Arkansas INBRE Research Conference

2024

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November 8-9

Arkansas INBRE Research Conference

Arkansas IDeA Network of Biomedical Research Excellence

Conference Schedule

Friday, November 8, 2024

Graduate Hotel & Fayetteville Town Center

12:00 – 1:30 PM	Registration – Second Floor Atrium, Graduate Hotel
1:30 – 3:00 PM	Invited Faculty Platform Plenary Session – Brodie Payne Ballroom, Graduate Hotel
3:30 – 5:00 PM	Invited Student Platform Sessions – Graduate Hotel Physics (Trammel), Chemistry (Brodie Payne A), Biology (Brodie Payne CD)
5:00 – 6:00 PM	Student and Faculty Reception and Networking – Graduate Hotel
6:30 PM	Banquet – Fayetteville Town Center
7:15 PM	Keynote Seminar: “Top-down Proteomics: Bridging the Silos between Chemistry, Biology and Medicine” – Fayetteville Town Center **Ying Ge**, Ph.D., University of Wisconsin–Madison

Saturday, November 9, 2024

University of Arkansas, Fayetteville Campus

7:30 AM	Breakfast – Hillside Auditorium and Physics Building
7:45 AM	Session A poster set up
8:00 AM	Poster Session A (posters come down at 9:00 a.m.) – Hillside Auditorium and Physics Building
9:00 AM	Session B poster set up
9:15 AM	Poster Session B (posters come down at 10:15 a.m.) - Hillside Auditorium and Physics Building
10:30 AM	Workshops and facility tours – assigned locations
11:45 AM	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 Holiday Inn Express,
1251 N Shiloh Dr, Fayetteville, AR 72704.

Parking:
Friday parking is complimentary in the Municipal Parking Garage, behind the Graduate Hotel, third level only (or first level card access for registered guests of the Graduate). Parking in the parking garage behind the Town Center is free from 12:30 pm until 9:00 pm Friday.

Saturday parking is free on the UA campus in designated yellow, green, and blue sign lots and parking decks. 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

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Abdel Bachri, Ph.D., Southern Arkansas University

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Cyndy Buckhaults, Media Specialist

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Participating Institutions

Abilene Christian University, Abilene
Arkansas State University, Jonesboro
Arkansas Tech University, Russellville
Harding University, Searcy
Hendrix College, Conway
John Brown University, Siloam Springs
Little Rock Central High School, Little Rock
Lyon College, Batesville
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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 Oklahoma, Norman
University of the Ozarks, Clarksville

Keynote Speaker

Friday, 7:15 p.m., Fayetteville Town Center
Chair: Julie Stenken, Ph.D. (Dept. of Chemistry and Biochemistry, UAF)

Top-down Proteomics: Bridging the Silos between Chemistry, Biology and Medicine

Ying Ge, Ph.D.

Vilas Distinguished Achievement Professor
Department of Cell and Regenerative Biology
Department of Chemistry, and
Human Proteomics Program
University of Wisconsin–Madison

Dr. Ge's research is highly interdisciplinary, transcending traditional boundaries in chemistry, biology, and medicine. Her group specializes in top-down mass spectrometry-based proteomics, a powerful technology for comprehensively characterizing proteoforms resulting from genetic variations, alternative splicing, and post-translational modifications. Their work aims to understand cardiac biology and translate bench discoveries into precision medicine applications. Addressing challenges in top-down proteomics, her lab has designed and synthesized new cleavable surfactants for protein solubilization, innovative materials and strategies for multi-dimensional chromatography separation of proteins, as well as novel nanomaterials for enriching low-abundance proteins. In this seminar, Dr. Ge will discuss the recent technology development and biomedical applications of top-down proteomics in bridging disciplinary divides, offering a comprehensive understanding of the proteome and fostering collaboration across diverse scientific fields.

Faculty Plenary Talks

Friday, 1:30 p.m. – 3:00 p.m., Brodie Payne Ballroom, Graduate Hotel
Chair: Susanne Striegler, Ph.D. (Dept. of Chemistry and Biochemistry, UAF)

Biology

Robert Shields, Ph.D. | Harding University

"A Functional Genomics Strategy to Unravel the Functions of Essential and Poorly Characterized Bacterial Genes"

1:30 PM Friday

In recent years, several microbial genomics techniques have been developed that have accelerated gene function discovery in bacteria. Our own research focuses on the study of critical but poorly characterized genes in *Streptococcus mutans*, a Gram-positive bacterium that colonizes the human oral cavity. Initially, by applying transposon sequencing (Tn-seq) and CRISPR interference (CRISPRi) we identified >200 essential genes that are required for the viability of the organism. With careful data inspection we determined that contained within the essential genome are eleven genes with unknown functions. Resolving the function of these genes is critical to understanding basic biology and molecular pathogenesis, and to developing more effective therapies against the pathogen. To begin to determine these functions, we have developed a strategy that allows us to characterize the phenotypic impact of loss of these genes on *S. mutans*. We begin by perturbing the amount of essential gene product using CRISPRi, and then we measure the phenotypic impact on cells with growth assays, ultrastructural microscopy, transcriptomics, and proteomics. We pair outcomes from these experiments with genetic suppressor screens. We attempt to mutate the essential genes and use genome sequencing to identify suppressor mutations which might highlight pathways/genes that interact with the hypothetical essential genes. Together, and with the inclusion of bioinformatic approaches, we have begun to understand the functions of some of the identified genes. For example, we have discovered a putative DNA-binding gene that may regulate aspects of the citric acid cycle. This gene is well conserved among Bacillota (formerly Firmicutes) bacteria. Our experimental strategy, and our findings, should identify critical essential functions in *S. mutans* and related Gram-positive microorganisms.

Chemistry

Tori Dunlap, Ph.D. | University of Central Arkansas

"Protein Disorder, Calcium Ion Signaling, and Neurodegenerative Diseases"

2:00 PM Friday

Structure leads to function, but sometimes lack of structure leads to function. In recent years a class of proteins known as intrinsically disordered proteins (IDPs) has been characterized. These proteins have no persistent secondary structure, and their 3D shapes exist on a continuum from expanded to compact. We now know that the lack of structure in these proteins is crucial for their function, and that IDPs are necessary for numerous cellular events. Also necessary for cellular function is calcium ion signaling. The main translator of the calcium signal is the protein calmodulin which, when bound to calcium ions, can then bind to and regulate an estimated 300 different proteins. Both disorder in proteins and calcium signaling are intertwined in neurodegenerative diseases. For many neurodegenerative diseases, the aggregation of an IDP has been implicated in the pathology, and calcium signal dysregulation also leads to neuronal cell disfunction or death. PEP19 is an IDP that is responsible for binding to calmodulin and regulating its ability to perpetuate the calcium signal. PEP19 concentrations are elevated in brain regions spared by Alzheimer's Disease, and high levels of PEP19 protect against cell death caused by calcium ion overload. We utilized fluorescence and circular dichroism techniques to determine how the crowded conditions of a cell might influence PEP19's 3D shape and how that would affect its ability to regulate calmodulin. We then investigated how the presence of neurodegenerative proteins involved in Alzheimer's Disease and Parkinson's Disease impacted PEP19's shape and ability to interact with calmodulin. We determined that PEP-19 is somewhat compact but is further compacted by the presence of neurodegenerative proteins, making it more difficult for PEP19 to bind to a regulate calmodulin, likely increasing calcium ion signaling in neurodegenerative cell states.

Physics

Puskar Chapagain, Ph.D. | Southern Arkansas University

"Synthesis and Characterization of Carbon Nanotubes-Alumina Nanocomposites"

2:30 PM Friday

Developing advanced materials with enhanced properties is crucial for various technological applications. Among these materials, carbon nanotubes (CNTs) are particularly promising due to their unique mechanical, thermal, optical, and electronic properties, which can significantly improve the performance of composite materials. Incorporating CNTs into ceramic matrices, such as alumina (Al_2O_3), we can create nanocomposites with multifunctional characteristics. This could potentially revolutionize electronics, medical devices, and energy storage. However, a major challenge lies in achieving a uniform distribution of CNTs within the Al_2O_3 matrix and understanding the behavior of these composites. To address this, we synthesized CNTs-Al_2O_3 nanocomposites using a chemical vapor deposition (CVD) process with nickel (Ni) catalysts to ensure proper bonding. We then analyzed the samples using various advanced techniques to study their structures and properties. Our findings show that the CNTs are evenly dispersed in the alumina matrix. Additionally, magnetic testing revealed that the composites with embedded Ni exhibit strong magnetic properties. This suggests that integrating CNTs with the alumina matrix in the presence of Ni could lead to innovative applications in magnetic sensors, data storage devices, and electromagnetic interference (EMI) shielding.

Student Oral Presentations

Undergraduates will give 12-minute oral presentations followed by 3 minutes of Q&A from 3:30 p.m. to 5:30 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
Chair: LaShall Bates, Ph.D.

3:30 PM. Salma Abdel-Karim
Arkansas State University
Anti-Inflammatory Activity of Isoflavones from Pigeon Pea Hairy Root Cultures in RAW 264.7 Macrophages

03:45 PM. Elijah DeCuir
Union University
Targeting MCL-1:BAK Pro-Survival Complexes in Apoptosis

04:00 PM. Avery Carter
University of Arkansas, Fayetteville
Assessment of nitrogen source utilization during nitrogen fixation and nitrogenase regulation by *Methanosarcina acetivorans*

04:15 PM. Allie Farrar
Hendrix College
The Molecular Basis of the Cooperativity Between the Anti-Apoptotic Protein MCL1 and the E3 Ubiquitin Ligase MARCHF5

04:30 PM. Kyrilos Sadaka
University of Arkansas at Little Rock
A Novel Cell Death Independent Mechanism of Acute Anthracycline Exposure in Human Cardiac Fibroblasts

04:45 PM. Kennedy Abanihe
University of Arkansas at Pine Bluff
Understanding the Complex Dynamics of Cigarette Smoking and Its Impact on Substance Use In the USA: Insights from Longitudinal Data Analysis

Chemistry Oral Presentations

Brodie Payne Ballroom A
Chair, Crystal Archer, Ph.D.

3:30 PM. Ethan Batey
University of Arkansas, Fayetteville
Attaining True Spectra Multicolor Images at the Nanoscale Using Phasor Analysis

03:45 PM. Danny Caceres
Hendrix College
Modifying Dipeptides to Investigate Aggregation Pathways: Developing Design Principles for Various Dipeptides

04:00 PM. Price Sheets
University of Arkansas at Little Rock
Design Development and Characterization of Polymer membrane Separator for Lithium-Ion Battery and Surface Modification using TiO2

04:15 PM. Bree Steinfeldt
Ouachita Baptist University
The Analysis of BPA Leaching in Various Types of Athletic Wear using Fluorescence Spectrometry

04:30 PM. Kennedy Foster
Harding University
SODIS: The bactericidal effect of UV radiation and thermal heating on water under real-world conditions in Arkansas

04:45 PM. Braden Glenn
Lyon College
Synthesis of Modified Rifamycins to Combat Drug Resistance Synthesis of Modified Rifamycins to Combat Drug Resistance

Physics Oral Presentations

Trammel Room
Chair, Hugh Churchill, Ph.D.

3:30 PM. Catherine Prabish
Rhodes College
Ultrasonic Characterization of the Human Scalp Using Backscatter Parameters

03:45 PM. Gabriel Reyna Garcia
Southern Arkansas University
Determining the Refractive Index of 2D Ferroelectric Material

04:00 PM. Joel Osho
Texas State University
Structure and Interface Analysis of Diamond on β-Ga_2O_3 Utilizing SiC Interlayer Grown by RF sputtering

04:15 PM. Aubrey McNiel
University of Oklahoma
Novel transferred Josephson junction fabrication using graphene monolayer

04:30 PM. Taksh Patel
University of Arkansas, Fayetteville
Exploring topological defects in Janus bilayers of $Cr(I,Cl)_3$ and $Cr(I,Br)_3$

04:45 PM. Sidney Kwame Osae-Asante
Abilene Christian University
Nanopore Device: Sensing the Shape of Protein Molecules

Poster Sessions

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

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 and Facility Tour

Saturday, November 9, 10:30 a.m. – 11:30 a.m.
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, Ph.D.**, 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. Funding opportunities, such as the Support for Research Excellence (SuRE) Program and SuRE-First Program (R16s) have been released with AR INBRE PUI faculty successfully obtaining NIH extramural support. 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 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: Maximizing Research Resources & Communicating Science for Broader Impact
***Amy Hopper Swan,** Program Director, Arkansas Research Alliance*
Location: Hillside 202

This interactive workshop will empower undergraduate researchers with the tools they need to both enhance their research productivity and communicate their findings with broader audiences. In the first part, participants will explore the Arkansas Core Facilities Exchange (CFE), a powerful database connecting them to over 350 cutting-edge research assets, from specialized equipment to world-class expertise, all designed to accelerate research and foster statewide collaboration. In the second part, participants will dive into the Message Box-a simple but effective framework developed by COMPASS-to communicate their research clearly and persuasively to funders, collaborators, and the public. By the end of the session, participants will have access to

valuable resources and sharpened communication strategies to maximize the impact of their work.

Workshop 3: Training future and current faculty in the art of scientific teaching -> the MoSI model
Mark Baillie, Ph.D., *Associate Professor, UA Little Rock Chemistry Program and STEM Ed Center, UALR*
Location: CHEM 147

Helping all of our students succeed in our classes can be extremely challenging. During this interactive 60-minute workshop, participants will engage in a deep dive on inclusive teaching and learn about how we can better support learning across various groups of students. This session is one of the first sessions that faculty and graduate students engage in during the week-long immersive Mobile Summer Institute on Scientific Teaching (MoSI) workshop, a week-long workshop that helps faculty bolster the support and impact for all students, especially those who typically struggle in our courses. This evidence-based workshop is a national model that is implemented around the country, and UA Little Rock has hosted the last 6 years training over 150 faculty.

Workshop 4: Cryo-electron Microscopy
Cody Brazel, *Dept. of Chemistry and Biochemistry, UAF*
Dylan Girodat, Ph.D.*, Dept. of Chemistry and Biochemistry, UAF*
Location: CHEM 201
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 spliceosomes. 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 of Cryo-EM, a hands-on demonstration of how samples are prepared, and how a 3D electron density can be generated from movies of particles. By the end, an attendee will have working knowledge of the Cryo-EM workflow. As an example, attendees will have the chance to use a manual plunger for sample preparation on practice grids.

Workshop 5: Preparing for Graduate School
Stefan Kilyanek, Ph.D., *Dept. of Chemistry and Biochemistry, UAF*
Location: CHEM 132

This workshop is targeted towards undergraduate 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:
Tiffany S. Weinkopff, Assistant Professor, Dept. of Microbiology & Immunology, UAMS
Aaron Kemp, Graduate student in Biomedical Informatics, UAMS
Eston Dunn, Graduate student in Biological Sciences, UAF
J. Chelsea Stephens, Graduate student in Chemistry and Biochemistry, UAF

Workshop 6: Molecular Modeling
Peter Pulay, Ph.D., *Dept. of Chemistry and Biochemistry, UAF*
Location: MAIN 205
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, NMR and VCD spectra, relative stability, NMR chemical shifts, reaction paths and barriers, etc.

The procedure has two steps. First, a qualitatively correct molecular geometry is constructed using a Graphical User Interface and a molecule builder. In the second step, a Quantum Mechanical program allows the determination of wavefunctions, molecular geometries and other properties.

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 U of 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.

The 33-page workshop document has a general discussion and describes several exercises (below) in detail. If everything goes well, we will be able to finish the first two.

1. Relative stability of the singlet and triplet states of methylene, CH2, and CF2
2. Distinguishing 2,3- and 2,5-dihydrofuran by comparing experimental and calculated infrared and NMR spectra
3. A molecule with a surprising structure: SF4
4. Energetics and reaction path of the cyclobutene thermal ring opening reaction
5. Geometry, infrared spectra, and NMR chemical shifts of cyclohexene

Workshop 7: Nanochemistry: Spontaneous versus electrochemical reduction at the nanoscale.
Jingyi Chen, Ph.D.*, Dept. of Chemistry and Biochemistry, UAF*
Location: DISC 418
Participant capacity: 10

Nanochemistry plays an important role in a wide variety of applications including drug delivery, sensing, environmental remediation, energy storage and conversion. In this workshop, the emphasis focuses on the synthesis of metal at the nanoscale. Two methods will be demonstrated including spontaneous and electrochemical reduction. The optical properties of the metal nanoparticles will be illustrated.

Workshop 8: Getting started on scorpion & spider genomics
Douglas Rhoads, Ph.D.*, University Professor, Dept. of Biological Sciences, UAF*
Location: SCEN 0408

We have recently published manuscripts on genome assembly and annotation for a scorpion species endemic to Arkansas. We are now working to do assemblies for two spiders. In this workshop we will provide advice and experiences. We will answer your questions on genomics based on our experiences with genomics in snakes, chickens, arthropods, and bacteria.

Workshop 9: Behavioral Neuroscience Approaches
Amy Rosetta Poe, Ph.D.*, Assistant Professor, Biological Sciences, UAF*
Location: SCEN 0606
Participant capacity: 16

The field of behavioral neuroscience involves the application of the principles of biology to study the genetic and developmental mechanisms of behavior. This workshop will provide hands-on experience in examining and quantifying animal behavior. First, I will provide an overview of ways in which behaviors like sleep and feeding can be studied in

organisms like Drosophila. Participants will then have the opportunity to learn to identify, analyze, and characterize behaviors at different biological time points using provided movies of freely behaving Drosophila larvae. Participants should bring a phone with a stopwatch feature.

Workshop 10: Investigating Metabolism with Multiscale Approaches: From Molecule to Tissue
***Timothy J. Muldoon, M.D., Ph.D.**, Dept. of Biomedical Engineering, Metabolic Imaging and Spectroscopy Core, Arkansas Integrative Metabolic Research Center (AIMRC), UAF*
***Narasimhan Rajaram, Ph.D.,** Dept. of Biomedical Engineering, Metabolic Imaging and Spectroscopy Core, AIMRC, UAF*
***Suresh Thallapuranam, Ph.D.,** Dept. of Chemistry and Biochemistry, AIMRC, 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. Recently acquired, our Raman confocal microscope enables characterization of molecular and chemical structures within intact 3D constructs, such as tissue or engineered cell culture platforms. 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 pf 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, the expertise available from the core directors and technicians, and details on how to access or get trained to use them.

Workshop 11: Confocal Microscopy
Payal Sanadhya, Ph.D.
***Fiona Goggin, Ph.D.**, Dept. of Entomology and Plant Pathology, UAF*
Location: AGRI 315 and AGRI 225

Confocal laser scanning microscopy (CSLM) is one of the most widely-used imaging techniques in biology. Through detection of naturally-occurring or artificially-added fluorescent chemicals (fluorophores), it allows the three-dimensional imaging of living tissues in real time, giving us a window into the structure, chemistry, and physiological functioning of these tissues. The Arkansas Bioimaging Core Facility at the University of Arkansas houses a state-of-the-art Leica Stellaris 8 microscope with a white light laser and Tausense technology for analysis of photon arrival time. These features provide enhanced sensitivity, reduced background noise, and the capacity to detect and distinguish a wider range of fluorophores than traditional confocal microscopes. This workshop will provide an introduction to the capabilities of the Stellaris 8 microscope and a tour of the Bioimaging Core Facility, which is available to investigators state-wide. Participants who wish to bring their own samples should contact Fiona Goggin: fgoggin@uark.edu.

Workshop 12: Quantifying the dynamics of cell division of bacteria and yeast at single cell
Pradeep Kumar, Ph.D.*, Dept. of Physics, UAF*
Location: PHYS 132 and PHYS Lab 126
Participant capacity: 15

The workshop will provide hands-on experience on working with yeast and bacterial cells under a microscope, and the methods to quantify their cell division dynamics. First, we will provide a brief introduction of the phase contrast microscopy and its usage in Biology. Participants will have the opportunity to learn to build and automate an autofocus system using a microscope and Arduino processor to capture focused long time-lapse movies of bacteria and yeast growing on a nutrient microchamber. Participants will then use a combination of image processing tools and obtained time-lapse movies to analyze and quantify cell division.

Workshop 13: Crystal growth
Jin Hu, Ph.D., *Dept. of Physics, UAF*
Location: PHYS: 133 & 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 14: Playing with lasers
Hiro Nakamura, Ph.D., *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 demonstrations including (1) looking inside a high-power laser; (2) creating higher order patterns from laser beam; (3) make a rainbow using CD, etc.

Workshop 15: Build a Robot at the MonArk Quantum Foundry
Hugh Churchill, Ph.D.*, Dept. of Physics, UAF*
Josh Goss*, MonArk NSF Quantum Foundry, UAF*
Location: NANO Lobby, NANO105/Lab
Participant capacity: 16

Workshop participants will use a sample transfer robot to collect starburst treats as they explore robotics, cartesian motion control, microcontroller programming, and automation using similar tools built at the MonArk Quantum Foundry to move semiconductor device chips through our fabrication pipeline. Participants will learn about the activities of the MonArk NSF Quantum Foundry that seeks to use robots and artificial intelligence to automate and accelerate the fabrication of quantum devices based on atomically thin two-dimensional materials. Time permitting, we will conclude with short tour of the MonArk Quantum Foundry Lab located in NANO 325, 731 W Dickson, Fayetteville, Arkansas.

Facility Tour 1: Department of Chemistry and Biochemistry
Ryan Tian, Ph.D.*, Dept. of Chemistry and Biochemistry, UAF*
Location: meet in Hillside foyer

Facility Tour 2: Arkansas High Performance Computer Center
Raymond Weldon*, Dept. of Chemistry and Biochemistry, UAF*
Pavel Wolinski, Ph. D. *Senior Linux Cluster Administrator*, AHPCC
Location: meet in Hillside foyer

Awards Ceremony

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.

Oral Abstracts

Biology Oral Presentations

03:30 PM. Anti-Inflammatory Activity of Isoflavones from Pigeon Pea Hairy Root Cultures in RAW 264.7 Macrophages

Salma Abdel-Karim, Gaurav Gajurel, Amit Raj Sharma, Mohammad Abrar Alam, Fabricio Medina-Bolivar
Dept. of Biological Sciences, Arkansas State University

Isoflavones are phenolic compounds produced by legumes as a defense mechanism against various stresses. Previous research has shown that these compounds exhibit bioactive properties, such as anticancer and antioxidant properties, thus making them of vital importance to the medical field. Extracting and purifying these metabolites from their natural sources, however, is challenging, making it imperative to utilize an alternative platform for the production of isoflavones. The aims of this study were to use hairy root cultures established from pigeon pea to produce isoflavones and to evaluate their anti-inflammatory activity in lipopolysaccharide-stimulated RAW 264.7 macrophages. Initially, hairy root cultures of pigeon pea were co-treated with cyclodextrin, methyl jasmonate, magnesium chloride, and hydrogen peroxide to stimulate the production of isoflavones in the hairy roots. Eight days later, the isoflavones were extracted from the culture medium. These compounds were identified using analytical high-performance liquid chromatography (HPLC) and purified using semi-preparative HPLC. Two isoflavones, genistein and its prenylated analog isowighteone, were first tested for their cytotoxic effect on the macrophages to establish an IC50 value. The lipopolysaccharide-stimulated macrophages were then exposed to genistein and isowighteone at concentrations of 10 μM and 25 μM for 24 hours, and the nitrite content in each sample was determined to assess their anti-inflammatory properties. The results showed that both genistein and isowighteone displayed significant anti-inflammatory activity, and isowighteone displayed greater activity than genistein at 25 μM. This study underscores the need for further research into pigeon pea isoflavones as potential anti-inflammatory agents.

03:45 PM. Targeting MCL-1:BAK Pro-Survival Complexes in Apoptosis

Elijah DeCuir, Tudor Moldoveanu, Shagun Srivastava, Elizabeth Ferreira, Raja Dey
Dept. of Biology, Union University

BCL-2 family proteins regulate apoptosis, a form of cell death often dysregulated in cancer. The pro-survival guardian BCL-2 family proteins, BCL-2,

MCL-1, and BCL-xL inhibit apoptosis by binding the BH3 domains of the pro-death BH3-only proteins, BIM, PUMA, NOXA, and the executioners of mitochondrial poration, BAK and BAX. These guardians are upregulated in cancer and selective inhibitors, known as BH3 mimetics, have been designed to displace the pro-apoptotic and executioner proteins from the guardians. BH3 mimetic compounds are in various stages of development, but only the BCL-2 inhibitor ABT-199 is FDA approved for cancer treatment. Although existing BH3 mimetics are supposed to exhibit high affinities for their guardians, there is evidence that they have surprisingly poor activities in neutralizing the complexes between guardian the executioner proteins. Here we used microscale thermophoresis and fluorescence polarization to determine both the potency of BH3 peptides and mimetics to neutralize MCL-1:BAK complexes. Thermal shift assays were also performed to probe the mechanism of the binding event. We found that while BH3 mimetics neutralized MCL-1:BAK complexes at higher concentrations than their reported direct affinity to MCL-1. It was also found that the presence of micelles in the preparation decreased the efficacy of BH3-mimetics. Thermal shift assays revealed poor stabilization of MCL-1 by binding to BH3-mimetics. Future studies should focus on developing drug screening that is accurate to the cellular environment and studying BH3 peptides to improve the binding favorability of their mimetics.

04:00 PM. Assessment of nitrogen source utilization during nitrogen fixation and nitrogenase regulation by *Methanosarcina acetivorans*

Avery Carter, Gary J. McIntosh, Jacob McLeod, Regan Massey, Faith H. Lessner, Ahmed Dhamad, Daniel J. Lessner
Dept. of Biological Sciences, University of Arkansas, Fayetteville

Nitrogen is a crucial element in biomolecules such as proteins and DNA, essential for all cellular life. Biological nitrogen fixation, a process utilized by certain bacteria and archaea, reduces dinitrogen (N_2) to ammonia (NH_3), enabling growth in the absence of fixed nitrogen sources like NH_3. This process is driven by the metalloenzyme nitrogenase, which catalyzes the reaction: $N_2 + 16ATP + 8e^- + 8H^+ \rightarrow 2NH_3 + H_2 + 16ADP + 16Pi$. Due to its high energy demand, nitrogenase production and activity are tightly regulated. Among archaea, nitrogenase is found exclusively in methanogens, where its regulation remains poorly understood. We employed *Methanosarcina acetivorans* as a model organism to investigate fixed nitrogen source utilization and nitrogenase regulation in methanogens. Using a mutant strain of *M. acetivorans* incapable of fixing N_2, we assessed the utilization of various nitrogen sources, including all 20 common amino acids and biologically relevant inorganic nitrogen compounds (e.g., nitrate). Surprisingly, only glutamine, trimethylamine (also a carbon source), and NH_3 supported the growth of the mutant strain, indicating a narrow range of fixed nitrogen source utilization in *M. acetivorans*. Notably, growth with glutamine as the sole nitrogen source was poor compared to NH_3. Further investigation using another mutant strain deficient in hydrogenase activity revealed H_2 production during growth with glutamine, suggesting functional nitrogenase activity despite the presence of glutamine as a fixed nitrogen source. Thus, in the absence of NH_3 or trimethylamine, *M. acetivorans* resorts to energy-intensive N_2 fixation, even when provided with glutamine, a usable fixed nitrogen source and key intermediate in nitrogen assimilation. These findings uncover new complexities in nitrogenase regulation and usage in methanogens.

04:15 PM. The Molecular Basis of the Cooperativity Between the Anti-Apoptotic Protein MCL1 and the E3 Ubiquitin Ligase MARCHF5

Allison Farrar, Justine Bersonda, Prasanth Viswanathan, Mark Manzano
Dept. of Health Science, Hendrix

Kaposi's sarcoma-associated herpesvirus (KSHV) causes Primary Effusion Lymphoma (PEL), a B cell malignancy often observed in people living with

HIV/AIDS. Dr. Manzano previously performed genome-wide CRISPR screens to identify cellular oncogenes that contribute to PEL cell survival and proliferation. The lab recently uncovered a strong genetic interaction between two of these oncogenes: the anti-apoptotic protein MCL1 and the mitochondrial E3 ubiquitin ligase MARCHF5. This is surprising because MARCHF5 primarily functions to regulate mitochondrial dynamics and antiviral signaling but has not been implicated in apoptosis. Our data supports the hypothesis that the functions of these genes converge in the same pro-survival pathway through the MARCHF5-mediated ubiquitination and proteasomal degradation of the MCL1 antagonist. The goal of my project was to determine (1) if NOXA is ubiquitinated in the presence of MARCHF5, and (2) if there is endogenous interaction between the proteins. Using HEK293T cells overexpressing epitope tagged MARCHF5, NOXA, and ubiquitin, I demonstrate that immunoprecipitation of tagged NOXA had a greater degree of ubiquitination in the presence of wild-type MARCHF5 compared to the E3 ligase-defective mutant H43W. Furthermore, I also captured endogenous interaction of MARCHF5 and NOXA by performing reciprocal co-immunoprecipitations followed by Western blotting of the proteins in the PEL cell line BC-3. This contribution to unraveling the mechanism of MCL1 and MARCHF5 cooperation is important to the fundamental biology of cell death pathways and better targeting the vulnerabilities of this rare but aggressive disease.

04:30 PM. A Novel Cell Death Independent Mechanism of Acute Anthracycline Exposure in Human Cardiac Fibroblasts

Kyrilos Sadaka, Rushita Bagchi, Ryan Holdiness
Chemistry, University of Arkansas at Little Rock

Doxorubicin (Dox) is a commonly used chemotherapeutic drug that is very effective in many forms of cancer throughout the human body. Despite its profound anticancer effects, Dox has been thoroughly cited to induce toxicity in the heart. Doxorubicin-induced cardiomyopathy (DIC) involves damage to the heart by generating reactive oxygen species and free radicals. The heart damage caused by DIC includes ventricular dysfunction, aberrant arrhythmias, and heart failure. Although there have been numerous studies on DIC pathways, the overall mechanism remains unknown, in addition to the effects of acute dosages of Dox. Additionally, research has been lacking on non-myocyte cells, including cardiac fibroblasts. This study aimed to identify and validate a potential cell death-independent mechanism for acute exposure of Dox on human cardiac fibroblasts (HCFs). HCFs maintain the structure and function of cardiac tissue via the production of extracellular matrix proteins such as collagens. By studying these cells, we can gain valuable insights into the mechanisms of drug-induced cardiac damage, particularly the cellular and molecular responses to Dox. Using a cell viability assay, we identified a nanomolar concentration of Dox that triggers proteome-wide changes in HCFs. We identified GDF15 as a potential target in these cells and conducted loss of function studies to determine the GDF15-regulated effects in Dox-treated HCFs. Patients with diabetes receiving chemotherapy are at a significant risk for DIC and heart failure. Thus, we also interrogated the GDF15-regulated mechanism in diabetic HCFs in response to Dox exposure. Using a combination of protein, gene expression, and mitochondrial function assays, our data provides evidence that GDF15 is a bona-fide target of Dox in HCFs and may serve as a biomarker for Dox-cardiotoxicity.

04:45 PM. Understanding the Complex Dynamics of Cigarette Smoking and Its Impact on Substance Use In the USA: Insights from Longitudinal Data Analysis

Peter Y. Wui, Corey Hayes, Kennedy Abanihe
Dept. of Nursing, University of Arkansas at Pine Bluff, University of Arkansas for Medical Sciences

This study investigates the complex nexus between addiction, economic factors, and public health outcomes, with a particular emphasis on the consumption patterns of cigarettes and the implications of marijuana legalization. Grounded in established economic frameworks proposed by Boyer (1978, 1983), Becker (1994), and Chaloupka

(1991), we construct a comprehensive utility function to unravel the behavioral dynamics of addictive consumption. By leveraging longitudinal data from the National Survey on Drug Use and Health (NSDUH) spanning the years 2014 to 2021, augmented by supplementary datasets from the Centers for Disease Control and Prevention (CDC), state-level repositories, and annual volumes of the Tax Burden on Tobacco (Orzechowski and Walker, 2023), we develop a nuanced model to dissect addiction trajectories and their societal ramifications. Our model conceptualizes cigarette consumption as a stock variable, intricately intertwined with addiction levels, market prices, regulatory interventions, marijuana usage trends, and a myriad of other life cycle variables. Utilizing a quadratic utility function, we derive demand equations that optimize consumption choices in the presence of addiction dynamics, shedding light on the intricate interplay between substance use behaviors and economic incentives. Key findings from our analysis illuminate the multifaceted impacts of marijuana legalization on cigarette consumption patterns. Through the estimation of demand equations and the meticulous examination of coefficient effects, we uncover significant relationships between cigarette consumption, marijuana use prevalence, pricing mechanisms, tobacco control program expenditures, and various socio-economic determinants. Our empirical insights offer valuable guidance for policymakers and public health officials seeking evidence-based strategies to mitigate substance abuse and its associated harms. Furthermore, we anticipate enriching our analytical framework by incorporating additional life cycle variables, such as unemployment rates and state-specific contextual factors, to provide a more comprehensive understanding of addiction dynamics and inform targeted intervention strategies. This iterative approach underscores our commitment to rigorously examining the complexities of addiction within the broader socio-economic landscape, with the ultimate aim of fostering healthier communities and promoting evidence-informed policy responses.

