-lability of the pendant base, substitution of this group may lead to improved activity. In this project, the pyridine rings were replaced with imidazole rings to synthesize EtImPDI. The ligand was then coordinated to nickel and evaluated for its activity in catalysis. Coordination and evaluation for the ligand with other common metals such as cobalt is also under investigation.

110A. Synthesis of a Novel Wound Healing Material Using Core-Shell Nanofibers Infused with AMD3100 and Tacrolimus

Rebekah Wendt, Sharon Hamilton
Chemistry, Ouachita Baptist University

The goal of wound healing is to create an environment that promotes the tissue's ability to regenerate. Since skin is the largest organ spanning the entire surface of the body it has a significant role in protection. When this organ is damaged, sterile bandages are used to aid the healing process; however, upon removal secondary wounds can occur. Core-shell nanofibers are electrospun materials that have been shown to be effective in drug release therapy which facilitates the delivery of a drug to a wound for a prolonged amount of time. As the fibers degrade a consistent distribution of the drugs are sent to the wounded tissue to promote efficient wound healing. Novel electrospun nanofibers have been infused with AMD3100 and a low dose of tacrolimus to mobilize cells for regeneration and to reduce the overall time needed to accomplish wound healing. For electrospinning, the drugs were spun with either a poly(lactic-co-glycolic acid) (PLGA) solution or a poly(vinyl alcohol) (PVA) and chitosan solution. PLGA, PVA, and chitosan, an antimicrobial natural polymer, were used because they are all biocompatible. Two drug-loaded fiber mats were prepared, one with PVA/chitosan + AMD3100 as the core and tacrolimus + PLGA as the shell. For the second type of fiber mat, the core and shell were reversed with the AMD3100 + polymer solution as the shell and the tacrolimus + polymer solution as the core. Additional nondrug-loaded mats were spun with the same configurations for negative controls. All fiber mat formulations were characterized and a cell mobility assay conducted to observe cellular responses to the novel fiber mats

110B. The Effect of Varying pH on the Leaching of BPA from Panty Liners

Kaydee Price, Sara E. Hubbard
Chemistry, Ouachita Baptist University

Bisphenol A (BPA) is an industrial chemical found in many everyday items, such as storage containers, food and drug packaging, and feminine hygiene products. BPA is an endocrine disruptor that has been linked to various health problems: reduced fertility, alterations in fetal development, and certain cancers. BPA can be absorbed dermally, which is a concern for women who use feminine hygiene products that contain BPA. Previous work in our lab determined that it is possible to monitor BPA leaching from panty liners over time into a 50% methanol/water solution using fluorescence spectrophotometry. My summer research project focused on determining the effects on the leaching of BPA from panty liners caused by changing the pH of the methanol/water solution to mimic variations in vaginal pH. BPA leaching was monitored by measuring the fluorescence emission of samples using the FS-5 spectrofluorometer from Edinburgh Instruments. BPA is a fluorescent compound that is excited at 278 nm and emits at 304 nm. A calibration curve was obtained for BPA emission versus concentration, which allowed us to determine the linear range, limit of detection and limit of quantitation for our method. Due to the complex sample matrix and small concentrations of BPA in pantiliners, the standard addition method was used. The top layer of netting from three pantiliners was collected, cut into small squares and placed into beakers that contained 100-mL 50% methanol/water. One beaker was used for each time analysis point, which ranged from 0 minutes to 6 hours. At each time point, aliquots of solution were removed from the beaker and used to prepare standard addition samples. Fluorescence emission data were obtained in quadruplicate and plotted in standard addition curves to calculate the concentration of BPA at each time point, which allowed us to monitor BPA release over time.

111A. Phosphine-Phosphinite Bidentate Ligands in Nickel Catalyzed Reactions

Savi Ahounou, Martin Quintero, Kerry Barnett
Chemistry and Biochemistry, University of Central Arkansas

