Arkansas INBRE Research Conference

2023

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November 3-4

Arkansas INBRE Research Conference

Arkansas IDeA Network of Biomedical Research Excellence

Conference Schedule

Friday, November 3rd, 2023

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: “Black Spot, Black Death, Black Pearl: Tales of Bacterial Pathogens” – Fayetteville Town Center **Kim Orth**, Ph.D., University of Texas Southwestern Medical Center

Saturday, November 4th, 2022

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.

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

INBRE Steering Committee

Lawrence Cornett, Ph.D., UAMS, PI & Chair
Jerry Ware, Ph.D., UAMS, PC & DRP Program Director
Alan Tackett, Ph.D., UAMS, Biotechnology Core Director
Feng Wang, Ph.D., UAF, Outreach Core Director
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Liz Pierce, Ph.D., UALR, Bioinformatics Co-Director & PUI Representatives
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Nathan Reyna, Ph.D., Ouachita Baptist University
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Stephen Addison, Ph.D., University of Central Arkansas
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Jason Ortega, Ph.D., UAFS
Sarah Gordon, Ph.D., Arkansas Tech University
Frank Knight, Ph.D., University of the Ozarks
Lance Gibson, Ph.D., Harding University
Samar Swaid, Ph.D., Philander Smith College
Mi-Seon Seong, Ph.D., Central Baptist College

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

Participating Institutions

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

Featured Speaker

Friday, 7:15 p.m., Fayetteville Town Center
Chair: Ines Pinto, Ph.D. (Dept. of Biological Sciences, UAF)

Black Spot, Black Death, Black Pearl: Tales of Bacterial Pathogens

Kim Orth, Ph.D.

Professor, Department of Molecular Biology

Investigator, Howard Hughes Medical Institute

University of Texas Southwestern Medical Center

The Orth lab is interested in deciphering molecular mechanisms used for signaling by the host and pathogen. We are interested in elucidating the activity of virulence factors from pathogenic bacteria so that we can gain novel molecular insight into eukaryotic signaling systems. In the past, we have discovered mechanisms such as Ser/Thr acetylation, AMPylation, irreversible actin assembly, bacterial phosphoinositide-binding domain mimics, and pore-forming V-ATPase inhibitors. The marine bacterium Vibrio parahaemolyticus is the worldwide leading cause of seafood-borne acute gastroenteritis. For decades, this pathogen has been studied exclusively as an extracellular bacterium. However, recent studies from our lab have revealed the pathogen's ability to invade and replicate within host cells. We find novel mechanisms used by the pathogen to manipulate

and exploit host signaling mechanisms so this bacterium can survive, proliferate, and escape. Our work at UT Southwestern is accomplished using a broad range of tools, including biochemistry, molecular microbiology, protein chemistry, structural biology, yeast genetics, cell biology and more.

Faculty Plenary Talks

Friday, 1:30 p.m. – 3:00 p.m., Brodie Payne Ballroom, Graduate Hotel
Chair: Christian K Tipsmark, Ph.D. (Dept. of Biological Sciences, UAF)

Biology

David Donley | Harding University

"I've got iron on my mind: Exploring factors that shape the neuroinflammatory response of microglia"

1:30 PM Friday

Microglia are highly plastic immune cells in the central nervous system that have multi-faceted responses to damage-associated signals. Chronic microglial activation and subsequent inflammation is linked to the progression of neurological diseases such as Alzheimer's disease (AD) by potentiating rather suppressing damage. Despite a well characterized phenotype of microglia, mechanism(s) that control their dynamic responses in disease are still poorly understood. To advance our understanding of the mechanisms underlying microglial activation in disease, we stimulate cultured microglia with iron and amyloid-beta due to their correlation with pathological inflammation and neurological disease progression. Amyloid-beta and iron accumulate concurrent with AD progression and are associated with detrimental inflammatory responses from microglia. However, the mechanism of how amyloid-beta and iron converge to induce microglial dysfunction remains elusive. The Normal Mucosa of Esophagus-Specific gene 1 (NMES1) protein and its gene, C15orf48, appear to be an intersection point of iron and amyloid-beta. Intriguingly, a proteomics analysis showed amyloid-beta stimulation increased expression of NMES1 while the addition of iron suppressed this effect in microglia. Further, we found that suppression of NMES1 leads to hyperactivation of microglia stimulated with amyloid-beta, suggesting that iron suppresses the ability of microglia to regulate inflammation downstream of amyloid-beta. These results indicate that NMES1 may be a critical regulator of inflammation in AD but more work is needed to elucidate how iron disrupts C15orf48/NMES1 function during disease. Our data expands on the emerging understanding of the impact of iron dysregulation on the inflammatory response of microglia to disease stimuli such as amyloid-beta. Broadly our work contributes to a better understanding of mechanisms underlying chronic microglial inflammation in the context of AD, and other neurological diseases.

Chemistry

Sharon Hamilton | Ouachita Baptist University

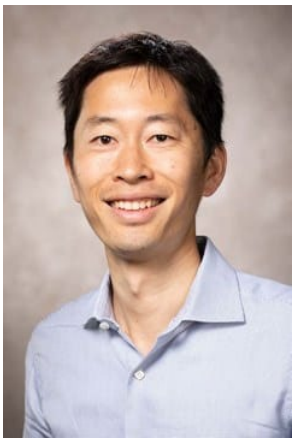
“Developing Modern Materials for Biomedical Applications”

2:00 PM Friday

Recent evolutions in the field of biomaterials have focused on developing materials that can facilely interface with biological systems to treat or replace tissues or functions of the body. Natural polymers including polysaccharides have been investigated as suitable biomaterials to mimic the environment of body tissues and facilitate tissue regeneration. Chitosan, collagen, and sodium alginate are water-soluble, natural macromolecules that have been used in applications such as cell scaffolding, drug delivery, and wound healing. Additionally, biocompatible synthetic polymers, such as poly(acrylic acid) and polylactones, are of significant importance within the fields of tissue engineering, drug delivery, and biomedical implants. Both natural and synthetic polymers can be modified to attach biomimetic and bioactive moieties to further enhance the final macromolecular product. Electrospinning polymers yields nanofibers that have shown promise in a variety of biomedical applications, including tissue scaffolds. Modern wound healing treatments have capabilities including preventing infection and encouraging cell growth; however, little research has been published on the development of synthetic analogs to costly biomolecules. Dr. Hamilton’s lab investigates the development of biomimetic polymers through the modification of commercially available polymeric backbones as well as the polymerization of functionalized monomers. It is anticipated that these biomimics will prove to be suitable materials for use in a variety of applications including wound healing.

Physics

Hiro Nakamura | University of Arkansas – Fayetteville



"Towards Quantum Frequency Conversion in 2D Materials"

2:30 PM Friday

Many modern optical technologies such as lasers and optical modulators have one component in common, which is called nonlinear optical materials. Recently, atomically thin two-dimensional (2D) materials were found to possess extremely large nonlinear optical properties, together with the ability to interact with light significantly despite being so thin. In this talk, first I will introduce the concept of nonlinearity in optics and some of the wonders of 2D materials focusing on strong light-matter interactions. Next, I will share ongoing efforts in our group to (1) explore nonlinear frequency conversion in various types of ultrathin materials and (2) develop unique experimental probe (laser ARPES) to uncover how light interacts with materials in ultrafast time scales. Our vision is that these fundamental insights will pave the way to quantum frequency conversion, a key element to build future quantum applications such as quantum computing in a scalable manner.

Student Oral Presentations

Undergraduates will give 12-minute oral presentations followed by 3 minutes 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: Jeannine M. Durdik, Ph.D.

3:30 PM. Tommy Caldarera
Hendrix College
Investigating HELB Activity in Response to Phosphorylation of Serine 1048

03:45 PM. Curtis Taussig
University of Arkansas at Fayetteville
Kinetic and Structural Characterization of Ribosomal Protection Protein Tet(S)

04:00 PM. William Winston
Northeastern State University
Determining a Novel Role of DNA Polymerase Epsilon in Nucleosome Dynamics at the Replication Fork by Investigating POLE3:POLE4 Interaction

04:15 PM. Patricia M. Fiedorek
University of Central Arkansas
Patterns of Host-Specificity Between Chlamydiae Bacterial Endosymbionts and Their Social Amoeba Hosts in Natural Populations

04:30 PM. Kelsey Steinmetz
Rhodes College
Elevated Carbon Dioxide Enhances the Growth and Reduces Antifungal Susceptibility of Histoplasma Yeasts

04:45 PM. Sydney Reynolds
Harding University
Decreasing Activation of Microglial Cells in the Presence of Pro-inflammatory Stimuli: A Role for Levetiracetam?

Chemistry Oral Presentations

Brodie Payne Ballroom A
Chair, Dylan Girodat, Ph.D.

3:30 PM. Kensley Flynn
Ouachita Baptist University
Developing a Novel, Biomimetic, Poly(δ-valerolactone)-based Wound Dressing

03:45 PM. Madeline Davidson
University of Central Arkansas
Investigating the Calcium Ion-induced Changes in the Calmodulin-binding Protein PEP-19 in the Presence of Neurogenerative Oligomers

04:00 PM. Elise Knight
Ouachita Baptist University
Light-Triggered Release of Indocyanine Green Using Polydopamine-Coated Gold Nanocages

04:15 PM. J. Ethan Batey
University of Arkansas at Fayetteville
High-Throughput Single Molecule Spectroscopy Reveals Cellular Structures with Exceptional Spatiotemporal and Spectral Resolution

04:30 PM. Sharae Gipson
University of Arkansas at Pine Bluff
Improving the Bioavailability of Sulforaphane as a Therapy for Melanoma

04:45 PM. Katherine C. Peters
University of Central Arkansas
Incorporating Sulfur-containing C-1 Feedstocks into Stereochemically-diverse Carbohydrates to Expand the Properties of Next-generation Sustainable Polymer Materials

Physics Oral Presentations

Trammel Room
Chair, Hugh Churchill, Ph.D.

3:30 PM. Eric Seglem
University of Arkansas at Fayetteville
Wait-time Distributions for Superposed Coherent States

03:45 PM. Arantxa Pardue
Belmont University
Electronic Transport Properties of Two-Dimensional Violet Phosphorus 11

04:00 PM. Gabriella Fields
Harding University
Autism and Agility: Analyzing Reaction Time in Individuals on the Spectrum

04:15 PM. Grace I Nehring
Rhodes College
Ultrasonic Technique for Measuring the Temperature-dependent Speed of Sound in Fluids

04:30 PM. Caleb E. Orr
Northeastern State University
Synthetization and Characterization of Misfit Layered Compounds

04:45 PM. Sam Sooter
University of Arkansas at Fayetteville
Searching for Signatures of Criticality Across the Sleep-Wake Cycle

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 4th, 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. New funding opportunities, the Support for Research Excellence (SuRE) Program and SuRE-First Program (R16s) have been released with the first-ever submission deadline of September 2021. Comparing the 2 FOAs and appropriateness for PUI faculty to apply for either will be discussed. Both the R15 and R16 have three main goals, ***1)*** to support meritorious science ***2)*** to strengthen the institution's research environment, and ***3)*** to expose students to research. Thus, special consideration for how/where to incorporate all three goals into the application will be discussed. The presenter has been part of recent NIH R15 Special Emphasis Panels and will share experiences with a goal of benefitting interested faculty and providing a perspective on how to write a competitive AREA application. Discussions will include what reviewers are "coached" to look for during peer review and some of the most common mistakes that can temper reviewer enthusiasm.

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

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

(dynamic) or too large to be solved by other techniques such as X-ray crystallography or NMR. Furthermore, structures of complexes in heterogeneous mixtures can be solved through 3D classification techniques.
This workshop will go over the fundamental theory for how a 3D electron density can be generated from movies of particles. By the end an attendee will be able to have working knowledge of the workflow for single particle 3D reconstruction. As an example, the workshop will go through the single particle reconstruction of the large protein beta-galactosidase.

Workshop 3: 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:
Julie Stenken, 21st Century Chair in Proteomics & Professor, Dept. of Chemistry and Biochemistry, UAF
Kusum Naithani, Graduate coordinator and Associate Professor, Dept. of Biological Sciences, UAF
Adnan Ali Khalaf Alrubaye, Associate Director of Graduate Program in Cell and Molecular Biology, UAF
Karl Boehme, Associate Professor, Department of Microbiology & Immunology, UAMS
Aaron Kemp, Graduate student in Biomedical Informatics, UAMS
Amanda Raley, Graduate student in Chemistry and Biochemistry, UAF
Eston Dunn, Graduate student in Biological Sciences, UAF
Colette Robinson, Graduate student in Cell and Molecular Biology, UAF

Workshop 4: 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 5: XRD New Capability for Art Restoration, Pharmaceutical Development, and Structure Determination of Pharmaceutical Targets Both Small and Large
Josh Sakon, Ph.D.*, Dept. of Chemistry and Biochemistry, UAF*
Location: CHEM 48
Participant capacity: 10

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

Workshop 6: CRISPR-Cas9-mediated Targeted Mutagenesis
Nagayasu Nakanishi, Ph.D.*, Dept. of Biological Sciences, UAF*
Location: FERR 214, 323 and SCEN 122
Participant capacity: 10

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

Workshop 7: Data Science Help Desk for the Arkansas INBRE
Phil H, Williams, Ph.D.*, Dept. of Information Science, UALR*
Location: HILL 202

A data Science Help Desk has been created using Spiceworks. Users can easily request help with projects in a variety of data science areas. These include general data science as well as Bioinformatics specific solutions. Examples include machine learning, high performance computing (HPC), RNA-seq analysis, internet of things (IoT), Linux OS, scripting in R, python and bash, systems integration, systems automation, and Cloud computing. The Help Desk enhances our ability to track trends in client needs and the solutions.
For help with data science, email your request to: help@arinbre-datahelp.on.spiceworks.com

Workshop 8: 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, UAF*
Narasimhan Rajaram, Ph.D., *Dept. of Biomedical Engineering, Metabolic Imaging and Spectroscopy Core, Arkansas Integrative Metabolic Research Center, UAF*
Suresh Thallapuranam, Ph.D., *Dept. of Chemistry and Biochemistry, Arkansas Integrative Metabolic Research Center, UAF*
Location: CHEM 144

The Arkansas Integrative Metabolic Research Center is a NIH-funded COBRE that was established in March 2021 to study metabolism in cells and tissue. As part of the AIMRC, two research cores were established as fee-for-service resources – an imaging and spectroscopy core and a bioenergetics core. This workshop will present the technologies and capabilities available within these two cores for utilization by universities and industry. The imaging and spectroscopy core currently houses state-of-the-art microscopes that allow high-resolution visualization of cell and tissue structure, function, and biomolecular composition. Two-photon microscopy enables quantification of cellular metabolism through endogenous fluorescence intensity and lifetime of the metabolic coenzymes, NADH and FAD. 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 9: Confocal Microscopy

Payal Sanadhya, Ph.D.
Fiona Goggin, Ph.D.*, Department 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 10: Dancing Bacteria
Yong Wang, Ph.D., *Department of Physics, UAF*
Location: PHYS 133 and PHYS Lab 115A

Participant capacity: 15

The capability of moving is critical to many bacteria for pursuing nutrients and avoiding hazards. Some bacteria, such as E. coli that naturally exist in human guts, rely on rotating flagella – filaments hooked on motors embedded on cell body – to move in different environments. In this workshop, we will have fun observing the rotation of bacterial flagella and their dancing using fluorescence microscopy.