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Chemistry Oral Presentations

03:30 PM. Attaining True Spectra Multicolor Images at the Nanoscale Using Phasor Analysis

James E. Batey, Elric D. Pott, Meek Yang, Bin Dong
Dept. of Chemistry and Biochemistry, University of Arkansas, Fayetteville

Over the past decade, super-resolution fluorescence microscopy techniques have been studied to overcome issues encountered in traditional fluorescence imaging techniques. When compared to traditional methods such as epifluorescence or confocal imaging, super-resolution excels at gathering spatial and temporal information with high resolution at the single-molecule level, allowing the resolution of tagged structures to be pushed beyond the theoretical diffraction limit. In recent years, there has been an increased focus on obtaining spectral information in addition to the spatiotemporal data at the single-molecule level. Spectrally enabled optical microscopy is crucial as it can distinguish multiple fluorophores with differing spectral emission distributions, enabling true multicolor imaging with applications in cellular biology, single-molecule catalysis, nanomedicine, and more. Current methodologies that can achieve multicolor imaging employ dispersive elements such as diffraction gratings or prisms to separate emitted light into its constituent wavelengths giving rise to spectral separation of fluorophores. However, these methods have limitations. When dispersive elements are used, a significant portion of signal is used for spectral determination. Because fluorophore localization is a result of the number of photons gathered in a single position over time, limiting the number of photons gathered for localization lowers the obtainable spatial resolution.

Further, because spectral determination relies on the first-order diffraction pattern being separated in space from diffraction patterns of other fluorophores, the labeling density of imaging probes must be kept low to prevent emission events occurring at the same time in proximity. Our method functions by splitting the emitted signal into three distinct optical paths. A reference channel with no modification and two modified channels composed of a sine and cosine path where a filter acting as each respective function within the expected emission wavelength range is implemented. A consequence of this setup is that each distinct wavelength emitted by a fluorophore has a different intensity ratio when comparing the sine and cosine channels to reference, allowing for high accuracy in spectral determination. Additionally, because there is no dispersion of signal, the three channels can be recombined to use all signal for localization with the same spatiotemporal resolution afforded to other super-resolution techniques. While other new systems can overcome photon inefficiencies using multiple objectives, these systems are complex and need specialized instrumentation not readily available in most lab settings. Here, we present the spectral phasor analysis utilizing an in-house constructed 3-channel system that can be adapted to most fluorescent microscopes to analyze complex fluorescence signals with high spectral and spatiotemporal resolution.

03:45 PM. Modifying Dipeptides to Investigate Aggregation Pathways: Developing Design Principles for Various Dipeptides

Danny A. Caceres, Jakob Anderson
Chemistry, Hendrix College

Abstract: The assembly process of dipeptides, specifically Diphenylalanine (FF), a dipeptide exhibiting aromatic and hydrophobic properties, is intricately studied to be a collective attempt to view trending patterns between monomers and determine potential medical proposals from these examinations. The properties of FF allow it to be one of the strongest biomaterials presently known due to its rigidity from its self-assembly into intricate, stable nanostructures. Additionally, due to these properties, FF has various proposed applications from selective biofilm eradication, drug delivery, and antibacterial effects. It is in great interest therefore, to optimize the structure of FF dipeptides and discover what modifications to its structure can be conducted in order to achieve applications of these proposals. This study considers the impact of modifying the relative amount of hydrophobic and aromatic properties within the aggregation process for FF-derived dipeptides. Thus, FF is rationally modified via changing its chemical compositions using either residues of Leucine (L), Phenylalanine (F), or Tryptophan (W), creating a series of trends based on aromatic and hydrophobic levels present in the system. Furthermore, modification on the N or C-terminal (LF/FF/WF and FL/FF/FW respectively) will create a series of trends based on sequence dependency, which in a previous study has been determined to be impactful with the usage of Valine and Phenylalanine residues. Thus, in this study we developed design principles based on aromaticity and hydrophobicity and design principles on the sequence dependency based on four, FF-derived dipeptide systems used. This is in order to determine what will occur to the aggregation process of dipeptides if we alter the sequence dependency and, separately, if we increase or decrease aromatic or hydrophobic levels on the system. We used explicit solvent to synthetically examine our systems with the usage of all-atom molecular dynamic simulations. By comparing the trends via conducting dihedral analysis, SASA plots, and radial distribution analysis on our systems during the initial aggregation phase. Our results determine that when viewing the monomeric conformations in our dihedral Ramachandran plots, there is an apparent increase when a phenylalanine is present on the N-terminal, which coincides with the previous Valine study. Additionally, when viewing early aggregation and the SASA plots of our systems for both the N and C-terminals, we can propose a design principle that as we decrease aromaticity on the N-terminal, the backbone-backbone association of monomers increases, meanwhile the same alteration on the C-terminal is less impactful on these same associations.

04:00 PM. Design Development and characterization of Polymer membrane Separator for Lithium-Ion Battery and surface modification using TiO2

Shahid Hussain Abro, Price Sheets, Noureen Siraj
Chemistry, University of Arkansas at Little Rock

The performance and safety of lithium-ion batteries are critically influenced by the properties of the polymer membrane separators used in their construction. This study explores the enhancement of these properties through the incorporation of titanium oxide (TiO_2) onto the polymer membrane surface. The primary objective is to improve the thermal stability, mechanical strength, and ionic conductivity of the polymer separators, thereby contributing to overall battery performance. Polymer separators are typically made from materials such as polyethylene (PE), polypropylene (PP), or blends of these polymers. These materials are chosen for their mechanical strength, thermal stability, and their ability to be manufactured into thin, uniform layers. We will synthesize polymer-TiO_2, composite membranes by incorporating varying concentrations of titanium oxide nanoparticles into a polymer surface via a solution casting method. The resultant membranes will be characterized using scanning electron microscopy (SEM) to examine morphological changes, and X-ray diffraction (XRD) to assess structural integrity. Thermal stability will be evaluated using thermogravimetric analysis (TGA), while mechanical properties will be determined through tensile tests. Ionic conductivity will be measured using electrochemical impedance spectroscopy (EIS). The expected results will indicate the incorporation of TiO_2, nanoparticles significantly enhance the thermal stability of the polymer separators, with a notable increase in the temperature at which decomposition begins. Additionally, the mechanical strength of the membranes improves with optimal TiO_2 content, leading to better performance under mechanical stress. The ionic conductivity of the composite membranes also shows enhancement, attributed to the increased surface area and improved interaction between the TiO_2 particles and the polymer matrix. This study demonstrates that titanium oxide is a promising additive for improving the surface properties of polymer membrane separators in lithium-ion batteries, potentially leading to more efficient and safer battery systems. Future work will focus on optimizing the concentration of TiO_2, and exploring other functional additives to further enhance separator performance.

04:15 PM. The Analysis of BPA Leaching in Various Types of Athletic Wear using Fluorescence Spectrometry

Bree Steinfeldt, Dr. Sara E. Hubbard
Chemistry, Ouachita Baptist University

Bisphenol A (BPA) is the most common endocrine-disrupting chemical that has been used in polycarbonate plastics and epoxy resins. BPA has been linked to several health issues due to binding to estrogen receptors. BPA is associated with an increase of ovarian, breast, prostate, and testicular cancer as well as low sperm count, motility and abnormal morphology of sperm, birth defects, early puberty, and Polycystic Ovary Syndrome. The item of focus for this research project was athletic wear. BPA can be absorbed dermally which is concerning because clothes have prolonged dermal contact with various types of tissue. Prior research at Ouachita Baptist University had found the presence of BPA in several brands of leggings. BPA leaching from different types of athletic wear were tested in a 50:50 methanol/water mixture as well as in artificial sweat. BPA leaching was observed and measured with a spectrofluorometer. BPA is a fluorescent compound, which means following excitation, it will emit radiation at a longer wavelength than the exciting wavelength. BPA is excited at 275 nm and emits at 306nm. This emitted light was measured and correlated to the concentration of BPA present in the sample. Fluorescence is a very sensitive and selective technique, which makes it possible to determine very low concentrations of BPA with few concerns about contamination. To compare the BPA leaching behavior of different types of athletic wear, a calibration curve was first established to help correlate the concentration of BPA in a standard solution to fluorescence emission intensity. The BPA leaching was monitored over the course of six

hours, and a leaching curve was prepared for each sample. BPA is found in very small concentrations in clothes; therefore, the standard addition method was used to calculate the unknown BPA concentration by the addition of a BPA standard solution to the testing solutions.

04:30 PM. SODIS: The bactericidal effect of UV radiation and thermal heating on water under real-world conditions in Arkansas

Kennedy Foster, Finneas Salazar, Daniel Atchley
Chemistry, Harding University

Solar disinfection of water (SODIS) has been used for treating and storing drinking water. SODIS relies on the combined effects of ultraviolet (UV) radiation and thermal heating to reduce the number of potential waterborne pathogens in water, thus making it safer to drink. Under optimal SODIS conditions, microbial decontamination can be significant, making this an attractive method for improving water quality in resource-limited settings. Arkansas, known as the Natural State, is largely rural and has many outdoor activities available. These factors make SODIS a potential viable option for purifying water in the field. However, the efficacy of SODIS is influenced by factors such as water turbidity, bottle material, and solar intensity, which can vary greatly in different geographic and climatic conditions. To determine the efficacy of solar disinfection under varying climatic conditions in Arkansas, real-world raw water samples were collected from Gin Creek, in Searcy, Arkansas, and subjected to SODIS treatment under a variety of weather conditions. To maintain the simplicity of this method in resource-limited settings, common plastic (polyethylene terephthalate/PET) water bottles were used. A six-hour kill-time study was conducted, and the quantity of potential waterborne pathogens (coliform bacteria) was determined every two hours. We observed that microbial killing was most effective under high solar radiation when the water temperature reached temperatures of 40°C, or higher. This study suggests the importance of optimal conditions when using this method. Further studies may need to be conducted to identify simple and cost-efficient ways to improve this method under non-optimal conditions.

04:45 PM. Synthesis of Modified Rifamycins to Combat Drug Resistance

Braden Glenn, Catherine Mills, Grant Beeser, Mai Lan Ho, Taylor Mitchell, Wyatt Treadway, Hannah Davison, Zane Fountain, Lola Beeser, Clara Nikkel, Ryan Holdiness, Jake Smith, Daniel Armstrong, Rachel Tyler, Jessie Parchman, Marissa Fullerton, Amanda Dragan*, Daniel Voth*, Ruud Dings*, Samir Jenkins*, Irosha N. Nawarathne (PI)*
Dept. of Chemistry, Lyon College

It is estimated that one-fourth of the population had latent tuberculosis (TB) infection. Not only is TB prolific but its danger is amplified by mutations which can result in antibiotic resistance, necessitating the development of new drugs. Mycobacterium tuberculosis (MTB)–the pathogen causing TB– has shown widespread resistance to rifampicin, making it futile in TB therapy as MTB RNA polymerase (RNAP) mutations disrupt key interactions between the drug and the target. Rifamycin and its derivatives, particularly rifampicin, have been a mainstay of TB treatment since the 1960's; it binds to the β subunit of the MTB RNAP and blocks RNA synthesis making it a resilient broad-spectrum antibiotic. We have exploited the rifamycin scaffold to target MDR (multidrug resistant) -TB and other bacterial infections. We propose that the addition of new functional groups to rifamycin S, both at the C-8 and C-3,4; will improve the RNA inhibition of these novel rifamycins against drug resistant bacteria. The new amino derivatives at C-8 of rifamycin S synthesized using click chemistry vary by azido, alkynyl, and triazole functional groups. The C-3,4 derivatives are benzoxazinorifamycins with the benzoxazino functional group formed on the C-3,4 carbons. We also conducted assays against both pathogenic Staphylococcus aureus (gram-positive) and non-pathogenic Escherichia coli (gram-negative) bacterial strains to evaluate the broad-spectrum antibiotic properties of these derivatives. Our work highlights the synthesis, isolation, purification, and antibiotic activity of novel

rifamycin derivatives with various functionalities and the innovative products of complex rifamycin chemistry.

Physics Oral Presentations

03:30 PM. Ultrasonic Characterization of the Human Scalp Using Backscatter Parameters

Catherine N. Prabish, Blake C. Lawler, Thomas H. Conroy, Cecille Labuda and Brent K. Hoffmeister
Physics, Rhodes College

Transcranial ultrasound has found many uses in the medical field. While there have been many research studies on the ultrasonic properties of the skull and brain, there are relatively few publications on the scalp. The goal of this study was to ultrasonically characterize the transmural structure of the scalp. Sixty-four formalin fixed specimens were prepared from four human donors and scanned in a water tank with a 25 MHz transducer to create parametric images of apparent integrated backscatter (AIB), frequency intercept of apparent backscatter (FIAB), and frequency slope of apparent backscatter (FSAB). Images revealed three distinct layers: a dermis/epidermis layer, a subcutaneous layer and a connective tissue layer. Measured values for the dermis/epidermis layer were AIB = -44.40 ± 3.26 dB, FIAB = -46.54 ± 6.13 dB, and FSAB = 0.1735 ± 0.3103 dB/MHz. Measured values for the subcutaneous layer were AIB = -45.35 ± 2.94 dB, FIAB = -49.88 ± 5.77 dB, and FSAB = 0.3671 ± 0.2843 dB/MHz. All parameters were significantly different between the two layers. Results from the connective tissue layer were not analyzed due to tissue damage concerns.

03:45 PM. Determining the Refractive Index of 2D Ferroelectric Material

Gabriel Reyna Garcia, Sudeep Puri, Dr. Hiro Nakamura
Engineering and Physics, Southern Arkansas University

Atomically thin SnS acquires ferroelectric and nonlinear optical properties. We evaluated the refractive index of thin SnS grown on SiO2/Si by analyzing the wavelength-dependent optical contrast of microscope images by using a theory that takes into account Fresnel interference in the dielectric layers. This work is supported by NSF through NSF-REU Award #2244130.

04:00 PM. Structure and Interface Analysis of Diamond on Î²-Ga2O3 Utilizing SiC Interlayer Grown by RF sputtering

Joel Osho, Ariful Haque
School of Engineering, Texas State University

In the expanding field of high-power electronics, beta Gallium Oxide (Î²-Ga2O3) emerges as a promising material for its robust properties, though its effectiveness is often curtailed by inadequate heat dissipation. This study introduces an ingenious approach to thermal management by integrating Silicon Carbide (SiC) and diamond layers into Î²-Ga2O3 devices, where SiC serves as a buffer layer between Î²-Ga2O3 and diamond to improve compatibility and thermal properties. The process involves depositing a Î²-Ga2O3 film by Pulsed Laser Deposition (PLD), adding a SiC interfacial layer by RF sputtering, and capping with a diamond film using Hot Filament Chemical Vapor Deposition (HFCVD). The innovation centers on

two main objectives: firstly, optimizing the SiC layer's thickness to minimize the thermal boundary resistance (TBR), which accounts for approximately 70% of total TBR at the interface, necessitating a smoother interface to enhance phonon transfer and device efficiency; secondly, developing a surface passivation technique for Ga2O3 during the thick diamond growth to mitigate radical species degradation. A significant aspect of our methodology is the optimization of seeding density for diamond growth, achieved using an electrostatic technique involving Polydiallyldimethylammonium chloride (PDDAC) and diamond nano slurries, achieving a high seeding density of approximately 5Ã—1011 cm-2. This enables uniform dispersion of diamond particles, essential for the robust growth of wafer-scale diamond films. Surface morphology and diamond quality are confirmed by Scanning Electron Microscopy (SEM), Atomic Force Microscopy (AFM), and Raman spectroscopy, ensuring high fidelity in structural and compositional analysis. Current findings have successfully optimized the interfacial layer thickness and demonstrated effective diamond growth with high seeding density. Future work will explore how these enhancements can directly improve thermal conductivity and overall device performance.

04:15 PM. Novel transferred Josephson junction fabrication using graphene monolayer

Aubrey McNiel, John Treusch, Hugh Churchill
Gallogly College of Engineering, University of Oklahoma

Josephson junctions are integral components of superconducting technologies, such as transmon qubits and superconducting quantum interference devices (SQUIDs) and are used for a variety of purposes ranging from providing the nonlinearity necessary for defining qubit states to reducing the sensitivity of superconducting qubits to charge noise. Ordinarily, these junctions are fabricated using either the Manhattan technique or the Dolan bridge technique, which often both result in devices with significant amounts of noise due to excessive residues on their surfaces. We aimed to build a Josephson junction with minimal residues by fabricating it on a silicon chip covered with a monolayer of graphene, transferring it to a gold lead, and depositing our second gold lead directly on top of the junction, avoiding shorting by depositing silicon dioxide as an insulator on all but our point of contact. We succeeded at the main goal of our project, the transfer, but further device fabrication and four-wire testing is needed to evaluate the effectiveness of this method. This work is supported by NSF-REU Award #2244130.

04:30 PM. Exploring topological defects in Janus bilayers of Cr(I,Cl)3 and Cr(I,Br)3

Taksh Patel, Dr. Suyash Rijal, Dr. Changsong Xu, Dr. Charles Paillard, Dr. Laurent Bellaiche
Dept. of Physics, University of Arkansas, Fayetteville

Magnetic materials can host novel spin textures such as skyrmions, bimerons, merons, etc. that are promising to be useful in novel memory devices for more efficient data storage techniques. One vital component needed for the formation of skyrmions, bimerons, and merons is typically a strong Dzyaloshinskii-Moriya interaction (DMI) – that originates from strong spin-orbit coupling. Chromium halides such as CrI3 have attracted interest recently. They possess the remarkable property of sustaining long-range magnetic order down to the thickness of only a few atoms. However, CrI3 lacks DMI due to inversion center present between the adjacently bonded Chromium atoms. One way the inversion center can be removed is through the fabrication of Janus Monolayers by adding another trihalide along with Iodine to synthesize the material, that is to grow Janus monolayers Cr(I, X)3 where X is another halide such as Cl or Br. In fact, our previous work has predicted non-trivial spin textures such as out-of-plane Néel-type cycloid with metastable Domain-Wall Skyrmions (DWS) in Cr(I,Cl)3 and Cr(I,Br)3. Furthermore, it was revealed there that a small out-of-plane magnetic field in Cr(I,Cl)3 leads to the stabilization of bimerons in the monolayer. Now, one may wonder what are the magnetic properties, not of monolayers, but rather of bilayers,

since 2D magnets are found to exist in layered form experimentally. Leveraging Density Functional Theory (DFT) and Monte-Carlo (MC) simulations, we explore in this work how Cr(I,Cl)3 and Cr(I,Br)3 bilayers are magnetically coupled. We reveal how these magnetic parameters are tuned by interlayer distance and stacking in these bilayer films. We will present our results regarding the tunability of interlayer parameters and consequently, the interaction of topological charge in bilayer films.

04:45 PM. Nanopore Device: Sensing the Shape of Protein Molecules

Sidney Kwame Osae-Asante, Dr Jiali Li, Haopeng Li, Sachinii Withanage
Physics, Abilene Christian University

In this research project, we will employ a solid-state nanopore-based sensing device. The central component of this device is a voltage-biased nanopore that we fabricate within a silicon nitride membrane. This membrane effectively separates two chambers filled with a conducting electrolyte solution (salt). The sole electrical conduction path between these chambers passes through the nanopore. The underlying principle of our method relies on Ohm's law. When a voltage is applied across the nanopore, an ionic current flows through the open pore. We achieve this by placing silver/silver chloride electrodes in each of the two reservoirs. Our goal is to study charged protein molecules of interest. These proteins are introduced into the chamber containing a grounded electrode. These molecules reach to the vicinity of the nanopore by diffusion and will be captured by the local electric field near it due to their charge. As a protein molecule interacts with the nanopore, the electric field within the pore drives the molecule to pass through to the other side. By recording the nanopore current over time during this event, We will gain insights into the protein's history of interaction with the nanopore. This information allows us to determine both the volume and shape of the protein. This work is supported by NSF-REU Award #2244130.

Poster Abstracts

Biology

1A. Genomic Strategies to Study Essential Biofilm Formation Genes in the Tooth Decay Pathogen *Streptococcus mutans*

Emanuel Emilio Cazano, Ana Karen Solano Morales, James Andrew Goode, Robert Colquhoun Shields
Biology, Arkansas State University

The bacterial species, *Streptococcus mutans* (*S. mutans*), is a heavily researched pathogen that is known to be one of the primary etiological agents of tooth decay (dental caries). Understanding the processes and specific genes responsible for *S. mutans* persistence within the human oral cavity is essential in designing better therapeutic strategies against dental caries. The goal of this project was to assemble an arrayed transposon (Tn) library to then use to screen for biofilm-defective mutants. An added goal is that the Tn library, once defined, will become an important tool for other researchers in the *S. mutans* research field. A total of 9,600 Tn mutant colonies were picked and placed into individual wells of 96-well microtiter plates. Assays used include the crystal violet (CV) assay to quantitate biofilm growth, planktonic growth measurements to ensure growth was not a factor in biofilm formation, and genome sequencing to locate Tn mutations. Z scores were calculated and used to select for the mutants that had a significant decrease in biofilm formation. (65% reduction in biofilm accumulation as measured with the CV assay, and Z scores within ±5 standard deviations from the mean). Out of the 9,600 colonies that were tested, 85 were found to have a mutation contributing to decreased biofilm formation. Once the 85 Tn mutants were selected and stored, mutants were then chosen to undergo genome sequencing. Once sequenced, several different genomic loci were identified as being required for wild-type biofilm formation. Future studies within this project include testing the mechanical properties (using a nanoindenter) of teeth exposed to defective and non-defective *S. mutans*. We anticipate the results of these studies will provide an understanding of the specific genes required for *S. mutans* to attach to the tooth surface, and then initiate the progression of dental caries.

1B. Suppression mutations of the essential gene, gpsB, suggest a relationship with protein phosphorylation in *Streptococcus mutans*

Sangam Chudal, Courtney Dover, Robert C. Shields
Dept. of Biological Sciences, Arkansas State University

Streptococcus mutans is a Gram-positive bacterium that resides in the oral cavity and causes tooth decay. Our recent studies have revealed the existence of several poorly characterized and essential genes in *S. mutans*. In this study, we focused on a single gene, SMU_471, that is putatively annotated as gpsB, a protein known to be involved in cell division in other Gram-positive pathogens. Using CRISPR interference, we were able to study the phenotypic impact of repression of gpsB on *S. mutans* via growth assays, transmission electron microscopy, and transcriptomics. In addition, we attempted to delete gpsB via allelic exchange mutagenesis to determine if we could select viable gpsB mutants that had acquired bypass suppressor mutations. We were able to isolate gpsB mutants, and after whole-genome sequencing, we discovered mutations in pppL (serine/threonine protein phosphatase) that might be responsible for allowing gpsB to be mutated. To investigate this further, we grew various mutant strains, including gpsB, knockdown gpsB, and several gene mutants involved in protein phosphorylation, and then used western blotting to probe the protein phosphorylation status of the cells. Our results indicate that repression of gpsB increases protein phosphorylation of PknB (serine/threonine protein kinase), DivIVA (cell division protein), and other unknown proteins. Interestingly, gpsB has even higher levels of protein phosphorylation compared

to the gpsB knockdown, with these levels not being restored to those seen in wild-type *S. mutans*. Our findings suggest a linkage between GpsB and protein phosphorylation status in *S. mutans*. Future work will aim to explore the functional implications of increased phosphorylation in these strains. This could further clarify how protein phosphorylation affects bacterial growth, protein regulation, and potential survival mechanisms through kinases and phosphatases.

2A. Analyzing the Role of GTPBP10 and PCDH1 in Kidney Morphogenesis

Kolby Payne Jasmeet Ghotra Mick Yoder
Biology, University of Central Arkansas

The kidney is an essential organ that filters soluble waste from the bloodstream. Without proper functioning, waste products would accumulate, and homeostasis would be impaired. It is estimated between 4 to 100 individuals per 10,000 carried to term are affected by congenital kidney anomalies. Due to the importance of the kidney, those affected by these defects suffer a low quality of life, or do not survive till adulthood. This makes understanding kidney development an important focus area of research. Xenopus laevis embryos are a model system that can be used to study embryonic development due to external development of embryos, ease of genetic manipulation with microinjections, and rapid development. In addition, many human disease genes are homologous to X. laevis genes with high sequence conservation. X. laevis has been used to model many common human kidney diseases. Previous studies show that the genes, GTPBP10 and PCDH1 are expressed in the embryonic kidney (pronephros); however, the roles of these genes have not been established. Research into these genes has shown indications that GTPBP10 mutants exhibit edema, a common sign of kidney failure. Other data show that GTPBP10 and PCDH1 have an in vitro interaction. The goal of this study is to characterize this interaction and determine the functioning of these genes in pronephros development. This will be done using microinjections of mRNA for overexpression and morpholino (MO) for knockdown in both wildtype and transgenic PAX8 GFP X. laevis. Their phenotypes will be analyzed against controls to identify disruption of pronephric development. Fluorescent images of the transgenic PAX8 GFP will be taken to determine precisely where pronephros development is disrupted. It is hypothesized that both genes are required, and their interaction is necessary for normal pronephros development.

2B. Histone Post Translational Modifications as Biomarkers for Resistance to Immune Checkpoint Inhibitor Therapies for Metastatic Melanoma

Elisabeth Hicklin, Katherine Bronson, Jake Edmonson, Billie Heflin, Megan Reed, Alan Tackett, Sean Taverna
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Metastatic melanoma has a five-year survival rate around 20%. Due to melanoma being highly immunogenic, the current standard of care is immune checkpoint inhibitors (ICI) that increase immune response against the tumor. However, half of patients have an innate resistance to ICI therapies. While resistance is apparent throughout the course of treatment, there is a lack of biomarkers to preemptively indicate resistance to ICIs. Therefore, to understand the mechanisms of ICI resistance within melanoma and develop new biomarkers for ICI responsiveness, we used Yale University Mouse Melanoma (YUMM) cells as models for human melanoma tumors due to available genotypes. YUMM1.7 and YUMM2.1 cell lines emulate human non-response and response to ICI therapies, respectively, and contain BRAFV600E and PTEN mutations. These cell lines provide a system for investigating innate and characteristic epigenetic marks between response types. The histone post-translational modifications (PTM) of a trimethylation of lysine 27 on histone 3 (H3K27me3) is associated with transcriptional repression of antigen presentation proteins within the major histocompatibility complex I (MHC-I) and activation of PD-L1. Additionally, previous studies reveal over-expression of H3K27me3 and its

modifier, the methyltransferase EZH2, positively correlates with metastatic melanoma growth and proliferation. As a proof of principle, we hypothesize that EZH2 and H3K27me3 can function as biomarkers for tumor recognition by the immune system. To evaluate the effect EZH2 has on antigen presentation, EZH2 will be inhibited using the FDA-approved drug Tazemetostat. Changes in transcript, proteome, and surface protein expression due to modified EZH2 function will be evaluated and compared between the two YUMM cell lines. Through this work we hope to better understand and identify potential mechanisms of ICI resistance in metastatic melanoma.

3A. Role of murine Rnd3 in Lewis Lung Carcinoma cells and its effects on cell migration and invasion in lung cancer

Faith Stephens, Noemi Garcia Garcia, Thanh Ha Vy Nguyen, Dane Richey, Cody Ashby, Katie R. Ryan
Dept. of Biological Sciences, Arkansas State University

In the US, lung cancer causes about 350 deaths a day and has the highest mortality rate out of all forms of cancer. Lung cancer metastasis leads to cancer cells invading the rest of the body, which greatly contributes to its lethality. Rnd3, a small Rho GTPase protein, has been shown to be a potential prognostic marker for patients with lung cancer. Rho GTPases regulate various cellular processes such as cell migration, gene expression, cell cycle regulation, and cell adhesion; these processes are commonly deregulated in cancer cells. Our data shows that in human lung adenocarcinoma cells, knockdown of Rnd3 decreases invasion and migration, two hallmarks of metastasis. Our goal is to understand how Rnd3 regulates migration and invasion in lung cancer cells and if Rnd3 regulates metastasis. We hypothesize that in murine Lewis Lung Carcinoma cells Rnd3 knockdown will decrease invasion and migration, recapitulating our data generated in human lung cancer cell lines, and lead to decreased metastasis in vivo. Through Rnd3 knockdowns and migration, invasion, and proliferation assays, we will evaluate the function of murine Rnd3 in the mouse cell line. Preliminary data generated here will aid in the design of our future in vivo experiments, determining whether we will perform xenograft or syngeneic in vivo experiments to study the effects of Rnd3 knockdown on lung cancer metastasis.

3B. eDNA Research collecting Guano samples to correctly identify The Ozark Big-Eared Bat

Maria Collins, Luke Brown Douglas, G. T. Yamashita
Dept. of Ecology and Evolution, Arkansas Tech University

Corynorhinus townsendii ingens, known as the Ozark Big-eared Bat, is an endangered species found in northwest and central Arkansas, eastern Oklahoma, and southern Missouri. Due to their sensitivity to human disturbance to their environment, finding a non-invasive way to identify the Ozark Big-Eared Bat species to prevent colonies from leaving their hibernacula has proven challenging. To counteract this reaction amongst the bats, collecting bat guano to identify the species of bat in a cave is the most suitable method. This is because collecting bat guano can be done at the entrance of the cave, ensuring no human disturbance during collection. Such methods are critical for the survival and conservation of the species. This study's purpose is to establish a reliable technique for DNA extraction and identification. To extract the DNA needed to identify the Ozark Big-eared Bats from their guano, the QIAamp protocol was used. After extracting the DNA, we tested three candidate primers to determine which was best suited for this species. These primers were used to bind targeted DNA sequences needed to identify the species and the DNA was amplified via PCR. We then visualized PCR products on agarose gels to identify which primer worked best. Finally, we purified and Sanger sequenced PCR products and determined bat identity via Blast-n search against the full GenBank nucleotide and BOLD database. As expected, the concentrations of DNA from individual pellets were lower than those from the pooled sample. We found that the “species from feces” primer showed the

best results compared to the other primers, and we demonstrated that these primers can accurately identify Ozark big-eared bats from guano samples. Overall, this research holds promise to advance our understanding of this endangered species and improve management efforts aimed at its conservation.

4A. Comparing Chloroform Methanol Extraction Digest and S-Trap Digest for Proteomics on B16-F10, MC38 and YUMM 1.7 melanoma cell lines

Emilia Moreno, Dennis Province
Biochemistry, University of Arkansas, Fayetteville

Discovery proteomics employs Chloroform Methanol Extraction (CME) and Suspension Trapping (S-Trap) to digest proteins into peptides by trypsin. CME is a tube-based protocol adapted for sample preparation because of its ability to clean up a variety of samples treated with upstream surfactants and can removed organic and aqueous contaminants before digestion; however, its single tube process is not compatible with automation. S-Trap is a commercially available protocol by ProtiFi that is 96-well-plate formatted. The S-Trap original is costly and uses the detergent Sodium Dodecyl Sulfate (SDS) for lysis, which can be difficult to rinse away before digestion and degrades the chromatography. Plate-based digestion is advantageous due to its ability to process up to 96 samples at once and lends itself to automation, offering greater reproducibility and time efficiency. Most proteomics core facilities, like IDeA National Resource of Quantitative Proteomics, are moving toward plate-based sample preparation, such as S-Trap. This project uses three melanoma cell lines (B16-F10, MC38, and YUMM 1.7), each is assigned to one of three treatment groups: a genetically modified group with ATF6-CA, which over expresses regulation of the unfolded protein response; a treated group with AA147, a drug that activates the ATF6 signaling molecule; and a control group. From a biological perspective, the data collected explores signaling pathways specific to unfolded protein response in melanoma immunosuppression. The processing of these biological groups by both the tube-based CME and plate-based S-Trap were compared based on total and unique protein IDs. S-Trap was found to obtain the greatest total number of protein identifications, but CME obtained the greatest number of significant protein identifications.