Transition metal catalysis plays a large role in the production of various materials including, plastics, agrochemicals, and pharmaceutical drugs. Palladium catalysts are commonly used because of the wide reactivity range, particularly for cross-coupling reactions that allow access to the formation of new C-C, C-X bonds. Palladium metal is considered a precious metal due to a limited natural abundance and is therefore a high cost element to use. The use of nickel in catalysis has received more recent attention as an alternative to palladium. Nickel is an earth abundant metal and is more cost effective. Studies focused on the design of ancillary ligands specific for use in nickel catalyzed cross-coupling are few. It is known that oxidative addition of Ni(0) complexes is aided by the presence of sigma donating ligands that create a more electron rich metal center. However, the challenging reductive elimination step from Ni(II) is promoted by electron poor groups coordinated to the metal center. Our group has proposed a target ligand for nickel catalysis that includes one electron-poor pi-accepting arm (phosphinite) and one electron rich sigma-donor arm (trialkyl phosphine). The target ligands are prepared from a straightforward synthetic route starting with commercially available compounds. The ligands will be applied in the nickel catalyzed cross-coupling of aryl halides (pseudohalides) and various nucleophiles.

111B. TiO2-based Nanotube and Nanowire: Syntheses, Characterizations, and Applications

Misriyani, Z. Ryan Tian
Biochemistry, University of Alkhairaat

The TiO2-based nanotubes and nanowires are two highly versatile one-dimensional (1D) nanomaterials, thanks to their easy-to-control morphology and applications in photovoltaics,

photocatalysis, sensing, energy storage and nanomedicine. By varying the nanosynthesis time, temperature, and sodium hydroxide concentration, for example, the crystallinity, morphology, surface functional groups, and lattice-doping of the 1D nanostructures can be readily controlled by design, each with a high reproducibility. Mainly, the nanotube lengths can vary from 3.4 μm to 46.5 nm diameter, while the nanowire length go up to 5-10 μm and width up to 50-100 nm. Although with similar X-Ray diffraction (PXRD) and scanning electron microscope (SEM) data, these two 1D nanomaterials showed very different surface functional groups and ion exchange properties, making them to be very different one another in nanomedicine applications, which is interesting.

112A. Fabrication, Photoelectrochemical Characterizations, and Anticorrosion Applications of Ag-TiO2 Nanotubes under Visible Light

Misriyani, J. Gunlazuardi, Z. Ryan Tian
Biochemistry, University of Alkhairaat

Photoelectrochemical application for a corrosion prevention of stainless steel under visible light has become an interesting topic recently. Here we report the synthesis and modification of Ag-TiO2 nanotube (Ag-TiO2 NT) electrodes for gain the noval photoelectrochemical properties. In experiment, the TiO2 nanotube (TiO2-NT) films were synthesized by anodization of titanium foil in an electrolyte solution containing water, glycerol, and fluoride ion, followed by a heating at 500oC. Then, an Ag-TiO2 NT film was formed on the TiO2-NT surface from a silver nitrate solution. The Ag-TiO2 NT film was characterized using the Diffuse Reflectance UV-Visible Spectrometer and electrochemical workstation. The electrode showed a corrosion speed under a visible light slower than that under the UV light, and about 2 times slower than that on the bare stainless steel coupled. Further, the Ag-TiO2 NT prevented the corrosion on the stainless steel 304 under visible light, concluding a facile way to the corrosion prevention in air under sunlight.

112B. Application of ETL in Five-dimensional Single Particle Orientation and Rotational Tracking

J. Ethan Batey, Meek Yang, Bin Dong
Chemistry and Biochemistry, University of Arkansas at Fayetteville

The use of parallax for accurate five-dimensional single particle tracking has been widely used to study dynamics of nanoscale processes with high spatial and temporal resolution. This imaging method either uses a series of strategically positioned mirrors or a wedge prism to create a duplicate-split image of one particle on a portion of the same detector. The difference in the relative lateral positions of these images is used to calculate the depth of the particle in the sample. To restore y-position differences and keep the object in focus, the sample stage must be moved. This stage migration risks movement of the subject and exposes the technique to inaccuracy of multi-dimensional data. Here, we employ an electronically tunable lens paired with SPORT for five-dimensional single particle tracking using parallax PSF engineering. This methodology eliminates the need to move the sample stage during data acquisition. The tunable lens works by modifying the optical power of the objective and therefore modifying the point-spread function by means of variable focal length. This variable focal length replaces the need to move the stage in the z-direction while maintaining resolution and depth of field.