Workshop 11: Quantifying the Dynamics of Cell Division of Bacteria and Yeast at Single Cell
Pradeep Kumar, Ph.D., *Department 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 12: Physics REU and Graduate Application
Reeta Vyas, Ph.D., Dept. of Physics, UAF
Location: PHYS 134
Participant capacity: 15

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

Workshop 13: Build a Robot at the MonArk Quantum Foundry
Hugh Churchill, Ph.D., *Department of Physics, UAF*
Location: NANO 105
Participant capacity: 16

Workshop participants will assemble a sample transfer robot and use it to collect treats as they explore robotics, cartesian motion control, microcontroller programming, and automation similar to 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 a 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

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. Investigating HELB Activity in Response to Phosphorylation of Serine 1048

Tommy Caldarera, Dr. Alicia Byrd, Ben May
Chemistry Department, Hendrix College

The helicase family contains numerous enzymes that are vital to processes involving DNA or RNA unwinding. DNA Helicase B (HELB) is one such enzyme that plays an essential role in maintaining genomic integrity. Although HELB is known to be crucial for genomic maintenance, preliminary data identified several sites of phosphorylation on the protein that reduce its enzymatic activity when phosphorylated. Furthermore, the effects of phosphorylating these sites individually are unknown. In order to investigate the effects of phosphorylation on serine 1048 (S1048) of HELB, we created a plasmid with a serine to aspartic acid mutation (S1048D) to mimic the effects of phosphorylation. We expect to see diminished activity of the S1048D HELB variant when tested with a DNA unwinding assay. We have developed a protocol to express and purify HELB from E. coli, and a DNA unwinding assays with the purified wild type HELB confirmed that active enzyme was produced. Alternatively, the S1048D HELB variant that we purified was completely inactive when analyzed by a DNA unwinding assay. In order to confirm this discovery, we will repeat the process with a HELB variant that includes a phosphoserine in place of S1048. Still, the current data collected with S1048D suggests that phosphorylation of S1048 regulates HELB activity.

03:45 PM. Kinetic and structural characterization of ribosomal protection protein Tet(S)

Curtis Taussig, Dr. Dylan Girodat, Teslie Sehorn
Biochemistry, University of Arkansas at Fayetteville

Antibiotic resistance is a burgeoning global threat with the CDC reporting 5 million deaths in 2019 alone being associated with antibiotic and antimicrobial resistance. Understanding mechanisms of antibiotic resistance is critical to diminish its impacts and provide strategies for novel therapeutics that can repurpose conventional antibiotics. Tet(S) is a proposed ribosomal protection protein (RPP), based on homology to other RPPs. These proteins grant antibiotic resistance by catalyzing dissociation of tetracycline antibiotics from the bacterial ribosome, thereby neutralizing the effects of the broad-spectrum antibiotic. Furthermore Tet(S) is homologous to the GTPase elongation factor G (EF-G), suggesting it is a GTPase and that GTP hydrolysis is essential to its function. Here we present findings on the first purification of Tet(S) from E. coli using Ni2+ Sepharose affinity

chromatography in tandem with size exclusion chromatography. We also report the rate of association and dissociation of GDP from Tet(S) using fluorescence resonance energy transfer (FRET) between mant-GDP and tryptophan using a stopped-flow apparatus. Towards achieving structural interpretations of Tet(S) we have begun crystallography for X-ray diffraction experiments as well as utilizing circular dichroism (CD), a form of absorption spectroscopy. The results of this research will provide insights into the role of GTP binding and hydrolysis by Tet(S) to confer antibiotic resistance formulating new strategies as to how to better combat antibiotic resistance.

04:00 PM. Determining A Novel Role of DNA Polymerase Epsilon in Nucleosome Dynamics At The Replication Fork By Investigating POLE3:POLE4 Interaction

William Winston, Lydia Ostmo, Sapna Das-Bradoo Department of Natural Sciences, Gregg Wadley College of Science and Health Professions, Northeastern State University

The mechanism by which chromatin is regulated at the advancing replisome is not fully understood. Previous work has revealed that two subunits of the Polymerase epsilon (Polε) complex: POLE3 and POLE4, work as replisome-associated histone chaperones and are important in chromatin maintenance during DNA replication. However, the consequences of the loss of interaction between POLE3 and POLE4 remains unclear in human cells. Our goal is to disrupt POLE3 and POLE4 interaction to investigate Polε stability at the replication fork. To accomplish this, we constructed POLE3 and POLE4 mutants and tested their efficacy in disrupting the interaction. GFP-tagged POLE3 and POLE4 genes were mutated at conserved nucleotides using site-directed mutagenesis. These mutations were confirmed by Sanger sequencing and protein expression in the HEK293T cell line by Western blotting. Protein-protein interactions were examined by co-immunoprecipitation using anti-GFP-tagged agarose beads. Our results show that in human cells, the POLE3 F44D mutation disrupts binding to POLE4, and the POLE4 F74D mutation disrupts binding to POLE3. Our data suggests that POLE3 and POLE4 interaction sites are conserved. Planned subsequent study may show if inhibition of POLE3:POLE4 interaction curtails the function of Polymerase epsilon as a histone chaperone at the replication fork.

04:15 PM. Patterns of Host-Specificity between Chlamydiae Bacterial Endosymbionts and Their Social Amoeba Hosts in Natural Populations

Patricia M. Fiedorek, Haley Garner, Hailee Gerner, James DuBose, and Tamara S. Haselkorn Biology, University of Central Arkansas

Symbiosis describes two species living purposefully together in close physical proximity. Social amoebae are eukaryotic bacterivores that can provide a strong selective pressure on environmental bacteria to survive digestion and adapt to an intracellular lifestyle. The bacterial phylum Chlamydiae consists of obligate intracellular bacteria including major human pathogens and diverse environmental representatives. Current estimates based on metagenomic and 16S rRNA gene-based surveys indicate that there are over 1000 chlamydial families, many of which are uncharacterized and their host ranges are unknown. Dictyostelium discoideum and other social amoeba species have been recently identified as natural hosts of novel Chlamydiae haplotypes. Interactions between these Chlamydiae endosymbionts and social amoebae may fall along a spectrum from parasitic to mutualistic depending on various factors, such as environmental conditions, relationship duration, and endosymbiont transmission pattern. We hypothesized that if Chlamydiae haplotypes are host-specific, then certain haplotypes would be more prevalent in particular social amoeba host species and cophylogenies would show matching topologies. Using wild social amoeba isolates collected throughout Arkansas, we amplified and sequenced the full-length 16S rRNA gene of our novel Chlamydiae haplotypes and approximately 600bp of the 18S rRNA gene from their social amoeba hosts. We then reconstructed molecular cophylogenies to infer any host-specific patterns. These cophylogenies suggest that both horizontal and vertical transmission of our Chlamydiae endosymbionts are occurring in nature, where certain haplotypes are indiscriminately

infecting social amoeba species and others may be more adapted to a particular host species. Additionally, we found that social amoeba species with high Chlamydiae prevalence tend to associate with specific haplotypes. Further study is required to determine if our Chlamydiae haplotypes confer any fitness effects on their social amoeba hosts.

04:30 PM. Elevated carbon dioxide enhances the growth and reduces antifungal susceptibility of Histoplasma yeasts

Kelsey Steinmetz and Qian Shen
Biochemistry and Molecular Biology program, Rhodes College

Histoplasma capsulatum is a thermally dimorphic fungal pathogen. It causes approximately 500,000 infections annually in the United States. Histoplasma is present as avirulent mycelia in the soil and transforms into pathogenic yeasts under the human body temperature upon inhalation. This elevated temperature triggers the expression of many virulence factors that enable Histoplasma yeasts to survive and proliferate within immune cells (i.e., macrophages) in the human lungs. In addition to elevated temperature, Histoplasma yeasts also experience other environmental changes within the mammalian hosts such as elevated CO2 (0.04% in the air vs. 5% within host tissues) during infections. However, the impact of elevated CO2 on Histoplasma yeasts remains completely unknown. In this study, our results showed that elevated CO2 enhanced Histoplasma's growth, particularly its enhanced ability to utilize certain amino acids (e.g., alanine) as the sole carbon source. We also found that elevated CO2 reduced Histoplasma's susceptibility to antifungals. Histoplasma's enhanced growth and reduced antifungal susceptibility under elevated CO2 were not pH dependent. Our findings suggest that the elevated CO2 within mammalian hosts could potentially enhance Histoplasma's virulence. Future antifungal susceptibility tests for Histoplasma should be performed under 5% CO2 rather than ambient air to obtain physiologically relevant results.

04:45 PM. Decreasing Activation of Microglial Cells in the Presence of Pro-inflammatory Stimuli: a Role for Levetiracetam?

Sydney Reynolds, Dr. David Donley
Harding University Biochemistry Department, Harding University

The neuroimmune system protects the central nervous system (CNS) by mobilizing defenses against pathologic material in response to proinflammatory stimuli. Microglia are the CNS's resident immune cells that bidirectionally modulate neurons and their environment by phagocytizing apoptotic neurons, unuseful synapses and pathologic agents. They can become "activated", engulfing offending materials and secreting proinflammatory intermediaries such as IFNγ and nitric oxide to predicate the proliferation and activation of more microglia. Neurons express complement proteins such as C3 and C1q on their plasma membranes to evoke microglial activation in disease states such as Alzheimer's disease (AD) and epilepsy. A brain with AD also characteristically exhibits high amyloid beta-42 (Aβ_{42}) concentrations, invoking activation of an abundance of microglia that inflict ever-increasing neurodegeneration by excessively engulfing neuronal material and potentiating exaggerated synaptic transmission, which further increases proinflammatory intermediary production. A potential remediation approach for neuroinflammation in AD is employing antiepileptic medications due to their ability to mitigate both signal transduction and immunomodulatory agent synthesis. One such medication is Levetiracetam (LEV) which mitigates activation of microglia in vitro. To elucidate LEV's utility in an AD environment, we measured phagocytic activity, cytokine and nitric oxide production in the presence of LEV and Aβ_{42} by doing phagocytosis, cytometric bead array, and inducible nitric oxide synthase assays, respectively. LEV beneficially mitigates phagocytosis, production of proinflammatory cytokines and nitric oxide. These outcomes were found to be highly dosage-dependent. Complement protein expression was found to increase in response to LEV, suggesting that microglial activity is modulated through neuronal response to LEV.

Chemistry Oral Presentations

03:30 PM. Developing a novel, biomimetic, poly(δ-valerolactone)-based wound dressing

Kensley Flynn and Sharon K. Hamilton, Ph.D.
Chemistry and Biology, Ouachita Baptist University

The development of biomimetic materials for use in the human body has been a point of interest for researchers over the past several decades. A prominent process for this is electrospinning because one can spin several components together into a non-woven nanofiber scaffold, similar to the architecture of the extracellular matrix. Polymers such as poly(δ-valerolactone) (PDVL), a biocompatible and biodegradable polyester, and biopolymers such as chitosan, a derivative of chitin known to have antibacterial properties, have been used to make such materials. Our research aimed to develop a collagen analog using a biomimetic PDVL (bPDVL) electrospun with chitosan to make nanofibrous wound dressings. We developed a practical, multi-step synthesis of our monomer, which was then polymerized into a PDVL derivative and modified with amines similar in structure to amino groups found in collagen to produce a bPDVL. Each synthetic step was analyzed using NMR and IR spectroscopies to confirm success. bPDVL/chitosan fiber mats were analyzed via scanning electron microscopy and IR spectroscopy. Previous studies in the Hamilton lab observed increased hemostatic properties for calcium chloride-treated fiber mats. In the earlier studies, though, the amount of calcium loaded on the scaffolds was unknown. Thus, a quantification method was developed to detect the amount of calcium chloride on the mats so that consistent results on the concentration of loaded calcium chloride could be determined. Additionally, in vitro studies were done on previously made materials to compare the bPDVL fiber mats. In future research, the bPDVL fiber mats will undergo cell and degradation studies to compare to our other fiber mats and similar commercially available products. It is predicted that the mats will help us develop a novel wound dressing that will resemble the extracellular matrix, have antibacterial and hemostatic properties, and be less expensive than a human collagen dressing.

03:45 PM. Investigating the calcium ion-induced changes in the calmodulin-binding protein PEP-19 in the presence of neurogenerative oligomers

Madeline Davidson, Victoria Dunlap
Chemistry and Biochemistry, University of Central Arkansas

PEP-19 is a small, intrinsically disordered protein (IDP) that regulates the binding response of Calmodulin (CaM) to calcium. Calmodulin is a central translator to the calcium ion signal, binding as many as 300 target proteins when in the presence of calcium. PEP-19's involvement with the calcium signaling process is to bind to CaM and increase the rate of calcium ion binding in the C-terminal lobe of CaM. PEP-19 levels are decreased in the brain in Parkinson's disease, and there is an increase of PEP-19 in brain areas spared in Alzheimer's disease. The presence of PEP-19 appears to help protect against calcium overload. Here, we investigate how neurodegenerative oligomers affect the CaM/PEP-19 complex using fluorescence resonance energy transfer (FRET) to measure the end-to-end distance of PEP-19 alone, in the complex, and in the presence of neurodegenerative oligomers of alpha-synuclein and amyloid beta peptide.