4B. Mathematics-AI Based Phylogenetic Analysis of Influenza Mutation Data

Emilee Walden, Jiahui Chen
Biology and Mathematical Sciences, University of Arkansas, Fayetteville

The influenza (flu) virus is a rapidly contagious virus resulting in seasonal epidemics, particularly in the H3N2 strain. The impact of virus mutations on public health is profound, leading to increased infectivity and vaccine resistance. Annually, the CDC characterizes approximately 2,000 virus strains to monitor their evolution and confirm vaccine effectiveness. Dimensionality reduction methods such as principal component analysis (PCA), uniform manifold approximation and projection (UMAP), and t-distributed stochastic neighbor embedding (t-SNE) combined with unsupervised machine learning algorithms such as k-means clustering offer solutions to the computational challenges posed by high-dimensional flu virus data. Clusters can forecast emerging flu variants by showing the most common mutation trends, provide insight into location-specific outbreaks, and allow scientists to prepare vaccine and antibody therapy for specific mutation types in different areas. Like the flu, COVID-19 is a single-stranded RNA virus that replicates in the respiratory tract epithelium. Thus, through the integration of genomic analysis, clustering, and dimensionality reduction methods, our study specifically investigates the influence of COVID-19 on flu virus mutagenesis by evaluating the evolution of flu mutations before and after the rise of COVID-19. Our findings reveal that a robust dimension reduction and clustering approach can yield promising results in deciphering the complex dynamics of virus mutations, providing valuable insights for future research and public health strategies.

5A. Ferrostatin alters ATP production and activation of cultured microglia

Naomi McNaughton, Alyssa Scott, Landon Gentry, David Donley
Biology, Harding University

Free radicals drive oxidation/reduction (redox) reactions that coordinate intracellular signaling. Buildup of radicals and/or dysregulation of redox pathways causes oxidative stress that damages cells. Microglial cells are Central Nervous System resident immune cells that are sensitive to oxidative stress at both the cellular and tissue level. Inflammation is associated with this stress in microglia and their response to disease-associated stimuli such as amyloid beta (AÎ²). Microglial dysfunction from long-term oxidative stress is implicated in the potentiation of neurodegenerative diseases such as Alzheimer's Disease (AD) and is associated with elevated iron. However, the interaction between redox-active iron, oxidative stress, and microglial inflammation is unclear. To study this relationship, we treated cultured microglia with ferrostatin, a transferrin receptor inhibitor and putative radical scavenger, with and without AÎ² stimulation. We found that ferrostatin decreases radical generation and suppresses activity of the pro-inflammatory enzyme, inducible nitric oxide synthase. This indicates that ferrostatin may push microglia towards an anti-inflammatory state. Metabolism is a determinant of activation state: pro-inflammatory states favor glycolysis and immuno-regulatory states favor oxidative phosphorylation. Consistent with suppression of inflammation, ferrostatin decreased AÎ²-induced glycolysis. Ferrostatin also increased basal oxidative phosphorylation and decreased maximal respiratory capacity. These results suggest that iron acts as a regulator of microglial inflammatory state, perhaps via regulation of mitochondrial respiration. The exact mechanism(s) of how iron contributes to disease-associated inflammation in microglia is unclear; however, our results indicate that iron dysregulation promotes inflammation and modulates responses to extrinsic stimuli in part by altering the response to stimuli such as AÎ². Future research will elucidate how iron-sensitive genes impact metabolic balance in microglia. Overall, our work details the relationship between iron and microglial inflammatory responses and provides insight into how iron, oxidative stress, and inflammation intersect to produce disease-associated inflammation.

5B. Development of a Novel Blood Test for Detection of Drug-Induced Liver Injury

Nyera Ali, Mitchell McGill
College of Public Health, University of Arkansas for Medical Sciences

Suspected drug-induced liver injury (DILI) ranks 4th among reasons for the termination of new drugs during clinical trials and is the primary cause for drug withdrawal from markets. The US FDA relies on alanine transaminase (ALT) in plasma as a biomarker to test for DILI and even transient ALT increases in very few trial subjects can result in discontinuing a new drug. However, elevations of this enzyme are not specific to liver injury, as fluctuations can occur for a variety of unrelated reasons. Discontinuation of drugs due to "false positive" ALT values may deprive patients of otherwise helpful treatments, accentuating the need for liver damage-specific biomarkers. Prior research indicated that during liver injury, proteases confined to lysosomes are dysregulated and cleave cytosolic proteins. Based on that, we hypothesized that some proteins should be fragmented only during real liver injury and that the fragments may appear in serum. To test this, mice were treated with acetaminophen (APAP) as a liver injury model, dexamethasone (Dex) as a drug yielding ALT elevations without liver injury, and their respective vehicle-controls. Using gel electrophoresis, serum proteins from the mice were separated by size and bands were extracted at regular intervals along the gel. While ALT was elevated in both the APAP and Dex groups, distinct fragmented proteins, specifically Glycogen Phosphorylase (Pygl), were detected only in serum from the mice with APAP injury. To quantify Pygl, we began developing an ELISA system, altering factors such as the capture and detection antibody and assay conditions using patient serum and synthetic Pygl. However, while fragmented Pygl is a promising biomarker with high

specificity for liver injury, additional experiments are needed to refine the ELISA system for clinical application.

6A. Determination of the Mechanism of Action of Bax Activation

Julie Schwartz, Archyshmaan Pattanaik, Jianhong Zhou, Yuchun Du
Physics, Hendrix College

Dysregulated apoptosis leads to many disorders, including tumorigenesis and neurodegenerative disorders. Bcl-2 associated X protein (Bax) is a pro-apoptotic member of the Bcl-2 family of proteins that regulate mitochondria-dependent apoptosis. When activated, Bax translocates from the cytosol to the mitochondria, where it oligomerizes and permeabilizes the mitochondrial outer membrane (MOM). MOM permeabilization allows the release of cytochrome C protein (Cyt C) from the mitochondria, which induces apoptosis. Although Bax is understood to play an important role in apoptosis, its mechanism of activation is not well understood. Using quantitative proteomic analysis and confocal microscopy, it has been demonstrated that inactive cytosolic Bax colocalizes with the Prohibitin 2 (PHB2) protein in vivo. A glutathione-s-transferase (GST) pull-down assay and Western blot analysis demonstrates that PHB2 does not physically bind Bax in vitro. These results suggest that the Bax-PHB2 association in the cells is potentially mediated by other factors. Flow cytometry-based cell assays demonstrate that PHB2 overexpression inhibits cell apoptosis.

6B. Examining *Caenorhabditis elegans* Ability to Form Conditioned Preferences to Caffeine

Sophia Smith, Rick Murray
Biochemistry/Molecular Biology, Hendrix College

Caffeine is recognized as the most used drug among humans and clinical studies have recently begun to highlight the similarities between the behavioral and physiological effects of caffeine and other drugs of abuse. Healthcare professionals are now starting to recognize dependence on caffeine as a clinical disorder which necessitates further research into the molecular and biological mechanisms underlying caffeine dependence. Recent animal models have demonstrated that behavioral responses to caffeine appear to be conserved among organisms: rats exposed to caffeine displayed preferential and withdrawal behaviors, and Drosophila displayed enhanced locomotor function and activity in response to caffeine. *Caenorhabditis elegans* (*C. elegans*) is a powerful animal model and has been shown to demonstrate cue-dependent conditioned learning to biological stimuli and certain drugs of abuse. Previous studies using chemotaxis assays have shown the ability of *C. elegans* to demonstrate associative learning through a conditioned preference for an environmental cue paired with psychostimulants, yet little is currently known about the effects of or the responses to caffeine in these organisms. In this study, we will pair a distinctive salt cue with caffeine to test the hypothesis that *C. elegans* will develop a conditioned preference for an environment containing a cue that was previously paired with caffeine. This invertebrate animal model could provide a new method for studying the behavioral and molecular mechanisms underlying caffeine dependence and caffeine use disorder.

7A. Social Amoebae Symbiont Prevalence in Southern Missouri

Lulu Quebedeaux, Johnna Hollis, Tammy Haselkorn
Biology, University of Central Arkansas

Symbiosis is when two organisms live together. Amoebae and bacterial interactions are a common symbiotic relationship. Free-living amoebae use bacteria as a food source where the bacteria will sometimes adapt to life within the amoeba. *Dictyostelium discoideum* is a soil-dwelling social amoeba that is the NIH model organism for experiments due to its macrophage-like nature. It is known for symbiotic relationships with the bacteria in the phylum Chlamydiae. This was discovered through sampling populations in Arkansas where Chlamydiae has been found in eleven different

species of amoebae. With Arkansas being the only place this is found so far, we wanted to see if it was prevalent across other states. Soil samples from South Missouri were collected and grown on hay plates and fruiting bodies were collected. These samples were run through DNA extraction and PCR with *Dictyostelium discoideum* primers and Chlamydiae symbiont-specific primers to determine Chlamydiae prevalence. Next, PCR samples were sent for sequencing of the Chlamydiae 200 base pair 16S rRNA gene. Phylogenetic analysis was then performed to see if Chlamydiae interactions are host-specific or geographically localized. The results of this study will lend insight into how Chlamydiae spreads beyond Arkansas.

7B. The Spread of Chlamydiae Symbionts in Natural Populations of Social Amoebas

Johnna Hollis, Alyssa Nolan, Tammy Haselkorn
Biology, University of Central Arkansas

Chlamydiae bacteria are best known as obligate intracellular parasites of many organisms, but metagenomic sequencing has revealed more extensive lineages within this bacterial phylum. Environmental Chlamydiae have been found to live intracellularly in an increasingly wide range of hosts, including amoebas, sometimes acting as defensive mutualists rather than pathogens. However, the role of different types of Chlamydiae in different species of amoebae is still being studied and has not been fully determined. *Dictyostelium discoideum*, a model host organism due to its macrophage-like nature, has been found to host novel Chlamydiae lineages. We have previously sampled over 1500 amoeba isolates of 11 different social amoeba species in damp soils across 11 parks in Arkansas and found an average infection prevalence of 40%. Chlamydiae prevalence is positively correlated with temperature. To expand on the potential symbiotic relationship between social amoebas and Chlamydiae, we are exploring how the Chlamydiae prevalence varies by location and host species across a latitudinal gradient. We sampled amoebae from 9 parks from Minnesota to Louisiana. The prevalence of Chlamydiae in social amoebas is variable but high, indicating a potential mutualistic relationship. Over 40 novel strains of Chlamydiae were found in these social amoebas, and specific Chlamydiae haplotypes are more associated with host species than geographic location. However, there is no obvious pattern of Chlamydiae prevalence across a latitudinal gradient. This lends insight into the epidemiology of Chlamydiae occurrence, and future work will explore its function in natural populations of social amoebae.

8A. Determining Viable Cells After Freezing of *Arthospira Platensis* Followed by Thawing

Isaac Devine, Dr. Jim Taylor, Cooper O'Briant
Biology, Ouachita Baptist University

Arthrospira platensis, also known as Spirulina, is a cyanobacteria that contains numerous proteins that can be used for nutritional benefits in the health industry today. As space travel develops plans for into the future, adequate oxygen levels and correct nourishment for astronauts are needed more than ever. Spirulina can provide space travelers with some of the health benefits needed to sustain life in space without the need for an extensive storage system. Spirulina produces oxygen through photosynthesis scrubbing carbon dioxide from the air. Spirulina contains two cell structures (straight and coiled). In space, every move must be calculated to prepare for catastrophic disasters. Temperature in space is -270.45°C. In the event of accidental freezing of Spirulina cultures, can the cultures possibly be revived? In this experiment, both straight and coiled Spirulina (Fig. 4 and 5) were studied when frozen to -78°C, then stored at -20°C and -80°C. Cultures were studied to determine if the cells were still viable after freezing and thawing to mimic the effect of low temperature on cell viability after recovery from the cold. Cell structure was observed by monitoring length of the pre and post frozen cultures using micro fluorescence.

8B. The Effect of Gravity on *Physarum polycephalum's* Ability to Solve 3D Printed Mazes

Cooper O'Briant, Dr. Jim Taylor, Isaac Devine
Biology, Ouachita Baptist University

Physarum polycephalum is an unicellular, fast moving slime mold that is commonly found in the forest. *Physarum* is found in the genus of mycetozoan and the family of Physaraceae. *Physarum* would be very instrumental for long-term space travel because of its ability to decompose and recycle. This would create better environments for other organisms to grow. The purpose of the experiment is to study the effect gravity has on *Physaryum's* ability to find food through a 3D printed maze. The 3D mazes were specifically created and designed to fit inside an 15mm/100 mm petri dish. *Physarum* is placed in the center of the 3D printed mazes that are being held down by bacteriological agar. In the center with the *physarum* a single oat was placed and multiple oats were placed at the end of the maze. The effect gravity has on the *Physarum* was studied using the clinostat. The mazes were split up to be either stationary/control group mazes and clinostat mazes that are constantly rotating. All growth was charted and recorded using a piece of yarn maneuvered around the maze every 24th. The experiment showed that gravity did not affect the growth of the *Physarum*, but it did affect the *Physaryum's* ability to solve the mazes. Because of the reduction of gravity, the *Physarym* loses its path throughout the maze and ends up taking the wrong turn. The final results were analyzed using the ANOVA test, in which all the p-values for each condition were analyzed.

9A. Polymerase Kappa-Mediated Fork Reversal in Glioblastoma Multiforme (GBM)

John Schaller, Reham Sewilam, Robert L. Eoff
Biochemistry-Molecular Biology, Hendrix College

Glioblastoma multiforme (GBM) is the most aggressive and invasive form of brain cancer, with bleak patient outcomes. Constant activation of the replication stress response (RSR) in GBM contributes to disease progression and treatment resistance. The Y-family member polymerase kappa (Pol κ) is a promising RSR factor to investigate due to its upregulation in GBM being correlated with worse prognosis and heightened resistance to the standard-of-care alkylating-agent temozolomide. Previous experiments in the Eoff lab showed an accelerated fork in GBM cells lacking Pol κ with no change in fork speed observed in other cell types, suggesting an exclusive role for Pol κ in slowing GBM fork progression. However, the mechanistic basis for Pol κ -mediated control of fork dynamics in GBM remains unknown. Fork reversal is known to slow the replisome, but a connection between Pol κ and fork reversal has not previously been made. We hypothesize that Pol κ slows replication by promoting fork reversal in GBM. To test this idea, we investigated whether the presence of Pol κ influenced the colocalization of SMARCAL1, a fork reversal factor, to nascent DNA in the presence or absence of the topoisomerase inhibitor camptothecin (CPT). We found that depletion of Pol κ led to a decrease in SMARCAL1 colocalization to sites of nascent DNA synthesis following treatment with CPT. This is consistent with the idea that loss of Pol κ produces a defect in fork reversal. We then used a DNA fiber spreading (DFS) assay to measure fork speed in an epistasis-type experiment assessing the effect of depleting Pol κ, SMARCAL1, or both factors simultaneously. Depletion of either Pol κ or SMARCAL1 alone each resulted in a fork acceleration phenotype. We found no additive effect on fork speed when both Pol κ and SMARCAL1 were depleted from GBM cells, suggesting these two proteins work in the same pathway to regulate fork dynamics in GBM. These results are the first to establish a link between Pol κ and fork reversal, helping to explain how GBM cells tolerate constant and high rates of DNA damage in the tumor microenvironment.

9B. Investigating Methylenetetrahydrofolate Reductase Gene Function in *Caenorhabditis elegans*

Kenedi Brunen, Sophie Smith, Dr. Richard Murray
Dept. of Biology, Hendrix College

The methylenetetrahydrofolate reductase (MTHFR) gene is an important enzyme in human folate and homocysteine metabolism. MTHFR catalyzes the biochemical conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which is required for the generation of folate and the conversion of homocysteine to methionine. Mutations in the MTHFR gene lead to reduced enzyme activity resulting in an increase of homocysteine in the blood. This has been shown to cause developmental delays and neural tube defects in humans. In order to develop an animal model to study MTHFR gene function, we are investigating the role of the MTHFR ortholog, MTHF-1, in *C. elegans*. Using RNAi to reduce gene expression, we will examine *C. elegans* for developmental delays or defects such as changes in body size, locomotion, egg laying, and life span. Examining phenotypic changes in the animals can help us to determine the role of the MTHF-1 gene in *C. elegans* development and could provide a powerful animal model of human neural tube defects.

10A. Efficacy of BCL-2 Guardian-Inhibiting Drugs

Handel Justus, Elisabeth Ferreira, Tudor Moldoveanu.
Biology, John Brown University

The BCL-2 family proteins regulate apoptosis initiation through mitochondrial poration, which releases apoptosis-inducing proteins such as cytochrome c, which activate the caspases that execute cell death. However, the overexpression of pro-survival proteins of the BCL-2 family leads to different malignancies. This has made the pro-survival proteins a well-known target for therapeutics. However, the Moldoveanu lab has recently revealed that some of the guardian inhibitors proposed to be potent and selective for MCL-1 are not as potent in inducing apoptosis in cells that contain only the effector BAK + MCL-1 and none of the other BCL-2 family proteins, which may explain why the inhibitors failed in clinical trials due to toxicity. Building on these observations, we set out to profile the most common guardian inhibitors in cells that contain only the effector BAK ± one of the guardians (MCL-1, BCL-XL, or BCL-2) to determine their potency and selectivity in inducing apoptosis.

10B. The Temporal Progression of Inflammatory Changes of Microglia in the Brain of the Rat Model of Alzheimer's Disease

Kaneeka Chakraborty, Sumit Sarkar, James Raymick
Little Rock Central High School

Background: Alzheimer’s Disease (AD) has been shown to lead to deposition of Amyloid Aβ plaques and neurofibrillary tangles (NFT) in the cerebral cortex and hippocampus of the brain. These have the potential to cause neurological damage and suggests a relationship to the neuropathology in an AD brain. To examine this, this study analyzes the characteristics of one of the key neurovascular units of the brain such as microglia in an AD brain. Microglia are macrophages in the brain that respond to pathogens and neurological damage, engaging in phagocytosis to regulate the brain environment. The Toll-like receptors (TLR) of the microglia recognize pathogens which leads to an ameboid shape and phagocytic response. The purpose of this study is to determine a causative relationship between the buildup of Amyloid Aβ plaques and the activation and proliferation of microglia. Methods: Both transgenic AD and non-transgenic female rat brain sections 25 micron thin were used and stained with a microglial marker, IBA1. Brain sections were additionally stained with Congo Red (CR) which detects amyloid Aβ plaques. Microglia labeling was visualized under light microscope (Nikon), and the CR staining was visualized under the fluorescence microscope to determine whether the increase in amyloid Aβ plaques was related to the activation/proliferation of microglia. Further quantitative analysis was performed using Image J

software. Results: In transgenic rats, microglial size significantly increased over time in the hippocampal and cerebral cortex regions. On the contrary, in non-transgenic rats, microglial size increased in the hippocampus and cerebral cortex, but was not significant. Conclusion: In AD brain sections, the hippocampus and cerebral cortex experienced a significant increase in microglial proliferation and inflammation over time. This was not seen in non-transgenic brain sections. This signifies a relationship between temporal changes of microglia during AD progression.

11A. Aeromicrobiology with High-power Rocketry

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

Aeromicrobiology is the study of microorganisms in the atmosphere. High-power rockets are capable of achieving impressive altitudes, even while carrying delicate payloads. For this series of experiments, our payload is the LADCAP (Launchable Automatic Device for Collecting Airborne Particles). LADCAP collects high-altitude microorganisms, called extremophiles, which can withstand low temperature, low pressure, desiccation, and increased UV flux. The data collected about extremophiles on Earth can potentially be extrapolated to extremophiles in other locations, including other celestial bodies. While the surface of Venus is extremely hostile, the cloud layer of the planet's atmosphere is much more hospitable to the possibility of life. This cloud layer has moderate temperatures of 0-60°C and pressures of 0.4 - 2 atmospheres. Extremophiles in earth's own atmosphere would have adapted to live under similar conditions. Therefore, the samples we collect on Earth could provide insight into the types of extremophile life that exist in the Venusian cloud layer. With the LADCAP proprietary system, our lab has aspirated airborne microorganisms from the atmosphere. Through repeated launches our lab has collected numerous airborne microbes, including three rhizoid bacterial colonies.

11B. CdSe/ZnS Quantum Dots – Actin Characterization, Interaction and Mechanism

Abhishu Chand, Nhi Le, Kyoungtae Kim
Biology, Missouri State University

Quantum Dots (QDs) are bright fluorescent nanoparticles that are highly sought after in biomedical applications due to their possibilities in drug delivery, cell labeling and tracking, and bioimaging. Despite such promise, QD's toxicity in cells has resulted in major utilization restrictions. Therefore, our study investigated the impact of CdSe/ZnS QDs on cellular proteins and their function. We identified several QD-binding proteins, including actin. Using a series of biochemical assays, we discovered that CdSe/ZnS QDs bind to G-actin spontaneously in vitro and compromise its function by altering the secondary structure of G-actin. We then further studied the potential effects that this structural alteration might have on actin dynamics, where we discovered the QDs' ability to behave in a biphasic manner. In doing so, we have also proposed a mechanism that showcases the QDs' biphasic property. We identified that high QD concentrations can inhibit the actin polymerization process, whereas lower QD concentrations stimulate the process. Furthermore, our results also showed that QDs can bind to F-actin and cause enhanced depolymerization of the filamentous actin. Overall, our study provides a novel aspect of QDs' toxicity and its interaction with intracellular proteins.

12A. Oxford Nanopore MinION based Complete genome sequencing of selected plant pathogenic bacteria and phage therapy

Andrew Welch, Dr. Dulanjani Wijayasekara
Dept. of Biological Sciences, Northeastern State University

Oxford Nanopore MinION based Complete genome sequencing of selected plant pathogenic bacteria and phage therapy Genome sequencing plays a crucial role in understanding the genetic makeup of pathogenic bacteria, enabling researchers to study virulence factors, track disease outbreaks, and develop targeted treatments. This study was focused

on sequencing the genomes of *Pantoea eucrina, Pseudomonas oryzihabitans,* and *Erwinia carotovora*, bacteria of significant agricultural and clinical interest. The primary objective was to establish a comprehensive genetic database for detailed analyses of the pathogenic traits exhibited by these bacteria. This was achieved through the utilization of the Oxford Nanopore MinION for the preparation and sequencing of DNA libraries specific to these bacteria. Additionally, investigations were conducted to explore bacteriophage interactions with the aim of identifying potential biological control agents for these pathogens. Initial plaque assays using *E. coli* B confirmed the efficacy of the assay protocol. Subsequent assays carried out on the target bacteria revealed limited plaque formation, indicating lower virulence. To address this, plans are in place to refine the assay methodology and to isolate bacteriophages with greater potency. All target bacteria were confirmed as Gram-negative, and successful genome sequencing facilitated data analysis for obtaining complete sequences. In future, we aim to confirm and annotate the complete genome sequences of the bacteria and identify highly virulent phages through refined plaque assays and sequencing. These endeavors are directed towards the discovery of effective bacteriophages serving as biological control agents against these plant pathogens, thereby contributing to both agricultural sustainability and clinical health.

12B. Investigating POLE1-Helicase Interactions at Replication Forks in Human Cells: Insights from Normal and Stress Conditions

Matthew Girard, Dr. Sapna Das-Bradoo
Biology, Northeastern State University

DNA replication and repair are critical processes in eukaryotic cells essential for growth and proliferation. Efficient and accurate DNA replication involves intricate protein complexes to ensure fidelity and prevent mutations that can lead to genomic instability and disease. The minichromosome maintenance helicase complex and Polymerase ϵ play crucial roles in initiating DNA replication. Previous studies in yeast have shown that Polymerase ϵ interacts with the helicase complex via its C-terminus domain, which is mutated in the patients with FILS syndrome (Facial dysmorphism, Immunodeficiency, Livedo, Short stature). Here, we aimed to investigate the interactions between the MCM helicase and Polymerase ϵ in human cells under normal replication conditions and during replication stress. In addition, we utilized Pole mutants (including FILS) to identify Mcm2 binding sites. Methods: Human embryonic kidney 293T cells (HEK293T) were co-transfected with plasmids overexpressing Polymerase ϵ and tGFP-tagged MCM2. Mutant variants of Polymerase ϵ, including FILS mutant and site-directed mutants, were also used to identify the MCM2 binding site. Protein interactions were assessed using co-immunoprecipitation with anti-tGFP agarose beads targeting MCM2-tGFP. Replication stress was induced by adding hydroxyurea to the culture medium. Results: Western blot analysis confirmed the overexpression of MCM2-tGFP, wild-type POLE1, POLE1 FILS, and POLE1 mutant proteins in HEK293T cells. Co-immunoprecipitation experiments demonstrated that MCM2 interacts with wild-type POLE1 and the FILS mutant under normal conditions, whereas replication stress attenuated this interaction. Conclusion: Our findings suggest that Polymerase ϵ collaborates with the MCM helicase complex during normal DNA replication but may not be actively involved under conditions of replication stress. Future investigations will focus on elucidating interactions between MCM2 and other Polymerase ϵ mutants to understand their roles in DNA replication dynamics. Relevance of the Study: Studying mutations in DNA replication proteins that leads to diseases like cancer and FILS syndrome could transform diagnostics and treatments. Our research aims to uncover how these mutations disrupt essential processes, potentially improving patient care through personalized medicine and targeted therapies.

13A. Chemotherapy-induced cognitive impairment associated with AC-T Drugs on Neuroplasticity: A study on Neurogenesis

Sofia Syed, Bailey Cronin, Antiño R. Allen
Biochemistry/Molecular Biology, Hendrix College

Breast cancer is the most common cancer diagnosed among women in the United States, with a 13% lifetime risk. With advancements in chemotherapy and proton radiation, survival rates have increased to 91%. As the survivor population increases, there is a greater urgency to further evaluate the long-term effects of chemotherapy and its impact on patients' Quality of Life. Chemotherapy-induced cognitive impairments, colloquially known as "chemobrain," can be a major impediment that survivors face post-chemotherapy. The objective of this study was to establish the relationship between treatment with AC-T regimen– Doxorubicin, Cyclophosphamide, Paclitaxel and changes in hippocampal-dependent behavior, gene expression, and brain structure. 12 weeks female C57/BL6 mice were treated with intraperitoneal (IP) injections weekly for 4 weeks of either saline (0.9% NaCl) or AC-T (2, 50, and 5 mg/kg), respectively. 30 days following the last AC-T injection, mice underwent behavioral testing. The three-chamber sociability test was used to assess social behavior and social memory. AC-T treated mice had no preference with the familiar mouse than the novel mouse during the social novelty stage, indicating a deficit in social memory. Dendritic spines are sites of excitatory synaptic transmission and changes in spine structure and dendrite morphology are thought to represent a morphological correlate of altered brain functions associated with hippocampal dependent learning and memory. Golgi-Cox staining was used to visualize changes in dendritic complexity and spine morphology, revealing significant morphological alterations associated with chemotherapy. Sholl analysis and dendritic spine morphology assessments within CA2 were conducted detect changes in dendritic complexity. To identify differentially expressed genes associated with neurogenesis, RNA sequencing was performed, revealing down regulated genes. We are currently validating these genes with RT-qPCR.

13B. CRISPR in Bdelloid Rotifers: Optimizing Uptake of sgRNA/Cas9 Complexes for Targeting DNA Repair Genes

Kailey R. Thurman, Rowan J. McCollum, Andrew M. Schurko
Biology, Hendrix College

Bdelloid rotifers are microscopic freshwater invertebrates with a noteworthy resistance to ionizing radiation and desiccation due to their ability to repair largely fragmented DNA. While potential DNA repair mechanisms have been postulated, identifying and silencing related genes is important to uncover how bdelloids recover from significant DNA damage. The objective of this project was to use CRISPR to knockout candidate DNA repair genes in the bdelloid rotifer *Adineta vaga*, to understand their effects on the ability of bdelloids to reassemble their DNA. Two candidate genes were selected for this study: DNA Ligase E (LigE), due to evidence of DNA damage response in bdelloids, and histone H2A variants, due to their abnormally long C-terminal tails that could play a role in DNA repair. Single guide RNAs (sgRNAs) were designed to target candidate genes, and in vitro cleavage assays showed efficient sgRNA-guided Cas9 cleavage of target sequences. To perform CRISPR, we then devised an uptake process of sgRNA/Cas9 complexes into bdelloids. In order to visualize this uptake process, we utilized Green Fluorescent Protein (GFP) and detected fluorescence in *A. vaga*. Plasmid pET28:GFP was modified to attach a 6×-histidine tag to the GFP gene, which was expressed in and purified from *E. coli* to obtain GFP. We tested transfection, electroporation, and desiccation methods to facilitate the uptake of GFP in *A. vaga*. Uptake of GFP was successful in both embryo and adult rotifers using transfection and electroporation. Upon identifying successful conditions for GFP uptake, we will then plan to use those same conditions for sgRNA/Cas9 uptake in *A. vaga*. Mutants, once identified, will be used in desiccation recovery assays to determine the effect of candidate gene silencing on DNA repair.

14A. Damage in Bladder Cancer Cells Post Uropathogenic Infection

Alejandro Lopez, Janaki K. Iyer
Dept. of Natural Sciences, Northeastern State University

Bladder cancer is the most common cancer of the urinary tract with the primary method of treatment employing the medication Bacillus Calmette-Guerin or BCG. BCG is introduced into the bladder tumor environment via a catheter. Recent shortages as well as evidence of an eventual resistance to treatment make it urgent to develop novel therapeutics to treat bladder cancer as according to the National Cancer Institute, chances of survival can drop down to just 8% when the cancer becomes metastatic. Responsible for over 70% of bladder infections, *Escherichia coli* (*E. coli*) is a Gram-negative bacteria that utilizes many virulence factors to aid in the successful infection of host cells. Thus, we hypothesize that virulence factors produced by a uropathogenic strain of *E. coli* will aid in the development of new therapeutics for the treatment of bladder cancer. We set out to identify potential strains of *E. coli* that could cause damage to bladder cancer cells. We infected 5637 bladder cancer cells with *E. coli* strain CFT073, CI5, JJ1886, or MVAST0072 and stained them with DAPI and fluorescently-labeled phalloidin to observe morphological changes in the nucleus and actin respectively of bladder cells upon infection. We then evaluated cell death in bladder cells by performing a lactate dehydrogenase (LDH) assay, which detects LDH in the extracellular media when cells die. We further detected cell damage by flow cytometry by staining the DNA of infected as well as uninfected bladder cells with propidium iodide (PI). Our results indicated that among all the uropathogens tested, *E. coli* CFT induced damage to bladder cells. Infection with *E. coli* CFT induced morphological changes and the release of significantly higher levels of LDH in the infected bladder cells. More than 50% of bladder cells infected with *E. coli* CFT displayed cell damage as evident by PI staining. We will determine if *E. coli* strain CFT induces DNA damage in bladder cancer cells by detecting breaks in DNA using a TUNEL assay. In the future, to evaluate the therapeutic potential of the unidentified virulence factor, we will design experiments to isolate the factor produced by *E. coli* CFT that causes cell death. Thus, these studies will enable us to achieve our long-term goal of designing novel therapeutics for the treatment of bladder cancer.

14B. Evaluating pathogenesis by utilizing fluorescently labeled uropathogenic *E. coli*

Victoria Espinoza, Tram-An Ho, Alejandro Lopez, Janaki Iyer
Natural Sciences, Northeastern State University

Bladder cancer is the sixth most prevalent cancer in the United States and the fourth most common cancer among men. The five-year survival rate for bladder cancer, in situ, is 96%. However, when the cancer is classified as regional or distant, this rate drops to 39% and 8%, respectively. Common treatments include radiotherapy, chemotherapy, and surgical procedures. There has been a rise in bladder cancers that are resistant to such treatments, thus highlighting the need for new therapies. The bladder is a common site for pathogens that utilize many strategies to infect the host cells. Based on previous studies, we found that one uropathogen, *E. coli* strain CFT073, causes morphological changes indicative of cell death in bladder cancer cells. We want to understand this process better by tracking the interactions of *E. coli* strain CFT073 with bladder cancer cells. We hypothesize that *E. coli* strain CFT073 adheres to bladder cancer cells and results in cell death. To test this hypothesis, experiments were performed to fluorescently label *E. coli* CFT073 with green fluorescent protein (GFP). We made chemically competent *E. coli* CFT073 and transformed a plasmid encoding the GFP gene. We then confirmed the expression of the GFP in the bacteria by way of fluorescence microscopy. We are currently performing experiments to determine if the transformation procedure has affected any properties of the bacteria in comparison to the untransformed *E. coli* CFT073, including the ability to induce morphological changes in bladder cells upon infection. We then plan to use confocal microscopy to evaluate the adherence and invasion of fluorescently labeled *E.*

coli CFT073 in bladder cancer cells. The results will provide insight into how the uropathogen causes damage to bladder cancer cells. This will ultimately provide a foundation to identify virulence factors employed by *E. coli* CFT073 that can be used as potential therapies.