113A. An Investigation of the pH-dependent Influenza Hemagglutinin Protein Conformational Changes using MD Simulations

Nada Tolba, Shadi Badiee, Mahmoud Moradi
Chemistry and Biochemistry, University of Arkansas at Fayetteville

Hemagglutinin (HA) is an antigenic glycoprotein found on the surface of influenza viruses. HA is a homotrimer that mediates the binding of the virus to the host cell and the subsequent membrane fusion. The HA trimer is synthesized as inactive HA0 to

prevent unwanted fusion activity. Prior to cell membrane fusion, HA0 must be cleaved to HA1 and HA2 by host proteases. HA binds to the monosaccharide sialic acid present on the surface of the target host cells. The cell membrane then engulfs the virus through endocytosis and forms an endosome. Subsequent acidification of the endosome is associated with a conformational change involving partial unfolding of the HA2 molecule and its movement away from HA1, exposing a hydrophobic fusion peptide. This fusion peptide had been previously sequestered within the protein. The loop-to-helix secondary structural transition of HA2 moves the fusion peptide away from the virion surface and facilitates its insertion into the target membrane. Preliminary research conducted using computer modeling and molecular dynamics simulations under various pH conditions characterized this mechanistic scheme of HA. pH conditions were simulated through creation of HA systems with varying protonation states at the site of three highly conserved HA2 histidine residues. As an extension of the preliminary models, we created models of isolated HA2 to investigate the pH-dependent conformational changes of the HA2 domain in the absence of HA1 using molecular dynamics simulations. The models are expected to further reveal the details of the mechanistic scheme for HA2.

113B. Developing and Testing a Biocompatible Material for Drug Delivery

Loren Adams, Zeeshan Habeeb, Ma'Kyah Goodlow, Kelvin Camp
Chemistry, University of Arkansas at Pine Bluff

This project explores the creation and testing of biocompatible materials to be used for drug delivery.

114A. Accelerating Tissue Regeneration with Protein-Loaded Fiber Mats

Caroline Cole, Sharon Hamilton
Chemistry, Ouachita Baptist University
Biology, Ouachita Baptist University

Nanofibrous webs produced by electrospinning polymers have long been investigated for potential biomedical applications. These fibers are ideal for wound healing as they mimic the primary characteristics of the extracellular matrix. Additionally, the natural polymer chitosan can be co-spun into fiber mats increasing the antimicrobial properties of the materials thereby reducing the risk of infection. Incorporating macromolecular therapeutics like proteins has the potential to enhance and accelerate the wound healing process. It is anticipated that introducing an external source of thrombin via fiber mats will promote a faster clotting time and ultimately promote better tissue regeneration. Thrombin is an ideal clotting factor for biomedical applications because it will induce a cellular response whether the pathway is intrinsic or extrinsic. The engineered protein s-FGF1 stimulates fibroblast activity thereby promoting an environment that is favorable for healing. This cascade from fibroblast activity ultimately produces an increase in native collagen that sustains healing. The first objective of this research is to optimize the chitosan and PVA formulation to yield a fiber mat with the highest possible amount of chitosan while maintaining the integrity of the fiber mat so that it is uniform in density and free of imperfections. Imperfections in the fibers may lead to an uneven distribution of fiber mat additives (e.g., co-polymers, therapeutics). Utilizing uniform fibers will allow for a better understanding of cellular responses to the engineered fiber mats. The second objective of this research is to integrate optimized fiber mats with proteins such as thrombin and s-FGF1. The protein-loaded fiber scaffolds were analyzed via infrared (IR) spectroscopy and ongoing in vitro studies include release rates and cellular responses. These results will be indicative of the protein-loaded fiber mat's potential application in treating active bleeds and chronic wounds.

114B. Developing and Optimizing a Degradable Collagen Mimic for Modern Wound Dressings

Josie White, Sharon K. Hamilton
Chemistry and Physics, Ouachita Baptist University

A major component of recent study into modern wound healing has been the production of materials that can mimic biofunctions in the wound healing process. By electrospinning nanofiber mats from biomaterials such as collagen, researchers have achieved materials that mimic morphology and components of the extracellular matrix. However, these dressings are not readily degradable, are not always antibacterial, and are expensive to produce. By using Polycaprolactone (PCL), a biodegradable polyester, and chitosan, an antibacterial biomacromolecule, the electrospun nanofibers developed would ideally be biodegradable, inherently antibacterial, inexpensive, and would promote rapid wound healing. The goal of this research is to develop a material with these properties that can be electrospun into a nanofiber scaffold. This project has focused on the optimization of the synthesis of a novel biomimetic polycaprolactone (bPCL). This bPCL was prepared by modifying caprolactone via amide coupling reactions to attach molecules that mimic the amino acids naturally occurring in collagen, then polymerizing that final product. By optimizing the steps of this synthesis, a purer monomer product could be obtained, leading to a better polymer for study. Additionally, electrospinning protocols for PCL and chitosan fiber mats were further studied and established through electrospinning trials. These protocols were applied to bPCL/chitosan solutions to produce nanofiber scaffolds. In the future the mats will be analyzed via degradation and in vitro assays. It is anticipated that these studies will further confirm that these mats are biomimetic, antibacterial, and degradable, which will dictate the utility of these mats in biomedical applications.