04:00 PM. Light-Triggered Release of Indocyanine Green Using Polydopamine-Coated Gold Nanocages

Elise Knight, Sarah York, Deborah Okyere, Jingyi Chen
J.D. Patterson School of Natural Sciences, Ouachita Baptist University

Antibiotic resistance is a rapidly growing problem in the medical field. Traditional antibiotics are becoming less effective for fighting off bacteria, but high-power antibiotics cause many negative side effects in the human body. One novel alternative method that could safely use strong antibiotics is drug delivery via gold nanocages combined with photodynamic therapy. The goal of this study is to develop a gold nanocage construct that can deliver a photosensitizer and/or a strong antibiotic to bacterial

cells that is then released with near-infrared-irradiation to harm the bacterial cells. Silver nanoparticles are used as the template for synthesis of gold nanocages through galvanic replacement. These gold nanocages are then coated with polydopamine to improve their functionality to conjugate to target bacterial cells. Newly coated gold nanocages are loaded with indocyanine green, a near-infrared photosensitizer that is harmless until irradiated, during which it produces singlet oxygen. Indocyanine green is released by near-infrared-irradiation of the gold nanocage aqueous suspension and compared to the full amount of indocyanine green loaded into the nanocages. It is found that in water, there is a positive correlation found between the amount of time the nanocage suspension was irradiated and the amount of indocyanine green released. However, the nanocages without irradiation still release small amounts of indocyanine green, so further studies must be done to optimize the photosensitization and release of indocyanine green from polydopamine-coated gold nanocages.

04:15 PM. High-Throughput Single Molecule Spectroscopy Reveals Cellular Structures with Exceptional Spatiotemporal and Spectral Resolution

J. Ethan Batey, Geun Wan Kim, Meek Yang, Darby Heffer, Elric Pott, Hannah Giang, Bin Dong
Chemistry and Biochemistry, University of Arkansas at Fayetteville

Single-molecule localization microscopy (SMLM) has become a strong technique in the toolbox of chemists, biologists, physicists, and engineers in recent years for its unique ability to resolve characteristic features quickly and accurately in complex environments at the nanoscopic level. Super-resolution multicolor imaging has seen the greatest advancement among SMLM techniques, drastically improving differentiation ability of nanostructures beyond the diffraction limit and increasing the precision with which previously unresolvable structures are studied. However, traditional multicolor SMLM methodologies present low spatial resolution, pseudo spectral resolution, and require complex optical systems. Here, we overcome these drawbacks by constructing an ultrahigh-throughput SMLM methodology that allows for fast and accurate multicolor imaging of complex environments at the nanoscopic level by a multichannel ratiometric analysis. This method overcomes traditional SMLM issues by separating signal used for spectral and localization analysis, permitting ultrahigh-throughput with high spatial and spectral resolution and true color analysis from a simple optical system. Our methodology can readily distinguish between close emitting fluorophores and achieves sub-10 nm localization precision with single molecule emission wavelengths at sub-5nm variance.

04:30 PM. Improving the Bioavailability of Sulforaphane as a Therapy for Melanoma

Sharae Gipson, Zeeshan Habeeb, Samir Jenkins and Ruud Dings
Chemistry, University of Arkansas - Pine Bluff

Melanoma, which translates to "Black Tumor", is a difficult to treat type of skin cancer. While melanoma is only reported for 1% of skin cancers, it is the cause of majority of skin cancer related deaths. It is harder to treat melanoma due to the resistance of the cancer cells to chemotherapy, caused by genetic pathways alterations. Sulforaphane, an extract derived from broccoli, has anticancer properties by inhibiting cancer cell growth through release of antioxidants that counteract carcinogens. However, sulforaphane is an oil with limited solubility in water. A peptide made from unnatural amino acids was developed in our lab to encapsulate sulforaphane and improve solubility and bioavailability. Cytotoxicity assays with the B16 murine melanoma cell line was conducted, and the encapsulated sulforaphane was found to have more efficacy than the free molecule.

04:45 PM. Incorporating sulfur-containing C-1 feedstocks into stereochemically-diverse carbohydrates to expand the properties of next-generation sustainable polymer materials

Katherine C. Peters, Ashley N. Braaksma, Autumn M. Andras, and Karen L. Wooley
Department of Chemistry and Biochemistry, University of Central Arkansas

Plastics are one of the most versatile materials used in modern society; however, current production methods rely significantly on the use of fossil fuels which has an extensive negative impact on the environment. One method to combat this persisting issue is to synthesize functional, biodegradable, and biocompatible polymers derived from naturally abundant products, such as carbohydrates, which have high degrees of functionality and stereochemical diversity. Over the last decade, the Wooley Lab has continued to innovate the use of D-glucose, developing methodologies that take advantage of the five available hydroxyl groups to transform glucose into various monomers, including six-membered bicyclic carbonates to be subjected to organobase-catalyzed ring-opening polymerization (ROP). Increasing interest has focused on the substitution of oxygen atoms with sulfur to provide compositionally-diverse polymer backbones yielding materials with varying chemical, physical and mechanical properties. Previously reported literature has demonstrated the use of CS2 insertion into a D-xylose derivative to produce five-membered cyclic xanthates and dithiocarbonates. This study will expand upon this work, targeting the formation of trans-fused six-membered cyclic xanthates from D-glucose and cis-fused six-membered cyclic xanthates from D-galactose to study how the stereochemistry of the sugar impacts the stability of the resulting monomer and the kinetics and degree of regiochemical control of the ROP. The thermal properties and degradation patterns of the resulting stereochemically-diverse sulfur-containing polymer materials will be explored to provide insight into the relationships among polycarbonates and their sulfur-analogs.

Physics Oral Presentations

03:30 PM. Wait-time Distributions for Superposed Coherent States

Eric Seglem, Reeta Vyas, and Surendra Singh
Physics, University of Arkansas - Fayetteville

Certain states of light exhibit properties which can only be accounted for by the quantum theory of light and not the classical theory. Such “nonclassical” states may reveal these properties through their photon counting statistics. It is possible to quantify the non-classicality of a state in terms of photo-detection wait-time distributions. An example of a nonclassical property which may be evident in a photon counting experiment is photon antibunching, where photons are unlikely to be detected within short time intervals of each other. We will present the photon statistical properties for the superposed coherent state of light with evenly distributed phases. With an analytical expression for the generalized superposed state, we calculate the photon number and wait-time distributions for a superposition of n coherent states. We then analyze these results for signatures of non-classicality and compare them with the results for the coherent and squeezed states of light.

03:45 PM. Electronic Transport Properties of Two-Dimensional Violet Phosphorus 11

Arantxa Pardue, Michael Mastalish, Ashby Philip John, Peter Gea, and Hugh Churchill
Physics and Chemistry Department, Belmont University

Violet Phosphorus (VP) is a 2D layered intrinsic p-type semiconducting Phosphorus allotrope[1]. Because most known 2D semiconductors are n-type, finding new intrinsic p-type structures will allow for the further development of complementary n−p architectures and p-electronics without requiring doping of the material[1]. This work explores the

electrical and optical properties of Violet Phosphorus 11. Mechanical exfoliation of violet-P11 into single-crystal flakes were performed in a controlled atmosphere of inert. From these flakes, Field-effect Transistors (FETs) were built using Hall Bar geometry to calculate mobility and resistivity as a function of hole density in a cryostat. Electric characterization will aid the understanding of violet-P11 and its potential applications. [1] Antonio Gaetano Ricciardulli, Ye Wang, Sheng Yang, and Paolo Samori. Two-dimensional violet phosphorus: A p-type semiconductor for (opto)electronics. Journal of the American Chemical Society, 144(8):3660–3666, 2022. PMID: 35179356. Supported by NSF-REU Grant \# 2244130.

04:00 PM. Autism and Agility: Analyzing Reaction Time in Individuals on the Spectrum

Gabriella Fields, Silas Foster, Dr. Taylor Williams
Biomedical Engineering, Harding University

Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder built upon the diagnosis of social deficits or restricted behavioral categories. These can include repeated speech or motor movements, patterns/routines, special interests, heightened sensory experiences, and these occur during development as a child according to the DSM-5 and the Harding University Speech Pathology department. This study explores a new potential diagnosis criterion for ASD—Reaction Speed. Individuals with ASD may have slow reaction speeds due to typical sensory processing disorders like Auditory Processing Disorder (APD). The Autism Spectrum Quotient test is a common tool used to screen for potential ASD traits in adults, with a score of 19 or higher indicating a need for further evaluation [2]. The control group in the study was tested and screened for scores less than 19 [6]. Eight people between the ages of 19 and 22 who are not diagnosed, nor self-diagnosed with a form of neurodiversity, and scored less than a 17 on the Autism Quotient (AQ) formed the control group. Seven people between the ages of 18 and 23 who were diagnosed with Autism Spectrum Disorder formed the autism group. The tests performed could be separated into three categories: physical, visual, and audio stimulus. The data failed to reject the null hypothesis on ASD and reaction speeds in adults, but with further research, a possible correlation could be explored between visual reaction speeds and ASD with a bigger sample size.

04:15 PM. Ultrasonic technique for measuring the temperature-dependent speed of sound in fluids

Grace I Nehring, Emily E Bingham, Ann M Viano, Brent K Hoffmeister
Physics, Rhodes College

The purpose of this project was to develop a technique to measure the speed of sound in fluids as a function of temperature using ultrasonic signals. The technique reflected 7.5 MHz ultrasonic pulses off an aluminum plate with a machined step of size Δd = 0.500 inches. The transducer, which transmits and receives the pulses, was mechanically moved to acquire echoes from both levels of the step plate. The speed of sound v was computed from the equation $v = 2\Delta d/\Delta t$, where Δt was the time difference between the echoes from each side of the step. The test fluid was contained in a 1 L tank surrounded by an 8 L thermostatically controlled water bath. Both tanks contained a pump to circulate water and improve temperature uniformity. To validate the system, measurements were made on distilled water in half degree increments from 15 to 25 degrees Celsius. The measured values of v were highly reproducible but systematically greater than previously published results for distilled water by approximately 0.3%.

04:30 PM. Synthetization and Characterization of Misfit Layered Compounds

Caleb E. Orr, Jin Hu, Gokul Acharya, Dinesh Upreti
Fulbright College of Arts and Sciences, Northeastern State University

The discovery of a group of 2D non-stoichiometric materials composed of alternating layers of two chemical compounds, named misfit layered compounds or MLC's, has fostered an explosion of research into synthesizing such materials due to their weird electronic and magnetic properties. One MLC, (FeSe)(NbSe2), for example, can better exploit the

FeSe's layer superconductivity by raising its critical temperature when compounded into the aforementioned MLC. Other applications for MLC's include the creation of semiconductors and thermoelectric power generation. The purpose of this experiment is to successfully synthesize such MLC compounds via chemical vapor transport CVT methods, which have been carried out successfully but rarely, leading to lack of experimental data on the compounds. Additionally, no method of synthetization has yielded enough of the target MLC's to be considered viable for commercial use. This study focused on transition metal dichalcogenides MLC's comprised of a cubic rock salt layer and a hexagonal layer, which take the form AX − BX2 with A as a transition metal or rare earth, B as group 14 transition metal, and X as the chalcogens Selenium and Sulfur. Successful synthetization wasn't accomplished during this study, but has yielded interesting results from the created compounds that give us a much better understanding of how exotic properties in materials affect one another. Particularly, dopant Fe atoms introduced into a superconductor NbSe2 were able to completely suppress its superconductivity. The Fe atoms completely erased the antiferromagnetic traits emblematic of all superconductors and caused the compound to display a neat, linear magnetization. Supported by NSF-REU Grant \# 2244130.

04:45 PM. Searching for Signatures of Criticality Across the Sleep-Wake Cycle

Sam Sooter (presenter), Antonio Fontenele, Nivaldo Vasconcelos, Woodrow Shew (mentor)
Physics, University of Arkansas at Fayetteville

It has long been known that collective neural activity in cerebral cortex exhibits large synchronous fluctuations during slow-wave sleep. Studies of population activity in awake animals have also revealed diverse coordinated fluctuations, sometimes called neuronal avalanches. How do the slow waves during deep sleep differ from neuronal avalanches in the awake state? Which of these states, if any, is consistent with the criticality hypothesis, which predicts that avalanches are scale-free? Here, we systematically compared the strength of signatures of criticality in the awake and NREM sleep states in primary visual cortex of freely behaving mice. In the awake state, we found power-law avalanche size and duration distributions whose exponents obey the crackling noise scaling relation, along with strong long-range temporal correlations. All of these markers of criticality are weaker in NREM sleep than in the awake state. We also examined the structure of the transition between the apparent critical dynamics in the awake state and non-critical dynamics in NREM, finding that, despite continuously varying variability and synchrony across cortical states, signatures of criticality abruptly change at the border between sleep and wakefulness.

Poster Abstracts

Biology

1A. Creating Cell Wall-Deficient Tobacco BY-2 cells with CRISPR/Cas9 for Enhanced Recombinant Protein Production

Jacqueline Vargas-Ulloa, Uddhab Karki, Jianfeng Xu
Biological Sciences, Arkansas State University

Plant cell culture has been established as a cost-effective alternative production platform for therapeutic proteins on an industrial scale due to its intrinsic safety, low cost, and the capability of post-translational modification. Due to its central role in bio-production and fundamental research, the tobacco BY-2 cell has been referred to as the "CHO-cell in molecular farming" and the "HeLa cell in the biology of higher plants". However, major challenges exist for the BY-2 cell bioproduction system, such as limited protein secretion, cell aggregation, the presence of sizeable vacuoles, and complications in cryopreservation. These problems can largely be attributed to the distinctive cell wall structure of plant cells, which is absent in animal cells. The complete cell wall structure may not be crucial for in-vitro-cultured plant cells because the optimized culture conditions support their rapid propagation. This project leveraged the CRISPR/Cas9 genome editing technology to create novel cell wall-deficient or "animal cell-like" plant cell lines, potentially better suited for therapeutic protein production. A BY-2 cell line with the cellulose synthase 3 (CESA3) genes knocked out, showed significantly reduced cellulose content (40.2% reduction) and significantly changed cell wall monosaccharide composition. Notably, these knockout cell lines exhibited distinctive phenotypic characteristics, such as the formation of large cell clumps (disappeared after >10 generations of subculture) and a shift towards a more spherical cell shape. The cell line also demonstrated desired bioproduction potential for recombinant proteins. Our transcriptome analysis further revealed the profound impact on the expression of some cell wall biosynthetic genes within the knockout cells. This study establishes proof-of-concept for cellular engineering of existing plant cells to improve the viability of plant cell-based bioproduction systems.