15A. Computational Simulations of Depletion Interactions for Adeno-Associated Virus Filtration Techniques

Emily Wheeless, Jeralyne Guerrero, Douglas Dougherty, Henry Fuentes, Jude Chidozie Obijiaku, Karthik Nayani, Jacob Monroe
Chemical Engineering, University of Arkansas, Fayetteville, NorthWest Arkansas Community College

The study of adeno-associated viruses (AAV) in biomedical applications and gene therapy techniques have gained increased interest in recent years. However, one of the major challenges in using AAVs for gene therapies is the development of effective filtration of full and empty viral capsids. In this project, several tests were conducted based on the proposed technique, directed by Dr. Karthik Nayani, involving the exploration of attractive forces between empty and full viral capsids. This approach investigates a new method by examining similar placeholders for AAV in the laboratory as well as utilizing computer simulations directed by Dr. Jacob Monroe. Previous research on disodium cromoglycate (DSCG) has shown that this compound has similarities in the phytochemistry and behaviors of different types of viruses making it a good placeholder and a cheaper option than AAV virus for laboratory experiments. Rod-shaped particles, such as DNA, have been proved in past studies to be good depletion candidates for their biocompatibility and their shape. Polyethylene glycol (PEG) is comparatively similar to DNA particles and also easier to use in laboratory experiments. Its effectiveness as a depletant in DSCG experiments further makes it a suitable placeholder for DNA. Computational simulations using a custom Linux program called FEASST were performed to test the attractive forces of DNA and AAV attractive forces. Experimentations using these methods hold promising potential for eventual virus crystallization and enhanced full and empty capsid separation by adjusting the volume concentrations of DNA and AAV. Utilizing both computational simulations and laboratory experiments provided robust models to optimize these interactions, laying the groundwork for improved AAV filtration techniques and future applications in gene therapy.

15B. Evaluation of the role of the Lateral Boundary Domain Transcription Factor GmLBD-A in Soybean Response to Sulfur Deficiency

Adrian Munoz, Jianxin Ma, Chancelor Clark, Leonie Trabert
Biology, NorthWest Arkansas Community College

Sulfur deficiency is an emerging problem in soybean (Glycine max) due to less atmospheric Sulfur deposition caused by stricter environmental regulations. Sulfur is an essential macronutrient for soybeans in part because it is required for symbiotic nodulation with nitrogen fixing Rhizobia bacteria. GmLBD-A is a class II Lateral Organ Boundary Domain (LBD) transcription factor, many members of which participate in abiotic stress responses. Preliminary results show that GmLBD-A is responsive to abiotic stresses and is highly expressed in nodules. To evaluate GmLBD-A's role in Sulfur deficiency, we grew soybeans in a hydroponic system under both normal and reduced Sulfur conditions. The expression GmLBD-A and its duplicate paralog, GmLBD-B, was measured in roots and nodule tissues under both Sulfur treatment levels. GmLBD-A overexpression and CRISPR/Cas9 knockout constructs targeting GmLBD-A and GmLBD-B were transformed from the soybean cultivar Williams 82. This study will deepen our understanding on how the GmLBD gene family responds to abiotic stresses, paving the way to future functional studies.

16A. The Role of MiR-127-3p in Cell Survival During Low Oxygen Conditions

Rachel Del Angel, John Hunter Crum, Dr. Nathan Reyna
Biology, Ouachita Baptist University

The primary objective of this study is to evaluate alterations in MiR-127-3p expression under hypoxic conditions and how it affects cell survival. Hypoxia is a condition in which the oxygen environment in a cell is reduced, causing cancerous cells to adapt and survive leading to more aggressive cell growth. The MiR-127-3p and hypoxia initiate metabolic reprogramming leading to epithelial-to-mesenchymal transition (EMT), thereby enhancing the invasive and metastatic capabilities of cancer cells. Additionally, hypoxia is one of the stimuli that can affect the production of miRNAs. However, the specifics regarding the impact of various forms of hypoxia on microRNA expression remain largely unknown. MiR-127-3p plays an important role in controlling the expression of certain genes. Within the context of cancer, this particular microRNA exhibits a dualistic function, it functions as both an oncogene and a tumor suppressor depending on the type of cancer. Collectively, it is believed that there is a relationship between hypoxia and MiR-127-3p in promoting tumor progression, metastasis, and the development of resistance to therapeutics in cancer cells. A cell viability assay will used to test the relationship between MiR-127-3p, hypoxia, and lung cancer. Results will be reported.

16B. Gordoniaphage Ruthy Infection Confers Increased Growth Rate in *Gordonia terrae* CAG3

Andrew Pierce, Dr. Ruth Plymale
Biology, Ouachita Baptist University

This study aims to investigate the infection dynamics of the temperate bacteriophage Ruthy and its target host, *Gordonia terrae* CAG3. Growth rates of phage-infected bacterial cultures are typically expected to be depressed as compared to uninfected cultures, even in episodes of lysogeny. However, it has been previously observed in this system, using microplate growth assays, that Ruthy-infected cultures grow at faster rates during exponential phase and exist in higher population densities during stationary phase than uninfected cultures. This study replicates these data through culturing uninfected and Ruthy-infected *G. terrae* CAG3 populations in larger volumes using 250mL baffled flasks. The consistency of this phenomenon was demonstrated across distinct populations of both host and phage. Samples were evaluated for optical density at multiple timepoints over the course of infection to provide relative population density data. Growth curve plots created from these data verify the previous observation that Ruthy lysogens exhibit enhanced growth. Additionally, patch assays prepared throughout the course of infection confirm lysogeny of infected populations, while streak plates prepared at multiple time points show the absence of contamination. Finally, because other temperate phage confer genes correlating to higher host metabolic rate in glucose-starved conditions, uninfected and Ruthy-infected populations of *G. terrae* CAG3 were cultured in defined M9 media to compare growth rates in glucose-starved and non-starved conditions. Preliminary data suggest enhanced growth of lysogens in glucose-starved conditions as compared to uninfected cultures. Ongoing research in this system aims to expand the investigation into the enhanced growth of lysogens in glucose-starved conditions, to define the effect of lysogeny on cellular uptake of carbon, nitrogen, and phosphorus, to characterize the host transcriptome throughout the course of infection, and to evaluate the prophage integration rate using qPCR.

17A. Effects of Early Infant Nutrition on Aperiodic Neural Activity from 2 to 12 Months Using EEG Analysis

Adam Andrews, Dr. Dylan Gilbreath, Dr. Linda Larson-Prior
Biochemistry/Molecular Biology, Hendrix College

Neural development begins in gestation and continues throughout early life. Infant nutrition is a topic of increasing concern, as it is the caloric fuel which supplies such developmental processes. Previous research in this lab has found slight

significant effects of nutrition on early cognitive developmental tests between children fed human milk (BF), soy-based formula (SF), and dairy-based formula (MF) for the first 12 months of life. This investigation consults this same data: a cohort study of 536 infants from 2 to 12 months of life. High-density electroencephalographic (EEG) recordings were taken at 2, 3, 4, 5, 6, 9, and 12 months of age using a five-minute silent video baseline. Using Specparam (formerly "FOOOF", aperiodic activity was parameterized in power spectral density (PSD) for each session, which were then averaged per dietary group over left, right, and medial frontal and parietal regions of interest (ROIs) and one occipital ROI. Aperiodic activity has been investigated as a potential marker of neuromaturation, as it relates to excitatory/inhibitory (E/I) balance and structural development in GABAergic systems. Consistent with previous findings, aperiodic activity decreased for the first five months in all dietary groups.

17B. Assessment of cingulum tract-selective myelination and neurometabolism by magnetic resonance spectroscopy imaging (MRSI) in adulthood and late life

Ella Kelly, Ashley Pike, Maegan B. Calvert, G. Andrew James, Tatiana Wolfe
Biochemistry and Molecular Biology, Hendrix College

Activity dependent myelination—or functional myelination—is a natural phenomenon by which myelin changes within neural circuitry to accommodate learning and memory processes throughout the adult lifespan. Myelination of the cingulum bundle (Cing)—a tract connected to all cerebral lobes which subserves cognitive functions in humans—can extend through periods of late life, presenting an intriguing relationship with age-related decline in cognitive abilities. Measures of neural and glial metabolism may offer a clue to adult mechanisms of functional myelination across the Cing. In this work, we pre-register the development and test of a multimodal framework to quantify Cing-specific levels of myo-Inositol (mIns) and N-acetyl aspartate (NAA) volumetrically by magnetic resonance spectroscopy imaging (MRSI), while estimating the corresponding fraction of tract-specific myelin. Data is being collected from 16 volunteer participants with ages 20-23 (n=3), 38-48 (n=5), and 60-78 (n=8). Using a Siemens Prisma 3T scanner (spatial field gradient 80 T/m) and a 64-chanels coil, semi-LASER pulse sequence is being used for MRSI acquisitions; 32-echoes GRASE sequence is being used for myelin quantification; and diffusion spectral imaging (DSI) data is being acquired using a 96-directions scheme with b-values = 650, 1350, 2000 s/mm2. Linear combination (LC) model will be employed for metabolite levels estimations; three-compartment relaxometry model will be used to estimate myelin fractions with T2=10-40 ms to encompass myelin patterns encountered in aged fibers; and a q-space diffeomorphic reconstruction model will be used to delineate fiber tracts in the cingulum bundle bilaterally. MPRAGE and T2-FLAIR scans will be used as anatomical reference and for estimation of age-related white matter hyperintensities (WMH), which will be considered as tissue of interest with distinct properties. We will investigate three related hypotheses: (H1) myelination in the cingulum bundle is correlated with levels of NAA (b1>0) and mIns (b1<0), where b1 is the linear fit coefficient for the modeled variables; (H2a-b) Cing WMH present in older adults modify the associations mentioned in H1. Furthermore, we will explore if (EH3) tissue within WMH volumes show significantly lower levels of NAA and mIns, and myelination compared to Cing normal appearing white matter in unimpaired adults between the ages of 20-80 years. Bayesian inference will be employed to estimate the uncertainty levels in these associations. The study is pre-registered in the Open Science Framework (OSF) repository. This study will test the feasibility of a novel, multi-modal, tract-selective approach that correlates measures of white matter neurometabolism with activity dependent myelination. Results from this experiment will elucidate possible applications and limitations of the proposed method for application in clinical mental health and aging research.

18A. Effects of linalool extracts on glioblastoma development

Konnor Wall, Simon Todd, Emily Wheeless, Erin Harders, Adrian Munoz, Hernan Campos, Allison Davidson, Adeola Abe, LaShall Bates, Gary Bates
Biology, NorthWest Arkansas Community College

Glioblastoma (GBM) is an aggressive brain cancer that attacks specialized support cells called astrocytes that support nerve cells in the brain and spinal cord. GBM has no cure currently. Treatments will slow the cancer growth and reduce symptoms. Linalool is a terpene alcohol found in several flowers and spic plants including basil and lavender. Linalool has demonstrated antiproliferative properties and is apoptotic in leukemia, cervical cancer, and breast cancer cells. Experiments were conducted comparing behavior of U87 malignant cells to differing amounts of commercial purchased linalool extract. Cell viability increased with an increase of linalool. Morphological changes were also observed based on concentration of linalool applied to the cells compared to the control cells.

18B. Identification of novel interacting proteins of toll-like receptor 8 using a proximity ligation strategy

Ahmed M. Tolba, Anisha Neupane, Aiiryel K. McCoy, Ryan M. Allen
Dept. of Biomedical Engineering, University of Arkansas, Fayetteville

Toll-like receptors (TLRs) recognize pathogen-associated molecular patterns (PAMPS) and activate pro-inflammatory signaling cascades in innate immune cells. Nucleic acids of viruses and bacteria are intracellular PAMPS that can be detected by TLRs embedded within vesicles of the endo-lysosomal network. Toll-like receptor 8 (TLR8) is expressed primarily by macrophages and neutrophils, where it recognizes single-stranded RNA (ssRNA) and RNA degradation products. Our lab recently reported that TLR8 is activated by microbial small RNA associated with low-density lipoproteins (LDL) and plays an important role in foam cell biogenesis and atherosclerotic cardiovascular disease (ASCVD). To better understand how TLR8 contributes to foam cell biogenesis, we sought to identify the interactome of TLR8 in cultured cells. We developed a proximity ligation strategy in which a split N-terminus of a biotin ligase (TurboID) was cloned to the cytosolic domain of TLR8 and the split C-terminus of TurboID was cloned to Rab5, an endosomal GTPase. HEK293T cells were transiently transfected with split-TurboID plasmids, treated with biotin for 24h, and biotinylated proteins were captured from protein lysates using streptavidin beads. Precipitated proteins were then quantified using an Orbitrap Exploris 480 mass spectrometer and identified using Spectronaut. We discovered 73 proteins enriched in cell lysates in which TLR8 was overexpressed in the presence of a ssRNA ligand. Unexpectedly, pathway analysis of TLR8-interacting proteins revealed enrichment for proteins localized to the nucleus, and more specifically the spliceosome. Moreover, our pathway analysis identified enrichment for genes linked to mRNA processing (30%) and splicing (27%). Putative TLR8-interacting proteins for ongoing validation are DEAD-box helicase 46 (DDX46), an RNA helicase linked to non-coding RNA splicing, and Cactin, a negative regulator of TLR signaling. In conclusion, our studies have identified surprising new facets for TLR8's role in the immune dysfunction of ASCVD.

19A. Establishing Working Protocol for Alcian Blue Staining in Zebrafish

Caleb Miller, Dr. Joshua Kwekel
Biology Research, Ouachita Baptist University

Zebrafish (*Danio rerio*) are freshwater fish native to southern Asia known to be an excellent vertebrate research model, as they are small, inexpensive, and are easily taken care of. For this reason, zebrafish are commonly found in lab environments to be used for histology techniques and other kinds of live vertebrate research. This research project focused on refining protocols regarding H&E staining of zebrafish and implementing new protocols to use Alcian Blue stain. Alcian Blue stains acid mucosusbtances (seen in blood vessel walls) as well as cartilage. Because of the ability to stain cartilage,

Alcian blue is more commonly used in embryonic and developmental biology, which lines up well with our future goal of studying early-stage sex differentiation in these fish. Ideally, these mucosubstances and cartilages would be stained blue, the nuclei stained pink/red, and the cytoplasm stained pale pink. The red and pink colors come from Nuclear Fast Red Stain, the counterstain for Alcian Blue. Great success and progress were made in obtaining good tissue sections in a repeatable way by developing successful protocols and picking up procedure tips along the way. In comparison to the H&E stain that was previously being used in this lab, the Alcian Blue appeared to be better in helping outline the cartilages in the fish, specifically in the head region. In the future, this new type of stain and improved staining procedures will better allow this lab at Ouachita to later investigate sex differentiation in zebrafish, in order to understand better why zebrafish sex ratios become skewed in high-stress environments, such as a lab.

19B. Optimizing Breeding Efficiency in Zebrafish

Tanner Radford
Dept. of Kinesiology and Dept. of Biology, Ouachita Baptist University

The Zebrafish research program was formed to investigate developmental biology and sexual differentiation in zebrafish. This laboratory was recently formed and challenges in producing new offspring have been a concern. This research project addressed the low reproductive capacity of zebrafish in our lab. The factors known to influence reproductive efficiency were identified and optimized. These factors include: water quality, tank cleanliness, nutrition, light/dark cycle, and breeding environment (water depth and vegetation). The reproduction phase consisted of breeding trials with repeated variable male/female pairings to see how many eggs could be collected efficiently and without damage. Methods for housing the fish were provided by a tanking/filtration system consisting of four active filters and reverse osmosis water for maintain water quality. Protocols were followed for cleaning the entire tank system. Nutrition was modified by providing live feed in the form of brine shrimp. Light/dark cycle conditions were improved by isolating breeding fish and improving darkness with dark plastic. For more detailed trials dealing with reproduction, experiments were set up away from the main system tanks. Early trials resulted in 37 fertilized eggs after two successful trials. Subsequent trials with different male/female pairings did not yield eggs. More trials are planned with continued modification of the water and light/dark apparatus and timing. The overall significance about this research is to improve reproductive capacity and efficiency to support research in developmental biology and sexual differentiation.

20A. Exploring the Gut Microbiota of Gray Bats in Kansas Following Culturable and Metagenomic Approaches

Ayushee Dasgupta, Bobbi Monroe, Andrew George, Anuradha Ghosh
Biology, Pittsburg State University

Humans have historically had an ambivalent relationship with bats. Bats perform important services by reducing populations of insect pests. They also act as reservoirs of diseases, as highlighted by the recent Coronavirus pandemic. This study aims to characterize the bacterial diversity associated with the Gray Bat (*Myotis grisescens*) in Southeast Kansas. A total of 32 bacterial isolates with different colony morphology were recovered from guano samples on tryptic soy agar media after enrichment. The majority (21/32, 65%) of isolates were Gram positive. All isolates were tested for growth on selective and differential media. Sugar fermentation profiles showed that 78% (25/32) 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. Urea was hydrolyzed by seven (21%) isolates while one isolate (3%) was positive for indole production. Pooled isolates were sequenced using an Illumina miniSequencer. A total of 2,909,555 reads were completed. The most common genus being Serratia (26.36%) followed by Achromobacter (20.17%), Lysinibacillus (19.93%),

and Bacillus (17.01%). Currently, sequencing experiments are underway to determine the microbiota of male and female bats GI tract. Identification of known and novel bacteria/fungi in bats is important for prevention of disease spread and long-term preservation of bat populations.

20B. Transcriptomic Analysis of EGFR and Downstream pathway expression in A549 and Healthy Lung Epithelium

Sebastian Henry, Dr. Christopher Ward
Dept. of Biology, Pittsburg State University

Introduction: Clinical tests utilizing EGFR isoforms as a method of cancer screening, primarily for lung, breast, and ovarian, have been uncertain. With these clinical tests lacking specificity and sensitivity. In particular, we have interest in intronic single nucleotide polymorphisms (SNPs) in intronic regions. This work is a an Insilco characterization and assessment of a lung adenocarcinoma cell line (A549) in association. With expression patterns of EGFR and associated pathways relative expression. Research Question: What associated proteins from downstream pathways are up or down regulated in A549 compared to normal lung epithelium. What SNPs in the intronic regions of the EGFR coding sequence may influence splicing activity. Methods: The expression pipeline was applied to lung adenocarcinoma and healthy lung epithelium from publicly available cDNA short reads. This pipeline involved sequence alignment with a splice aware aligner (HISAT2) and feature counting algorithm (featureCounts) and normalization/filtering/plotting with limma. Feature counts were plotted in a log of counts per million with heteroscedasticity adjustment (voom). The SNP pipeline applied typical genomic aligner (BWA) using GRCh38, Variant calling (Varscan), and Mpileup were used and annotated with vcf2maf. Variance in the coding sequence were plotted with the use of Gviz. Results: Transcriptomic expressions trended in favor of under expression, with the log fold change in gene expression of EGFR being statistically insignificant. SNP mutations have been identified with the mutation, c.2625+196A>G seen as phenotypically benign. Discussion: Overall, the lung adenocarcinoma cells show a general trend towards under expression. However, the consistent expression of EGFR, comparable to that of healthy lung epithelium, remain distinctive. The stability highlight's EGFR's potential for possible detection of different isoforms.

21A. Characterization of Snake Immunity for a Novel Animal Model

Hallie Nielsen, Dr. Daniel McDermott, Dr. Jeremy Chamberlain, Alana Hedden, Rylee Griffis
Dept. of Biology, Southern Arkansas University

Immune research commonly utilizes inbred animal models, which do not represent inherent variability in natural populations. Our previous research aimed to use outbreed snakes as a novel vertebrate model, matching typical variability seen in populations. We characterized immune cell populations in blood of two species of North American watersnakes (*Nerodia rhombifer* and *fasciata*), collected at various locations throughout southwest Arkansas. Results from flow cytometry showed distinct cell populations of lymphocytes, heterophils, and azurophils. These populations were overall consistent both within and between the two species. Despite this consistency, there are significant numbers of dead cells and cell debris within each sample, making further characterization difficult. To address this issue, LIVE/DEAD stains distinguish live cells from the debris and dead cells by binding free amines on the cell surface and inside the cell. This stain results in brighter contrast between dead cells and the live immune cells, which can be used to improve flow cytometry results. Although the watersnake samples provided reliable results, sample collection was limited seasonally to warm summer months. Therefore, to test effectiveness of the LIVE/DEAD stain for future work, we utilized outbred African House Snakes (*Boaedon fuliginosus*) maintained in the snake colony at SAU. We initially assessed blood samples from *B. fuliginosus* using flow cytometry and confirmed similar populations in the *B. fuliginosus* samples as our previous data. Our data also demonstrate that LIVE/DEAD staining is able

to differentiate live and dead cells as well as cellular debris.

21B. Nanoplastics from food containers and their effects on cultured SHY5Y cells

Hannah Bearden, Dr. James Hyde
Dept. of Biology, Southern Arkansas University

Nanoplastics comprise plastic particles < 1 micrometer in diameter and can have a variety of negative effects on our bodies. Previous studies have shown that these particles are regularly shed by plastic food containers and that they can accumulate within the brain and other organs. The overall goal of this project was to analyze the amount of shed neoplastic using flow cytometry and gather preliminary data on the effects of nanoplastics on SHY5Y cells, a neuron like immortalized cell line. Distilled water was boiled in three different types of plastic food containers (two polypropylene and one polycarbonate) and one glass container. Water samples were microwaved in four samples of each type of container for 2 minutes. Samples were stained with lipophilic nile red stain to fluorescently label plastic particles. Particle counts were taken with a flow cytometer. Cells were also incubated with 100mg/ml polystyrene or polypropylene (mix of sizes <1μm in diameter) for 24 hours and tested for DNA damage with a COMET assay. Early results showed that polypropylene releases between 1 to 7 million nanoparticles per square centimeter of water exposure while polycarbonate was comparable to glass controls. The majority of these particles were between 200 to 500 nm in diameter. Preliminary COMET results demonstrate significant amounts of DNA damage from 24 hour plastic exposure in both polypropylene and polystyrene. In upcoming work, the cells will be exposed plastic nanoparticles and we will measure changes to cell activity, oxidative stress, and metabolism.

22A. Pollution Diffusion: A Look at Northwest Arkansas's Watersheds

Christopher Edwards, Analise Black, Vanessa Gonzalez, Jasmine Rosa, Camelia Vela
Dept. of Biology, University of Arkansas at Fort Smith

Water quality plays a crucial role in safeguarding public health, preserving ecosystem functions, and fostering sustainable economic growth. As the population of Arkansas grows, there is a concurrent increase of land use for industry, agriculture, and residential functions. These shifts in land use bring along potential impacts to waterways that may impact overall water quality. Wherein water runoff from these altered sites may have a detrimental effect on water quality. We set out to build a data set of water quality parameters in an effort to model how altered land use will impact water quality in Northwest Arkansas. Water samples were collected using a water column collector from various localities in the following Arkansas counties: Washington, Crawford, Sebastian, and Franklin. Each site was assessed for pH, turbidity, chemical oxygen demand (COD), nitrate, phosphorous, and presence of pathogens (Coliforms). To date we have collected samples from over 30 sites. Ultimately all locality and water quality data that is collected will be used by the Computer Science program at UAFS to generate a model to predict how land use will impact water quality.

22B. Isolation and Identification of Species and Mating Type Dynamics of *Dictyostelium* Wild Isolates from the Arkansas River Valley

Libbi Cusimano, Alexus Ferguson, Caden Fox, Sandhya Baviskar
Dept. of Biology, University of Arkansas at Fort Smith

Soil amoebae *Dictyostelium* transit back and forth between unicellular and multicellular stages during their life cycle hence they are commonly used model organism to address questions about cell biology, multicellularity, and development. For these studies, axenic strains of *Dictyostelium* are used. In recent years, there is growing interest in

studying wild isolates of *Dictyostelium* to understand how these bactivorous amoebae interact with soil microbes and impact soil microbial composition and dynamics. During its developmental life cycle, *Dictyostelium* starving amoebae go through several stages to form a multicellular fruiting body which has a basal disc and stalk comprising of dead cells with living spore cells at the top. Also, studies have shown that sexual reproduction is very common among wild isolates. Two genetically distinct isolates from the same location can undergo developmental cycle where one isolate could be a cheater, producing mainly spores but inducing the other to produce stalk. Thus, cheaters have evolutionary advantage. The goals of this project are 1) to isolate and identify species and mating types of wild isolates of *Dictyostelium* from the river valley region of Arkansas.2) to determine the behavior of cheater strains during sexual cycle. We have collected soil samples from LeFlore County, OK, and Sebastian County, AR. Based on the morphological features of the fruiting bodies, we confirm successful isolation of at least three wild isolates of *Dictyostelium*. To identify mating types, we plan to set up sexual crosses between wild isolates and *Dictyostelium* strains of known mating types. Using PCR and DNA sequencing techniques we will identify the species of these newly found natural isolates.

23A. Natural variation in transformation efficiency in the model yeast *Saccharomyces cerevisiae*

Mary Kathryn Cheek, Jeffrey A. Lewis, Stephanie E. Hood, Tara N. Stucker
Biological Sciences, University of Arkansas, Fayetteville

Horizontal gene transfer—the movement of genetic information across species—has played a long-standing role in the evolution of bacteria. Horizontal gene transfer is an important addition to the Mendelian vertical transfer of genetic material from parents to offspring, as it allows for the transfer of genetic material from species to species. While originally believed to be a primarily bacterial phenomena, it is now understood to happen in eukaryotes, where it can mediate large evolutionary changes. Single cell eukaryotes, like fungi, are the most common eukaryotes to participate in horizontal gene transfer, but even plants and animals can experience rare horizontal gene transfer events through their parasites, which has led to acquisition of new traits ranging from increased metabolic capacity to disease tolerance. While horizontal gene transfer clearly plays an important role in trait acquisition, the precise mechanisms behind horizontal gene transfer are still not fully understood. It has been long known that cells can be "transformed" phenotypically by taking up DNA from the environment, and laboratory transformation is a key tool in molecular genetics. The budding yeast *Saccharomyces cerevisiae* will take up DNA if made "competent" through chemical treatments and mild heat shock. I have found that our commonly used laboratory strain is more efficient at transformation compared to a panel of wild strains. This is exciting because it suggests that some strain backgrounds may be more transformable than others, and hence more likely to be "evolvable" due to an increased capacity to undergo horizontal gene transfer. I am currently performing experiments to understand the genetic basis of high transformation efficiency, which will lead to a new understanding of the molecular mechanisms in nature that can drive increased likelihood of horizontal gene transfer events.

23B. Examining the mechanisms of cortisol control of intestinal Na^+,K^+,$2Cl^-$ cotransporter 2 in Atlantic killifish

Angelina Ke, Karma Hine, Christian Tipsmark
Biological Sciences, University of Arkansas, Fayetteville

Atlantic killifish (*Fundulus heteroclitus*) are euryhaline teleosts, which means they can adjust cellular transport of water and ions in response to environmental salinity fluctuations and are found in both saltwater (SW) and freshwater (FW) environments. Within the concentrated marine environment, killifish must rehydrate by swallowing seawater while increasing the rate of water

absorption along the esophageal and intestinal tracts and actively secreting excess ions across the gills. Water reabsorption is facilitated by transport proteins along the apical and basolateral membranes of hormone-responsive enterocyte cells within the intestinal lumen. Previous research in our laboratory has indicated that Nkcc2 is upregulated in response to an increase in environmental salinity, an effect that is mirrored in cells artificially treated cortisol, a stress hormone associated with both FW and SW acclimation in teleost fish. The focus of this research concerned the mechanism of control for differential regulation of the Na+, K+, 2Cl- cotransporter type 2 (Nkcc2) within intestinal cells, particularly the cortisol receptors responsible for observed phenotypic changes. Two types of corticosteroid receptors have been identified within the killifish: the glucocorticoid receptor, which has two isoforms (Gr1 and Gr2), and the high-affinity mineralocorticoid receptor (Mr). Using a short-term acclimation experiment, I investigated the effects of environmental salinity on the relative mRNA expression of Mr, Gr1, Gr2, Nkcc2, and other select transport protein transcripts associated with transcellular and paracellular (via tight junction proteins) water transport. By selectively blocking the activity of specific cortisol receptors and evaluating the effect on Nkcc2 transcript levels, I was able to elucidate the receptors likely responsible for our observed phenotype using an ex-vivo explant experiment and in-vivo injection experiment, the results of which are anticipated to be presented at the 2024 INBRE conference.

24A. Investigate the effects of diffusible signals from different plant growth-promoting bacteria on rice

Hannah-Grace Fritz, Stephanie Long, Samuel Hoggard, Matthew Calhoun, Dylan Neuhaus, Anna Bommes, Dr. Arijit Mukherjee
Biology, University of Central Arkansas

Plants form associations with beneficial microbes, including arbuscular mycorrhiza (AM), rhizobia, plant growth-promoting bacteria (PGPB). In these associations, the host plants benefit from improved growth in exchange for carbohydrates for the microbe. Studies in legume-rhizobia symbiosis (LRS) and AM symbiosis have shown that a molecular dialogue between the symbiotic partners is required to initiate these interactions. Furthermore, genetic and biochemical studies identified the plant and microbial signals and the host genetic pathways involved in these symbioses. For instance, 'Nod factors' are secreted by rhizobia bacteria during LRS, and 'Myc factors' are secreted by AM fungi during mycorrhizal symbiosis. Interestingly, the direct application of these microbial signals on plants can promote their growth, and naturally, these are already commercialized. The same level of understanding doesn't exist for interactions between plants and PGPB. One recent study showed that diffusible signals from *Azospirillum brasilense*, a PGPB, stimulated growth in *Arabidopsis thaliana*. We established an experimental system where diffusible signals from *A. brasilense* could promote rice growth. We are currently investigating if diffusible signals from other PGPB, such as *Azotobacter vinelandii* and *Azorhizobium caulinodans*, can be recognized and perceived by rice, leading to enhanced growth. In the future, we will identify the underlying transcriptomic changes regulating the effects of these microbial signals on their host plant. We expect plant genes encoding receptor kinases, transcription factors, and hormone pathways to be differentially expressed. Our results will identify the host genetic pathways regulated by the microbial signals. In the long term, we plan to identify the chemical nature of these microbial signals, which can have important implications for improving agriculture sustainably and preventing human health concerns.

24B. Investigating the molecular mechanisms via which the plant growth-promoting bacterium, *Azospirillum brasilense*, improves growth in salt-stressed rice

Dylan Neuhaus, Matthew Calhoun, Samuel Hoggard, Hannah-Grace Fritz, Avery Gilkey, Stephanie Long, Anna Bommes, Dr. Arijit Mukherjee
Biology, University of Central Arkansas

Major food crops, such as rice and maize, display severe yield losses (30-50%) under salt stress. Furthermore, problems associated with soil salinity are anticipated to worsen due to climate change. Therefore, it is necessary to implement sustainable agricultural strategies, such as exploiting beneficial plant-microbe associations, for increased crop yields. Plants can develop associations with beneficial microbes (e.g., mycorrhiza, plant growth-promoting bacteria (PGPB)). PGPB improve plant growth via multiple mechanisms, including protection against biotic and abiotic stresses. *Azospirillum brasilense*, one of the most studied PGPB, can mitigate salt stress in different crops. However, little is known about the molecular mechanisms by which *A. brasilense* mitigates salt stress. Previously, we established an experimental system in which *A. brasilense* inoculation improved plant mass in rice grown under high salt concentrations (100 mM and 200 mM NaCl), seven days post-inoculation (dpi). We hypothesized that *A. brasilense* inoculation would regulate the expression of rice genes involved in salt-stress response, nutrient and ion transport, and abscisic acid and jasmonic acid signaling, among others. Using RNA sequencing, we identified the transcriptomic changes in rice plants during *A. brasilense*-mediated salt stress tolerance at seven dpi. Our results identified key gene expression patterns in rice via which *A. brasilense* help improve growth in rice. To identify the early plant transcriptomic changes in salt-stressed rice upon *A. brasilense* inoculation, recently we completed an RNA-seq experiment and are currently analyzing the results. In this study, we expect to identify differentially expressed genes in salt-stressed rice involved in the initial perception and response to *A. brasilense*. Our findings will provide essential insights into salt stress mitigation in rice by *A. brasilense.*

25A. The Use of Plasmid qPCR in the Standardization of Phage Quantification

Jenna Malone, Nathan Reyna
Biology, Ouachita Baptist University

MicroRNAs are biomarkers for various clinical uses such as diagnosis, prognosis, treatment plans, disease risks, and progression. To better understand the implication and application of microRNAs, bacteriophage RNA was amplified and quantified to obtain quantitative plasmid data rather than a virion basis. While plasmid isolation may be an extensive process, phage plasmid quantification produces reliable results and, therefore, can be used to create a standard of comparison. By standardizing this process, future phage analysis will have more statistical relevance, less quantification variance due to lysate factors, and the quality of the experiment can be assessed against the universal standard. Experimental techniques include plasmid amplification through the growth and isolation of competent *E. coli* cells, plasmid purification, and quantitative PCR procedure and analysis. The standardization results of the experiment were inconclusive due to various factors, including negative control amplification, technical error regarding annealing temperatures, and lack of stability testing.