115A. Hydrogen Production Using Nickel Complexes with Substituted Thiosalen Ligands

Alex Hemphill, Nate Hames, and William Eckenhoff
Inorganic Chemistry, Rhodes College

As our global population grows, our need for cleanenergy also grows. One new energy source can be found through the use of artificial photosynthesis to produce hydrogen gas. In our lab, we have investigatedthe effectiveness of nickel complexes with thiosalen ligands acting as a catalyst for the artificial photosynthetic process. While unsubstituted thiosalen complexes show protonreduction to occur electrocatalytically at ~-2.0 to -2.5V vs Fc+/Fc., addition of electron withdrawing substituents can lower the overpotential. Ni(II) thiosalen and thiosalphencomplexes with 3-CF3and 5-CF3groups were synthesized, characterized, and tested for efficacy of hydrogen production. While the substituents did lower the Ni(II/I) redox couple in accordance with their electron withdrawing ability, this effect did not greatly affect the overpotential of proton reduction as we supposed. DFT calculations were carried out to better understand the mechanism of proton reduction.

115B. Synthesis of 6-substituted Dopamine Analogues to Probe L-DOPA Dioxygenase Function

Leah G. Borders, Trinity L. Liaw, Gabriella Krisanic, Kameron L. Klugh, Keri L. Colabroy, Larryn W. Peterson
Chemistry, Rhodes College

Dopamine is an essential compound in the human body which has been able to serve as the blueprint for various important synthetic drugs. The enzyme L-DOPA dioxygenase that breaks down dopamine is a member of vicinal oxygen chelate superfamily which can cleave aromatic rings in catechols through metal chelation. This mechanism of action is not well known because of the lack of diverse substrates. This work incorporates the addition of different substituents to the 6-position of dopamine's catechol core which have been found to

change the properties including pKa values and hydrophobicity of the molecule that are crucial to the overall reactivity of the compound. Substantial progress towards the synthesis of these dopamine analogues has been made in good yields starting from the commercially available compound 3,4-dimethoxyphenethylamine. This toolkit of dopamine derivatives provides access to investigate use as enzyme substrates, inhibitors, or even in nonbiological applications.

116A. Synthesis of Multimodal Drugs to Combat Trypanosoma Parasites

Jamie Chen, Gregory Naumiec
Chemistry and Biochemistry, University of Central Arkansas

At least one billion people around the world are infected with a neglected tropical disease (NTD), and these people are usually in underdeveloped countries that either cannot afford funding for cures or the pharmaceutical companies do not have incentives to work with those countries. NTDs such as Chagas disease (CD) and Human African Trypanosomiasis (HAT) are caused by a parasite which affects work and health development along with possible damage to the nervous system and heart. This research project aims to synthesize a cost efficient compound drug to combat both CD and HAT through synthesis of N,N'-disquaramides. Commercially available diethyl squarate (DES) has been reacted with one equivalent of N-methylpropargylamine in ethanol solution at room temperature to attach an amino group via a substitution reaction with 53% yield. One equivalent of propargylamine was also substituted onto DES with 77% yield. Future work will include the use of a nickel catalyst NiCl2(PPh3)2 in Sonogashira coupling to install anti-HAT substrates. Triazole click-chemistry will be used to install triazole rings known for anti-parasitic effects onto the compound drug.

116B. In the Spotlight: Cost-Effective Treatment for Chagas Disease

Hannah Malone, Gregory Naumiec
Chemistry, University of Central Arkansas

This project is dedicated to finding a more cost effective treatment for Chagas disease, one of seventeen neglected tropical diseases (NTDs) recognized by the World Health Organization (WHO). Benznidazole and Nifurtimox are the two drugs currently used to treat the disease. The former requires patients to take daily doses for 60 days and the latter for 90-120 days. Patients often lose interest once the medicine begins to work, give up on the treatment prematurely, and quickly relapse. These medications become extreme physical and financial burdens on those who need it most. Chagas disease mainly plagues poverty-stricken countries that often lack medical resources and/or the education to control the spread of the disease on their own. The goal of this research is to create a treatment for Chagas disease using organic compounds that ideally lowers production and consumer costs.