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

Andrew Goode Co-author- Ana Karen Solano Morales Mentor- Robert Shields
Biological Sciences, Arkansas State University

Genomic Strategies to Study Essential Biofilm Formation Genes in the Tooth Decay Pathogen Streptococcus mutans 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. After creating the library, we will complete biofilm assays to discover mutants that are unable to form competent biofilms in the presence of sucrose. Currently, approximately 3,360 unique mutans (of 9,216 needed) have been isolated and stored in long-term ultracool freezer storage as triplicates. Of these

mutants, the first 960 have been screened using biofilm assays to examine their competence in forming biofilms in the presence of sucrose. Mutants observed with poor biofilm growth will undergo genetic identification methods, arbitrary PCR and CP-CSeq, to understand the location and significance of the transposon insertion. Understanding genomic differences between mutants that cannot construct biofilms will allow for the determination of essential and non-essential genes in biofilm growth. 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 Streptococcus mutans to attach to the tooth surface, and then initiate the progression of dental caries.

2A. Studying bypass of essential genes in the dental caries pathogen Streptococcus mutans

Sangam Chudal, Beatrice Rono and Robert C. Shields
Biological Sciences, Arkansas State University

Title: Studying bypass of essential genes in the dental caries pathogen Streptococcus mutans Authors: Sangam Chudal, Beatrice Rono, and Robert C. Shields Address: Department of Biological Sciences, Arkansas State University, Jonesboro, USA In recent studies we discovered several uncharacterized essential genes (genes required for survival) in the dental caries pathogen Streptococcus mutans. As a first step to determining the function of these genes, we are investigating if we can bypass essentiality through mutagenesis screens. We began by creating oligonucleotide primers for allelic exchange mutagenesis against the following S. mutans hypothetical essential genes: SMU_415, SMU_419, SMU_368, SMU_369, SMU_393, SMU_471, SMU_734, SMU_775, SMU_958, SMU_1801 and SMU_1802. Using standard molecular biology techniques (PCR, gel electrophoresis and restriction enzyme digest), we amplified PCR fragments, digested the fragments, and then purified the fragments. Next, an antibiotic marker, aphA3 (kanamycin resistance), was digested from the Escherichia coli plasmid pALH123. Afterwards, PCR fragments and the aphA3 gene were combined in a ligation reaction. Lastly, ligation products were transformed into competent S. mutans before selection on brain heart infusion agar containing kanamycin. From the genes tested, putative mutant colonies were visible for SMU_415, SMU_471 and SMU_369. To determine if gene essentiality has been suppressed, we will sequence the genomes of the mutant strains and compare them to the reference genome of S. mutans UA159. We anticipate that we may find mutations that render the essential component non-essential, as well as discovering possible gain-of-function variants. In the near future we will also test whether introducing transformation products into a transposon library will increase the mutability of genes for which we have not yet obtained mutants.

2B. The Mechanism of BAK Activation by PUMA in Apoptosis Initiation

Daniela PerezLaguna, Adedolapo Ojoawo, Shagun Srivastava, Elisabeth Ferreira, Seetharaman Jayaraman, Tudor Moldoveanu
Biological Sciences, Arkansas State University

Mitochondrial apoptosis initiates through mitochondria membrane poration, a process orchestrated by pro-apoptotic BCL-2 family proteins. To induce membrane permeabilization, the pore-forming protein BAK is activated from a dormant state by BH3-only BCL-2 family proteins including BID, BIM, and PUMA through protein-protein interactions. How PUMA activates BAK remains unclear, and we sought to investigate the molecular mechanism of BAK activation by PUMA. A crystal structure of the BH3 domain of PUMA bound to BAK has revealed that binding of the BH3 at the

hydrophobic groove of BAK destabilizes the inhibitory helix α1 of BAK, as observed in other BH3 complexes with BAK. In addition, the AlphaFold structure of the complex of full-length BAK and PUMA has indicated a C-terminal tail following the BH3 domain, which forms a short α-helix, possibly implicated in atypical membrane tethering. We tested these structure-based hypotheses using binding and functional assays with PUMA BH3 mutant peptides, truncated PUMA constructs, and a BAK mutant refractory to direct activation by BH3 ligands. Fluorescence polarization groove-binding assays showed wild-type (WT) PUMA BH3 peptide bound to BAK with similar affinity as the prototypical direct activator WT BID BH3 peptide, confirming BH3 in-groove binding. Both peptides triggered BAK-mediate liposome permeabilization to the same extent. Compared to the WT PUMA BH3, rationally designed missense PUMA BH3 mutations that exhibited a higher or lower affinity for BAK promoted diminished or enhanced BAK-mediated liposome permeabilization. The contributions of the disordered regions outside of the BH3 region are also being investigated mechanistically considering the AlphaFold structure of the complex. Our results support the hit-and-run weak affinity nature of the PUMA BH3–BAK interaction underlying efficient direct BAK activation and membrane poration.

3A. Outcome of Metabolomics Study in Nepl15KO flies

Surya Jyoti Banerjee. Please note that, I am the PI and would like to be considered for faculty presentation.
Biology, Arkansas Tech University

The Drosophila Nepl15 is a unique non-catalytic neprilysin that regulates nutrient storage. Upon knock-out of Nepl15, the mutant adult male fruit flies store significantly low levels of glycogen and glycerolipids, whereas the mutant adult female flies store higher amount of glycogen compared to the control flies, although the both male and female mutant flies uptake same amount of food like their control counterparts. As a result, the mutant male flies have same life-span but the mutant females have extended life span in culture, and both they remain significantly more active in their older age relative to the control flies. These attributes in the mutant resemble positive, anti-obesity health effect. Therefore, it becomes imperative to find out the effect of Nepl15 mutation on the nutrient metabolic pathways. To investigate the metabolic changes, I have performed primary metabolomics analysis using age-matched mutant and control adult male and female flies. The result shows that, overall primary metabolites are different in the male vs female flies irrespective of Nepl15 mutation is present or absent in the Principal Component Analysis. A significant overall separation of primary metabolites between mutant and control male and female flies is evident in sPLSDA and oPLSDA analyses. The initial analyses identified changes in the amino acid metabolism pathways between mutant and control male and female flies. Further dissection of this data will provide important information of signaling pathways that regulate nutrient metabolism and obesity.

3B. Specifications grading for equity in microbiology course

Suparna Chatterjee
Biology, Arkansas Tech University

Specifications grading is a grading system based on the mastery of specific educational outcomes that determine the final grade a student can earn in a course. I have designed a specifications grading strategy for the undergraduate Microbiology for Health Sciences course, creating 16 individual learning outcomes (LOs). Most of the students in this course are Nursing majors for whom this course is mandatory. It implemented two design principles: (i)

detailed feedback on completed work, what is done well, and what needs improvement through practice or review, and (ii) additional opportunities to practice skills that are challenging but can be achieved by resubmitting assignments. The grade earned in the lecture depended on the number of LOs the students mastered. A student's final class grade depended on the number of LOs mastered combined with the grade earned in the final exam. Implementing this grading system it was found that students showed positive attitudes towards learning microbiology and the DFW (students receiving D, F, and withdrawal) rate dropped.

4A. Determining the roles of DNase I and EndoG in DNA autohydrolysis in isolated cell nuclei

Dallas Fuller, Randal S. Shelton, Olena Levurdiak, Shenyang Li, Alexei G. Basnakian
Biology, Harding

During and after cell death, DNases cause nuclear internucleosomal DNA fragmentation, which is visualized as a 200bp DNA ladder in agarose gels. Overexpression of apoptotic DNases, in particular DNase I and EndoG, in cells and tissues was shown to induce DNA fragmentation. This DNA destruction makes cell death irreversible, while genetic knockout or chemical inhibitors of apoptotic DNases usually prevent cell death. Search for new DNase inhibitors as anti-cell death drugs requires simple quantitative methods for their testing. The goal of the current study was to evaluate isolated cell nuclei as a potential model for testing apoptotic DNase inhibitors and to determine whether DNase I or EndoG directly cause the 200bp ladder. Cell nuclei were isolated by Triton X-100 method from kidneys (expressing DNase I) and brains (with DNase I inactivated by alternative splicing) of wild-type (WT), DNase I knockout (KO), or EndoG KO mice and subjected to autodigestion for varying periods of time from 0 to 240 min in the presence of Ca2+ and Mg2+ ions, which universally activate DNases. Four previously developed inhibitors were tested, including DNase I inhibitors, IG17 and ZnNAC, and EndoG inhibitors, PNR-3-80 and PNR-3-82. DNA was then purified and subjected to 1.4% agarose gel electrophoresis. The gels were stained with ethidium bromide, photographed, and quantified by densitometry using the ImageJ program. EndoG KO or inhibitors did not affect the 200bp-ladder DNA fragmentation indicating that EndoG is not directly involved in it. DNase I KO also did not mitigate DNA fragmentation compared to WT, but DNA fragmentation in the brain and in the presence of DNase I inhibitors was suppressed (likely due to effects on several/other DNases). In conclusion, neither DNase I nor EndoG seems to be involved in DNA fragmentation in isolated normal cell nuclei.

4B. Analyzing the Role of Oncomodulin in Cochlear Rat Microglial Cells during Inflammation

Evan Paltjon, Dr. David Donley
Psychology, Harding University

The organ of Corti, the auditory sensory organ found in the cochlea, consists of various types of cells that allow sound wave impulses to be transmitted to the brain. Overstimulation due to mechanical damage can lead to calcium influx that damages or destroys the cell, eventually inducing hearing loss. Expression of the calcium buffering protein, oncomodulin (OCM) protects against damage but its role and mechanism are not fully understood. Oncomodulin has been found in macrophages and is associated with recovery from inflammation. However, it is unknown whether oncomodulin plays the same role in cochlear macrophages or microglial cells after mechanical damage or inflammatory insult. Macrophages and microglial cells may contribute to further cochlear damage or remediate it. The current study aimed to determine if and to what extent OCM plays a role in cochlear immune cells. Previously, macrophages have been found to infiltrate the

cochlea after lipopolysaccharide (LPS) administration or acoustic injury. elevated toll-like receptor 4 (TLR4) expression is associated with OCM expression and has been observed after both acoustic injury and inflammatory damage that leads to hearing loss. Presumably, the TLR4 pathway leads to the recruitment of macrophages and microglial cells whose role is currently unknown. Herein we report the response of cultured cochlear microglial cells (MOCHA) to inflammatory stimuli. Further, the role of OCM will be tested to determine if elevated OCM after damage contributes to the inflammatory response. These data are critically important because they contribute to our understanding of the pathology of hearing loss. An understanding of oncomodulin's role in the damaged cochlea may lead to a remedy for hearing loss, which is helpful in itself and also plays a role in the development of neurodegenerative diseases like Alzheimer's.

5A. Mechanisms Connecting Inflammation to Astrocytic Glucose Transport: Relevance to Alzheimer's Disease

Andrew Shelton
Biochemistry, Harding University

Alzheimer's disease (AD) is a neurodegenerative disorder characterized by progressive cognitive decline, memory loss, and neuronal death. A predominance of the evidence indicates that AD is precipitated by accumulation of the amyloid β-peptide (Aβ), which elicits an inflammatory response in the brain that includes an elevation in the levels of cytokines such as interleukin-1β (IL-1β) and tumor necrosis factor (TNF). Growing research also suggests a relationship between the dysregulation of brain glucose metabolism and the pathology of AD. Astrocytes, the most abundant glial brain cells, are essential for maintaining homeostasis in the brain, especially the conveyance of glucose from blood vessels to neuronal elements deeper in the brain parenchyma. Astrocytes primarily transport glucose through glucose transporter 1 (GLUT1) enzyme. Aβ can disrupt GLUT1 trafficking to the plasma membrane, resulting in attenuated glucose transport. This effect is replicated by a combination of IL-1β and TNF. Findings in other systems suggest that thioredoxin-interacting protein (TXNIP) or another protein termed GRP78/BiP may respond to cytokines and influence GLUT1. In primary cultures of astrocytes, TXNIP was manipulated through a molecular approach (RNAi) and GRP78/BiP pharmacologically (small-molecule inhibitor) to test the impact on glucose uptake in the presence and absence of cytokines. Initial results indicate a role for TXNIP but not GRP78/BiP, findings being tested through ongoing experiments. Determining the mechanisms involved in glucose dysregulation in AD may provide therapies relevant to both symptoms and progression of AD.

5B. NMES1 is a regulator of neuro-inflammation in cultured murine microglial cells

Jules Sinzi, Bre Bishop, Savannah Ewing,David Donley
Biology, Harding University

Beta-amyloid42(Aβ42) is a peptide that accumulates in the brain of Alzheimer's disease (AD) patients and is closely associated with disease-potentiating pro-inflammatory responses of microglial cells. While the inflammatory response to Aβ42 is extensively studied, the precise mechanisms and cell signaling pathways that trigger and regulate this response remain poorly understood. Consistent with prior literature, our preliminary data identified Normal mucosa of esophagus-specific1(NMES1) as a putative regulator of microglial activation in response to Aβ42. NMES1 is a mitochondrial cytochrome c oxidase subunit that is increased in cultured microglia by Aβ42. Consistent with its anti-inflammatory properties, NMES1, replaces the NDUFA4 subunit of cytochrome c oxidase, resulting

in lower efficiency of electron transport. Paradoxically, decreased mitochondrial respiration is often associated with elevated inflammation, but increased NMES1 is implicated in the suppression of inflammation. Therefore, we modulated NAMES1 expression in cultured microglial cells with and without Aβ42 stimulation. Herein we report on the impact of NMES1 on inflammatory markers and metabolic regulation in microglia. Notably, we found that the knockdown of NMES1 by silencing RNA resulted in an increase in the expression of CD68, a marker of inflammatory activation. Together our data is consistent with NMES1 acting as an inflammatory braking mechanism. Overall, we postulate that NMES1 has been previously underappreciated as an inflammatory regulator in microglial cells. However, more work is required to investigate the impact of NMES1 on microglial activation and proinflammatory responses during disease.