25B. Molecular Diagnostics to Uncover the Prevalence of Pertussis Infections in Central Arkansas

Luke Wood, Noah Pruitt, Elizabeth Seek, Dylan Clayton, Dr. Nathan Reyna
Biology, Ouachita Baptist University

Whooping cough is a highly contagious respiratory disease. While several *Bordetella* sp cause whooping cough-like symptoms, only *Bordetella pertussis* causes "Pertussis" or whooping cough. Unfortunately, not all *Bordetella* sp. respond similarly to treatment. Further, the misconception

that whooping cough only infects children often leads to underdiagnosis in adults. The difference in symptoms between adults and children exasperates this misconception. Accurate detection of a causative organism is essential for proper diagnosis and subsequent treatments. Central Arkansas Genetics and Molecular Diagnostics (CAR:GM) is a molecular lab that uses Quantitative-PCR to identify bacterial and viral infections. CAR: GM's new comprehensive respiratory infection panel uses species-specific primers to differentiate between *Bordetella* sp. In three months (April-June 24), 63 patients in Saline, Jefferson, and Hot Springs Counties tested positive for *B. pertussis* infection, with a high percentage being adults. Infection rates did not correlate with gender. However, a majority of patients were in rural areas. Interviews with clinicians revealed many positive adult patients were initially unsuccessfully treated for a viral respiratory infection. Only after symptoms persisted were they referred for molecular diagnostics. While molecular diagnostics is non-evasive, quicker, and more sensitive than traditional bacterial culture methods, it is not often available in rural areas. Our research took a public health approach to document the spread of Whooping Cough in rural Central Arkansas. By reporting the prevalence of specific *Bordetella* sp in an area, we can help clinicians make informed decisions when identification is unavailable. An analysis of our findings will be reported.

26A. The effect of temperature on the symbionts between a Chlamydiae symbiont and its social amoeba host

Kevin Leal, Donovan Clark, Matt Curtis, Dasha Young, and Tamara Haselkorn
Biology, University of Central Arkansas

Symbiotic relationships are close associations made between organisms from two distinct species, and these relationships can range from mutualistic to parasitic. Their effects on each other are not always obvious and can vary under different environmental conditions. One model organism used to study symbioses are amoebas and their bacterial symbionts. Natural populations of social amoebas have been found to harbor symbionts in the phylum Chlamydiae with infection levels up to 40%. How Chlamydiae affect their hosts, however, is unknown. There does not seem to be a cost to infection in most social amoeba species when grown under standard laboratory conditions, and in one species of social amoeba with the highest Chlamydiae prevalence, *Dicyostelium giganteum*, Chlamydiae may improve spore production. One distantly related social amoeba species, *Cavendaria aerostipes*, has the second highest infection rate for Chlamydiae in the field, suggesting there also might be a positive relationship between infection and viability. Furthermore, there is a positive correlation between temperature and Chlamydiae prevalence in the field. Thus we hypothesize that Chlamydiae may be conferring a benefit to its host under a range of temperature conditions. We are testing this by curing three Chlamydiae-infected *C. aerostipes* lines, measuring their spore production under room and elevated temperatures, and comparing the results to those from their infected counterparts. Studying the effects of temperature on this relationship could lead to a better understanding of host-symbiont relationships and how Chlamydiae may be spreading in natural populations of amoebas.

26B. Exploring the role of a functional Taok3-Pcdh1 protein complex in Xenopus development

Jesus Hernandez Meza, Hayden Hall, Mick Yoder
Biology, University of Central Arkansas

Embryonic development is a complex and dynamic process that relies on the coordinated interplay of signaling pathways, cell movement, and regulatory mechanisms to form tissues and organs. Among these, cell adhesion is a critical factor that facilitates tissue morphogenesis and cell migration. Protocadherins, a family of cell adhesion molecules, play an essential role in various developmental processes. In particular, Protocadherin-1 (Pcdh-1) has been identified as crucial for proper notochord cell sorting. The notochord is a key structure in early development that contributes to the formation of the nervous system, and previous studies have shown that the loss of Pcdh-1 results in the absence

of the notochord, leading to severe developmental defects. In our current research, we have identified Taok3 as a potential interactor with Pcdh-1 through in vitro experiments designed to discover Pcdh-1-associated proteins. Taok3 is a kinase that is part of the MAP kinase signaling pathway, which regulates several important cellular processes. This suggests a possible role for Taok3 in embryonic development through its interaction with Pcdh-1. The primary goal of our study is to validate the interaction between Pcdh-1 and Taok3 in vivo, using the model organism *Xenopus laevis*, to test the hypothesis that the Taok3-Pcdh-1 interaction is required for proper notochord development. To achieve this, we will employ a variety of experimental techniques, including microinjections into embryos, co-immunoprecipitation (Co-IP), western blotting, and immunofluorescence. These experiments will provide valuable insights into the molecular mechanisms that regulate notochord formation and broader developmental processes.

27A. Reduced Immunosuppresion with Partial Heart Transplantation

Eli Contorno, Herra Javed, Louis Steen, Konrad Rajab
Dept. of Biomedical Engineering, University of Arkansas, Fayetteville

Partial Heart Transplantation is a novel procedure aimed at providing growing heart valves to children by transplanting the root of the valve from a donor into a recipient. In order to study immune response and growth related to varied immunosuppressive regimens, PHTs were performed using porcine animal models. Pigs received one of three immunosuppressive regimens, consisting of no treatment, tacrolimus only, or triple immunosuppression with tacrolimus, prednisone, and mycophenolate. Weekly echocardiography was performed to analyze growth throughout the life cycle of the piglets with twice weekly tacrolimus levels to maintain adequate trough levels. Once the piglets doubled in weight, the hearts were explanted. Flow cytometry, immunohistochemistry, and immune fluorescence were performed on the explanted heart leaflets to gain insight into the cell viability and immune response associated with the different immunosuppressive treatments. The results of this showed that transplanted valves grow with triple immune suppression, it also revealed that valves can function successfully even with severe immune infiltration.

27B. Analyzing Transcriptional Control of IL-10 in Macrophages using CRISPR-Cas9

Jayita Ujjaini, Christopher Nelson, Abbey Stokes
Biomedical Engineering, University of Arkansas, Fayetteville

Macrophages are known to have a plastic nature where they can change from M1 to M2 states and vice-versa. M1 and M2 states are partially characterized by their pro-inflammatory cytokines and anti-inflammatory cytokines, respectively. Notable examples of anti-inflammatory cytokines that can be efficiently used for regenerative medicine include IL-10 and IL-4. This study focuses on the possibilities of manipulating macrophages to optimize immune responses. IL-10 promotes healing by preventing uncontrolled immune responses. In diseases such as diabetes, this process gets dysregulated and macrophages struggle to induce M2 state. The catalytically inactive CRISPR-Cas9 system, known as dCas9, can be used to upregulate or downregulate cytokines to promote an anti-inflammatory phenotype. In this study, we aim to promote the upregulation of IL-10 in RAW 264.7 macrophage lines. Previously, using VP64, a virally derived transcriptional activator, we were able to induce IL-10 activation. In this study we will compare P300, a human-derived histone acetyltransferase, against VP64 to analyze if one has a higher efficiency depending on their mechanism. The RAW 264.7 cells will be transduced with lentiviruses encoding dCas9-P300 and undergo antibiotic selection. We will transduce CRISPR guide RNAs targeting IL-10 in each macrophage line- RAW 264.7 with dCas9-VP64 and RAW 264.7 with dCas9-P300 and go through a second selection using cell sorting. RT-qPCR will be done to confirm both the presence of dCas9-P300 and IL-10 gRNAs. Then IL-10 expression will be analyzed using RT-qPCR. We will normalize

against GAPDH, a constitutive gene, and compare the IL-10 levels to when RAW264.7 cells are in a proinflammatory and unstimulated state. These results will show which transcriptional activator, VP64 or P300, is more likely to induce an anti-inflammatory state through IL-10 activation. This technology can then be analyzed in the context of wound healing and immunotherapy to improve patient outcomes.

28A. Bird Species Diversity and Abundance at Big Timber WMA

Luke Robbins, David Dixon, Dr. Christin Pruett
Biology, Ouachita Baptist University

Bird populations are declining in the United States with an estimated 3 billion individuals lost since the 1970s. Wildlife management areas (WMA) such as Big Timber in south-central Arkansas provide areas of undeveloped habitat for bird species. Big Timber at 45,000 acres is a large wildlife management area that has upland pine tree forests as well as many low-lying areas with deciduous woodlands, creeks, and marshes. To understand how habitat influences bird populations, we conducted bird surveys and any birds seen or heard were recorded in a 10-minute window. One hundred random locations were surveyed throughout Big Timber WMA. In addition, at each point a habitat survey was conducted determining the type and density of the habitat. Initial results suggest that the mixture of habitat types has led to a wide diversity of bird species. For example, Northern bobwhite, hooded warbler, pine warbler, and summer tanager prefer pine habitats while Acadian flycatcher and prothonotary warbler are commonly found in deciduous, water associated habitats. We will present an evaluation of the relationship between species diversity and the abundance of species in relation to habitat variables such as canopy cover, shrub density, and ground cover. Our findings will be used in the management of habitats that are key to the recovery of bird species.

28B. Developing a Protocol for Bacteriophage Guided Evolution

Hannah Matthews, Ruth Plymale
J.D. Patterson School of Natural Sciences, Ouachita Baptist University

Experimentation was done to generate a protocol for expanding the host ranges of bacteriophages based on the Appelmans Protocol. Temperate bacteriophages were introduced to multiple species of *Gordonia* bacteria in a 96-well plate. Lysis was determined using spectrophotometer absorbance values for each well and compared to the known host range of each phage. The spectrophotometer results were compared at 48 hours post infection and 72 hours post infection, and 48 hours was found to be the optimal time post infection to record data. A ratio of 100 phage to 1 bacteria was effective for determining bacterial lysis in the protocol.

29A. Tumor microenvironment reprograming strategy by combining dichloroacetic acid (DCA) and photodynamic therapy (PDT) to exerts synergistic anti-cancer responses in PANC1 Cells

Adeolu Oluremi, Sukhbir Singh, Nawab Ali
Biology, University of Arkansas at Little Rock

Pancreatic cancer (PC) has emerged as a leading cause of tumor related deaths in the USA. Despite multi-dimensional treatment approaches developed in the last decade, prognosis of PC remains poor due to its heterogeneity, rapid growth, infiltration and location of the pancreas. Cancer cells exhibit mitochondria dysfunction due to the abnormal metabolic phenotype of anaerobic glycolysis- the Warburg effect. Reprogramming this pathway appears a promising strategy. This can be achieved by dichloroacetate (DCA) treatment in combination with photodynamic therapy (PDT) using 5-aminolevulinic acid (5-ALA), a precursor of protoporphyrin IX (PPIX). PDT is now clinically employed to achieve synergistic effects. Our hypothesis is that the combined effect of DCA and 5-ALA in a PDT approach will exert synergistic apoptotic effects in PANC 1 cells. Our results suggest that this combination treatment indeed produces synergistic cytotoxic effects via the

generation of reactive oxygen species (ROS) due to sensitization of PPIX. The combined effect in PDT-5-ALA – DCA treatments serves as a key metabolic regulator in the inhibition of PANC 1 cell proliferation, enhancing antitumor efficacy by inducing apoptosis and causing mitochondrion membrane depolarization. This combination treatment releases significant amounts of ATP implicating an involvement of immunogenic cell death mechanism. Our study provides a potent strategy to reprogramming tumor microenvironment and enhancing anticancer efficacy in pancreatic cancer treatment.

29B. Identifying Factors That Contribute to Zebra-fish Embryonic and Larval Survival

Phillip "Christian" Dunger, Tyler Melton, Stefanie Leacock
Biology, University of Arkansas at Little Rock

Zebrafish are widely used in universities and research labs around the world. These little fish have become a popular model organism in many areas of biology including genetics, development, and neuroscience. Zebrafish undergo embryonic development in approximately 72 hours, then progress through larval stages for about 6 weeks, becoming sexually mature adults by 3 months of age. The zebrafish lab at UA Little Rock was established in 2022 and now breeding is necessary to provide new generations of zebrafish and embryos. The adults are used in Zoology courses and embryos are used in a Developmental Biology course to enhance student learning, so generating a large breeding population will benefit our department and university by supporting student laboratory experiences. Over the course of the Fall semester, we will investigate what physical characteristics of individual fish lead to more desirable breeding outcomes. A number of protocols for raising embryos and larvae exist, but have not been experimentally optimized in our facility. For example, different larval food types and timing for transitioning the fish through their larval stage diets will be tested. The preliminary work on this project over the summer has already resulted in four surviving juveniles, our goal is to have a minimum of 70 adult zebrafish to support biology courses over the next year. The data collected from these experiments will be used to create a standard protocol for breeding and rearing zebrafish in our facility. Such a protocol will benefit future students at this University and others to increase productivity of breeding and allow more labs and classes to use the zebrafish in research and learning. Our lab will also be generating new experiments for students taking Developmental Biology in the Spring 2025 semester. The lab is an important part of this class and being able to provide educational and interesting experiments to students is the ultimate goal. Before any of this can happen, viable embryos must be obtained and this is why our breeding and embryo and larval maintenance methods need to be researched and improved.

30A. Elucidating the Role of miR-127/3p in the Tumor Microenvironment

Jackson Lipscomb, Nathan Reyna, Kassidy Gray, Tuesday Melton, Parker Nelson, Alyssa Rye, Christin Pruett
Biology, Ouachita Baptist University

MicroRNAs are small noncoding nucleotides that serve as intracellular and extracellular signaling molecules. A previous collaboration found miR-127/3p circulation in the blood of breast cancer patients correlated with improved patient recovery and prognosis. While this study exclusively focused on breast cancer patients, data mining of the TCGA databases indicated that miR-127/3p may be positively associated with outcomes in other cancer types. In our study, A549 lung adenocarcinoma cells were transfected with miR-127/3p using Cell Block protocols produced by the Cell Biology Education Consortium (CBEC). After transfection, cell migration (scratch/wound healing) assays were used to determine the role miR-127/3p plays in the tumor microenvironment. To mimic and test this environment, transfected cells were incubated in normal oxygen (normoxia) and low oxygen (hypoxic) environments. We found that miR-127/3p inhibited cell migration in both normal oxygen and hypoxic environments. These results help elucidate the role miR-127/3p plays in the prevention of

metastasis, and further highlight its potential as a positive biomarker.

30B. An alternative to flow cytomtery: Piloting a novel Apoptosis assay in context of cell stress

John Hunter Crum, Nathan Reyna, Rachel Del Angel
Biology, Ouachita Baptist University

Understanding the role of programmed cell death (apoptosis) under stress conditions is important to cancer researchers. However, most apoptosis assays utilize cell flow cytometry. The expense and technicality of this method is a barrier to many research labs. We have partnered with a start-up company, Sampling Human (SH), to pilot a novel apoptosis assay that is affordable and as sensitive as flow cytometry. We did this in the context of hypoxia and miRNA 127 expression. Hypoxia is known to induce apoptosis through regulation of mRNA transcription. MiRNA-127 is a micro RNA that was previously shown to be associated with apoptosis inducing vesicles. Previous work in our lab has shown MiRNa-127 to have an inhibitory effect on cell migration. The SH-apoptosis assay was used to investigate the effects of miRNA-127 in A549 (small-cell lung cancer) cell lines grown under hypoxic conditions. Apoptosis was measured after cells were grown under hypoxic conditions as an endpoint assay. The results of this study are to be reported.

31A. Interactions between lytic and latent gene products in murine gammaherpesvirus 68

Eli Shepherd, Shana Owens, Steven Murdock Jr., J. Craig Forrest
Chemistry, University of Arkansas, Fayetteville

EBV has been found in all cases of the endemic form of Burkitt's lymphoma, and KSHV has been found in all cases of Kaposi's sarcoma. KSHV is more prevalent in sub-Saharan Africa with a prevalence larger than 50% in some countries but below 10% in North America and Northern Europe. GHVs are associated with cancers, especially in individuals that are immunodeficient. For instance, several human cancers are closely linked with EBV and KSHV in immunosuppressed individuals like AIDS patients. In preliminary studies, the Forrest lab determined that MHV68 MTA enhances the production of MHV68 RTA. I am attempting to confirm this result for the homologous proteins of human virus KSHV. An additional aim of my project is to synthesize an RTA- and LANA-null virus as a potential vaccine. The goal of this vaccine strain would be to expose the host to the viral structural proteins but using a virus that is unable to undergo lytic replication and establish latency.

31B. Berberine Mitigates Cisplatin-Induced Hepatorenal Mitochondrial Dysfunction through Preservation of Electron Transport Chain Integrity

Bhavana Sridharan, Kimberly M. Krager, Nukhet Aykin-Burns
Biology, University of Arkansas, Fayetteville

A high incidence of hepatorenal impairment in cancer patients treated with cisplatin has been reported. Berberine, a plant alkaloid possesses wide range of medicinal properties. Mitochondrial accumulation of cisplatin and subsequent damage to electron transport chain (ETC) plays a key role in cisplatin-induced cell death. This study was aimed to elucidate the mitigative role of berberine against cisplatin-induced hepatorenal mitochondrial injury. Clone 9 and Human renal mesangial cells (HRMC) were treated with 10 μM berberine for 24 h followed by 20 μM cisplatin (24 h). Mitochondrial ROS and antioxidant status (RTPCR & Western Blotting), apoptosis (Incucyte), mitochondrial membrane potential (TMRM uptake), respiration and oxygen consumption rate through basal and state 4 respiration (Seahorse Pro analyzer), protein expression and activities of complex II, III and IV were measured. An increase in mitochondrial oxidative stress and reduced antioxidant enzymes by cisplatin subsequently induced apoptosis, mitochondrial membrane depolarization, and inhibition of electron chain complexes leading to reduced oxygen consumption and respiration. Berberine effectively mitigated these deleterious

effects, ameliorated mitochondrial functions and prevented cell death. In conclusion, this study has provided significant preliminary evidences that berberine preserved the integrity of ETC and mitigated cisplatin-induced hepatic and renal mitochondrial dysfunction. However, future studies in animal model is required to elucidate the potential of berberine to be considered as an adjuvant drug during and after chemotherapy with cisplatin.

32A. The Effects of Common Chemicals on Zebrafish Embryonic Development

Tyler Melton, Stefanie Leacock
Biology, University of Arkansas at Little Rock

There are chemicals that many humans around the world consume, sometimes while pregnant, and the effects of these chemicals on embryonic development have not been thoroughly studied. Chemicals such as caffeine and nicotine, or L-theanine, which is used in many energy drinks to combat some effects of caffeine, and Erythrosine B, which is a main chemical in red food dye #3, are used widely around the globe. Due to the frequent consumption of these chemicals, this study on their embryonic developmental effects could lead to new advancements in how diets for pregnant women are recommended, along with general information about how chemicals affect biological molecules and pathways. Zebrafish embryos are a quick and accessible way to test the chemical effects on living vertebrates, due to production of large numbers of transparent embryos that are externally fertilized. We will breed adult zebrafish and expose the embryos to different dosages and timing of the selected chemicals. Then we will track the formation of the endoderm, mesoderm, and ectoderm germ layers by examining overall progression through development and the formation of structures from these layers such as the brain, somites, heart, and melanocytes. We will collect quantitative data such as for heart rate, length, and embryonic viability in the different treatments from 0 to 72 hours post fertilization (hpf). This study will be applied to build a new module for Developmental Biology students. This lab course uses principles of Course-Based Undergraduate Research which allows students to conduct real research on embryonic development, and help students understand how different areas of an organism are affected by various environmental factors.

32B. Exploring EARP: a tethering complex in endosomal trafficking

Jackson Lewis, Walter Aragon, Vladimir Lupashin
Dept. of Biology, University of Arkansas at Little Rock

Endosome associated recycling protein (EARP) is a tetrameric protein complex consisting of four different proteins: VPS50 (EARP exclusive), VPS51, VPS52, and VPS53. It is a close relative of the Golgi associated retrograde protein (GARP). Although prior research suggests that EARP functions similarly to GARP, aiding vesicle fusion, the exact localization and function of EARP is an enigma. To investigate EARP, we have tested the stability of its subunits and their co-localization with transferrin receptor (TfR) during recycling. Using hTERT-RPE1 EARP knock-out (KO) cell lines, we discovered that VPS53 is essential for the stability of other subunits, particularly VPS50. We found that EARP co-localizes with TfR early during the recycling process and that EARP subunits may be more mobile and adaptable than previously believed. We have also created and validated mitochondria-targeted VPS53 and VPS50-degron hybrid constructs that will be instrumental for future studies of the EARP complex.

33A. Interaction of a Fatty Acid Desaturase and a ROS Sensor in the Chloroplast to Influence Photosynthesis and Plant Development

Alexandra L. Barnett, Fiona Goggin, Jiamei Li
Dept. of Mathematics and Natural Sciences, University of Arkansas at Monticello

Fatty Acid Desaturase 7 (FAD7), which is found in the chloroplast of all higher plants, catalyzes the conversion of dienoic fatty acids (18:2 and 16:2) to

trienoic fatty acids (18:3 and 16:3). It increases membrane fluidity and influences the functioning of membrane-associated proteins. FAD7 expression levels influence host plant resistance to abiotic and biotic stresses, increasing resistance to some stresses and decreasing resistance to others. Null mutations in the FATTY ACID DESATURASE 7 gene (FAD7) enhance resistance to aphids in *Arabidopsis thaliana*. The fad7 null mutation also increases accumulation of singlet oxygen (SO), which appears to contribute to aphid resistance. SO is among the most potent reactive oxygen species (ROS) and it accumulates in response to a variety of stressors that disturb chloroplast metabolism. SO participates in stress-responsive retrograde signaling by interacting with a sensor protein in chloroplast, EXECUTER1 (EX1), to relay a message to the nucleus and reprogram gene expression. Aphid resistance is eliminated when null mutations in EXECUTER signaling (the ex1 and ex2 mutations) are introduced into the fad7 mutant to create the fad7ex1ex2 triple mutant; therefore, it appears that the fad7 mutation requires EX signaling to confer aphid resistance. It was found that the fad7 mutation and EX signaling interact to influence flowering time, and differences in photosynthetic parameters were not due to an interaction between them.

33B. Understanding the Complex Dynamics of Cigarette Smoking and Its Impact on Substance Use In the USA: Insights from Longitudinal Data Analysis

Peter Y. Wui, Corey Hayes, Kennedy Abanihe
Dept. of Nursing, University of Arkansas at Pine Bluff, University of Arkansas for Medical Sciences

This study investigates the complex nexus between addiction, economic factors, and public health outcomes, with a particular emphasis on the consumption patterns of cigarettes and the implications of marijuana legalization. Grounded in established economic frameworks proposed by Boyer (1978, 1983), Becker (1994), and Chaloupka (1991), we construct a comprehensive utility function to unravel the behavioral dynamics of addictive consumption. By leveraging longitudinal data from the National Survey on Drug Use and Health (NSDUH) spanning the years 2014 to 2021, augmented by supplementary datasets from the Centers for Disease Control and Prevention (CDC), state-level repositories, and annual volumes of the Tax Burden on Tobacco (Orzechowski and Walker, 2023), we develop a nuanced model to dissect addiction trajectories and their societal ramifications. Our model conceptualizes cigarette consumption as a stock variable, intricately intertwined with addiction levels, market prices, regulatory interventions, marijuana usage trends, and a myriad of other life cycle variables. Utilizing a quadratic utility function, we derive demand equations that optimize consumption choices in the presence of addiction dynamics, shedding light on the intricate interplay between substance use behaviors and economic incentives. Key findings from our analysis illuminate the multifaceted impacts of marijuana legalization on cigarette consumption patterns. Through the estimation of demand equations and the meticulous examination of coefficient effects, we uncover significant relationships between cigarette consumption, marijuana use prevalence, pricing mechanisms, tobacco control program expenditures, and various socio-economic determinants. Our empirical insights offer valuable guidance for policymakers and public health officials seeking evidence-based strategies to mitigate substance abuse and its associated harms. Furthermore, we anticipate enriching our analytical framework by incorporating additional life cycle variables, such as unemployment rates and state-specific contextual factors, to provide a more comprehensive understanding of addiction dynamics and inform targeted intervention strategies. This iterative approach underscores our commitment to rigorously examining the complexities of addiction within the broader socio-economic landscape, with the ultimate aim of fostering healthier communities and promoting evidence-informed policy responses.

34A. Comparative Biochemical Studies of Four Plants to determine Antibacterial and Antifungal Properties

Taryn LaGrone, Dr. Joseph Onyilagha
Dept. of Biology, University of Arkansas at Pine Bluff

Plants contain a plethora of chemical compounds with various properties. Some of these compounds offer significant health benefits, including anti-inflammatory, anti-cancer, and anti-diabetic effects. A plant such as bitter leaf is a medicinal plant native to the tropical region of Africa that has been used for its health benefits. The aim of this research is to determine whether common leafy greens have the same properties as bitter leaf, and if they can be utilized in treating certain conditions such as diabetes, cancer, arthritis, and malaria. In this study, four plant species were used: bitter leaf (*Vernonia amygdalina*), spinach (*Spinacia oleracea*), kale (*Brassica oleracea* var. *Sabellica*), and lettuce (*Lactuca sativa*) to determine and compare their antioxidative capacity and phenolic content compared to bitter leaf. The powdered form of each plant was used to execute the phenol method. Extracts from each plant in ethanol were used to determine its antioxidant capacity and estimated phenolic content. Subsequent studies will include phenol extraction using methanol and ethyl acetate from *Vernonia amygdalina*. These extracts will be tested against three different strains of bacteria and fungi: *Streptococcus pyogenes, Staphylococcus aureus, Escherichia coli, Mucor hiemalis* (+), *Penicillium notatum,* and *Aspergillus niger*. This is to test bitter leaf's antibacterial and antifungal properties. In upcoming investigations, the same extracts will be utilized to determine if there are any influences on glucose concentrations over time based on its anti-diabetic properties. This work can further educate people on the effectiveness of plant extracts on bacteria, fungi, and diabetes.

34B. Interaction between Tumor-Derived Exosomes and Macrophages through Scavenger Receptor Class A

Carvis Campbell III, Fariba Jousheghany, Laurie Lacer Defoor, Vinay Raj, Behjatolah Karbassi
Regulatory Science, University of Arkansas at Pine Bluff

Despite significant advancements in medical research, cancer remains one of the most decisive battles in medicine, accounting for nearly 10 million deaths annually. [1] Breast cancer among women is estimated to have 2.3 million new cases annually and over 685,000 deaths. It is a cancer affecting women worldwide, estimated to account for 30% of all new cancer diagnoses in women. [2] Following, lung cancer proves to be the second most common cancer in both men and women, with an estimated 2.2 million new cases annually and responsible for more than a million deaths annually. [1] The development of novel therapeutics for cancer is vital in the process to combat the medical condition and can further be explored through the observation of the tumor microenvironment (TME). Exosomes are seen to be a key factor in the progression of cancer though their role of communicating with the tumor immune microenvironment. Exosomes are small, membrane-bound vesicles that are released by cells into the extracellular environment. They transfer their molecular contents to recipient cells, thereby influencing the behavior and function of these cells. Tumor-derived exosomes carry molecules and factors known to affect immune cell functions. [3] The ability of exosomes to transport bioactive contents and their presence in biofluids has led them to be innovative clinical research tools. However, for exosomes to be utilized properly in the research industry, it is paramount that they are isolated with the highest purity. This can be deemed challenging as existing methods presents problems such as low yield or purity, long periods of processing, high cost, and difficulties in standardization. [5] Thus, this project is aimed to establish alternative methods of exosome isolation using novel techniques. The ExoQuick method (System Biosciences, LLC) is what will be the subject of study in this project, with the ultracentrifugation method to be the control. [6]

Exosome size characterization and morphological analysis will be performed and compared to the original isolation method of ultracentrifugation used before. Following, the exosomes isolated can then be characterized regarding their glycan contents through immunoblot/immunofluorescence and ELISA assays using plant lectins. It is studied that tumor-associated glycans (TAG) act to suppress the host's immune response to tumor cells, thus solidifying its importance in the study of exosomes. [8-14] M1 and M2 macrophages are two major functional states of macrophages that exhibit distinct roles in the immune response. These states are part of the macrophage polarization spectrum, which describes how macrophages can adopt different phenotypes depending on environmental signals. In the context of cancer, M2 macrophages can support tumor growth and metastasis by creating an immunosuppressive environment. M1 macrophages are generally associated with anti-tumor activities. They can recognize and destroy cancer cells. Skewing the M1/M2 ratio towards M1-like phenotype is an attractive strategy in the treatment of cancer. [7] With supporting data from previous research, it states that tumor cells express glycans on their cell surface that are recognized by a macrophage specific pattern-recognition receptor. This establishes a secondary aim in characterizing exosomes to primarily identify the presence of TAGs and how its exosomes interact with SR-A on macrophages, while additionally recording the consequences the interactions may produce.

35A. Exploring the Function of DJ-1 Protein in Mitochondrial Dynamics in *Dictyostelium discoideum*

Martin Ugarte, Dr. Kari Naylor
Dept. of 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. Past studies of fission and fusion 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 our model *Dictyostelium. 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. Parkinson conditions were induced with rotenone, and DJ-1 antisense and overexpressed cells were stained with MitoTracker Red CMXRos for visualization of mitochondria under a confocal microscope, and further analyzed with Fiji from ImageJ2 software. Fission and fusion of four DJ-1 antisense strains and seven overexpressed DJ-1 strains were quantified in 30 cells. DJ-1 decrease alone does not affect fusion and fission but there is a synergistic effect when both DJ-1 levels are decreased, and cells are exposed to oxidative stress via rotenone. This preliminary data supports the idea that loss of DJ-1 contributes to PD if oxidative stress is also present. In contrast, overexpression of DJ-1 upon rotenone exposure suggests that oxidative stress is reduced, with fusion and fission events resuming normal values.

35B. The Effect of Chlamydiae in the Social Amoeba *D. giganteum*

Dasha Young, Kevin Leal, Donovan Clark, Matt Curtis, Tamara Haselkorn
Dept. of Biology, University of Central Arkansas

Bacteria in the phylum Chlamydiae are symbionts and require a host to survive. They are pathogenic in humans but have been found thriving in many natural populations of social amoebae, seemingly without harming the amoebae. We suspect the relationship between amoebae and chlamydiae is mutualistic rather than parasitic. Previous work in the lab found *D. giganteum* produces more spores when infected with chlamydiae than without. However, this was with a single *D. giganteum* clone. We are trying to reproduce those results with other *D. giganteum* clones to ensure the chlamydiae is the cause for that advantage and that this effect is

consistent. To do so, we cured additional clones of amoebae to compare chlamydiae infected and uninfected lines. The spores produced from each line are in the process of being counted to compare the reproductive differences. The results of this investigation are ongoing but we hope they are consistent with the first trials and give us more insight into the relationship between these two organisms.

36A. Identification of dysregulated E3 ubiquitin ligases in exhausted T cells

Anna L. Bolding, Jessica L. Kelliher, Daniel Fil, Lora Rogers, Sydnye L. Shuttleworth, Brian Koss Dept. of Biological Sciences, University of Arkansas, Fayetteville

Applications of T cell-based immunotherapies are largely limited to hematologic cancers and efficacy in solid tumors remains limited. Tumor-infiltrating lymphocytes (TILs) face a much harsher environment within solid tumors, which contributes to the loss of cytotoxic function and upregulation of inhibitory receptors, ultimately leading to terminal T cell exhaustion and inhibiting the ability to control tumor growth. We aim to understand the proteins that are essential for T cell phenotypic plasticity, ensuring ample adaptability for TILs under these environmental stressors. In this project, we hypothesize that E3 ubiquitin ligases play a crucial role in proteome homeostasis and preventing T cell exhaustion. Using an established in vitro model of chronic stimulation induced T cell exhaustion, we have generated exhausted T cells from three healthy human donors for proteomic analysis. E3 ligase expression in exhausted T cells will be compared to acutely stimulated T cells and T cells that receive a single restimulation. Concurrently, in an effort to protect T cell function, we will stably over express previously identified E3 ligases which are lost in exhausted T cells. E3 over expressing T cells will be used in a series of in vitro co-culture T cell killing experiments. Co-culture experiments will be performed in a repetitive fashion to determine if the upregulation of specific E3 ligases enhances the ability of T cells to control tumor growth. These findings will further establish the role of E3 ligases in preventing T cell exhaustion and nominate candidate protein for cell engineering strategies.