117A. Computational Analysis of a Titanium Monoxide Reaction

Brennan Friesenborg, Michael Gutierrez
Chemistry, Harding University

Titanium monoxide has been shown to react with acetone resulting in Titanium monoxide and propyne. In the current research literature, how the reaction progresses is unknown. This research theorized that the reaction takes place in an excited energy state. Using gaussian and density functional theory, the steps in the reaction were computationally determined through evaluation of the energy state and the energy surfaces. The reactants, Titanium monoxide and acetone, and the products, Titanium monoxide and propyne, have been computationally determined to be favorable. The transition state calculations suggest evidence of possible proton tunneling. Continued testing of the transition states is needed to further explore how the reaction progresses.

117B. ZnO Nanostructures by Hot Water Treatment for Photocatalytic Bacterial Disinfection

JoAnna Campbell, Cindy White; Dakota Ungerbuehler, Tansel Karabacak
Chemistry and Biochemistry, Harding University

Photocatalysis with zinc oxide (ZnO) nanostructures has received significant attention as an alternative method for microbial disinfection in water. However, most ZnO nanostructure synthesis methods are expensive, non-scalable, and use toxic chemicals. Besides that, ZnO photocatalysts are often synthesized in nano-powder form that are suspended in water. Nanostructures suspended in water have various disadvantages such as tendency to agglomerate and difficulty of recovery and reuse. Here we introduce a simple and chemical additive-free nanostructure synthesis method called hot water treatment (HWT) to produce immobilized ZnO nanostructures on Zn surfaces. In this study, Zn plates were immersed in DI water at 75^{o}C for different durations, which resulted in the formation of ZnO nanostructures of different lengths and diameters. Reduction in E. coli growth was observed on HWT ZnO nanostructured surfaces that were irradiated with UV light, which is believed due to the photocatalytic activity of the HWT ZnO nanostructures.

118A. Cloud Condensation Nuclei (CCN) Activity of Model Insoluble Atmospheric Aerosols

Kyle Bounds, Kouadio Kondo, Adam De Groot, Courtney D. Hatch
Chemistry, Hendrix College

Of the factors that contribute to climate change, the aerosol indirect climate effect remains the least understood. Cloud condensation nuclei (CCN) activity measurements that provide cloud formation modeling parameters are important for reducing uncertainty of the effect of atmospheric aerosols on climate change through the mechanism of cloud formation. Of particular interest is the cloud activation of insoluble mineral aerosol, which comprises the largest fraction of atmospheric aerosol by mass. The goal of the presented work was to measure the CCN activation of silica nanospheres as spherical model insoluble atmospheric aerosols. Aerosols were generated using a constant output atomizer, dried by passing through two diffusion dryers, size selected at the nominal particle diameter using a differential mobility analyzer (DMA), and counted using a CCN counter and a Condensation Particle Counter (CPC). The results presented include CCN calibration results using ammonium sulfate as the standard aerosol, CCN activation curves from CCN activation measurements of size-selected silica nanospheres, and critical activation parameters that can be used to model cloud activation of insoluble atmospheric aerosol. Future studies will explore the effect of surface microstructure of silica on CCN activation.

Physics

201A. Ultrasonic Scattering Properties of Brain Tissue

Shona C. Harbert, Will R. Newman, Kiera Downey, Jessica Myat, Lauren Boughter, Kate Hazelwood, Cecille Labuda, Brent K. Hoffmeister
Physics, Rhodes College
Physics and Astronomy / National Center for Physical Acoustics, University of Mississippi

The goal of this study was to characterize the ultrasonic scattering properties of brain tissue. 1-cm thick slices of brain tissue were prepared from 12 preserved sheep brains. Slices were oriented along the transverse, sagittal and coronal planes. Ultrasonic backscatter measurements were performed in a water tank at room temperature using a 5 MHz transducer. The transducer was mechanically scanned to acquire measurements from multiple locations on the specimens. A two-dimensional map of the integrated backscatter coefficient (IBC) was created from the data. IBC is a fundamental measure of ultrasonic scattering caused by tissue heterogeneity. Measured values of IBC ranged from 9.94×10^{-5} - 3.88×10^{-4} $cm^{-1}str^{-1}$ depending on specimen. IBC also varied greatly within each specimen. These results indicate that the ultrasonic properties of brain tissue are highly heterogeneous.