6A. Comparative Analysis of Microglial Responses to Beta-Amyloid Fibrils and Oligomers: Implications for Neurodegenerative Diseases

Tayler B. Appleton Dr. David W. Donley
Biochemistry & Molecular Biology, Harding University

Alzheimer's disease, and other similar neurodegenerative diseases, are linked to the aggregation of beta-amyloid beta (Aβ) peptides in the brain. There are multiple structural isoforms of Aβ, ranging from small soluble oligomers to intermediate fibrils and large, insoluble aggregates., each associated with distinct pathological outcomes. Aggregation is thought to be partially driven by a compensatory response to the toxicity of small monomers and oligomers. The generation of reactive oxygen species (ROS) in response to Aβ structures plays a pivotal role in neurotoxicity, yet the nuanced differences in ROS production and their implications for neurodegeneration remain enigmatic. This study presents a comparative analysis of ROS production in Aβ42 fibrils and oligomers within the IMG cell line which is utilized due the recapitulation of key features of microglial cells such as surface markers, phagocytic capacity, and morphological properties. Our study of ROS generation in Aβ42 fibrils and oligomers, utilizing the IMG cell line, has far-reaching implications for neurodegenerative disease research. Tailoring therapeutic strategies to target specific ROS pathways associated with each Aβ42 structure could lead to more effective treatments addressing different stages of disease development. Additionally, this research emphasizes the influence of environmental factors, including the ratio of sodium sulfate to stress, on Aβ42 fibril formation, offering novel avenues for preventive interventions. In conclusion, our research advances the understanding of ROS production within Aβ42 fibrils and oligomers, using the IMG cell line, providing valuable insights into their distinct roles in neurodegenerative diseases. These insights can guide the development of precision-targeted therapies while highlighting the significance of environmental influences on Aβ42 aggregation. This work contributes to a deeper comprehension of neurodegenerative disorders and lays the foundation for future therapeutic breakthroughs, recognizing the disparate contributions of Aβ42 oligomers and fibrils at various stages of disease progression.

6B. Determination of the Viability and Nutritional Content of Plants Grown in Martian Regolith

Abby White, Hannah Davidson, Dr. Rebekah Rampey, and Dr. Cindy White
Biology, Harding University

As NASA continues its plans to send men to Mars in the near future, there are still many aspects of the journey that remain left to be studied. One such example is how astronauts will be able to self-sustain

on the long journey in space as well as when they finally reach their destination on the planet's surface, including a source of food that will provide the nutrients needed to remain healthy. The intent of this project is to find crop options which would produce good sources of nutrients for the astronauts that plan to inhabit the surface of Mars. Current research includes determining which plants are capable of germinating and growing in Martian regolith soil as well as focusing on plants that are high in essential nutrients, specifically Vitamin C (ascorbic acid). Differences in growth rates between potting soil and Martian soil were evaluated as well as different germination processes. In addition, plants known to contain high amounts of Vitamin C were analyzed for their viability for growing in Martian regolith, as well as evaluating the concentrations of the Vitamin C produced in these plants.

7A. Investigation into the Role of Rev1 and Interacting Partners in Resolution of G4 Sequences

John Schaller, Dr. Amit Ketkar, Bethany Paxton, Reham Sewilam, Dr. Julie E.C. Gunderson, Dr. Robert L. Eoff
Biochemistry and Molecular Biology, Hendrix College

Translesion DNA synthesis (TLS) is a vital process to bypass replication stress or DNA damage. An inability to respond effectively to these stressors can lead to replication fork stalling, mutations, double-stranded breaks, or cancer. One such stressor is a G-quadruplex (G4) structure, a non-canonical DNA structure frequently encountered in G-rich regions of the genome. G4 structures have been shown to be potent blocks to DNA replication and require proteins that are specialized in binding and resolution of these structures. Rev1, a Y-family polymerase, is heavily involved in this activity, and allows replication to continue unhindered at sites of G4 sequences. We have previously shown using a supF mutagenesis assay with a G4 containing sequence placed in the lagging strand of a pSP189 plasmid that in HAP-1 cells deficient in Rev1, there is a >200-fold greater mutation frequency compared to Rev1-proficient cells (Ketkar et al., 2021). We will now investigate the positional effect on mutation frequency when G4 is placed in the leading strand of the pSP189 plasmid and compare results to a lagging strand G4 plasmid. Our previous work, using site-directed mutagenesis has also shown the important role played by residues E466 and Y470 in the insert-2 motif of human Rev1 in binding and resolving G4 DNA. We will conduct similar mutagenic studies to produce catalytically inactive Rev1 (D570A/E571A) either by itself, or in combination with the insert-2 mutations, to investigate whether catalytic activity of Rev1 is essential for binding and replication of G4 sequences. Questions surrounding the mechanism by which Rev1 works, particularly with respect to its recruitment of other proteins to resolve G4 sequences, remain. The C-terminal domain of Rev1 is believed to play a crucial role in protein interactions. Towards this end, a cell line that stably expresses Rev1 with C-terminal deletion (1-1040) will be generated. This cell line, together with similar cell lines expressing other mutant forms of Rev1, will be used in techniques like isolation of proteins on nascent DNA (iPOND), as well as immunofluorescence microscopy approaches like proximity-ligation assays to investigate the role of various Rev1 motifs in protein recruitment at G4 sites.

7B. Investigation into the Role of DHX36 in Rev1-mediated G4 Resolution

Kate Jackson, Julie E.C. Gunderson, and Robert L. Eoff
Biochemistry and Molecular Biology, Hendrix College

G-quadruplexes (G4s) are non-canonical nucleic acid structures that form in guanine-rich regions and present an endogenous barrier to replication. Failure

to bypass G4s during DNA replication may result in an increase in single-stranded DNA gaps and double-stranded breaks, which can lead to genomic instability. Rev1 is a translesion synthesis (TLS) polymerase that disrupts and replicates G4 DNA, though the precise mechanism is unclear. Ongoing work in the lab has implicated DEAH-box helicase 36 (DHX36) as a factor in Rev1-mediated G4 resolution through isolation of proteins on nascent DNA coupled with mass spectrometry (iPOND-MS). We validated these results in a Rev1*DHX36 proximity ligation assay (PLA) coupled with 5-ethynyl-2′-deoxyuridine (EdU) immunofluorescence detection, in which we confirmed Rev1-DHX36 association and found Rev1*DHX36 foci counts to be independent of EdU incorporation. This suggests that Rev1-DHX36 interactions may not be cell cycle-dependent. To evaluate G4-associated Rev1-DHX36 association, we conducted proximity ligation assays with pyridostatin (PDS), a selective G4-stabilizer. We found that Rev1*DHX36 foci decreased with prolonged treatment with PDS. We then performed a series of PLAs, including BG4*PCNA, Rev1*PCNA, and DHX36*PCNA, to assess proximity. BG4 is a G4-binding antibody. These results suggest that DHX36 is recruited to G4 sites and plays a role in Rev1-mediated resolution of G4 structures. Our findings have implications for novel cancer therapies that target TLS pathways as well as bypass mechanisms of endogenous fork barriers.

8A. The Plausible Role of Histone H2A Proteins in Bdelloid Rotifer DNA Repair

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Multiple DNA double-strand breaks caused by desiccation are lethal to most eukaryotes. Bdelloid rotifers, however, are an exception. These microscopic, aquatic animals possess unique DNA repair capabilities that allow them to survive desiccation. Their DNA repair mechanism is unusually efficient and not yet understood. In other eukaryotes, chromatin - specifically histone proteins - plays a key role in DNA repair. Bdelloids have seven histone H2A proteins with longer C-terminal tails than in other animals, so these proteins are good candidates for having a role in DNA repair. The objective of this project is to determine which bdelloid histone H2A proteins are likely involved in DNA repair. First, to identify polyadenylated histone mRNAs, 3’ random amplification of cDNA ends (3’ RACE) was used to sequence 3’ UTRs of histone genes in the bdelloid Adineta vaga. Transcripts with poly-A tails likely represent histone variants that might regulate DNA repair. Next, the function of histone H2A proteins H2Abd and H2Abd1 in A. vaga were investigated by using CRISPR genome editing to inactivate the genes. Single-guide RNAs (sgRNAs) designed to excise each gene were first tested using an in vitro Cas9 cleavage assay. A DNA template was also designed to replace each histone gene with the GFP gene during homology-directed repair. CRISPR was carried out by electroporating rotifer embryos with the sgRNA/Cas9 complexes and the GFP repair template. Fluorescence microscopy was used to find evidence of genome editing via GFP expression in rotifers. Once a histone mutant is identified, CRISPR will be used to inactivate histone H2A genes that are potentially involved in DNA repair. Mutant rotifers will be desiccated to cause DNA damage, then rehydrated to induce DNA repair. Ultimately, a reduced recovery rate in mutant rotifers relative to wild type rotifers would suggest that the targeted histone H2A gene has an important role in DNA repair.

8B. Role of platelet glycoprotein Ibα in radiation-induced cytogenetic damage

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In a large-scale nuclear event, individuals could be exposed to high levels of irradiation, which can have detrimental effects on the cytogenetic makeup of bone marrow, stem, and progenitor cells responsible for generating various blood cell types, including platelets. Platelets play a crucial role in communication with hematopoietic cells and carry numerous proteins and biologically active compounds. This study aims to investigate the potential impact of platelet glycoprotein Ibα (GPIbα) in modifying radiation-induced cytogenetic damage. Female mice, including wild-type and hIL-4R/Ibα mice, were exposed to a total body irradiation dose of 8.0 Gy. Bone marrow cells were collected from the femur and tibia for eight days after exposure for conventional and molecular cytogenetic analysis. The types and total number of chromosomal aberrations between hIL-4R/Ibα mice and age-matched wild-type mice were compared following irradiation. Data findings suggest that platelets play a role in modifying radiation-induced chromosomal damage. Preliminary data show that mice with dysfunctional GPIbα (hIL-4R/Ibα mice) exhibit increased inflammation, which is one of the major contributors of cytogenetic damage.

9A. Aeromicrobiology With High-power Rocketry

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

Aeromicrobiology With High-power Rocketry Katherine Hunter, Taylor Mitchell, Braden Glenn, and Dr. David Thomas Science Division, Lyon College, 2300 Highland Rd., Batesville, AR 72501

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. In addition to the LADCAP system, we are developing an alternate method of sampling for airborne particles. This method would function without a flight computer and would be designed for amateur microbiology in classrooms without access to the same resources as our research lab.

9B. The Catecholaminergic Component Within Cervical Vagus Nerve Influences Heart Remodeling: A Pilot Study

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The tandem of two antagonistic divisions of the autonomic nervous system, parasympathetic and sympathetic, controls cardiac functions such as heart rate, contractility, and coronary blood vessel diameter. Increased sympathetic outflow is involved in cardiac remodeling leading to the development and progress of congestive heart failure. Concurrently, parasympathetic activity may exert a protective effect on the heart. The Vagus Nerve (VN) is known as a principal source of preganglionic parasympathetic fibers to the heart. However, the presence of catecholaminergic fibers, presumably postganglionic sympathetic, ranging from 0% to 22%, has been detected through immunohistochemical assessment of the VN with anti-tyrosine hydroxylase (TH) antibody. The present study aimed to evaluate the correlation between the quantity of TH+ fibers within the cervical VN and the degree of heart remodeling. METHODS. Human cervical VN samples were collected bilaterally from 6 embalmed cadavers (male n=3, females n=3) at superior and inferior cervical ganglia levels for histological examination. All samples were evaluated for TH reactivity. Heart dimensions and wall thickness were measured before collecting myocardium for histological processing. Samples were harvested from both ventricles, interventricular septum and stained with trichrome to evaluate the presence of Connective Tissue (CT). All slides were photographed for quantitative analysis using ImageJ. SUMMARY. The linear regression showed a significant positive correlation between the thickness of the right ventricular wall and the number of TH+ fibers in the left VN ($p=0.02$). A trend towards increased CT within both ventricles and TH+ fibers within the right VN was apparent. CONCLUSIONS. The results of our pilot study revealed a positive correlation and trends between changes associated with heart remodeling and the number of TH+ fibers within the cervical VN.

10A. An Evaluation of Sympathetic Fibers within the Orbital Cranial Nerves

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Biology, Missouri Southern State University

The ophthalmic effects of disruptions in sympathetic outflow are characterized by a constricted pupil, drooping of the upper eyelid, and a sinking of the eyeball. Moreover, sympathetic outflow can influence various aspects of ocular function, including accommodation, blood flow regulation, and aqueous humor production. Despite the broad impact of sympathetic innervation (SI) on eye function, there remains ongoing debate regarding the precise anatomy of SI within the orbit. Previous studies have utilized immunohistochemical methods with anti-Tyrosine Hydroxylase (TH) antibodies to qualitatively examine sympathetic fibers within orbital nerves. However, a comprehensive quantitative analysis of these fibers has been lacking. This study aims to shed light on the presence, distribution, and quantity of catecholaminergic elements within the cranial nerves of the orbit. Methods. The frontal, nasociliary, and lacrimal branches of the ophthalmic nerve, as well as the superior and inferior divisions of the oculomotor nerve, the trochlear nerve, and the abducens nerve bilaterally from the orbits of five formalin-preserved adult human cadavers (3 males and 2 females) were collected for histological examination. All sections were validated through Luxol Fast Blue staining and assessed for TH reactivity. Photographic documentation of histological slides was performed,

and quantitative analysis was carried out using ImageJ software. Summary. Catecholaminergic fibers were consistently identified in all bilateral frontal nerves, with their presence ranging from 0.2% to 11.45%. The mean area of TH-positive fibers in the right frontal nerve was comparable to that in the left (0.022 ± 0.003 mm2 and 0.04 ± 0.019 mm2, respectively, $p>0.05$). TH+ fibers were also detected, either bilaterally or unilaterally, in the other collected samples, with a prevalence ranging from 0% to 25%. Conclusions. The number and distribution of TH+ fibers within orbital cranial nerves exhibit significant individual variations. Our study contributes to a deeper understanding of the morphology of these nerves within the orbit, which is crucial for the development of pharmacological agents and surgical techniques aimed at treating ophthalmic diseases.