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Chemistry

100A. Synthesis and Characterization of Copper Complexes Supported by Binucleating Ligands for CO2 Activation

Nathan Taylor, Lei Yang
Dept. of Chemistry and Biochemistry, University of Central Arkansas

There is an overabundance of carbon dioxide (CO2) gas within the atmosphere; therefore, this project aims at trying to turn carbon dioxide from a contaminant within the air into other building block molecules such as methane, carbon monoxide, formate, methanol, oxalate, ethylene, etc. To achieve this, researchers on this project focused on the development of binuclear copper (I and II) complexes for CO2 activation. While other rare earth metals have shown some success with CO2 activation, copper's high number of redox states (0, +1, +2, +3) along with its ability to form complexes with a plethora of different coordination geometries make it a viable transition metal for CO2 activation studies. In addition to its ideal chemical properties, copper has a relatively low toxicity and cost which makes it an ideal catalyst to research. A group of copper(I) and copper (II) complexes have already been synthesized by the reaction of copper salts and the 1,3-bis-(2-pyridylmethyl)acetamidinato ligand. The resulting products were characterized through methods such as X-ray crystallography, FT–IR, solid/solution UV–vis, EPR, NMR, and cyclic voltammetry. Furthermore, some preliminary tests using the copper (I) complexes exposed to CO2 gas showed some interesting results with dramatic color changes and GC-mass spec data from a collected gas sample; however, the characterizations of the products are still under investigation.

100B. Synthesis and characterization of copper complexes supported by polydentate amide ligands

Olivia Benefield, Lei Yang
Dept. of 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. Two polydentate amide ligands were employed in order to construct polynuclear 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.

101A. Computation of short term interactions between proteins and interactive compounds

Jeremy Garcia, Adem Behi, Dr. Koizumi
Chemistry and Physics, Arkansas State University

Understanding the interactions between proteins and their ligand compounds is essential for clarifying biological mechanisms and guiding drug design. This research employs molecular dynamics (MD) simulations to investigate the dynamic interactions between selected proteins and their interactive ligands. Focusing on protein-ligand complexes, we utilized advanced MD techniques to explore binding affinities, conformational changes, and the stability of these interactions over time. Key proteins involved in metabolic pathways were selected for study, and various ligands of interest were modeled. Our simulations provided critical insights into the binding dynamics and conformational flexibility of proteins in response to ligand interactions. This work highlights the effectiveness of MD simulations in enhancing our understanding of protein-ligand interactions, laying the groundwork for future experimental studies and therapeutic applications.

101B. Characterize the behavior of FAB proteins through the docking studies with the Thiazole series compound as antibacterial agents

Siam Chowdhury, Shailesh Bhudhathoki, Mohammad A. Alam
Chemistry and Physics, Arkansas State University

Novel antibacterial agents are now necessary to fight the menace of antibiotic-resistant bacterial infections. Computer-assisted drug design is now becoming more convenient with the help of molecular docking technology. It allows to predict the binding scores for selecting the potent compound for the proteins. We have found thiazole derivatives (e.g., HTM-18) as potent antibacterial agents, particularly active against methicillin-resistant Staphylococcus aureus (MRSA). Based on our CRISPRi studies of our potent compounds. Docking studies the targeting proteins were selected from the Fatty Acid Biosynthesis (FAB) series: FABK (PDB ID: 2Z6I), FABG (PDB ID: 6T60), FABZ (PDB ID: 3LBE). Whereas the compound HTM-18 belongs to the Thiazole derivatives. Autodock Vina(1.5.7) and Autodock Tools were used for computational docking studies in this research. Moreover, Discovery Studio was used for observing the binding of protein and compound in the 3D mode. According to the docking results we get a very strong score -10.6 kcal/mol during synthesized the FABZ (PDB ID: 3BLE) with HTM-18. The other proteins also show the acceptable binding scores with HTM-18, and this report will help figure out more potent antibacterial agents for future research.

102A. Cold storage-mediated p38MAPK activation: a potential contributor to kidney damage after transplantation

Demah Yousef, Dinesh Bhattarai, Nirmala Parajuli
Dept. of Chemistry, Hendrix College

The majority of donor kidneys require cold storage (CS) prior to transplantation. While CS is a necessity for preserving organs between harvest and transplantation, the process usually leads to suboptimal outcomes due to CS activating cellular pathways that damage kidney tissue. Previously, our laboratory demonstrated that the CS followed by transplantation decreases graft function in rat kidney grafts; however, the mechanism of this dysfunction is not known. The p38MAPK pathway is known to induce inflammation and cellular death during the disease process. Here, we hypothesized that the CS activates p38MAPK pathway and leads to kidney damage following transplantation. To address this hypothesis we used in vivo rat kidney models with or without CS followed by transplantation, and in vitro models of normal rat kidney (NRK) cells with CS and rewarming (RW). Pharmacological inhibition of p38MAPK (SB202190) was performed during CS of NRK cells followed by RW. NRK cells exposed to CS showed a time-dependent increase of p38MAPK phosphorylation (a marker of p38MAPK activation). This result indicates inhibition of p38MAPK increases the cell viability compared to the CS+RW condition, suggesting p38MAPK negatively regulates tubular cell viability during CS+RW. Together, our results suggest that CS-mediated activation of the p38MAPK leads to renal injury following CS+Tx. Therefore, p38MAPK could be a novel therapeutic target during CS to reduce CS+Tx-mediated graft failure. Future studies are warranted to inhibit p38MAPK signaling during kidney preservation (CS) to prevent renal injury in the transplants.

102B. Antimycin-like effects of isothiocyanates on liver submitochondrial particles

Aubrey Bailey, Andres Caro
Dept. of Chemistry, Hendrix College

Isothiocyanates (ITCs) are small biomolecules with the general structure R-N=C=S, where R represents either an aliphatic or aromatic group. These compounds are primarily produced through the enzymatic breakdown of sulfur-containing compounds found in plants of the Brassica genus (Brassicaceae family) by human intestinal bacteria. ITCs have demonstrated anticancer effects across various cancer types, with one key mechanism being the induction of apoptosis via oxidative stress driven by mitochondrial reactive oxygen species (ROS). However, the precise mechanism by which

ITCs promote mitochondrial ROS generation remains unclear. To investigate whether ITCs elicit a direct, antimycin A-like effect on complex III of the mitochondrial respiratory chain—leading to increased ROS and oxidative stress—we used submitochondrial particles, a cell-free model ideal for studying mitochondrial ROS production without interference from cytosolic or matrix enzymes. In this study, we examined the impact of both aromatic (benzyl isothiocyanate, BITC) and aliphatic (sulforaphane, SFN) ITCs on mitochondrial electron transport using bovine liver submitochondrial particles. Unlike SFN, BITC and antimycin A inhibited complex III activity and enhanced mitochondrial oxidant production in the presence of succinate and NADH, suggesting a potential direct antimycin-like oxidative effect of aromatic ITCs.

103A. Size dependent activity of doxorubicin based combination nanomedicine for tumor treatment

Sara Mateen, Noureen Siraj
Biology, University of Arkansas at Little Rock

Combination nanodrugs utilizing various sizes have garnered significant attention in the biomedical field for their enhanced therapeutic potential in cancer treatment. By optimizing the size and morphology of the nanoparticles, the cellular uptake and therapeutic efficacy of the nanodrugs can be significantly improved. In this study, these multifunctional nanocarriers are engineered to deliver a synergistic chemo-photothermal therapy (chemo-PTT) using a combination of Doxorubicin (DOX) and indocyanine green (ICG). The nanoparticles are characterized by using transmission electron microscopy (TEM) to determine their shape and size distribution, and dynamic light scattering (DLS) is employed to assess their hydrodynamic diameters. Zeta potential measurements are conducted to evaluate the surface charge, which influences their stability and interaction with cells. Ultraviolet-visible (UV-Vis) absorbance spectroscopy and fluorescence spectrometer are used to evaluate the size-dependent photophysical properties of the DOX-ICG combination nanoparticles which is very important to investigate their phototherapeutic potential. Additionally, the heat efficiency of the three different sized nanoparticles is assessed to determine their photothermal therapeutic activity. In the future, in vitro studies will be performed to assess the effect of size on cancer cells toxicity.

103B. Combination Drug Coated Gold Nanoparticles for Improved Cancer Therapy

Nistha Neupane, Noureen Siraj
Biology, University of Arkansas at Little Rock

Gold nanoparticles (AuNPs) have been extensively utilized in the biomedical field for a wide range of applications, including bioimaging, photothermal therapy (PTT), biosensors, catalysis, drug and gene delivery, and surface-enhanced Raman spectroscopy (SERS). The morphology and size of these nanoparticles are crucial factors affecting their cellular uptake and bioactivity. In this study, sphere shaped AuNPs are synthesized. Furthermore, these AuNPs are functionalized with chemo-PTT combination drugs based on Doxorubicin (DOX) and indocyanine green (ICG) to enhance their therapeutic properties. The nanoparticles are first characterized using transmission electron microscopy (TEM) to determine their shape and size, followed by dynamic light scattering (DLS) to assess their hydrodynamic diameter. Zeta potential measurements are conducted to evaluate the surface charge of the nanoparticles. The functionalized AuNPs are further characterized by using FTIR and XPS to quantify [DOX][ICG] ionic material based combination nanomedicine on the surface of AuNPs. Finally, in vitro studies will be performed to evaluate their therapeutic activity.

104A. Preparation of Innately Antibacterial Chitosan-Based Hydrogels for Wound Care Applications

Alexander Browning, Sharon Hamilton, Tatum Smith
Dept. of Chemistry, Ouachita Baptist University

In the past decade, research has shown the effectiveness of biopolymers for medical applications such as wound dressing, suturing, promoting cell proliferation, and controlled drug administration (Baranwal et al., 2022). Chitosan is a natural biopolymer of high functionality that is comprised of repeating Î²-(1,4)-2-amino-D-glucose and Î²-(1,4)-2-acetamido-D-glucose units that are linked by 1,4-Î²-glycosidic bonds. Chitosan is a highly biocompatible, cost effective, and versatile biopolymer that has merit in several medical applications, including hydrogels (Nicolle et al.,) Due to chitosan's large number of functional groups, it is possible to functionalize the polymer with antibiotic and therapeutic compounds through a reversible mechanism. This study explores the effectiveness of chitosan functionalization for drug delivery for wound care. It is possible to functionalize the chitosan at primary alcohol groups with primary amine containing drugs, which includes many antibiotics like amoxicillin, so that they can later be released at the wound site for therapeutic effects. The functionalized chitosan would retain its cross-linking capabilities and allow for comparison of effective drug delivery between an antibiotic functionalized chitosan hydrogel and a traditional antibiotic loaded chitosan hydrogel.

104B. Analyzing the Degradation Rates of Natural Polymer-Based Novel Materials for Use in Biomedical Applications

Tatum Smith, Sharon Hamilton
Dept. of Chemistry, Ouachita Baptist University

Modern research towards wound dressings has shown that alternatives to standard bandages have proven more successful at healing injuries. One such alternative is the use of electrospun fiber scaffolds. Polymer solutions can be spun into a construct that has a random configuration of fibers which closely resembles the architecture of the extracellular matrix (ECM). Additionally, the composition of the polymer solution can be changed to tailor the resulting nanofibers to facilitate wound healing and polymer degradation. In this experiment, the natural polymer alginate was modified to create an ideal compound for wound dressings. Amines similar to amino acids in collagen, a protein found in the ECM, were attached to the alginate to make it biomimetic and to yield free amines which are known to have antibacterial properties. The modified alginate (bAlg) was oxidized to increase its rate of degradation under physiological conditions. Modified alginate (bAlg) and oxidized modified alginate (oxbAlg) were analyzed via IR and NMR spectroscopy to verify the successful modification of the polymer backbone. An advanced polymer chromatography (APC) system was used to compare the degradation rate of the oxbAlg versus bAlg and commercially available alginate (Alg). Post modification, the alginates (Alg, bAlg, and oxbAlg) were electrospun with poly(vinyl alcohol) (PVA) to yield nanofibrous mats of three different compositions (Alg/PVA, bAlg/PVA, oxbAlg/PVA) and the degradation of the fiber mats were analyzed in vitro. Morphology changes of the mats over time were observed via scanning electron microscope (SEM). In addition to the above experiments, these fiber mats will be analyzed for their cellular responses and antimicrobial properties. These materials are anticipated to be used in a variety of future biomedical research applications. As a comparison, alginate was also modified with the four most prominent amino acids found in collagen Type II.

105A. Investigating changes in compaction of PEP-19 by neurodegenerative oligomers

Emma Brown, Tori Dunlap
Dept. of Chemistry and Biochemistry, University of Central Arkansas

PEP-19 is a disordered protein that regulates the binding of Calmodulin (CaM) to calcium. With calcium signaling, PEP-19 is able to bind to CaM, increasing the rate of calcium binding in the C-terminal lobe of CaM. PEP-19 is strongly associated

with neurodegenerative diseases. It is found in higher levels in brain areas spared in Alzheimer's Disease and found at a deficit in brain areas affected by Parkinson's disease. PEP-19 has also been shown to prevent excess calcium signaling caused by an overload of calcium ions within the brain. However, excess PEP-19 can lead to premature neuronal differentiation and learning deficiencies. We investigated how PEP-19 and the CaM/PEP-19 complex are affected by neurodegenerative oligomers through the use of fluorescence resonance energy transfer (FRET). We used this to measure the end-to-end distance of PEP-19 by itself, in complex with CaM, and with the neurodegenerative proteins alpha synuclein and A-beta peptide.

105B. Investigating the Impact of PEP-19 on Calmodulin Target Binding

Rachel Harmon, Tori Dunlap
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Pep-19 is a small, intrinsically disordered protein (IDP) that regulates calmodulin's (CaM) response to calcium ion influx. Calmodulin is a central translator of the calcium ion signal and binds to up to 300 target proteins in the presence of calcium ions. The only known signaling function of PEP-19 is to bind to CaM and increase both the Kon and Koff of Ca2+ binding to the C-terminal lobe of CaM without significantly altering calcium ion binding affinity. Overexpression of PEP-19 can lead to learning impairment and premature neuronal differentiation while PEP-19 knockdown can be linked to increased susceptibility to calcium overload and several neurodegenerative diseases. Given differences in PEP-19 conformation when bound to apo-CaM vs. Ca2+ -CaM, we hypothesize that PEP-19 will impact CaM target binding. Despite knowing the phenotypic effects of varying PEP-19 levels, little is known about how PEP-19 impacts CaM signaling pathways. Here, we investigate how PEP-19's different CaM binding modes affect CaM binding to common target peptides using FRET and fluorescence anisotropy to determine the types of complexes formed.

106A. Microwave-Assisted, Solvent-Free Synthesis of Azole Heterocycles for Antifungal Applications

MaryGrace McAfee, Brian Walker
Chemistry, University of Arkansas at Little Rock

Traditionally, antifungal resistance has been largely overlooked as a public health threat, despite posing critical risks to human health comparable to those of bacterial resistance to medications. According to the World Health Organization, fungal infections account for 3.8 million deaths annually, with many responsible pathogens already showing resistance or quickly evolving resistance to current antifungal treatments. The four classes of antifungal drugs are azoles, polyenes, echinocandins, and allylamines, with azoles being the most widely used due to their affordability and broad-spectrum efficacy. Consequently, this work is concerned with exploring new azole-containing scaffolds that may bypass known resistance mechanisms. However, traditional synthesis methods for azole-containing antifungals, taking 24–72 hours to complete, often depend on large amounts of volatile, toxic solvents and are energy-intensive. To address this, our project leverages solvent-free, microwave-assisted synthesis in developing a small library of novel azole scaffolds through the ring-opening of epoxides, followed by alcohol derivatization. For example, reacting phenyl glycidyl ether with imidazoles and pyrazoles in one minute under solvent-free conditions. This green process not only reduces environmental impacts but also significantly shortens reaction times, promising a green alternative to traditional methods and a path toward novel antifungals.

106B. Derivatization of Gepotidacin to Evade Efflux in Gram-Negative Bacteria

Joshua L. Pack, Jonathan C. K. Quirke, Rebecca J. Ulrich, Paul J. Hergenrother
Chemistry, University of Arkansas at Little Rock

In a recent report by the World Health Organization outlining the top pathogens posing a significant threat to human health, all "critical" priority pathogens were Gram-negative bacteria. This is a consequence of the incidence of multidrug-resistant strains of Gram-negative pathogens and the diminishing treatment options for infections; a new class of FDA-approved, Gram-negative targetting antibiotics has not been introduced into the clinic since the fluoroquinolones in the 1960s. A major contributing factor to the inefficacy of antibiotics against Gram-negative pathogens is attributed to a lack of their accumulation in the cell, which is partly the consequence of broad-specificity efflux pumps embedded in the cell membrane of Gram-negative bacteria. Minimum inhibitory concentration data for wild-type and efflux knockout strains of *E. coli* with approved antibiotics suggests that drugs, such as fusidic acid, are only ineffective treatments for Gram-negative bacteria because they are efflux substrates. Therefore, this work is concerned with engineering out efflux-liabilities from an efflux-liable antibiotic, gepotidacin (which has passed Phase II clinical trials for the treatment of urinary tract infections), using a systematic set of rules–EffluX Propensity EvaLuation (EXPEL) guidelines–that could be applied to future generations of antibiotics to increase their potency against Gram-negative pathogens.

107A. Progress Toward the Synthesis of 5-nitrodopamine to Determine Activity and Significance in Biological Settings

Jennifer D. Bui, Emma G. Gruss, Larryn W. Peterson
Dept. of Chemistry, Rhodes College

Catecholamines are aromatic rings identified by their ortho-substituted alcohols and differing side chain amines. Substituted catecholamine analogues demonstrate varying effects on the cardiac and endogenous modulators of vascular systems. Specifically, 6-nitrodopamine has been found in human vas deferens and umbilical cords, acting as a contractility modulator. It has also shown to be a positive chronotropic agent in rat hearts, 10,000x more potent than dopamine. It is believed to interact with D2-like receptors to modulate chronotropic and contractility effects. The development of substituted catecholamines is motivated by these various biological applications. This work details the ongoing synthesis of 5-nitrodopamine through two different pathways, with the most recent intermediate synthesized at an 81.9% yield. Catecholamine derivatives such as these provides key insight into biological settings and is necessary to further elucidating certain biological mechanisms.

107B. Synthesis of dopamine derivatives to further elucidate biological catecholamine significance and physiological activity

Trinity L. Liaw, Larryn W. Peterson
Dept. of Chemistry, Rhodes College

6-Nitrodopamine has recently been found in various locations of the body, acting as a major mediator of tissue contractility in the rat and human vas deferens and as a positive chronotropic agent in the heart. To aid in further elucidation of the physiological significance of catecholamines and their analogues, this work details the synthesis of the dopamine derivatives 6-cyanodopamine and 6-carboxydopamine, which are synthesized through a series of reactions starting with the commercially available 3,4-dimethoxyphenethylamine. 6-Cyanodopamine was synthesized in six steps with an overall yield of 25.2%. The synthesis of 6-carboxydopamine is currently in progress with three steps toward the final dopamine analogue having been made. When completed and fully characterized, these dopamine derivatives, along with others, will be sent to collaborators where they will be used to determine the biological relevance of catecholamines and serve as standards to quantify them in the body.

108A. Synthesis and Effects of Amine Substituted Thiazole Molecules

Gavin Brown, Shailesh Budhathoki, Mohammad A. Alam
Chemistry and Physics, Arkansas State University

Antimicrobial resistance (AMR) has slowly developed as a global threat in the past 70 years; with more than 4.95 million deaths occurring worldwide each year. One of the goals of the CDC is to produce novel antibiotics to fight AMR. Responding to this we have created a novel series of small molecule thiazole molecules. Thiazole, is highly valuable in the use of small molecule pharmaceuticals, the medicinal interest in it's derivatives has surged due to its antimicrobial properties and therapeutic potential against a wide range of psychotic and physical diseases. These derivatives exhibit a diverse array of beneficial characteristics such as; antioxidant, analgesic, antibacterial, anticancer, antiallergic, antihypertensive, anti-inflammatory, antimalarial, antifungal, and antipsychotic activities. With more than 18 FDA approved drugs in the market. We are synthesizing a series of amine conjugated thiazole derivatives based on the structures of potent compounds. The molecules will be tested against an array of drug resistant bacteria to report their in vitro activity in this presentation.

108B. Characterization of c-type cytochrome in Yersinia enterocolitica

Tawni Bacorn, Newton Hilliard, Caitlin Drake
Dept. Physical & Earth Sciences, Arkansas Tech University

Yersinia enterocolitica is a human pathogen with the capability to survive the acidity of the stomach (pH 2), and migrate to its infection site in the middle region of the small intestine (pH 8.5). This represents a drastic shift in environmental pH, which has steep energy demands in switching from an acid tolerance response (ATR) to moderately basic pH. To meet these demands, *Yersinia enterocolitica* contains genes for two separate and distinct low molecular weight, mono-heme c-type cytochromes (Ga0077840_11951 and Ga0077840_111766). These two genes produce two proteins with highly different sequences, leading to differing properties. Both genes produce proteins with an aspartic acid triad on one side of the c-type cytochrome. Gene number 11951 sees a uniform distribution of charged residues across the surface of the protein, which is substantially different from gene_111766. This difference potentially influences differences in redox binding partners. The gene was amplified by PCR, cloned into the pF1K plasmid, and transformed into E. coli HB101. After induction of genes while grown at 30 °C, highly colored cell pellets were noticed. SDS-PAGE of cell lysate shows bands at approximately 10 kDa.

109A. Characterization of protein expression levels in Diamond-Blackfan anemia models

Seth Eubanks, Divya Sapkota, Lauren Van Dee, Dylan Girodat
Dept. of Chemistry and Biochemistry, University of Arkansas, Fayetteville

Diamond-Blackfan Anemia (DBA) is a rare disease, characterized by erythroblastopenia physical malformations, and an increased rate of cancer. Treatment options for DBA include steroid administration, blood transfusion, or hematopoietic stem cell transplantation. DBA is caused by mutation in or haploinsufficiency of ribosomal proteins, which are components of ribosomes, the ribonucleoprotein complexes responsible for protein production in all cell types. Models of DBA display elevated reactive oxygen species and oxygen consumption rates, indicating a modulation to metabolism. However, it is unclear as to the molecular mechanism by which defects in protein synthesis are coupled to altered metabolic profiles. Here we have isolated knockdowns of rpl5, rpl11, and rps19 genes in *S. cerevisiae* and in *H. sapiens* and performed proteomic analysis to characterize differential expression of metabolic genes. Proteomic analysis was carried out using R and The Database for Annotation, Visualization, and Integrated Discovery (DAVID). It was found that that the rpl5, rpl11, and rps19 haploinsufficiency leads to differential expression in several genes

associated with metabolism, particularly for those that are regulated by mTOR signaling. Therefore, we speculate that haploinsufficiency of ribosomal proteins leads to elevated ribosomal assembly, requiring increased energy production, and stimulating mTOR activation.

109B. Single Particle Diffusivity Through Enhanced Five-Dimensional Single Particle Tracking

Jackson Brandt, James E. Batey, Meek Yang, Bin Dong
Chemistry, University of Arkansas, Fayetteville

Translational and rotational diffusion coefficients of single molecules and metal nanoparticles have been of significant study to physical and analytical chemists alike for their ability to resolve chemical kinetics, dynamics, and catalysis properties. The acquisition of these metrics is obtained experimentally by a variety of techniques and predicted theoretically by the Einstein-Stokes relation. Experimental proceedings employ methods such as UV-Vis spectrometry, flow cytometry, dynamic light scattering, and more. Typically, these methodologies can obtain translational diffusion coefficients with great precision. However, traditional techniques fall behind in their ability to quickly and accurately resolve rotational diffusion coefficients of particles. Here, we employ a two-channel optical microscopy system and single particle orientation and rotational tracking (SPORT) methodology to obtain both translational and rotational diffusion coefficients of gold nanoparticles (AuNP) in diverse media with sub-10 nm and 10o precision. This allows for readily available diffusion information using a common optical microscope under darkfield illumination.

110A. Design Development and characterization of Polymer membrane Separator for Lithium-Ion Battery and surface modification using TiO2

Shahid Hussain Abro, Price Sheets, Noureen Siraj
Chemistry, University of Arkansas at Little Rock

The performance and safety of lithium-ion batteries are critically influenced by the properties of the polymer membrane separators used in their construction. This study explores the enhancement of these properties through the incorporation of titanium oxide (TiOâ,,) onto the polymer membrane surface. The primary objective is to improve the thermal stability, mechanical strength, and ionic conductivity of the polymer separators, thereby contributing to overall battery performance. Polymer separators are typically made from materials such as polyethylene (PE), polypropylene (PP), or blends of these polymers. These materials are chosen for their mechanical strength, thermal stability, and their ability to be manufactured into thin, uniform layers. We will synthesize polymer-TiOâ,, composite membranes by incorporating varying concentrations of titanium oxide nanoparticles into a polymer surface via a solution casting method. The resultant membranes will be characterized using scanning electron microscopy (SEM) to examine morphological changes, and X-ray diffraction (XRD) to assess structural integrity. Thermal stability will be evaluated using thermogravimetric analysis (TGA), while mechanical properties will be determined through tensile tests. Ionic conductivity will be measured using electrochemical impedance spectroscopy (EIS). The expected results will indicate the incorporation of TiOâ,, nanoparticles significantly enhances the thermal stability of the polymer separators, with a notable increase in the temperature at which decomposition begins. Additionally, the mechanical strength of the membranes improves with optimal TiOâ,, content, leading to better performance under mechanical stress. The ionic conductivity of the composite membranes also shows enhancement, attributed to the increased surface area and improved interaction between the TiOâ,, particles and the polymer matrix. This study demonstrates that titanium oxide is a promising additive for improving the surface

properties of polymer membrane separators in lithium-ion batteries, potentially leading to more efficient and safer battery systems. Future work will focus on optimizing the concentration of TiOâ,, and exploring other functional additives to further enhance separator performance. : Lithium-Ion, Membrane, Titanium oxide, Polyetherimide, safety, mechanical strength. Etc

110B. Synthesis and Characterization of ionic material based combination nanodrugs

Zane Austin, Noureen Siraj
Biology, University of Arkansas at Little Rock

Synthesis and Characterization of ionic material based combination nanodrugs Student: Zane Austin; Mentor: Noureen Siraj, Chemistry, CSTEM Abstract: Nanomedicine is an ever-growing field due to the advantages that nanodrugs have over traditional medicine such as: greater selectivity towards cancerous tissue, facile delivery of hydrophobic drugs, and controlled drug release. We have designed several ionic materials-based combination nanodrug previously and saw superior cytotoxicity compared to parent drug. Herein, we are developing for the first time a combination nanomedicine by combining two non- invasive phototherapies i.e. Photodynamic Therapy (PDT) and Photothermal Therapy (PTT). These ionic materials will be characterized in detail by using nuclear magnetic resonance and mass spectrometry. We will also prepare nanoparticles and then characterize it using Transmission electron microscopy (TEM), Dynamic light scattering (DLS) and Zeta potential. We will assess their phototherapeutic activities by measuring their PTT activity light to heat conversion efficiency) and PDT activity reactive oxygen species (ROS) quantum yield. In future, in vitro studies will be conducted to assess the cellular uptake as well as cell viability of the compound to determine the IC50 value. Materials & methods We will perform ion exchange reaction to synthesize the compound. The purified and dried compound will be used for further characterization. We will perform heat efficiency experiment by measuring the temperature of the solution upon irradiation with the laser. We will use the probe to investigate the reactive oxygen quantum yield of the compound.

111A. Neglected Tropical Diseases: Synthesis of Urea Analogs for Schistosomiasis

Eva R. Palmer, Gregory R. Naumiec
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Schistosomiasis, or snail fever, is a neglected tropical disease that affects millions of people worldwide with only one approved treatment option, praziquantel (PZQ). This creates the problem of drug immunity that will eventually render PZQ ineffective in treating this disease. My research aims to synthesize new drug candidates that could potentially act as an alternative to PZQ. To date, this has been done by synthesizing diarylureas from varying aniline and isocyanate compounds, since this class of compounds have been shown to have antischistosomal properties. Thus far, I have synthesized over 20 potential drug candidates with percent yields ranging from 30.6% to 99.9%. In addition to building an expansive drug library of diarylureas, I have also been exploring the thermal and microwave synthesis of highly functionalized ureas via Sonogoshira coupling. This has been accomplished in yields as high as 54.3%. All compounds were analyzed using 1H and 13C nuclear magnetic resonance (NMR), infrared spectroscopy (IR), and HRMS MALDI mass spectrometry (MS). In future research, I plan to further my experimentation with Sonogshira coupling, especially via microwave synthesis, as well as expand my drug library to potentially include thioureas and diureas.

111B. Development of a Wax Microfluidic device for Investigating the Flow Dynamics of Calmodulin Protein

Lucas Yarbrough, Gabriella Toland, Ahmad Zaman Qamar
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Capillary microfluidics is an expanding field focused on developing efficient and accessible fabrication methods. This study investigates the use of Parafilm as a material for creating open-channel capillary microfluidic devices and explores the application of a cutting plotter in their production. While Parafilm presents certain fabrication challenges, it can be optimized to produce inexpensive, easily assembled devices. Our optimization process involved evaluating various design parameters, such as channel dimensions and substrate materials. For one optimized model, we achieved ideal dimensions with a 0.5 mm channel width, 10 mm channel length, and 1.2 mm inlet width. PET sheets were used as the bottom substrate, while different brands of PET and PE were tested as top-sheet materials. Additional optimization efforts included exploring heating time, channel shapes, sealing techniques, clamping methods, and cutting devices. We tested both water and Calmodulin (CaM) solutions in these devices. CaM is a protein that undergoes conformational changes in the presence of calcium ions (Ca 2+), regulating various cellular processes. We hypothesized that these conformational changes would alter flow velocity in the channels. Our final devices were used to compare CaM samples with and without calcium in aqueous solutions as well as to ensure consistency with 10% trifluoroethanol solutions. We were successfully able to confine the samples in the wax micro-channels without leakage. This research highlights the potential of Parafilm-based microfluidic devices as cost-effective and efficient platforms for capillary flow dynamics.

112A. Determining the effect of atmospheric pollution on Sphagnum in North England peatlands

Lizzie Horton, Jennifer Clear, Angela Creevy, Alex Treadway
Chemistry, Physics and Engineering, Biological Sciences, Ouachita Baptist University

Peatlands are a type of wetland ecosystem covering less than 3% of the terrestrial land surface. They are ombrotrophic systems fed only by rainfall and are therefore very acidic, nutrient poor environments. Sphagnum, a genus of moss typically found in this type of environment are ecosystem engineers that further promote acidic conditions. Due to the acidic and waterlogged conditions, microbial decomposition is very slow. As a result, carbon accumulates at a rate of approximately 1 mm/year. This makes peat bogs a very good environment to study past pollution and environmental change. Eight sample cores approximately 20 cm long were taken from a site on Winter Hill, Lancashire, UK, an area that has long been a center of industry in the UK. These cores were cross-sectioned and scanned using X-ray Fluorescence (XRF) to detect the presence of heavy metals. In addition, the samples were examined microscopically to determine botanical composition. Initial findings indicated that the majority of heavy metals were deposited 50-80 years ago. The results of this study suggest that atmospheric pollution may have caused Sphagnum growth to decline, and Heather *Calluna vulgaris* growth to increase.

112B. Determining the effect of atmospheric pollution on Sphagnum in north England peatlands II

Alexander Treadway, Lizzie Horton, Angela Creevy, Jennifer Clear
Dept. of Chemistry, Ouachita Baptist University

Peatlands are a type of wetland ecosystem covering less than 3% of the terrestrial land surface. They are ombrotrophic systems fed only by rainfall and are therefore very acidic nutrient poor environments. Sphagnum, a genus of moss typically found in this type of environment are ecosystem engineers that

further promote acidic conditions. Due to the acidic and waterlogged conditions, microbial decomposition is very slow. As a result, carbon accumulates at a rate of approximately 1 mm/year. This makes peat bogs a very good environment to study past pollution and environmental change. Eight sample cores approximately 20 cm long were taken from a site on Winter Hill, Lancashire, UK, an area that has long been a center of industry in the UK. These cores were cross-sectioned and scanned using X-ray Fluorescence (XRF) to detect the presence of heavy metals. In addition, the samples were examined microscopically to determine botanical composition. Initial findings indicated that the majority of heavy metals were deposited 50-80 years ago. The results of this study suggest that atmospheric pollution may have caused Sphagnum growth to decline, and Heather, *Calluna vulgaris* growth to increase.