202A. EPR Characterization of NO Reduction by YtfE

Dillon Simmons, William A. Gunderson
Physics, Hendrix College

As bacteria continue to evolve resistance to antibiotics, developing alternative therapeutic treatments for bacterial infections is essential. In response to a bacterial infection, the mammalian immune system targets iron-sulfur (FeS) clusters inside the bacteria by producing high concentrations of reactive oxygen and nitrogen species (in particular, NO) to disrupt FeS activity which inactivates proteins and kill the bacteria. Some drugs utilize this process to fight infection, but bacteria have evolved defenses against NO. Thus, understanding the mechanisms behind this defense is essential to developing effective treatment. Here, electron paramagnetic resonance (EPR) spectroscopic techniques were employed to study the mechanisms of NO reduction and FeS cluster repair by YtfE, a non-heme diiron enzyme that is essential to the bacterial response system. EPR serves as a site-specific probe for the active site of YtfE. The spectral results suggest that the NO reduction occurs at the diiron site, and the electronic structure and local coordination geometry play important roles in NO reduction by YtfE.

203A. Ultrasonic Characterization of the Human Scalp using the Speed of Sound and the Frequency Slope of Attenuation

Blake Lawler, Shona C. Harbert, Cecille Labuda, Ann Viano, Brent K. Hoffmeister
Physics, Rhodes College

There is interest in developing transcranial ultrasonic techniques for therapeutic and diagnostic applications involving the brain. Ultrasonic waves must propagate through the scalp as well as the skull. While the ultrasonic properties of the skull have been investigated extensively, the ultrasonic properties of the scalp are unknown. The goal of this study was to investigate the ultrasonic properties of scalp tissue, specifically the speed of sound (SOS) and the frequency slope of attenuation (FSA). 32 specimens from four human cadaveric donors were prepared from the frontal, parietal, temporal, and occipital regions of the scalp. Ultrasonic measurements were performed using a broadband transducer with a center frequency of 7.5 MHz. Measured values for SOS ranged from 1523 m/s to 1564 m/s with a mean + standard deviation of (1536 + 9.713) m/s, and measured values for FSA ranged from 1.219 dB/cm/MHz to 2.891 dB/cm/MHz with a mean + standard deviation of (1.886 + 0.4890) dB/cm/MHz. This study represents the first study to characterize the ultrasonic properties of human scalp tissue.

204A. Second Harmonic Generation and Down Conversion Using Mode-locked Laser

Apoorva Bisht, Hiro Nakamura
Physics, University of Arkansas, Fayetteville

A non-linear crystal, β-Barium Borate is used for generating second harmonic generation (SHG) from a mode-locked laser of frequency 740 nm. A SHG beam of frequency 370 nm with conversion efficiency of 18% is obtained. SHG beam is incident on another crystal for spontaneous parametric down conversion (SPDC). Based on theoretical calculations we expect SPDC to be around few pW. We have attempted to generate SPDC photons by adjusting the phase matching angle. The images generated will depict the cones of down converted photons generated in type II SPDC. We will use the SPDC photons with the existing setup for correlation measurements, Hanbury Brown and Twiss type experiments to confirm and utilize the single photon nature. Supported by Honors College Research Grant and Fui T. Chan and Kaiyuan Chen Endowed Research Scholarship

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Director of Outreach

Tara Dean
Director of Client Success

Kaye Trout
Outreach Specialist

Shelley Reh
Implementation Manager

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2023 UPCOMING EVENTS

May 14-19: INBRE Sponsored Health Sciences Entrepreneurship Boot Camp.

A week-long educational program held on the campus of UCA where students will learn the fundamentals of entrepreneurship and formulate new health science ventures.

- **Website: https://inbre.uams.edu/**

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2023 UPCOMING EVENTS

The week of May 22nd (exact date TBA): A one-day workshop focusing on bone diseases.

Spend a day with clinicians and scientists exploring what it takes to do osteoporosis research or to study cancer metastasis to the bone.