10B. Qualitative and Quantitative Assessment of G-actin – Quantum Dots Interaction

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Quantum dots (QDs) are a type of nanoparticle with excellent optical properties, suitable for many optical-based biomedical applications. However, their toxicity limits the potential of quantum dots to use in clinical settings. As such, much effort has been invested to examine the mechanism of QDs' toxicity. Yet, current literature mainly focuses on ROS- and apoptosis-mediated cell death induced by QDs, which overlooks other aspects of QDs' toxicity. Thus, our study aimed to provide another way that QDs negatively impact cellular processes by investigating the possibility of protein structure and function modification upon direct interaction. Through Shotgun proteomics, we identified a number of QD-binding proteins, which are functionally associated with essential cellular processes and components, such as transcription, translation, vesicular trafficking, and actin cytoskeleton. Among these proteins, we chose to closely examine the interaction between quantum dots and actin, as actin is one of the most abundant proteins in cells and plays crucial roles in cellular processes and structural maintenance. We found that CdSe/ZnS QDs spontaneously bind to G-actin in vitro, causing a static quenching of G-actin's intrinsic fluorescence. Furthermore, we found that this interaction favors the formation of QDs-actin complex with a binding ratio of 1:2.5. Finally, we also found that CdSe/ZnS QDs altered the secondary structure of G-actin, which may affect G-actin's function and property. Overall, our study provides an in-depth mechanistic examination of the impact of CdSe/ZnS QDs on G-actin, proposing that direct interaction is another aspect of QDs' toxicity.

11A. Determination of Quantum Dots Effects on Downregulation of Yeast Transmembrane Transport Proteins

Emma Braun, Nhi Le, Dr. Kyoungtae Kim
Biochemistry, Missouri State University

Quantum dots are semiconductive nano crystals that produce a variety of fluorescent colors under UV light. Because of their versatility QDs can be used in various biological applications. Although QDs are useful recent studies have linked quantum dots to toxicity in cells. Since these findings have become apparent it is important to further study the mechanism of action of quantum dots to further understand and develop a safer alternative. The research surrounding QDs and how they enter cells is ever growing but not many studies have investigated how QDs interact with cellular components. Therefore, this study aims to further understand the interactions between QDs and transmembrane transport proteins. Our preliminary research has shown that upon addition of QDs in normal conditions Can1-GFP exhibited a statistically significant increase in membrane to vacuole fluorescence intensity ratio as compared to the control. This suggests that QDs may interfere with

the trafficking of Can1-GFP to the vacuole. We also tested the effects of QDs in starving conditions and found that the membrane to vacuole fluorescence intensity ratio was not statistically different. This suggests that when nutrients are not present the addition of QDs does not have a significant effect on downregulation. Moving forward we will investigate the effects on downregulation of Ste2-GFP, a receptor for α-factor pheromone, when treated with quantum dots.

11B. Changes in Soybean Associated Diazotrophic Community in Response to Land Use Change and Organic Matter Amendment

Erin Harrelson Scott David McElveen Dr. Michael Burton Dr. Babur Mirza
Biology, Missouri State University

Biological nitrogen fixation (BNF) by rhizobial endophytes is one of the main sources of nitrogen for legumes. The efficiency of BNF relies on the selection of rhizobial endophytes with soybean root nodules. The selection of rhizobial endophytes in root nodules can be influenced by several biotic and abiotic factors. In the current greenhouse study, we explored the potential influence of organic matter and previous crop rotation practices on the selection of rhizobial endophytes within soybean root nodules. We used Illumina paired-end DNA sequencing of 16S rRNA and nifH gene amplicons to assess the bacterial diversity within soybean root nodules and rhizosphere soil. The results of 16S rRNA gene sequencing suggested that there was no direct influence of preceding crop and compost amendment on the selection of rhizobial endophytes with soybean root nodules. In all treatments, Bradyrhizobium spp. were the dominant rhizobial symbionts, accounting for 95.9% of all 16S rRNA sequences retrieved from soybean root nodules. This suggests a strong role of the host plant in the selection of endophytes. Currently, we are assessing the nifH gene sequences to determine the distribution of diazotrophs within the rhizosphere of soybean plants.

12A. The toxic effects of perfluorooctane sulfonate (PFOS) on HepG2 and THLE-2.

Phuong D. Tran, Kyoungtae Kim
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Perfluorooctane sulfonate (PFOS), one of the most widely detected human-made perfluorinated organic compounds, has garnered increasing attention due to its widespread distribution and potential health risks. While PFOS occurs as a complex chemical in the environment, its toxicological interactions remain largely unknown. The current study utilized two immortalized cell lines, HepG2 and THLE-2, as experimental models that can mimic the conditions under which PFOS accumulates in the liver. The XTT viability assay results showed that both HepG2 and THLE-2 demonstrated a dose-dependent decrease in cell viability when treated with increasing concentrations of PFOS. The calculated IC50 concentrations of PFOS were approximately 100 micromolar. An elevation of reactive oxygen species (ROS) is expected in these cell lines.

12B. Constructing a Novel Human Cell Line Harboring POLE1 Patient Mutations

Chalisa Longden, Dr. Sapna Das-Bradoo
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Polymerase Epsilon is an enzyme responsible for leading-strand synthesis during DNA replication. Mutations of the central catalytic subunit, POLE1, have been implicated in connection with a disease causing facial dysmorphism, immunodeficiency, livedo, and short stature (FILS). Specifically, a single base pair substitution in intron 34 of POLE1 results in a truncated protein causing the impairment of T lymphocyte proliferation from G1 to S-phase. In order to better understand the mechanisms behind

these pathogenic mutations, our goal is to construct a novel cell line that mimics the FILS patient mutation. However, POLE is an essential gene, meaning a direct insertion of a FILS mutation to endogenous POLE could result in cell death. To circumvent this issue, we are constructing a novel HEK293T cell line where a POLE-FILS mutation will be inserted into the genome at the AAVS1 safe harbor site using Cas-9 transgene knock-in technology. To begin this process, a donor vector, pAAVS1-puro-DNR and a guide (gRNA) vector, pCas-Guide-AAVS1 were purchased from OriGene. pAAVS1-puro-DNR contains AAVS1 homologous arms, puromycin resistance for selection, and Myc-DDK tags. pCas-Guide-AAVS1 contains a Cas9 gene and a validated AAVS1 targeting sequence. Currently, we are in the process of cloning the POLE gene with FILS mutation into the pAAVS1-puro-DNR plasmid. The correct ligation of the FILS mutation into the donor vector will be verified via Sanger sequencing. Next, both the pAAVS1-puro-DNR (carrying POLE1-FILS) and pCas-Guide-AAVS1 plasmids will be co-transfected in mammalian cells. Colonies will be screened for the successful integration of the FILS mutation into the genome at the AAVS1 safe harbor locus. Ultimately, using Cas-9 technology, the endogenous POLE1 will be knocked out, allowing for the sole expression of POLE-FILS mutant genes in HEK293T cells.

13A. Fluorescently Tagging Proteins to Study the Function of Polymerase Epsilon Complex

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Natural Sciences, Northeastern State University

During DNA replication, the leading strand is synthesized by DNA polymerase epsilon. POLE1, POLE2, POLE3, and POLE4 are the subunits of DNA polymerase epsilon. Of these subunits, POLE1 and POLE2 are essential for cell viability. POLE3 and POLE4 are nonessential proteins but have an important function as histone chaperones (H3 and H4) during nucleosome assembly at the replication fork. Despite the relevance of Pole in DNA replication and nucleosome assembly, the formation of the polymerase epsilon complex in human cells remains undeciphered. Our research project seeks to fill this gap by studying Pole complex assembly using fluorescence microscopy and Pol epsilon mutants. Specifically, we are interested in determining if mutations in POLE3 and POLE4 disrupt interactions among the polymerase epsilon subunits. To accomplish this, we constructed GFP-tagged POLE3 and YFP-tagged POLE4 vectors. DNA sequencing confirmed the successful construction of the POLE3-GFP and POLE4-YFP vectors. Additionally, expression of the tagged proteins was confirmed in human embryonic kidney (HEK) 293T cells by western blotting. Currently, we are using fluorescence microscopy to study the co-localization of the mutated and wild-type versions of polymerase epsilon subunits in HEK293T cells. These results will be discussed at the meeting.

13B. Effect of Uropathogenic Escherichia coli on Bladder Cancer cells

Alejandro Lopez, Tram-An Ho, Shaariq Iqbal, Janaki K. Iyer
Natural Sciences, Northeastern State University

According to the American Cancer Society, it is estimated that there will be nearly 83,000 new cases of bladder cancer and nearly 17,000 deaths in 2023. Depending on the stage and type of bladder cancer, surgery, radiotherapy, and/or chemotherapy are commonly used for treatment. However, there is a rising incidence of radio-resistant and chemo-resistant bladder cancers. This increases the costs associated with treatment dramatically. In fact, it is estimated that more than $6 billion is spent annually on treatment of bladder cancers. Thus, there is a need for alternative and more effective therapies to treat bladder cancers. The bladder is a common target for uropathogens that possess virulence factors, which

facilitate infection in bladder tissues. Different strains of Escherichia coli (E. coli) are known to cause more than 70% of bladder infections. We hypothesize that certain virulence factors made by bladder cells may be promising therapeutics to treat bladder cancer. To this effect, we obtained different strains of uropathogenic E. coli (UPEC) and characterized their antimicrobial resistance and growth properties. We then infected bladder cells with these different strains and observed any changes in cell morphology. Out of 4 UPEC strains tested, bladder cells infected with E. coli CFT073 showed drastic changes in cell morphology within one hour of infection. Immunofluorescence studies demonstrated that there was dramatic reduction in microfilaments and the nuclei appeared smaller, which may indicate that the cells are undergoing cell death. Such changes were not observed in bladder cells infected with other UPEC strain. Further experiments are being performed to confirm that E. coli CFT073 causes cell death and evaluate the properties of the factor produced that causes these changes in bladder cells. These findings will enable us to determine if the factor produced by E. coli CFT073 can be used as a therapeutic to treat bladder cancer.

14A. Evaluating pro-inflammatory cytokine responses in bladder cells infected with uropathogens

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Urinary tract infections (UTIs) are common bacterial infections with high treatment costs associated. Escherichia coli (E. coli) is the most prevalent causative agent followed by Klebsiella pneumoniae (K. pneumoniae). Upon infection, bladder cells respond by producing pro-inflammatory cytokines. Despite the similarities in properties between E. coli and K. pneumoniae, there are differences that can influence the infection process and resulting response of the host to these pathogens. To better understand the hosts' immune responses to different uropathogens, we performed an Enzyme-Linked ImmunoSpot (ELISpot) assay that allowed us to determine the expression of multiple pro-inflammatory cytokines. We hypothesize that infection with different uropathogens will result in differential expression of pro-inflammatory cytokines. To test this hypothesis, we infected human 5637 bladder cells with uropathogenic E. coli and K. pneumoniae strains for 24 hours and determined cytokine protein expression. The results of the ELISpot revealed that uropathogenic E. coli induced the secretion of IL-1ra, IL-6, IL-1a, and IL-1b as compared to uninfected but the corresponding induction of IL-6, and IL-1b was reduced in bladder cells infected with K. pneumoniae strains. In order to understand the cytokine production and secretion process better, we determined that intracellular cytokine staining and evaluation by flow cytometry would be better. To detect cytokine production inside bladder cells, we used brefeldin A (BFA) to prevent the secretion of cytokines into the media. We determined if BFA was toxic to our bladder cells by an MTT cell viability assay. Our results revealed that there was no statistical significance between the different concentrations of BFA tested. Further experiments are being performed to determine the optimal conditions to detect cytokine production by flow cytometry. The findings will enable us to gain better insight into how uropathogens modulate innate immune responses in bladder cells during the infection process, which in turn will aid in developing more effective therapies for the treatment of UTIs.

14B. Comparisons of wheat seedling vigor by pathogen, environment, and genotype

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Significant stand loss in cereal grains has a deleterious effect on establishment as well as crop yield. Factors that effect stand include vigor, weather, disease, fertility management, planting date and variety. This study compared vigor for different varieties of wheat including perennial varieties. The experiments consisted of saturated cold tests, cold soil tests, as well as direct inoculation of seedlings for comparisons. Results demonstrated no difference between perennial lines and the standard wheat varieties tested for vigor. Environmental effects had stronger effects on all varieties compared to pathogens in these studies. Disease resistance variance was observed in non-homogeneous lines and could hold potential for the future.

15A. Evaluation of Extracellular Vesicle Isolation from 3 Mammalian Cell Lines

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Extracellular vesicles (EVs) are non-reproducing subcellular compartments produced and secreted by cells in the body as part of cellular signaling. EV therapies have the potential for replacing current synthetic drug delivery systems, invasive prognosis procedures, and various immunotherapies. Conventional immuno-marking techniques and other isolation methods for developing these therapies are limited between quantity of samples or specificity of samples due to the extensive variety in EV biophysical properties and composition. Comparisons were made and evaluated using harvested spent media from NIH-3T3 fibroblast cells, human Schwann cells, and human mesenchymal stem cells that underwent two methods of EV isolation: chemical isolation and chemical isolation with centrifuge filtration. Results indicate chemical isolation combined with centrifuge filtration further purified and filtered samples for EVs closer to the target smaller EVs which have been implicated in intercellular communication.

15B. Development of a Continuous Downstream Process for the Isolation and Purification of Proteins

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Bioreactor cell production is an efficient method to produce valuable proteins at high throughput. However, recovering these proteins can be an inefficient and tedious process due to the speed and efficiency limitations of traditional bioprocessing techniques such as ion exchange chromatography. Replacing these inefficient steps with alternative membrane technologies has been shown to dramatically improve the processing speed and recovery of important biomolecules such as proteins. By combining tangential flow filtration and membrane chromatography, a bioreactor downstream purification process was modeled for bovine serum albumin (BSA) and green fluorescent protein (GFP). Proteins were isolated from larger cellular contaminants using tangential flow filtration (TFF), then further purified from other similarly sized contaminants through membrane chromatography. Operating conditions such as membrane flux were optimized to increase protein recovery over multiple regeneration cycles. Membrane fouling was observed while separating BSA from Saccharomyces cerevisiae cells, but flux was able to be restored by regeneration cycles. A

maximum of 80% of BSA was recovered using TFF from a solution containing BSA and S. cerevisiae. Following the first separation step, a maximum binding capacity of 2.5 mg of BSA from a solution containing BSA and lysozyme was observed with membrane chromatography. BSA was then recovered with a 93% efficiency during elution. Similar high recovery values were reported using the fluorescence of GFP. This model downstream purification process has the potential to improve the scale of the production of valuable proteins and similar biomolecules of interest.