113A. Deoxyribose Assay to Measure Antioxidant Capabilities of Methimazole

Kolten Kluesner, Jaime Murphy
Chemistry and Biochemistry, Harding University

This research aimed to clarify an efficient protocol for testing anti-oxidant capabilities using the deoxyribose assay and obtain a greater sense of the mechanism by which Methimazole, a known anti-oxidant, inhibits oxidative damage. The assay works by introducing iron (II) into the solution along with hydrogen peroxide. The hydrogen peroxide will be reduced to form hydroxyl radicals by oxidizing iron (II) to iron (III). Hydroxyl radicals are well known for the oxidative damage they can cause. These hydroxyl radicals then react with the deoxyribose sugar and break into smaller organic compounds. With the addition of Thiobarbituric acid and a period of high temperatures, these fragments of deoxyribose, known as malondialdehyde, link two molecules of Thiobarbituric acid together, which create a chromophore that can be measured ~530nm through UV-Vis Spectroscopy. Adding a known anti-oxidant or pro-oxidant shifts the absorbance, higher for pro-oxidants and lower for anti-oxidants. Gallic acid showed pro-oxidant properties, while Methimazole displayed anti-oxidant properties.

113B. Synthesis of Tautomerically Ambiguous Nucleosides and Overcoming Challenges of Dichloromethane Regulation

Oscar Jose Jimenez de las Heras, Vincent Dunlap
Division of Science and Mathematics, McKendree University

The prolonged COVID-19 pandemic brought to light the critical need for potent antiviral medications, particularly against resilient viral strains such as HIV. This research aims to create tautomerically ambiguous nucleosides that will enhance viral replication efficiency to an unfavorable degree, causing an error catastrophe and eradicating the virus. Our research employed a wide range of techniques, such as column chromatography and thin-layer chromatography (TLC), to produce and evaluate several nucleoside analogs. Problems surfaced after dichloromethane (DCM) was recently outlawed, necessitating the use of substitute solvents for chromatography. The study employed 2'-deoxycytidine derivatives modified with protecting groups, to achieve the desired tautomeric ambiguity. Future work will focus on amination of the 2'-deoxycytidine derivatives and advancement to the next synthesis phase. This presentation will cover the synthesis process and adaptations to changing regulations of DCM.

114A. Synthesis of novel Chalcones and their Antimicrobial Properties

Casi Gee, Isbel Ritter, Kennedi Burns, Dane Richards, Latorya Hicks
Dept. of Biochemistry, Hendrix College

Chalcones have been of great interest lately, not only due to their synthetic perspective, but due to their biological and potential pharmacological activity. Chalcones have been used for thousands of years through plants and herbs to treat medical disorders, such as anti-hypertensive, anti-retroviral, anti-inflammatory, anti-fungal, antioxidant, and anti-bacterial properties. Drug resistance and the increase of infectious diseases is one major concern today. There is an increase in the demand for the discovery of new drugs with potent anti-microbial

activity, particularly against resistance strains. Recently, there have been reports that chalcones have anti-microbial properties. Reports have shown that derivatives of chalcones, particularly ring fused chalcones, have been shown to have antimicrobial activity. In particular, 3-(carboxylalkyl) rhodanine showed high antimicrobial properties against both *Staphylococcus aureus* and methicillin resistant *S. Aureus*. Chalcones were determined to be enhancers of antimicrobial agents in the treatment of oral microbial infections. Today sulfonamide derivatives have been shown to have anti-HIV, anticancer, antimicrobial, and hypoglycemic biological activity. Currently, thousands of derivatives have been synthesized and have shown varying pharmacological properties. The biological activity is due to the main structure where where R′ hydrogen, alkyl, aryl, or hetero aryl, etc. It is the lipophilicity of the amino group that demonstrates the largest effect in protein binding. Numerous reports have shown the antimicrobial properties activity of chalcones. Sulfonamides, in particular, N-sulfonamide derivatives have been reported to demonstrate antimicrobial properties; however, there is little data on derivatives of chalcones with an N-sulfonamide moiety to test their anti-microbial properties. These novel chalcones have demonstrated antimicrobial properties with a range of 60 – 80 μM.

114B. CYP2E1 overexpression protects HepG2 cells against ferroptosis.

Kaleigh Coker, Andres Caro
Dept. of Chemistry, Hendrix College

Ferroptosis is a recently identified form of regulated cell death, initiated by iron-mediated one-electron reduction of lipid hydroperoxides (LOOH). The induction of Cytochrome P450 2E1 (CYP2E1) may promote ferroptosis by increasing the cellular levels of LOOH. However, CYP2E1 induction also upregulates anti-ferroptotic genes that regulate glutathione peroxidase 4 (GPX4), the primary inhibitor of ferroptosis. Based on this, we hypothesize that the effect of CYP2E1 induction on ferroptosis depends on the balance between the pro- and anti-ferroptotic pathways activated by CYP2E1. To test this, we induced ferroptosis in hepatoma HepG2 cells—both in cells lacking CYP2E1 (Mock cells) and cells engineered to express human CYP2E1 (WT cells)—using class 2 inducers (RSL-3 or ML-162). We then assessed cell viability and levels of reduced glutathione (GSH), the substrate for GPX4. Overexpression of CYP2E1 protected HepG2 cells from ferroptosis, as indicated by an increase in the IC50 of WT cells compared to Mock cells following exposure to the inducers. Additionally, CYP2E1 overexpression resulted in an 80% increase in GSH levels. These findings suggest that CYP2E1 overexpression protects HepG2 cells against ferroptosis, likely through GSH induction.

115A. Synthesis of Novel N,N'-Disquaramides Toward the Development of Leishmanicidal Agents

Natasha M. Moreland, Gregory R. Naumiec
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Leishmaniasis is a neglected tropical disease found in about 88 countries affecting more than 12 million in the world. The disease is spread through infected sand flies. The three forms of leishmaniasis are: cutaneous leishmaniasis(CL), mucosal leishmaniasis (ML), and visceral leishmaniasis (VL). Currently, there are a few treatment options for leishmaniasis. However, with so few resources, the effectiveness of the drug is declining and the cost is expensive. The goal of my research is to develop a more effective drug at a lower cost. The common core of my compound is a squaramide. Currently, I am making a drug library with varying amino side chains to see what combination is the most potent against the leishmania parasite, specifically *L. major* and *L. braziliensis*, in vitro. When suitable candidates are identified, they will then be tested in vivo in mice models. To make each drug, sequential addition-elimination reactions are performed from diethyl squarate to monosquaramide to disquaramide. More specifically, ethanol is added into a round bottom flask with diethylsquarate or monosquaramide which is over a stir plate. Then, a solution ethanol

and primary or secondary amine are added in an additional funnel and added to the round bottom flask slowly. Once combined, I let it mix overnight and then purify by precipitation or flash chromatography. Identity is confirmed by TLC, 1H and 13C NMR spectroscopy. As of now, 13 potential drugs have been successfully synthesized in moderate to high yields (77%-99%) and are currently waiting to be tested against the disease, hoping one is more successful than what is available now for treatment choices.

115B. Studying how conformational changes in the protein PEP-19 may contribute to neurodegenerative diseases

Luke Hinson, Victoria Dunlap
Dept. of Chemistry and Biochemistry, University of Central Arkansas

PEP-19 is a protein that helps regulate calcium ion (Ca2+) homeostasis within our bodies by binding to the calcium translating protein calmodulin (CaM) and altering its calcium binding kinetics. Certain characteristics of PEP-19 structure require further research to fully understand its function. Components of PEP-19 were sampled in various concentrations of calcium, trifluoroethanol (TFE), and EGTA— all of which were analyzed using circular dichroism spectroscopy to study their resulting conformation. Collected data allows for a better understanding of the CaM/PEP-19 complex structure and how it modulates Ca2+ signaling within our cells. The significance of this understanding lies in the correlation that exists between Ca2+ dysregulation and neurodegenerative diseases. It is possible a causal relationship between abnormal CaM/PEP-19 complex structure in-vivo and neurodegeneration. This determination may identify a potential target for future therapeutics aimed at helping alleviate the onset and progression of diseases such as Alzheimer's Disease and Parkinson's Disease.

116A. Chemical Manipulations of Rifamycin Core Providing New Solutions to an Old Problem: Multidrug Resistant Tuberculosis

Taylor Mitchell, Grant Beeser, Braden L. Glenn, Wyatt Treadway, Jessie, Marissa Fullerton, Amanda Dragan, Daniel Voth, Irosha N. Nawarathne
Chemistry, Lyon College

Amid the antibiotic resistance crisis, *Mycobacterium tuberculosis* (MTB)–the pathogen causing TB– has shown widespread resistance to rifampicin, making it futile in TB therapy as MTB RNAP mutations disrupt key interactions between the drug and the target. Rifamycin, particularly rifampicin, has been a mainstay of TB treatment since the 1960's; it binds the B subunit of the MBT RNA polymerase (RNAP) and blocks RNA synthesis. By utilizing the 'enabling reaction' of the rifamycin core and coupling it with click chemistry, we have exploited the thoroughly studied rifamycin scaffold to target MDR-TB and potentially treat other bacterial infections. Though click chemistry and other means we have added numerous functional groups to Rifamycin S. Assays have been conducted to test the antibiotic properties of these derivatives, both in vivo and in vitro, against both common bacteria genera as well as drug resistant strains of pathogens. In vivo data suggests some derivatives are highly effective against *Staphylococcus aureus*. Our work highlights the first report of synthesis, isolation, and purification of rifamycin derivatives with azido, alkyne, triazole, and benzoxazino functionalities, the innovative products of coupling complex rifamycin chemistry and simple click chemistry. 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.

116B. Napthoquinone Derivatives as Novel Lung Cancer Therapeutics

Megan Bean, Maria Cervantes, Whitney Mitchell, Rachel E. Tyler, Lola Beeser, Nikkolette Perkins, Samir V. Jenkins, Amir Mortazavi, Marissa Fullerton, Daniel Voth, Ruud Dings, Irosha N. Nawarathne
Dept. of Chemistry, Lyon College

Each year, more people die of lung cancer than of colon, breast, and prostate cancers combined. Since the 1980s, it remains the most common cancer in terms of mortality in the United States with an estimated 127,070 deaths in 2023. Despite worldwide efforts for cancer prevention, diagnosis, and treatment, the need for new lung cancer therapeutics is clear and pressing. Naphthoquinones and their derivatives, both naturally occurring or created, possess a wide range of activities, including anticancer and antimicrobial properties. However, they also represent the challenge to develop clinically relevant anticancer molecules due to the untamed redox properties. Any modification to the naphthoquinones has to be designed carefully, by adding nitrogen and oxygen, both highly electronegative atoms to moderate the redox activities. We have created a wide array of new biologically significant aminonaphthoquinones, including rifamycin derivatives. Select derivatives were further modified using click chemistry to create triazoles, which are good additions when attempting to further increase biological activities. After the products were purified, they were then tested against Lewis Lung Carcinoma (LLC) cell lines, fibroblasts (3T3), and embryonic mesenchymal stem cells (10T1/2) in cell viability assays to determine their effectiveness against lung cancer cells and noncancerous cell lines. In this presentation we aim to describe the synthesis, purification, characterization, and activity against a variety of cell lines of naphthoquinone derivatives. We also plan to take a data driven approach to identify the mechanism of action of modified naphthoquinones in lung cancer cells. 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.

117A. Analysis of BPA Leaching from Feminine Hygiene Products into Simulated Vaginal Fluid using Fluorescence Spectrophotometry

Maryann Rettig, Sara E. Hubbard
Dept. of Chemistry, Ouachita Baptist University

Bisphenol-A (BPA) is a chemical compound commonly used to produce several plastics and epoxy resins. Recently, BPA has also been detected in feminine hygiene products. Because of a structural resemblance to estradiol, BPA can act as an endocrine disruptor, which has linked BPA to several health complications such as cancer development, reduced fertility, and early puberty. In recent summer research at Ouachita Baptist University, it was determined that fluorescence spectrophotometry could be used to monitor BPA leaching over time into a 1:1 methanol/water solvent from panty liners, tampons, and tampon applicators. BPA is a fluorescent compound with excitation and emission wavelengths of 278 nm and 304 nm, respectively. Due to the small amount of BPA leaching from feminine hygiene products and the resulting complex sample matrix, the standard addition method was used to calculate the BPA concentrations obtained from these samples. The leaching of BPA from multiple brands of menstrual pads was analyzed over a six-hour time period in the 1:1 methanol/water; the fluorescence emission intensity of each sample was determined using the FS-5 spectrofluorometer from Edinburgh Instruments. Analytical figures of merit: linear range, limit of detection, and limit of quantitation were determined. To further analyze the leaching effects, a simulated vaginal fluid was utilized as the solvent to mimic the pH and proteins of the female vagina. The standard addition method was repeated using the simulated vaginal fluid to compare to previous results using the 1:1 methanol/water solvent.

117B. Treating lung cancer with ZnTPP-6AH as a PDT agent

Madison Goff, Dr. Olivia Owens, Dr. Joe Bradshaw
Dept. of Chemistry, Ouachita Baptist University

Photodynamic Therapy (PDT) is a novel method of cancer treatment. It uses light, oxygen, and a photosensitizer to target and kill malignant cancer cells. In this research, a novel porphyrin, ZnTPP-6AH, has been synthesized for use as a possible photosensitizer for PDT treatment of A549 lung cancer cells. This novel compound is synthesized by the coupling of ZnTPPC with 6-amino-1-hexanol. The new water-soluble zinc porphyrin was purified using Sephadex LH-20 and G-50 column chromatography. After purification, the porphyrin was characterized using ultraviolet-visible (UV-vis), nuclear magnetic resonance (NMR), and infrared (IR) spectroscopies. The final purity of this compound was then determined using HPLC. Additionally, cyclovoltammetry (CV) and fluorescence spectroscopy were carried out on the ZnTPP-6AH. Finally, cell viability using A549 lung cancer cells with ZnTPP-6AH as the photosensitizer was determined using a Presto Blue assay.

118A. Synthesis of (arylamino)disquaramide compounds: A potential class of anti-leishmaniasis drugs

Kathryn N. Hicklin, Gregory R. Naumiec
Dept. of Chemistry and Biochemsitry, University of Central Arkansas

Neglected tropical diseases are a group of conditions that typically effect impoverished areas due to lack of sanitary resource. Leishmaniasis is a major NTD caused by the Leishmania protozoan, which is transferred to hosts by the bite of a sand fly. Symptoms can range in severity and typically include slow-healing ulcers, and in severe cases enlargement of the spleen and liver. Treatment options are available, such as amphotericin-B, but drug toxicity and resistance are becoming more prevalent issues and new drugs are needed. There is little monetary incentive for pharmaceutical companies to develop new treatment options for this condition. The objective of our research is to synthesize cost-efficient anti-parasitic drugs for use in these endemic areas. Success has been seen with adding aromatic groups to diethyl squarate. There is current works on making a drug library from diethyl squarate by substituting on two amino arms via addition-elimination chemistry: an arylamino group and a diamino group. Future directions include adjusting the sterics and electronics of the benzylamino group through the addition of R-groups. These new drugs will then be tested on Leishmania parasites to assess their effectivity on the extracellular version of the parasite. To date, I have successfully synthesized, purified, and characterized my precursors in 45.73 and 73.57% yield and have used them to start on the syntheses of my target drug libraries.

118B. Optimization of N-heterocyclic carbenes for the synthesis of CO2-reducing electrocatalyst

Gotre Bi Boti, Christ Ivan Traye, Owen Bussell, Katherine Peters, Robert Winzerling, Elisabeth Hicklin, Noah Taylor, Imani Mbong, Dasha Young, Marsha Massey
Dept of Chemistry and Biochemistry, University of Central Arkansas

Natural gas combustion significantly contributes to the rise of CO2 in the atmosphere. This greenhouse gas can be transformed into useful substances like carbon monoxide (CO) by using catalysts. Our research focuses on enhancing the N-heterocyclic carbene (NHC) part of our catalyst, a manganese tricarbonyl bromide catalysts, fac-Mn(NHC-pyridine)(CO)3Br. It's composed of a bidentate NHC-pyridine and four monodentate ligands (3 CO and a Br). By changing the structure of the NHC, we hope to improve the durability and stability of the catalyst. We plan on assessing the properties of the NHC and the resulting catalyst through NMR spectroscopy and cyclic voltammetry.

119A. Harnessing Natural Amino Acids for Eco-Friendly Dye Degradation: A New Approach to Iron(III) Catalysts

Karie E. Sanford, Raja Shekhar Kondrapolu, Taiwo Oluwanifemi A. Fashina, Anindya Ghosh, Ambar B. Rangumagar
Dept. of Chemistry, Philander Smith University

This study explores the development of iron(III) catalysts derived from natural amino acids, marking a shift from traditional synthetic precursors. By utilizing L-valine, L-leucine, and L-phenylalanine, we synthesized three unique catalysts and tested their effectiveness in degrading synthetic dyes in water. Our findings show that the most stable catalyst achieved 98% degradation of indigo carmine dye within 45 minutes, operating via a second-order reaction. This approach offers a greener alternative to conventional methods, contributing to more sustainable water purification processes. Gas chromatography-mass spectrometry (GC-MS) analysis identified potential degradation byproducts such as ethylene glycol and N-benzylbenzamide, highlighting the catalysts' efficacy and environmental benefits.

119B. Effect of Stereochemistry on Antibacterial Activity Against Gram-negative Bacteria

Mia J. Farraday, Joseph C. Hane, Gabriella A. Krisanic, Elaine R. Frawley, Larryn W. Peterson
Dept. of Chemistry, Rhodes College

The high antibacterial resistance of Gram-negative bacteria is a growing concern, but there is a lack of development of novel compounds with broad spectrum activity. The resistance of these Gram-negative bacteria is largely due to a high outer-membrane impermeability and the excretion of antibacterial compounds from the bacteria through efflux. Previous work confirmed that the lack of antibacterial activity of our compounds was due to TolC-mediated efflux. To avoid efflux, a next generation of potential antibacterial compounds have been designed with increased hydrophilicity for better binding in the polar region of the LpxC active site, as well as a hydrophobic tail for increased interactions in the hydrophobic pocket of the enzyme. Several analogues have already been synthesized and tested as potential antibacterial agents. Studies have shown the importance of specificity in these compounds, with stereochemical changes to the side chain drastically changing the antibacterial properties.

120A. Characterizing the Mixture Effects of Perfluorinated Alkane Systems (PFAS) with Microplastics from an All-Atom Molecular Dynamics Simulation

Elise Remerscheid, Jakob Anderson
Dept. of Chemistry, Hendrix College

Perfluoroalkane substances (PFAS) are a class of molecules characterized by strong carbon fluorine bonds, low polarizability, and weak dispersion forces. These properties make PFAS highly useful in industrial applications such as drug delivery, non-stick surfaces (e.g., Teflon), surfactants, textiles, and upholstery. Despite their utility, PFAS has been considered by the US Environmental Protection Agency (EPA) as substances of significant concern due to their bioaccumulation in humans, animals, and environmental sources such as groundwater and soil. In addition to PFAS having adverse effects on biologically relevant systems, it has recently been demonstrated that PFAS will also induce a structural change on microplastics—another increasingly prevalent pollutant. While studies are being conducted for PFAS and the interactions with naturally occurring chemicals, the study of PFAS interactions with microplastics is largely understudied. It has been hypothesized that the PFAS-induced structural change will have significant mixture effects that alter the fate and transport properties, toxicity, and associated health risks for pollutant PFAS's. To investigate these mixture effects, we utilize all-atom Molecular Dynamics (aaMD) simulations to model PFAS and microplastics at varying concentrations. The OPLS force field was used to maintain consistency with other experiments. Simulations of polyethylene (hexane) systems with PFAS at concentrations of 0%, 25%, 50%, 75%, and 100% were systematically performed and analyzed. Our results demonstrate the need for a modified potential and

additional insights into the mixture effects of PFAS and microplastics.

120B. Investigation of Reaction Mechanisms of Carbocation Chemistry

Erin DeWald, Bin Dong, Brooke Rainwater
Dept. of Chemistry, Hendrix College

Carbocations are a valuable source of information. There are links between the unstable intermediates and possible breakthroughs in the development of olefins and a synthetic source of oil. It is believed that the intermediate carbocations formed in oligomerization could be a sustainable source of oil. Using UV-Vis spectroscopy, the reactions of furfuryl alcohol and 4 types of H-ZSM-5 zeolites are able to be monitored and analyzed to determine a possible reaction mechanism. Through visual spectroscopy, the identification and investigation into the intermediates will allow for a better understanding of the mechanisms present in acid catalyzed reactions through zeolites. ZSM-5 has a correlation between zeolite acidity and the formation of polymers including the dimer and trimer of furfuryl alcohol. The acidity of the zeolite, found in the molecular ratio of silicate to aluminum, seems to indicate a relationship with the catalytic activity of the zeolite. The information will be further used in the investigation into single molecule reactions using these zeolites.

121A. Synthesis of 6-Substituted Dopamine Analogues to understand the Substrate Tolerance of L-DOPA Dioxygenase

Ella Petit, Leah Grace Borders, Connor Bronze, Larryn W. Peterson
Dept. of Chemistry, Rhodes College

Catecholamines are a vital organic compound for both humans and plants. In humans, catecholamines are neurotransmitters and other regulatory compounds, while in plants they have an important role in the plant's overall growth. The enzyme L-DOPA dioxygenase has the ability to break down these compounds by catalyzing the cleavage of their catecholic rings. The substrate tolerance is not fully known due to a lack of diverse catechols. We report on the synthesis of 6-substituted dopamine to attain greater understanding of the requirements for substrate selectivity. Synthesis of the 6-substituted analogues has been achieved from the starting compound 3,4-dimethoxyphenylethylamine. The completed compound provides a way to further the investigation of the L-DOPA dioxygenase pathway and the possibility for continued research on bioremediation, as well as the use of the enzyme in the semisynthetic preparation of novel compounds.

121B. Generation of Aza-Crown Ethers Using 2,6-bis-hydrazinopyridine

Peyton Cely, William Constantine, Leven Greene, Dr. Kimberly A. Brien
Dept. of Chemistry, Rhodes College

Hydrazinopyridines have remarkable promise as platforms for the construction of new transition metal ligands. The synthesis of 2,6-bis-hydrazinopyridine (BHP) is presently being used in preparation of chelating ligands that are otherwise more difficult to generate through other means. The generation and isolation of BHP occurred through the reaction of 2,6-difluoropyridine with anhydrous hydrazine to generate the crude product, followed by treatment with NaOH to isolate the BHP. Previous research has implicated BHP as a useful reactant in the preparation of 2,6-bispyrazoylpyridines, but further research has indicated that it may also provide a useful way to generate Nitrogen based azo-ethers (crown ethers) through reaction with 1,2-dibromoethane.

122A. (Neopentylamino)disquaramide-based drug library: assessing the effects of steric hindrance and polarity as anti-leishmanial properties

Molly K. Johnson, Gregory R. Naumiec
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Leishmaniasis, an endemic disease most prevalent in areas of high poverty and high levels of compromised immunity and malnutrition, is a neglected tropical disease caused by various strains of the leishmania parasite. The facile transfer of this protozoan parasite from its vector, the sand fly, to humans leads to over a million infections each year across 98 different countries. Antimonial salts (sodium stibogluconate and meglumine antimoniate) and a variety of repurposed drugs (pentamidine, paromomycin, amphotericin B, fluconazole, ketoconazole, miltefosine, etc) have been used for decades resulting in resistance, as well as undesired side effects, unideal administration, and low efficacy. To effectively treat leishmaniasis, a new drug must be developed that is easily administered, with low cost, and high efficacy against this disease. Current research shows there are several proposed disquarimide-based compounds that have shown potential leishmanicidal activity. This study aims to further understand the chemical and structural characteristics of such disquarimide-based compounds and how these properties lead to antileishmanial behavior. This understanding will guide the development of new compounds with similar functionality, but with significantly lower costs of fabrication and higher efficacy. Through the use combinatorial chemistry methods, we developed an array of structurally diverse (neopentylamino)disquaramide-based compounds with potentially enhanced functionality as our (butylamino)disquaramide lead compound, predominantly employing back-to-back addition-elimination reactions starting from commercially available diethyl squarate and utilizing equipment readily available in our research laboratory (vacuum filtration, rotary evaporation, automated flash chromatography). 1H and 13C NMR spectroscopy and IR spectroscopy was then used to confirm the structure of the synthesized molecules. Through these techniques, we developed synthetic pathways with greater than 95% purity and moderate to high yield (72.44% - 99.54%) for a drug library, consisting of 12 unique members, as a preliminary exploration of the effects of polarity and steric hindrance on antileishmanial behavior. This study is an important step towards the development of new antileishmanial drugs with higher efficacy and lower costs of fabrication.

122B. The Synthesis of (Hexylamino)squaramides for Treatment of Leishmaniasis

Mia Clark, Gregory Naumiec
Dept. of Chemistry, University of Central Arkansas

Neglected Tropical Diseases (NTDs) affect approximately 1.7 billion people per year and those most affected by these diseases are in impoverished tropical areas. Funding for research into cures for NTDs is very limited, therefore, the goal is to find ways to synthesize organic compounds to be used in treatment with a low cost and high yield. We created a common precursor using diethyl squarate and hexylamine via addition-elimination chemistry and used this precursor to create a drug library of squaramides. Thus far, I have created a library of 6 squaramides with yields ranging from 66.1% to 80.2%. The monoamino precursor was purified using a CombiFlash and the squaramides were purified through precipitation and vacuum filtration. These products have been confirmed by both TLC and 1H and 13C NMR spectroscopy.

123A. Quantitative Analysis of the Purity and Composition of Lavender Essential Oils

Leven Greene, Areej Khan, Peyton Cely, William Constantine, Matthew Coulson, Kim Brien
Dept. of Chemistry, Rhodes College

Essential oils are intended to be used topically or in diffusers, but they are often misused as flavor additives. As these oils are not designed for consumption, nor for any potential medicinal

properties, the FDA does not monitor their production. As such, they might contain harmful volatile organic compounds (VOC) that are not suitable for human ingestion. This experiment was conducted to evaluate the purity and composition of essential oils by comparing data obtained from three different brands all listed as pure *lavandula angustifolia* oil. Samples were analyzed using 1H-NMR and GC-MS, and the data was compared between samples, as well as to literature references to prove or disprove the purity of each essential oil sample.

123B. Testing Raw (Influent) Wastewater as a Seed Control for the CBOD Method

Rylee Griffis
Dept. of Chemistry, Southern Arkansas University

Carbonaceous biochemical oxygen demand (CBOD) tests for organic pollution in effluent (treated wastewater) and treated drinking water by looking at how microorganisms use dissolved oxygen when metabolizing organic pollutants. This process can be affected by temperature, pH, the presence of certain organisms, and the types of organic/inorganic compounds in the water. This test also ensures that the organisms in the receiving body of water are not deprived of oxygen. Synthetic seeds provide microorganisms capable of oxidizing the oxygen in the samples; these synthetic seeds can be stored for an extended period at relatively high/low temperatures and provide a seed without using raw (influent) wastewater. However, with rapidly increasing prices, the variability of the synthetic seed from capsule to capsule, and the inability to match the matrix of the effluent wastewater, synthetic seeds introduce errors in glucose-glutamic acid (GGA) recovery. This is used to determine the accuracy of the CBOD test and has to be included in every batch of samples run. Influent seed is more cost-effective, matches the matrix of the effluent wastewater, and varies, along with the samples, with changes in the environment (pH, temperature, weather, etc.). This experiment aimed to determine if raw (influent) wastewater acted as a better seed source than synthetic seed by comparing the accuracy, provided by the comparison of the GGA recoveries.

124A. The Effects of Dual Anti-Cytokine Tk-850 against RILF in Mice

Blake Wright, Brandon Frett, Marjan Boerma, Vijayalakshmi Sridharan
Dept. of Cancer, Tennessee State University

Patients who undergo radiotherapy in the thoracic region of the body are at increased risk of contracting radiation induced lung fibrosis (RILF). The condition causes the lungs to become dysfunctional and ineffective in proper respiration. This is caused in part by the cytokines tumor necrosis factor alpha (TNF-Î±) & transforming growth factor beta (TGF-Î²) which, respectively, cause inflammation and excessive collagen production in the lungs. Hypothetically, the reduction of these cytokines could reduce the symptoms of RILF. An anti-dual cytokine drug was synthesized to limit these cytokines with the ideal to reduce RILF. This drug was tested in a mouse model of RILF. In past studies, Tk-850 was injected into mice three times a week for four weeks after irradiation of the thorax. The time frame for these injections were weeks 1-4, weeks 4-7, and weeks 12-15 after irradiation. This study will be analyzing the effects of Tk-850 when administered through weeks 8-11. The results show that the effects of Tk-850 on lung histology was inconclusive. Nonetheless, Tk-850 reduced the protein levels of the macrophage marker CD68 in the irradiated lung. Next, we will measure the mRNA levels of TNF-Î± & TGF-Î². In conclusion, while TK-850 administered through weeks 8-11 after radiation may have some effects in the lung, further experiments are needed to determine the optimal dosage and administration time frame for the drug. Also, additional testing might be needed to see if a different drug needs to be created.

124B. Activity-Based Protein Profiling on Nucleophilic Amino Acid Residues with Pyrocarbonates

Alex Van Horn, Shang Jia, Paul Adams
Dept. of Chemistry and Biochemistry, University of Arkansas, Fayetteville

Genome sequencing initiatives, like the Human Genome Project, have provided comprehensive lists of anticipated proteins in both eukaryotic and prokaryotic organisms. Proteomics builds on genomics by assigning functions to these proteins, but the complexity of the proteome presents significant challenges. Analyzing every amino acid in every protein is inefficient, so targeting key amino acids that play significant roles in protein function is crucial. Activity-Based Protein Profiling (ABPP) has emerged as a powerful chemical proteomic approach to directly investigate enzyme functions in biological systems. This project focuses on developing a histidine-specific probe for ABPP, given histidine's crucial roles in enzymatic catalysis, metal ion coordination, and protein-protein interactions. The project proceeds through three stages: (1) testing histidine reactivity with a pyrocarbonate probe on individual amino acids, followed by attaching an azide tag via copper-catalyzed alkyne-azide cycloaddition (CuAAC), (2) applying the probe to a model protein and analyzing results via mass spectroscopy, and (3) testing the probe on a lysed cell proteome using traditional ABPP protocols, with analysis also by mass spectroscopy. This work aims to enhance our understanding of the proteome by selectively probing histidine reactivity in complex biological systems.

125A. Correlating pH and buffer effects with the apparent antimicrobial efficacy of nanogels on *E. coli*

Alexander Rahal, Susanne Striegler
Dept. of Chemistry and Biochemistry, University of Arkansas, Fayetteville

The surge in antibiotics after the discovery of penicillin in the 20th century sparked the beginning of what is often referred to as the “Golden Era of Antibiotics”. Since then however, the frequency and misuse of antibiotics and antimicrobials has led to a rapid growth in antimicrobial resistance in many bacteria, which now poses a global threat to human health. This is shown in the emergence of superbugs, who’s development of strong resistances to many current antibiotics have made the targeting of these pathogens difficult. As opposed to gram-positive bacteria, the presence of antimicrobial resistance is even more pronounced in gram-negative bacteria, due to the presence of an outer covering of peptidoglycan and lipopolysaccharides, which provides a layer of protection from antimicrobial agents. The presence of phosphate groups in the membrane leads to a large negative charge in the outer layer, which then becomes stabilized from the insertion of metal cations, such as Mg(II) or Ca(II), into the structure. A new approach to develop bactericidal agents to circumvent this stabilization will be discussed.

125B. Analysis of Collagenase

Pixie Hickerson, Osamu Matsushita
Chemistry, University of Arkansas, Fayetteville

Collagens are key molecules for multicellularity, and major constituents of the extracellular matrix (ECM) in animals. Unicellular life has been present since at least 3.5 billion years ago. This bacteria has adapted to break down and consume the collagen present in multicell organisms. The bacteria has enzymes with multiple domains which achieve this goal. The crystal structure of this catalytic module is being derived from *Hathewaya histolytica* class II collagenase (ColH). The way the bacteria moves and functions is being derived from the crystal structure.