- **Website: https://inbre.uams.edu/**

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2023 UPCOMING EVENTS

May 22 – July 28: INBRE Undergraduate Summer Research Fellowship Program.

Intensive 10-week research program. Competitive stipend included. Applications now being accepted.

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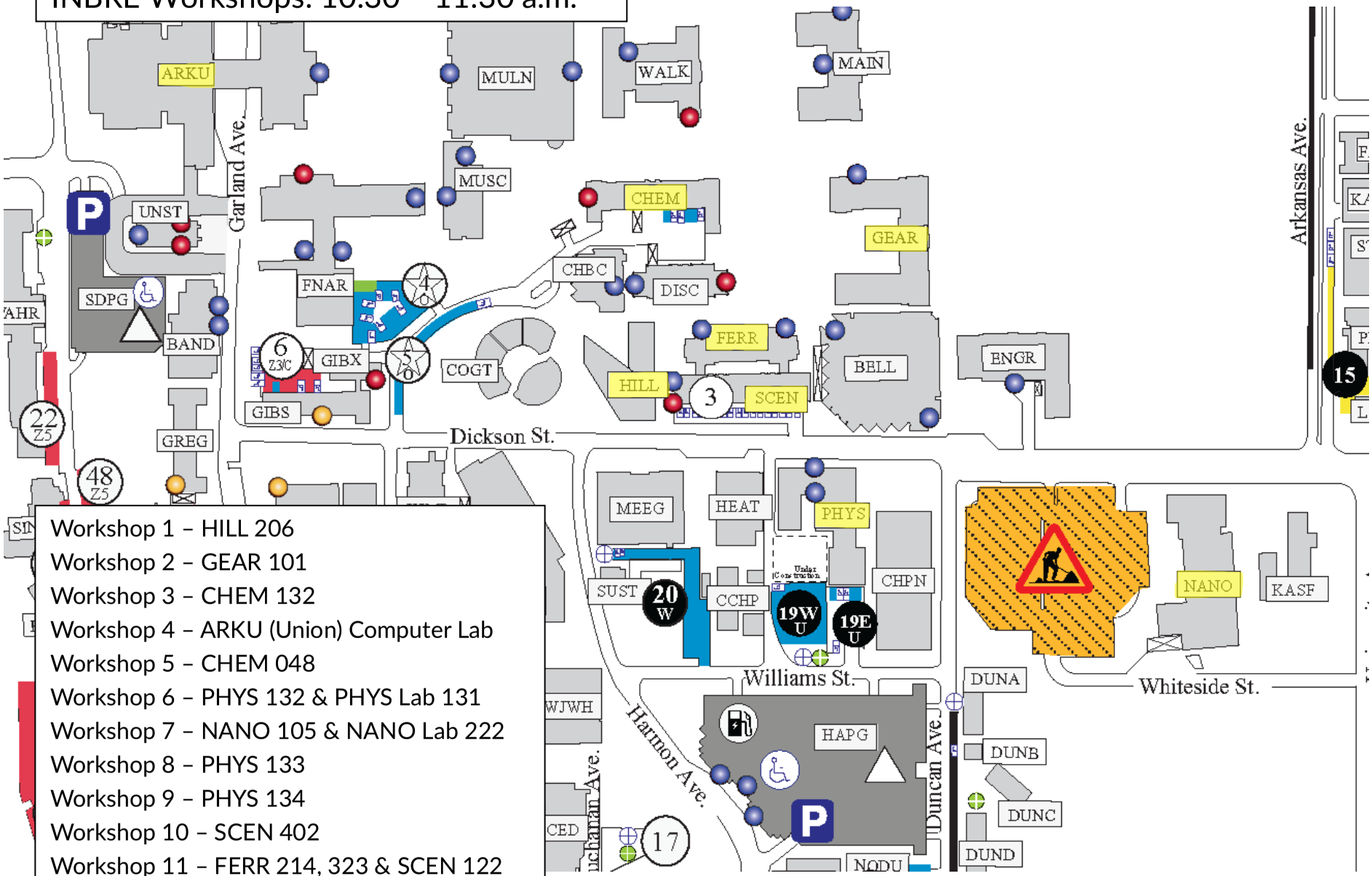
INBRE Workshops: 10:30 – 11:30 a.m.



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Workshop 2 – GEAR 101
Workshop 3 – CHEM 132
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