16A. Inhibition of Cytokine Production by uropathogenic Klebsiella pneumoniae

Jacob I. Castañeda, Jonathan Crosse, and Janaki K. Iyer
Biology, Northeastern State University

Inhibition of Cytokine Production by uropathogenic Klebsiella pneumoniae Jacob I. Castañeda, Jonathan Crosse, and Janaki K. Iyer Department of Natural Sciences, Northeastern State University, Broken Arrow, Oklahoma Different uropathogenic strains of Escherichia coli and Klebsiella pneumoniae cause most urinary tract infections. Of the two pathogens, infections caused by Klebsiella pneumoniae are harder to treat due to biofilm production and rising antimicrobial resistance. Upon infection with uropathogens, host cells induce the expression of pro-inflammatory cytokines as part of the innate immune response. Proinflammatory cytokines like interleukin (IL) 1β and IL6, produced in response to infection, induce inflammation resulting in an effective immune response. The purpose of this study is to characterize the modulation of cytokine production by different strains of Klebsiella pneumoniae. Since bladder cells express pattern recognition receptors that can identify the presence of different pathogen associated molecular patterns, we hypothesize that infection with different strains of Klebsiella pneumoniae will induce proinflammatory cytokine production when compared to uninfected cells. We obtained uropathogenic strains of Klebsiella pneumoniae from BEI resources and determined the antimicrobial resistance and growth characteristics of three strains: Kp UCI-19, Kp UCI-20, and Kp UCI-41. Out of the three strains, Kp UCI-19 and Kp UCI-41 were resistant to multiple antibiotics that are commonly used for the treatment of UTIs. We analyzed the production of IL1β and IL6 upon infection for 6 or 24 hours by enzyme-linked immunosorbent assays (ELISAs). Additionally, cytokine production in bladder cells infected with heat-killed Kp UCI-20 was evaluated. Statistical analyses were performed to determine significance. All three strains of Klebsiella pneumoniae showed significantly increased IL1β levels for both time periods, however, there was no significant induction of IL6 in bladder cells infected with these strains. Infection with Kp UCI-20 showed the least induction of IL-1β and IL-6. To determine if the viability of Kp UCI-20 was responsible for decreased cytokine production, bladder cells were infected with heat-killed Kp UCI-20. Heat-killed Kp UCI-20 decreased IL1β production but increased IL6 production. Based on our results, 2 out of the 3 strains of Klebsiella pneumoniae were multi-drug resistant and all three prevented the induction of IL-6 production. Further analysis of Kp UCI-20 showed that viability was a requirement for interfering with IL6 production in bladder cells. Future experiments will be designed to evaluate the mechanism of IL6 cytokine suppression by Kp UCI-20. These findings will identify targets and pathways that can be used for designing therapies for treating UTIs.

16B. The Effects of Light and Hypo-Gravity on the Devlopment and Movement of Dictyostelium discoideum

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Dictyostelium discoideum is a prevalent eukaryotic slime mold that has been utilized in many experiments because of its distinct development as an organism. Dictyostelium d.'s life cycle (figure 2) starts as spores which develop into amoebae, which feed on bacteria and when conditions are right, they will develop into multicellular structures referred to as slugs. The focal point of this experiment is to observe the movement and development of the slugs in response to light and the influence of gravity using a clinostat. To conduct the experiment, ten slugs were placed in the center of each lactose peptone plate and were either attached to a clinostat which rotated at 1 rpm or placed in a stationary position inside a clinostat box. Each plate was either treated to white light or darkness for a period of two days. Slugs on the stationary plates showed movement towards the light vector against the influence of gravity. There was little movement downward due to gravity's influence in dark conditions. Plates on the clinostat were not affected by gravity in the light conditions as they moved toward the vector. The plates without light, did not display much movement from the center.

17A. Nutrition Assessment of Pre-School and School-Aged Children

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One in three US children's body mass index (BMI) fits into the category of overweight or obese. Childhood obesity may lead to serious health risks associated with poor mental health and reduced quality of life. A multi-component approach involving dietary modification and advocacy for a healthy lifestyle comprised of regular physical activity, minimizing screen time and behavioral intervention found beneficial in preventing obesity.

17B. Quantification of Gordonia terrae Bacteriophages using Lysate qPCR

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Biology, Ouachita Baptist University

Bacteriophages are viruses that infect and replicate only in bacterial cells. Quantitative PCR was used in this experiment to count the number of DNA copies in the phage lysate sample. In this project, the more rapid lysate qPCR method was compared to standard plate count titer assays using the double layer agar method, to match the number of genomic copies with the plaque forming units in the lysate. Initially, multiple primer sets were designed to amplify the best primers and reaction conditions to use for phage detection. Because qPCR is sensitive to contamination, there were multiple controls to ensure no contamination. Subsequently, a standard curve was generated by comparing the phage concentration determined from titer assays with that measured using SYBR Green qPCR. The optimized lysate qPCR method will be a faster method to determine the number of bacteriophage DNA copies in phage lysate, allowing the rapid determination of phage concentration for optical density-based infection growth curve experiments.

18A. Peak aerobic capacity and dietary composition are related to the bioenergetic profile of platelets in children

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In the absence of a nucleus, platelet (PL) health is highly dependent on the health of their mitochondria. PL contribute to cardiovascular disease and ischemic events. Also, emerging evidence suggests that PL mitochondria may be used to study the bioenergetic health of vulnerable populations for whom tissue biopsy is not an option. Objective: The purpose of this study was to characterize the association of measures of PL mitochondria function with markers of cardiovascular health and dietary intake in 8 to 10-year-old children. Study Design/Methods: Children (n = 87) attended one study visit in the fasting state. Anthropometrics, cardiorespiratory fitness [incremental cycle ergometer test, VO2peak (ml·kg-1·min-1)], and physical activity [accelerometers, activity counts (AC), moderate to vigorous physical activity (MVPA)] were measured. Body mass index percentiles (BMI-P) were calculated using CDC standards. Dietary intake was estimated (Block Food Frequency Questionnaire). PL mitochondria respiration [oxygen flux analyzer, oxygen consumption rate (OCR) (pmol/min)] was measured: a) Basal respiration (B) b) Leak respiration (L) c) Maximal respiration (M) d) Reserve capacity (RC), e) non-mitochondrial respiration (NM) f) ATP linked respiration (ATP), and g) coupling efficiency (CE). The bioenergetic health index (BHI) was calculated. Spearman correlation coefficients were used to measure the correlation of PL mitochondria function with variables of interest. Results: Children (60% boys) were 9.52±0.86 y/o and predominantly Caucasian (64%). Mean BMI percentile was 75.37±23.52. VO2peak directly associated with L (rho= 0.21, p=0.049) and negatively associated with CE (rho= -0.24, p=0.025). BMI-P, total AC, and MPVA did not correlate with measures of PL mitochondria function. L decreased with increasing fruit consumption (rho= -0.23, p= 0.033), NM negatively correlated with % fat intake (rho= -0.35, p= 0.0008) and positively correlated % carbohydrate intake (rho= 0.31, p= 0.003). ATP positively correlated with saturated fat consumption (rho= 0.23, p=0.027). CE was positively correlated with fruit consumption (rho= 0.25, p= 0.017). The BHI did not associate with measures of fitness and dietary intake. Conclusions: The bioenergetic profiles for PL is influenced by dietary composition and peak aerobic capacity. Whether these findings translate in changes in PL activation will be determined in the ongoing MI-Energy study. Funding: This work was funded by USDA-ARS 6026-51000-012-06S

18B. Characterization of temperate bacteriophage infection of Gordonia species utilizing an optical density-based approach

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Bacteriophages are viruses that infect and replicate within bacterial hosts; phage-host interactions, including successful infections, play a role in shaping bacterial populations. This research aims to describe bacteriophage infection in Gordonia, a soil actinomycete. The infection efficacy of a phage is determined by analyzing the growth of infected bacteria and comparing it to an uninfected host. Optical density measurements are used to describe bacterial growth, with virus infection metrics determined by analyzing optical density values of uninfected and infected cultures over time. These experiments evaluated temperate Gordonia phages Goib, GrandSlam, and Ruthy on host species Gordonia terrae CAG3, Gordonia lacunae, and Gordonia rubripertincta. Preliminary results confirm

findings previously observed in phage lambda, that temperate phages "choose" lysogeny over lysis at a high multiplicity of infection. This research will provide insights into how phage infection dynamics vary among different Gordonia host species, contributing to the understanding of phage-host interactions. The outcomes have implications for fields such as microbial ecology and phage biology, furthering our knowledge of phage infection dynamics and bacteriophage-host interactions.

19A. Progress Towards Phage Stability for Possible Oral Phage Therapy

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Oral cavities or caries is a localized deterioration of the tooth caused by an accumulation of harmful bacteria. This research intends to integrate bacteriophages onto unwaxed dental floss as a possible future preventative treatment for oral cavities. Bacteriophages are viruses that degrade the composition of bacterial populations by invading and reproducing inside bacterial hosts. The experimental framework involves soaking unwaxed floss in bacteriophages, Phrick and Stonehill. The effectiveness of infection is measured by applying the phage-infused floss on an agar plate with Gordonia terrae CAG3, then analyzing the diameter of the plaque around the floss. This research will provide insight on the interactions between bacteriophages and bacterial pathogens, focusing on stability of phage within the oral solutions. Preliminary results confirm phage stability on filter paper, successfully lysing bacteria on an agar plate. The result carries significance in areas of dentistry and microbiology.

19B. Nutrition Assessment of Older Adults Using the Nutrition Focused Physical Exam

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As a person ages, the body transitions into a less active state with lower energy levels and a decreased appetite. Nutritional deficiencies are a result of this physiological decline in food intake. The nutrition focused physical exam (NFPE) is an in-depth examination of a patient from head-to-toe by a trained nutrition professional. The exam identifies muscle wasting, subcutaneous fat loss, and edema. The objective of this research study was to determine the prevalence of malnutrition and its severity in elderly adults using body mass index (BMI), hand grip strength, NFPE, and 24-hour dietary recall.

20A. Tick and tick-borne pathogen surveillance as a public health tool updating Kansas geographic distribution map

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Ticks transmit a wide variety of pathogens including viruses, bacteria, protozoa, and helminthes to vertebrates. Their life cycle depends on blood meals from various hosts as well as on environmental conditions such as the temperature and habitat type. With climatic changes, the expansion of tick habitat is apparent and thereby a need arises for annual surveillance of ticks and periodic update of geographic distribution maps. The present study conducted tick surveillance using flag-drag technique in both Crawford County and Anderson county, Kansas as well as collected ticks from a

veterinary clinic in the Crawford Co. during March-August 2023. Locations surveyed in the Crawford Co. were a mined land area, a recreational park, and a farm. Surveillance in Anderson Co. was conducted in recreational areas. Environmental data (temperature, humidity, etc.) were collected on-site at each visit. Collected ticks were identified in the laboratory using taxonomic keys at the species level and differentiated by sex and life stages. A total of 499 adult and nymph ticks were collected, the majority of which were identified as Amblyomma americanum (90.4%, Males-204, Females-173, Nymphs-74) and a significant number of Dermacentor variabilis (9.6%, Males-25, Females-23) were also obtained. More than one species of Amblyomma were identified from the vet clinic. Identified ticks will be pooled and tested for selected bacterial pathogens using real-time PCR. The outcome of this study will help our Kansas State agency in updating the geographic distribution map of ticks in Kansas. Knowledge of pathogens carried by this tick population will assist in management programs and efforts to reduce the risk of tick-borne diseases.

20B. Elucidating the role of type I collagen mutations on respiratory function in osteogenesis imperfecta

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Respiratory failure is a leading cause of death in patients with Osteogenesis Imperfecta (OI), yet the primary phenotype of OI is bone fragility and malformation. It has long been thought that bone deformities alone, particularly rib cage and spinal distortions, restrict ventilation, yet recent research suggests that abnormalities in the lung itself may exist and lead to respiratory problems in OI patients. We previously showed morphological and functional changes in the lungs of OI mouse models. Specifically, OI lungs had enlarged alveolar structures perhaps due to defective alveolar septation compared to WT mouse lungs, resulting in less surface area for gas exchange. We hypothesize that defective type I collagen in matrix-synthesizing lung fibroblasts, cells that produce the majority of collagen and play a role in alveolar development, will lead to dysregulation of lung alveolar morphogenesis and alteration in mRNA expression levels of genes involved in this process. Our goal is to 1) confirm if a lung-specific collagen mutation in mice leads to altered lung morphology and respiratory function independent of skeletal defects and 2) identify cellular and molecular dysregulation leading to improper alveolar development using single cell RNA-sequencing. Identification of differentially expressed mRNA/proteins may offer new therapeutic targets to improve health and quality of life for OI patients.

21A. Exploring Genomic Convergence for Adaptations to Freezing Environments in Polar Fish

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Convergent evolution provides valuable insights into how natural selection shapes species traits. A remarkable example of convergent evolution is the independent development of antifreeze proteins (AFPs) in phylogenetically distant polar fish lineages. While AFPs themselves are relatively well studied, the full genomic context of adaptation to freezing conditions in fish remains largely unexplored. One interesting approach to investigate genomic convergence is by analyzing the dynamics of gene family size over evolutionary time. Leveraging the whole genome sequences previously assembled in our lab, along with other high-quality genomes available in GenBank, we examined the gene family size in the AFP-bearing species and their closely

related AFP-lacking outgroup species across multiple teleost fish lineages. Our goal was to identify gene families that have either expanded or contracted in AFP-bearing species, those capable of withstanding freezing temperatures, in comparison to their respective outgroups. Through the identification of shared expanded and contracted gene families and a thorough exploration of their functions, we aim to uncover valuable insights into the molecular mechanisms underlying the convergent freezing adaptations in these species.

21B. Phosphonate Recycling

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Phosphorus plays a vital role in cell physiology and biochemistry. It is found in various forms, including the carbon-oxygen-phosphorus (C-O-P) linkage and the chemically inert, lysis resistant carbon-phosphorus (C-P) bond. Organophosphorus compounds containing the C-P bond are referred to as (organo)phosphonates. Phosphonates occur both naturally and synthetically, and they are often used as antibiotics, agrochemicals, coolants, and industrial additives. It is estimated that in the US alone, more than 20,000 tons of phosphonates are released annually into the environment in the form of herbicides and detergent wastes where it becomes toxic. There is a significant interest in understanding the mechanisms by which phosphonates are degraded by bacterial species. This will help to resolve phosphonate pollution. There are three known classes of enzymatic systems that have been mechanistically characterized which can lyse the C–P bonds of phosphonate compounds. These include phosphonate hydrolases, the C-P lyase complex, and an oxidative pathway. Unfortunately, those enzymatic systems of phosphonate degradation are insufficient to break down those phosphonates released into the environment. The goal of my project is to engineer and mechanistically characterize novel enzymes/microorganisms that will degrade phosphonates more efficiently in order to minimize the environmental impacts of these compounds. The approach is to clone and express the promising phosphonate degradation genes from different wild type bacteria, select highly efficient ones for further enhancement by various genetic methods including mutagenesis and evolution.