126A. Tryptophan Fluorescence Quenching in Human Serum Albumin by Quinclorac

Le Nguyen, Rahul Yadav
Dept. of Biological Sciences, University of Arkansas at Fort Smith

Human serum albumin (HSA) is the most abundant plasma protein. It binds and acts as a transporter/reservoir of endogenous ligands such as fatty acids, heme, bilirubin, prostaglandins, metal ions, etc. HSA also binds to various exogenous ligands, including pharmacological drugs, affecting their pharmacokinetics/ADME. HSA is a 66 kDa monomeric, multidomain (domains I, II, and III) protein and characterized by two primary ligand binding sites, Sudlow-I and -II. The Sudlow I binding site contains the only tryptophan (Trp214) present in the HSA, which can be used to probe ligand binding in the Sudlow I binding site. Here, we have used tryptophan fluorescence spectroscopy to characterize the interaction of an organochlorine herbicide quinclorac (QNC) with HSA. The binding of QNC with HSA is characterized by concentration-dependent quenching of intrinsic tryptophan fluorescence in HSA, which indicates the binding of ligand to the HSA's Sudlow-I binding site. Insights into the quenching mechanism were investigated by determining the extent of quenching at three different temperatures. A decrease in the slope of the Stern-Volmer plot at higher temperatures suggests static quenching of fluorophore upon ligand binding and moderate affinity (Kd < 100 Î¼M) of QNC for HSA. Next, we plan to confirm the quenching mechanism in the HSA-QNC complex by fluorescence lifetime measurements. These results show the utility of intrinsic tryptophan fluorescence in characterizing protein-ligand interaction.

126B. Discovery of Novel DNA-PKcs Inhibitors for Transplant Recipients

Jackson Frederick, Brendan Frett, Daniel Armstrong
Dept. of Biology, University of the Ozarks

DNA-Protein Kinase catalytic subunit (DNA-PKcs) is an enzyme that repairs double stranded breaks (DSB) in DNA via non-homologous end joining. Overexpression of this enzyme is observed in many cancers such as melanoma, carcinoma, and multiple myeloma. The role of DNA-PKcs in cancer has prompted researchers to investigate inhibition of this enzyme as a cancer treatment. Many potent inhibitors such as NU7441 failed clinal trials due to poor pharmacokinetic profiles. DNA-PKcs has a wide range of functions and inhibition of this enzyme has the potential to improve modern medicine beyond just treating cancer. One such function is the role of DNA-PKcs in immunity. V(D)J is a type of recombination which is vital for diversification of antibodies and T cell receptors, and this process is reliant on DNA-PKcs activity. Upon investigating DNA-PKcs in immunity, researchers found that DNA-PKcs inhibition disrupts the production of IL2, a cytokine that regulates the production of B and T cells. These findings later prompted studies to investigate the effects of DNA-PKcs inhibition on preventing allogenic skin graft rejection in organ transplant patients. In this project, we report the discovery of second-generation DNA-PKcs inhibitors to prevent graft rejection in organ transplant patients. Using NU7441 as a scaffold, we have made novel analogues of these inhibitors with improved pharmacokinetic profiles/properties and show high selectivity for DNA-PKcs.

127A. Eliminating Resistant Bacteria with Photothermal and Chemical Therapy

Armin Mortazi, Noureen Siraj, Ahmed Hikal, Ashraf Khan
Chemistry, University of Arkansas at Little Rock

The surging issue of bacterial resistance to conventional antibiotics poses a significant threat to public health worldwide. Traditional treatments are

increasingly ineffective, leading to a rise in persistent infections and deaths. This study focuses on addressing the urgent need for innovative treatments by exploring a novel approach that combines two distinct antibacterial mechanisms in a single therapeutic compound. This research involved the synthesis of a novel compound integrating a commercial antibiotic with a near-infrared dye, through ionic synthesis. In this study, [IR-780][NOR] was synthesized from their parent compounds: Na-Norfloxacin and IR780-Iodide. The synthesized combination drug is tested in a 96-well plate against Na-Norfloxacin as well as IR780-Iodide. For effective drug uptake, each drug was turned into nanoparticles using a sonicator. Different concentrations were achieved through serial dilution. This study tested the drugs in both dark and light conditions. Each well in the light trials was lasered for 5 minutes in a dark room to mimic in vivo conditions. The model bacteria that was used was NOR-resistant *Salmonella entercia* 75. The effectiveness of the compound was measured through bacterial inhibition concentration. Preliminary findings indicate a significant enhancement in the eradication of our resistant bacteria. The compound's dual mechanism drug, both in light and dark studies has been very successful compared to its traditional, single-mechanism counterpart.

127B. Using Tamoxifen-Based Nanomaterial Drugs to Enhance Chemo Drug Efficacy

Muhammad Rayaan, Noureen Siraj
Biology, University of Arkansas at Little Rock

In this study, a detailed investigation of nanodrugs derived by combining chemotherapy (chemo) and photothermal therapy (PTT) to enhance chemo drug efficacy is presented. Tamoxifen and its metabolite; N-desmethyltamoxifen are the selected chemo drugs that were combined separately with a PTT agent, NaIR820, via a metathesis approach to develop two different ionic material (IM)-based chemo-PTT drugs which does not exhibit Förster resonance energy transfer phenomena. Ionic nanomaterials (INMs) were synthesized using reprecipitation method, and these carrier-free nanoparticles were characterized in detail. Photophysical properties of the free parent compound, both IMs and their INMs revealed significant alterations in absorption and fluorescence emission spectra of IR820 in different forms. Photophysical results demonstrated that INMs exhibited promising characteristics that are beneficial for light mediated therapy. Photothermal conversion efficiency and reactive oxygen quantum yield of INMs and IMs also improved significantly in comparison to the parent IR820 compound. In vitro cell viability studies demonstrated better dark and light cytotoxicity of INMs as compared to treatments that involved either the mixture of the soluble drugs and chemo or PTT drugs independently.

128A. Synthesis of SnO2 3D hollow nanobeads and their cytotoxicity assessment on human lung cells

Fidaus Razak, Alexei Basnakian, Olena Levurdiak, Qinglong Jiang, Dallas Fuller, Shenyang Li, Dept. of Chemistry and Physics, University of Arkansas at Pine Bluff

SnO2 3D hollow nanobeads can be used for drug delivery due to the hollow structure, in which medicines can be released slowly with better efficacy and lower adverse toxic effects than unpacked drugs. Before developing this new drug delivery approach, the absence of toxicity in the nanobeads must be established. The goal of this study was to synthesize SnO2 3D hollow nanobeads and test their toxicity on cultured human lung epithelial A549 cells, which are the most commonly used model for the toxicity assessment of nanomaterials, drugs, tobacco products, and environmental agents. The SnO2 3D hollow nanobeads 100 nm in diameter were prepared by the template method, labeled with Cy5.5 fluorophore for intracellular localization, and exposed at varying concentrations with the A549 cells for 24 hours. The toxicity was measured by the TUNEL assay in two modifications, the classical TUNEL and denaturing TUNEL (dTUNEL), recently developed by our team.

128B. Paramagnetic Cobalt-Cobalt Dimers Leading to Highly Magnetic Oligomers and Molecular Magnets

Ian T. Blair, Patrick J. Desrochers
Dept. of Chemistry and Biochemistry, University of Central Arkansas

Cobalt(II) is an ion with magnetism useful in spectroscopic probes for metalloproteins. This same quality can be exploited as the core of molecular magnets. A new paramagnetic cobalt-cobalt dimer will be described in which two cobalt(II) centers are held together by three bridging 3,5-dimethylpyrazolide ions. These dimers are synthesized by the direct reaction of potassium 3,5-dimethylpyrazolide and cobalt(II) salts in dry DMF and isolated as stable K-salts, deep blue K[XCo-dimer-CoX] solids. This general synthetic process was replicated with three different halides/pseudohalides, using CoX2 (X= Cl, Br, SCN). These new dimers were characterized by UV-visible electronic and infrared spectroscopies. The addition of excess (10:1) potassium 3,5-dimethylpyrazolide converts the dimers to deep purple oligomers, thermally and moisture stable deep purple solids. Spectroscopic (UV-vis and IR) and elemental analyses indicate this oligomer is devoid of KX (from the dimer), and consists exclusively of Co-pyrazolide units, with cobalt(II) adopting typical pseudo-tetrahedral geometries. Room temperature magnetic measurements of this oligomer indicate a highly paramagnetic material. Ongoing work is investigating development of these materials as molecular magnets.

Physics

201. Ultrasonic Characterization of the Human Scalp Using Backscatter Parameters

Catherine N. Prabish, Blake C. Lawler, Thomas H. Conroy, Cecille Labuda, Brent K. Hoffmeister
Dept. of Physics, Rhodes College

Transcranial ultrasound has found many uses in the medical field. While there have been many research studies on the ultrasonic properties of the skull and brain, there are relatively few publications on the scalp. The goal of this study was to ultrasonically characterize the transmural structure of the scalp. Sixty-four formalin fixed specimens were prepared from four human donors and scanned in a water tank with a 25 MHz transducer to create parametric images of apparent integrated backscatter (AIB), frequency intercept of apparent backscatter (FIAB), and frequency slope of apparent backscatter (FSAB). Images revealed three distinct layers: a dermis/epidermis layer, a subcutaneous layer and a connective tissue layer. Measured values for the dermis/epidermis layer were AIB = -44.40 ± 3.26 dB, FIAB = -46.54 ± 6.13 dB, and FSAB = 0.1735 ± 0.3103 dB/MHz. Measured values for the subcutaneous layer were AIB = -45.35 ± 2.94 dB, FIAB = -49.88 ± 5.77 dB, and FSAB = 0.3671 ± 0.2843 dB/MHz. All parameters were significantly different between the two layers. Results from the connective tissue layer were not analyzed due to tissue damage concerns.

202. Developing a Single Photon Detection System Using SPDC in BBO

Andrew Files, Vinayaak Balasubramaniam, Apoorva Bisht, Hiro Nakamura
Physics, University of Arkansas, Fayetteville

Detecting single photons is challenging, but possible. I have developed a system that generates a two-dimensional plot of the pattern of photons emitted from a point source. The function of the photon-imaging system is being tested using spontaneous parametric down conversion (SPDC) from a Barium Borate crystal (BBO). Using a 405nm laser to pump SPDC, I focused on the 810nm converted photons. The spatial resolution of the system has been demonstrated to be around 10 microns. Once SPDC has been confirmed using BBO, down converted photons from other highly nonlinear crystals will be tested using this apparatus.

203. Low loss InP/GaP Waveguides for Sapphire-based Photonic Integrated Circuits Platform

Joel Ruzindana, Wisdom Ariagbofo, Shrawan Roy, Qinglong Jiang, Manoj Shah, Mansour Mortazavi
Dept. of Chemistry and Physics, University of Arkansas at Pine Bluff

Photonic Integrated Circuits (PICs) have the potential to deliver a chip with reduced size-weight-power-and-cost. PICs have been demonstrated in various material systems such as III-V, Si, Si3N4 LiNbO3 with varying levels of functionality. The thermal expansion mismatch between the epitaxial film and substrate is a factor responsible for large numbers of defects and eventually, device failure. Matching the linear coefficient of thermal expansion of sapphire to that of InP and GaP shows sapphire is a favorable substrate for the growth of III-V materials. Thus, a sapphire-based platform has the potential for use in large-scale integration platforms just like silicon-based platforms. We studied an InP/GaP-on-Sapphire waveguide for a Sapphire-based PIC platform by Finite-Element Method (FEM) using Ansys software. The materials InP, GaP, and Sapphire were used for core, buffer, and substrate layers respectively to design rib and strip waveguides. Using FEM, we numerically investigated multi-mode, single-mode, and cut-off conditions and single-mode propagation loss in the InP/GaP-on-sapphire straight waveguides over a broad optical wavelength (900nm to 2500 nm). We presented the investigated operation conditions of rib and strip waveguides. The higher index contrast between the core and substrate layer allowed us to design compact, low-loss waveguides in the mid-infrared regime. The presented low-loss, InP/GaP-

on-sapphire PIC platform would enable a range of applications in defense systems, and civilian applications like machine learning, fiber optic communication, RF photonics, space exploration, and nuclear applications. Keywords: Group III-V materials, optical waveguides, photonic integrated chips, Finite-Element Method.

204. Optical properties of Ultrathin Silver Iodide

Leonardo Landivar Scott, Leonardo Landivar, Hiro Nakamura, Christopher Klenke, Sudeep Puri, Rodrigo Rodriguez
Dept. of Physics, University of Arkansas, Fayetteville

Silver iodide (AgI) is a non-centrosymmetric semiconductor with promising nonlinear optical properties. We grow AgI crystals using physical vapor deposition (PVD) and characterize their morphology using X-ray diffraction (XRD) and atomic force microscopy (AFM). Our study focuses on the evolution of second harmonic generation (SHG) and two-photon absorption photoluminescence (2PPL) as the crystals approach the ultrathin limit. We aim to gain insight into the relationship between crystal thickness and nonlinear optical efficiency at the nanoscale by analyzing how these phenomena change as the crystal approaches the bidimensional limit. These measurements will help interpret the behavior of halides in ultrathin regimes, offering potential for advancements in photonic and optoelectronic applications.

205. Detection of micro-algae cells using automated deep learning techniques

Jack Harper, Yong Wang, Hemanta Pradhan
Dept. of Physics, Rhodes College

There has been a recent growth in the popularity of object detection using deep learning algorithms in a broad range of fields. Models are trained using convolutional neural networks (CNNs) to classify objects in images and videos, and they can even be trained to detect single cells. Detecting and tracking single-celled organisms has become important as bacteria grow resistance to antibiotics. Putting single-celled organisms in different conditions and tracking the differences in shape and motion could give insight on methods of fighting bacteria without antibiotics. Current research has revealed that silver ions and nanoparticles may slow the growth of single-celled organisms. To give more insight into this phenomena, Mask R-CNN and YOLOv8 models were trained to detect micro-algae cells. The accuracy and loss functions were compared, and both models can adequately detect micro-algae cells in videos, although Mask R-CNN seems to detect more cells. The models will be used to track algae that are exposed to silver ions and nanoparticles. This work is supported by NSF-REU Award #2244130.

206. Studying Nanoscale Vibrations Using Lasers

Michael Marking, Sneha Patel, Hiro Nakamura
Dept. of Physics, Middle Tennessee State University, Institute for Nanoscience and Engineering, University of Arkansas, Fayetteville

Two-dimensional (2D) transition metal dichalcogenides (TMDs) such as MoS2 display unique lattice vibrations at ultralow frequencies. An ultralow frequency Raman system was aligned and used to measure shear and breathing interlayer lattice vibrations of 2D atomic layer thick MoS2. Two different polymorphs of bilayer MoS2 (2H & 3R) were grown in a PVD furnace on SiO2 wafers, in which 2H structures have inversion symmetry whereas 3R structures do not. 2H structures displayed more intense Raman intensity and greater Raman shifts for shear-modes than those for 3R structures. This work was supported by NSF REU Program #2244130.

207. Progress in Autonomous Vehicle Engineering

Eric Nguyen, Jeremy Abbott, Ashton Johns, Lin Zhang
Dept. of Physics, Astronomy, and Engineering, University of Central Arkansas

Engineering Physics students in Senior Design 1 and 2 at the University of Central Arkansas (UCA) have been engineering autonomous vehicles for five years. Our team, UCA Jetson, tasked us to design a better self-driving platform. This involved a new mock of the RC platform, such as an off-the-shelf RC car and microprocessor. Due to the expensive nature of the hardware, we improved the mechanical design by creating a robot base and crash cage brace on computer-aided design (CAD) to protect the hardware from a given environment. We have adjusted from a Raspberry Pi to an NVIDIA Jetson Orin Nano, with AI capabilities for improved computation. A new inclusion of computer vision includes the depth camera and lidar to improve the self-driving robot's performance. Additionally, this necessitated upgrades to the battery, motor, servo, and electronic speed controller.

208. The Scintillation of Pulsars

Katelyn Bryant, Dr. Julia Dusk Kennefick
Physics, University of Arkansas, Fayetteville

I will be presenting research conducted over this summer at the Pulsar Search Collaboratory camp on pulsar scintillation and further research that I have continued in an approach to get a better model of the interstellar medium. Scintillation is a common phenomenon present in astronomy due to electromagnetic radiation being scattered by particles such as electrons or ionized particles. One example of such is the twinkling of stars due to the light being refracted by the ionized particles in the earth's ionosphere. Pulsars are the remnants of semi high in mass stars that have already undergone a supernova explosion and is left with the shrunken, highly dense, dead core, or a neutron star. This neutron star spins extremely fast and therefore produces electromagnetic radiation from north and south poles that we can detect as radio signals. We receive these radio signals by using radio telescopes at observatories like the one I went to at Green Bank Observatory in West Virginia at the Pulsar Search Collaboratory (PSC) summer camp. The PSC is a collaborative effort between West Virginia University, NANOGrav, and the Green Bank Observatory. They have been using the Green Bank Telescope to do pulsar timing arrays in order to detect gravitational waves, millisecond pulsars, and other pulsar events such as scintillation or fast radio bursts. Pulsar scintillation is caused primarily by two different types of interference, refractive and diffractive, which type of interference is distinguished by the timescale of the signal. At this camp, I studied pulsar J2313+4253 to detect scintillation using the 20m radio telescope at the observatory. I put the observation obtained for the pulsar from the software system Skynet into our shared NANOGrav JupyterHub notebook to get a visual representation of the dynamic spectrum of the interstellar medium and the free electrons between us and the pulsar that caused the scintillation to occur. We were able to get a scintillation bandwidth of frequencies that we could use to find the scattering screen distance. I will be showing more examples that I continued on with pulsar J0332+5434 and an interesting, unplanned, telescope observation that occurred where four observations happened within a day and gave a different dynamic spectrum for each, showing just how dynamic the interstellar medium is.

209. A theoretical model for estimating errors in ultrasonic backscatter measurements of bone

Keith T. Hoffmeister, Kate E. Hazelwood, Layla A. Lammers, Hugh E. Ferguson, Brent K. Hoffmeister
Dept. of Physics, Rhodes College

Ultrasonic backscatter measurements are being developed to detect changes in the porosity of cancellous bone caused by osteoporosis. One source of error in measuring the backscattered power may be power loss effects caused by the cortical bone layer that overlies the cancellous bone tissue. The errors range from approximately from 5 to 15 dB depending on the angle of incidence of the

ultrasonic wave on the bone surface. These errors are much larger than changes caused by osteoporosis (approximately 5 dB). A theoretical model finds that the observed errors in backscatter measurements of cancellous bone are consistent with reflection and attenuation losses caused by the cortical layer.

210. Advancements in Additive Manufacturing and Industry 4.0: Enhancing Biomedical Applications through Real-Time Monitoring, Agent-Based Systems, and Digital Twins

Daniel Riggs, Hayder Zghair
Engineering & Physics, Southern Arkansas University

Additive manufacturing (AM) and Industry 4.0 (i4.0) technologies have significantly impacted various fields, including biomedical applications. Integrating advanced i4.0 technologies into AM processes can significantly enhance efficiency, reduce waste, optimize operations, and provide robust monitoring and control mechanisms, thus paving the way for smarter, more responsive production systems. This research review synthesizes findings from research papers that have been recently published to highlight the advancements, methodologies, and applications in AM, particularly focusing on integrating IoT, agent-based systems, digital twins, and other intelligent production frameworks. Kakade, Mulay, and Patil (2022) discuss the development of an IoT-based real-time online monitoring system for openware Fused Deposition Modeling (FDM) 3D printers. This system addresses common issues such as material jamming and flow runout, using Raspberry Pi, rotary encoders, and load cells to remotely monitor and control the printing process. The proposed system enhances the reliability and efficiency of FDM printers, which are extensively used in biomedical applications for producing prosthetics and anatomical models. Giunta et al. (2023) introduce a Living Lab platform for evaluating agent-based manufacturing strategies in AM systems. This platform supports empirical validation of strategies to manage distributed manufacturing systems, crucial for producing customized biomedical devices. The study demonstrates the platform's effectiveness in coordinating manufacturing tasks and highlights the need for further optimization to improve system behavior and job selection protocols. The article by Hossain et al. (2022) presents a CNN-based warping detection system for Fused Filament Fabrication (FFF) 3D printing. Ensuring the quality of biomedical devices is critical, and this system allows for real-time detection of defects, ensuring that printed devices meet the required standards. This technology is particularly relevant for applications where precision and reliability are paramount, such as in the production of medical implants. Mulla, Rajamanickam, and Gujar (2019) explore the optimization of energy consumption in the FDM process. Reducing energy consumption is essential for sustainable manufacturing practices, especially in the biomedical field, where the production of devices must be both efficient and environmentally friendly. The study’s findings contribute to developing more sustainable production methods for biomedical applications. Zhang, Chu, and Wei (2020) explore the digital twin concept for additive manufacturing systems. Digital twins provide a virtual replica of the manufacturing process, allowing for precise control and monitoring. This technology is particularly beneficial in the biomedical sector for producing customized implants and devices with high accuracy and quality. These articles collectively highlight the importance of advanced monitoring, control, and optimization techniques in the AM of biomedical devices, aiming to improve production processes' quality, reliability, and efficiency. In conclusion, integrating advanced i4.0 technologies into AM processes has significantly enhanced biomedical device production's efficiency, reliability, and quality. Real-time monitoring, agent-based strategies, defect detection, energy optimization, and digital twins are pivotal in advancing the field. Future research should continue to refine these technologies and explore new applications to fully realize their potential in the biomedical sector.

211. Inkjet-Printed MOF-Graphene Nanocomposite for Organic Solar Cells: Improving Electrical Conductivity through Solution-Processable 2D Materials

Vu Pham, Haque Ariful, Halim Md Abdul
Ingram School of Engineering, Texas State University

This research focuses on addressing the limitations of traditional high-cost, high-temperature semiconductor thin film deposition techniques by developing a solution-processable inkjet printing method for organic solar cells (OSCs). Specifically, using exfoliated two-dimensional (2D) metal-organic frameworks (MOFs) combined with graphene nanocomposites to create a cost-effective and efficient photoactive layer. Tetracyanonickelate (TCN) based MOFs, which exhibit intrinsic porosity and alterable optoelectronic properties, are exfoliated using liquid phase exfoliation (LPE) to form conductivity ultrathin nanosheets. The conductivity of nanosheets can be improved by adding commercially available carbon-based materials such as graphene or reduced graphene oxide (rGO), thus forming a nanocomposite. The nanocomposite material will be studied using techniques like X-ray Diffractometry, Raman spectroscopy, and UV-Vis Spectrophotometry; their electrical conductivity and electronic band gap will be measured by using a four-point probe and UV-Vis Spectrophotometry. This approach offers a scalable, flexible, and low-cost deposition method for organic solar cells (OSCs), with the potential for improved performance and mass customization through inkjet printing. The study aims to overcome current challenges in improving conductivity while leveraging the processability and flexibility of organic solar cells.

212. Assessing Novel Uses of Controlled Underfitting for Improved Prediction Accuracy of Bone Density Using Convolutional Neural Networks and Time-Frequency Analysis

Hugh E. Ferguson, Carl D. Herickhoff, Ann M. Viano, Brent K. Hoffmeister
Dept. of Physics, Rhodes College

Early detection of osteoporosis is crucial for implementing preventive measures. This study investigates the effectiveness of undertraining convolutional neural networks (CNNs) in analyzing time-frequency representations of ultrasonic backscatter signals from bone to predict bone density. CNNs were used to analyze time-frequency representations of ultrasonic signals from 55 bone samples. The CNNs were trained to varying degrees by adjusting hyperparameters. Interestingly, under-trained CNNs achieved better overall results in terms of root mean square error (RMSE), slope, and correlation coefficient when predicting bone density. These findings suggest that mild underfitting may lead to improved accuracy in bone density prediction using this approach.

213. Investigation and Characterization of a Complex AlGaN/GaN HEMT Structure: Pioneering Source, Drain, and Gate Integration for Optimized Electrical Performance

Mahfuz Ahmed Azmain, Ariful Haque
Electrical Engineering, Texas State University

In this study, we present the novel integration of source, drain, and gate contacts on a complex Metal Organic Chemical Vapor Deposition (MOCVD) - grown AlGaN/GaN high electron mobility transistor (HEMT) structure, a venture yet unexplored in semiconductor device fabrication, as per the author's knowledge. The HEMT configuration is grown by MOCVD in situ with successive layers of varying Al composition, aimed at optimizing electron mobility, thermal stability, and operational efficiency through tailored bandgap engineering and strain management. The device structure begins with a Si (111) substrate, topped with sequentially grown in situ AlN, GaN, and dual AlGaN layers, each refining the electron gas channel and

enhancing the surface states. Anticipating the experimental results, we aim to measure the drain-source current (Ids) as a function of gate-source voltage (Vgs), exploring our experiment's electrical characteristics and potential superior performance metrics. The ultimate goal is to demonstrate this patterning approach's feasibility and potential advantages in terms of device functionality and performance, particularly in high-frequency and high-power applications. Our motivation stems from the gap in existing research regarding the integration of gate contacts in our well developed and optimized AlGaN/GaN HEMT structure. By detailing the fabrication process and expected outcomes, this presentation will not only shed light on the innovative aspects of our design but also serve as a foundational study for future research in advanced semiconductor technologies.

214. Assessing the impact of non-normal angle of incidence on backscatter parameters for ultrasonic bone assessment

Layla Lammers, Brent Hoffmeister, Ann Viano, Hugh Ferguson, Kate Hazelwood, Emily Bingham, Keith Hoffmeister
Dept. of Physics, Rhodes College

Ultrasonic backscatter techniques are being developed to detect changes in bone caused by osteoporosis. This study investigates the effect of non-normal angle of incidence as a source of error for three backscatter parameters that have been identified as potentially useful for bone assessment: apparent integrated backscatter (AIB), frequency slope of apparent backscatter (FSAB) and frequency intercept of apparent backscatter (FIAB). Specimens for the study were prepared from an open-cell rigid polymer foam that simulates cancellous bone. A thin (~3 mm) epoxy layer was added to one surface of the foam to simulate the bone cortex. Ultrasonic measurements were performed in a water tank with a 3.5 MHz broadband transducer. The transducer was mechanically scanned in a horizontal plane over the specimen with and without the cortical layer as the incident surface. Scans were performed for angles of incidence that ranged from 0 to 30 degrees relative to the normal. The cortical surface caused large errors in AIB and FSAB that increased as angle of incidence was increased. Errors in FIAB were much smaller (< 25%) in comparison.

215. Methodological Advancements in Light Sheet Microscopy for Enhanced Cellular Imaging

Parker Foley, Bin Dong, J. Ethan Batey
Physics, University of Arkansas, Fayetteville

Since its creation, Light Sheet Fluorescence Microscopy (LSFM) has been used to image the dynamics of cellular and subcellular processes. It has held a high value in the world of microscopy due to its minimal photodamage on the specimen and its ability to image rapidly compared to traditional fluorescence microscopy methods. However, traditional LSFM has faced challenges in achieving high spatial resolution across all dimensions (specifically the z-axis) due to the primary use of horizontal light sheet illumination. To address this limitation, our lab is developing an advanced LSFM method that uses a vertically oriented light sheet, allowing for better resolution along the z-axis while keeping the advantage of minimal photodamage. We are also introducing an Electronically Tunable Lens (ETL) into the system for dynamic focus control. This will reduce the need for mechanical adjustments and increase the imaging speed. This method will also require the development and use of custom software to control electronics such as the ETL and acquire data seamlessly. This software would be capable of rapid autofocus, allowing high precision across different depths without diminishing temporal resolution. This presentation will focus on the methodology behind our improved LSFM technique. Specifically, I will discuss the final steps of fine-tuning our physical setup and how we will begin creating the software for these physical components to use the microscope most effectively. It will also mention potential applications of this technique for live-cell imaging which can be essential to many other research fields that require the use of cellular and subcellular imaging with minimal disturbance to the specimen.

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2025 Upcoming Events
May (Dates TBA)

INBRE-Sponsored Healthcare Innovation Sprint Bootcamp

A four-day educational program is held on the UCA campus, during which students learn the fundamentals of entrepreneurship and formulate new health science ventures.

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2025 Upcoming Events
May 28

Workshop on training opportunities leading to careers in cancer research

Participants will learn about recent advances in cancer diagnosis and treatment through interactions with clinicians and, scientists, and their trainees

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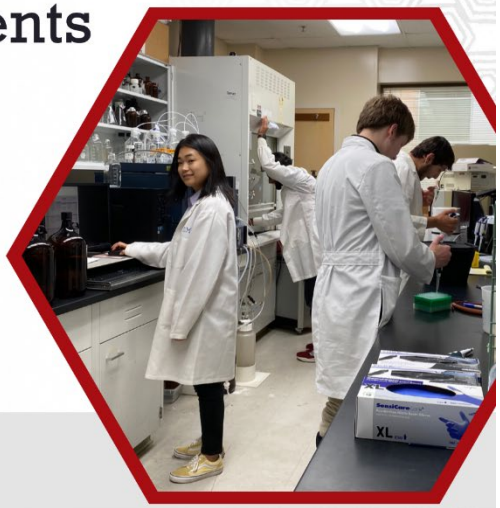
2025 Upcoming Events
May 27-July 25

INBRE Undergraduate Summer Research Fellowship Program

Cancer Fellowships are also available

Intensive 9-week research program.
Competitive stipend included.
Applications are now being accepted.



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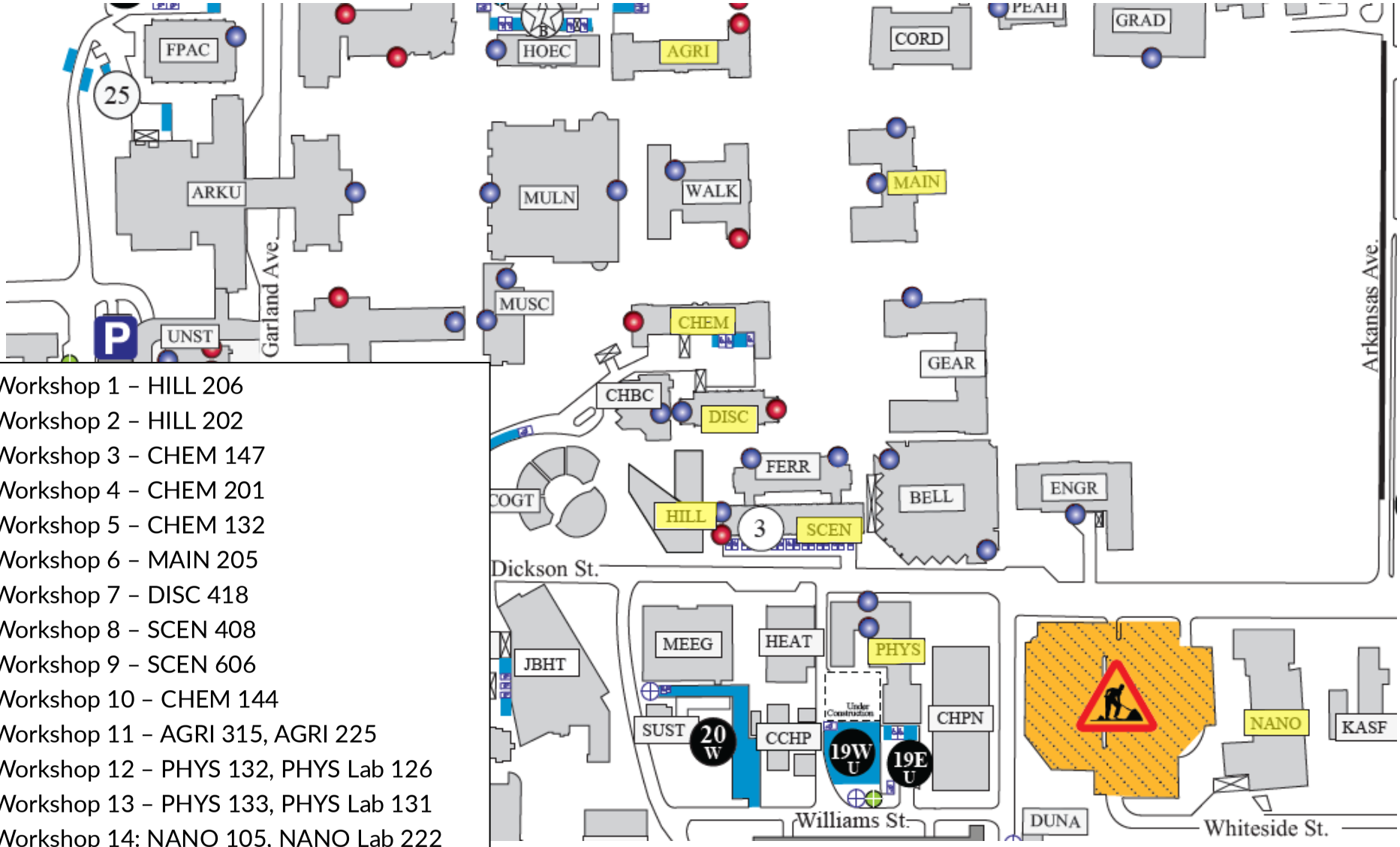
How many grant and funding opportunities have you passed on because you didn't have access to special equipment and expertise?

INBRE Workshops: 10:30 – 11:30 a.m.



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