22A. Identification of the cellular proteins that determine the activation state of the proapoptotic protein Bax in human cells.

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Dysregulated apoptosis plays a pivotal role in numerous human maladies, encompassing tumor genesis, neurodegenerative diseases, and autoimmune disorders. Within this context, Bax stands as one of the principal proteins of the Bcl-2 family, alongside Bak, serving as a crucial conduit for mitochondria-mediated programmed cell death. In non-apoptotic, Bax's transmembrane domain is sequestered within a hydrophobic pocket of its own molecular structure. However, during apoptotic stimuli, Bax undergoes a series of conformational shifts, transitioning from the cytosol to the mitochondria, thereby instigating mitochondrion-dependent apoptosis. However, the precise mechanism governing Bax activation remains an area of ongoing inquiry. The objective of this project is to understand the molecular mechanism of Bax activation. Our hypothesis is that one or more cellular proteins interact with the Bax protein and keep Bax in the inactive state in healthy cells. Traditionally, biochemical and genetic methodologies, such as co-immunoprecipitation, have been employed to investigate proteins that associate with Bax, yet these techniques bear

fundamental limitations. A proximity-dependent biotin identification (BioID) method has been developed to overcome these limitations based on the fusion of a protein of interest to a promiscuous biotin protein ligase. Through the application of BioID, we found that prohibitin 2 was associated with or physically proximate to Bax in the non-apoptotic cells. PHB2 has been shown to inhibit apoptosis in various cell types. Immunostaining using antibodies against Bax and PHB2 and followed by confocal microscopy image analysis demonstrate that PHB2 and Bax colocalize in the cells. Currently, we are working on examining the potential role of PHB2 in regulating the activation state of Bax in human cells by using a combination of biochemical, molecular, and cell biology techniques. By elucidating the mechanisms steering Bax activation, we aim to enhance our understanding of cellular apoptosis, paving the way for therapeutic advancements in related pathologies.

22B. Utilizing CRISPR/Cas9 to Investigate Putative Meiotic Recombination Hotspots in Schizosaccharomyces pombe

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High rates of homologous recombination during meiosis are required for the faithful segregation of chromosomes and to generate genetic diversity upon which natural selection acts. Meiotic recombination is clustered at "hotspots" that are irregularly distributed across the genome. To further elucidate how discrete DNA sequences direct hotspots, we are using the CRISPR/Cas9 gene-editing system to introduce specific sequences into the model organism Schizosaccharomyces pombe. We have incorporated two previously identified DNA motifs, known as HES92 and HES95, that are potential hotspots into the reporter gene ade6. To accomplish this, we transformed wild-type fission yeast with a plasmid that expresses both the Cas9 endonuclease and a guide RNA that directs it to the desired region of ade6. The plasmid was co-transformed with a short DNA fragment containing the motif of interest flanked by sequences homologous to the target region. Transformants were selected by resistance to the drug G418, as well as screened for red colony color, indicating the successful incorporation of mutations in ade6. The resulting ade6 gene of selected transformants was analyzed by Sanger sequencing. The sequences obtained revealed that some of the candidates contained only a subset of the desired mutations, while others harbored all of them. The latter strains were then utilized in recombination tests to determine whether the inserted motifs elevate recombination levels. Recombination test results were inconclusive but did suggest that the incorporated DNA motifs elevated levels of recombination. Further recombination tests must be conducted to draw conclusive results.

23A. Evaluation of promotor-driven Factor IX expression in skeletal muscle for hemophilia therapeutics

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As medicine and technology improve, the standard of care for patients evolves. Many researchers are vying to switch treatments from symptom minimization to curative therapies. Gene therapies are an emerging option for the curative treatment of genetic diseases and cancers. Hemophilia B is one such disease, with an estimated 6,000 men suffering in the U.S. alone. It causes a coagulation factor IX (FIX) deficiency, a protein vital to the blood clotting cascade. The lack of FIX leads to episodes of prolonged and spontaneous bleeding. Current treatments for hemophilia B consist of infusions of

coagulation concentrates administered as often as every other day. While this treatment is adequate for a short time, a curative treatment would mitigate the treatment burden. The FDA has only approved one curative hemophilia B treatment, Hemgenix, a gene therapy directed towards the liver, the endogenous FIX producer. However, skeletal muscle (SM) is a promising candidate as a regenerative protein factory. SM accounts for over 30% of the body's mass, is easily accessed for therapy administration, and expresses proteins needed for FIX processing and export. This indicates that SM could be utilized as a non-endogenous protein factory. To prove this, we will deliver a construct with the human FIX (hFIX) coding sequence into mouse skeletal muscle cells and evaluate the muscle-generated-hFIX expression. This study will also examine the effect of two muscle-specific promoters on FIX expression in SM, a creatine kinase promotor (CK8e) and the synthetic muscle-specific promotor (SPc5-12), compared to a ubiquitous cytomegalovirus promoter (CMV). Use of the CMV promoter, while inducing strong expression, could lead to oncogene activation due to its ubiquitous nature. SPc5-12 and CK8e are inactive in non-muscle tissue and thus are a safer option for viral vector-mediated gene therapy. In addition to this, we also analyzed the hFIX expression of two different FIX variants, the K5A variant, a muscle-specific mutation, and Padua, a hyperactivity mutation. Based on qRT-PCR, there was no significant difference between FIX gene expression under CMV and CK8e promotors after normalization with peptidylprolyl isomerase (Ppia), a housekeeping gene. A continued study will show the protein expression capacity under promoter and the ability of SM to post-translationally modify non-endogenous protein.

23B. Prolactin and cortisol and the molecular control of gill ion transport

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Atlantic killifish is an estuarine fish that can handle changes in salinity ranging from dilute freshwater to double strength seawater. To keep constant plasma ion concentrations in a changing environment, specific gill cells secrete salt in seawater and take up ions in fresh water. In fresh water, these ionocytes express Na-Cl cotransporter (ncc) and Na-H exchanger (nhe) that are responsible for NaCl retention, as well as epithelial calcium channel (ecac) involved in calcium uptake. In seawater ionocytes, Na-K-2Cl cotransporter (nkcc), Na-K-ATPase (nka1a) and cystic fibrosis transmembrane conductance regulator (cftr) are needed to secrete salt. These genes were evaluated, along with tight junction proteins and aquaporin-3 (aqp3) controlling gill permeability and cell volume. The salinity dependence of the genes was examined in killifish acclimated to fresh water, brackish water, and seawater. A series of organ explant experiments examined the role of two osmoregulatory hormones (prolactin and cortisol) in molecular control of gill function. It was discovered that cortisol stimulates the markers of seawater ionocytes (cftr and nka1a), while prolactin had no significant effect on the expression of these genes. Prolactin in conjunction with cortisol stimulated ncc2b and aqp3 both associated with the freshwater gill phenotype. Cortisol stimulated ecac suggesting it to be a hypercalcemic hormone in killifish in contrast to its role in mammalian calcium homeostasis. Our data so far indicate that prolactin promotes freshwater acclimation while cortisol plays a dual role; and that this is done in part by organizing the expression of multiple transport proteins in the gill.

24A. Synthetic mechanical loading on autophagy-deficient osteocytes in vitro

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Macroautophagy maintains cellular homeostasis by recycling cytoplasmic contents including lipids, organelles, and protein aggregates. Macroautophagy contributes to osteoblast to osteocytes differentiation. In previous studies, macroautophagy was eliminated in the entire osteoblast lineage via conditional knockout of Atg7 in mice utilizing the protein cre recombinase (Cre) under the Osterix1 (Osx1) promoter. After the conditional knockout of Atg7 a significant decrease of periosteal diameter was observed indicative of a reduced response to load. Further investigation showed low bone formation in conjunction with decreased bone resorption as well. This decrease in bone turnover was due to decreased effector bone cell number. Further investigation revealed there was decreased osteocyte cellular projections and enlarged cell body in Atg7 flox;Osx1-Cre mice. We hypothesize that the morphologically altered osteocyte network leads to improper sensation and response to load and contributes to low bone mineral density in vivo. To start testing this we will examine if mice lacking autophagy in the osteoblast lineage can respond to synthetic mechanical loading in a normal fashion. Piezo1 is a calcium sensing receptor in osteocytes that is involved in the influx of calcium ions for a proper response to load. This receptor can be allosterically activated by a small molecule named Yoda1, such activation is speculated to mimic mechanical loading. Stimulation of bone organ cultures in vitro with Yoda1 was performed. Afterward, Atg7 flox;Osx1-Cre cells that are treated with Yoda1 effectively simulating mechanical load, were analyzed for the expression of genes responsive to mechanical loading and compared to control groups. It was discovered that Yoda1 induced load on macroautophagy deficient osteocytes in vitro increases expression of genes responsive to mechanical loading.

24B. KSHV-transformed Primary Effusion Lymphoma Cells Exhibit Oncogene Addiction to the Mitochondrial Ubiquitin Ligase MARCHF5

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Primary Effusion Lymphoma (PEL) is an AIDS-associated cancer caused by the Kaposi's Sarcoma-Associated Herpesvirus (KSHV). Our previous work has shown that PEL cell lines require the expression of the oncogene MCL1 to promote tumor cell survival by inhibiting intrinsic apoptosis. Furthermore, ongoing work in our laboratory reveals that MCL1 may synergize with another oncogene MARCHF5. This is surprising since MARCHF5 has not been linked to apoptosis; it is instead known as a mitochondrial E3 ubiquitin ligase that regulates mitochondrial fusion/fission. Our goal is to define how the mitochondrial oncogenes MCL1 and MARCHF5 function together in PEL cell lines. Using a doxycycline-inducible Cas9 system, we showed that CRISPR knockout (KO) of MARCHF5 led to a significant decrease of live cells accompanied by increased caspase 3/7 activity without affecting proliferation. Western blot analysis reveals that the total protein levels of the pro-apoptotic and MCL1 antagonist NOXA increases upon MARCHF5 KO. The stabilization of NOXA protein suggests that it may be a direct client of the MARCHF5 E3 ligase thus linking MARCHF5 with MCL1 in preventing intrinsic apoptosis. Since intrinsic apoptosis leads to loss of mitochondrial activity, MARCHF5 KO decreased mitochondrial membrane potential but not total mitochondrial content as revealed by staining with MitoTracker dyes followed by flow cytometry. In sum, our results indicate the oncogene MARCHF5 is essential for the

survival of PEL cells by limiting the levels of the pro-apoptotic protein NOXA thereby synergizing with MCL1 function. MARCHF5 should be further studied for a potential therapeutic target for PEL.

25A. Determining Gene Expression Profile of Dedifferentiated Cells of Dictyostelium discoideum

Analise Black, Nelly Ortiz, Maria Salas, Elizabeth Willhite, Evan Wittig & Sandhya Baviskar
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One of the multicellular stages during Dictyostelium development life cycle is the slug stage which is formed at 14 to 16 hours of development. A slug is a 1-2 mm long tubular structure consisting of differentiated cells. We conducted experiments to explore if slug cells can undergo dedifferentiation, and we found that differentiated cells when kept in a nutrient medium undergo dedifferentiation but not in a non-nutrient medium like phosphate development buffer. These findings have led to these two important questions. 1. Would these differentiated slug cells dedifferentiate in the presence of bacteria, their natural food source? 2. Is there a reversal in expression of developmentally regulated genes in dedifferentiated cells? To answer the first question, we will plate physically disaggregated slug cells with Klebsiella aerogenes on a solid media (SM) agar plate. Using an inverted microscope, the test plate will be compared to a control plate containing normal Dictyostelium cells and Klebsiella aerogenes. To determine if there is a reversal in expression of developmentally regulated genes in dedifferentiated cells, we plan to study and compare the expression of two developmentally regulated genes: ecmA and pspA because their expressions are required to form a slug. Using RT-PCR and DNA sequencing techniques we will confirm the presence or absence of these genes in dedifferentiated cells.

25B. Effect of Tallgrass Prairie Restoration on Soil Microbiomes – Fungal Diversity

Le Nguyen, Elham Hejaz, Jeff Shaver
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The native tallgrass prairie once occupied a large area of the midwestern U.S., but agriculture has virtually eliminated the biome and microbial diversity that once supported it. Recent developments in microbial analysis indicate that soil communities may also serve as indicators of restoration effectiveness. However, there is currently little knowledge of important fungal and functional processes in both wild and restored ecosystems. This project seeks to create a baseline for analyzing the effects of present-day prairie growth, maintenance, and restoration on soil microbial populations. In this study, fungal diversity and abundance at 12 locations, including virgin, remnant, restored, and non-restored (turfgrass) tallgrass prairie, will be characterized and compared using ITS (Fungal) amplicon sequencing. In Ben Geren Park (Fort Smith, AR), soil samples were collected from four restored prairie sites, one non-restored (turfgrass) site, three remnant prairie sites, and four neighboring virgin prairie sites (Massard Prairie). Additional soil samples were also collected and analyzed from three other virgin prairies within Sebastian County, including Dillon, Long, and Walker prairie. The 12 soil samples were collected and stored in Zymo Research DNA/RNA Shield Lysis Collection Tubes. The sample tubes were then shipped to Zymo Research for total soil DNA extraction and sequencing of ITS (Fungal) amplicons. The ITS sequencing report delivered by Zymo Research provides assessments of alpha- and beta-diversity (within- and between-samples), taxonomy heatmaps, and soil fungus compositional bar plots. The ITS amplicon sequencing service report will contain group comparisons and LefSe biomarker finding. In other studies, soil fungal diversity and microbial resilience has been shown to be boosted by plant biodiversity. Therefore, we

expect higher fungal taxonomic diversity in virgin and restored tallgrass prairie compared to non-restored (turfgrass) tallgrass prairie. The restoration of tallgrass prairie biodiversity is expected to enhance fungal diversity in the soil by promoting mycorrhizal symbiotic relationships, which is characteristic of virgin tallgrass prairie.

26A. Least Flycatchers Under Reported in Fall Migration in Arkansas--A Citizen Science Conundrum

Luke Barnes, Ragupathy Kannan, and Jack Jackson II
College of Arts and Sciences, University of Arkansas at Fort Smith

The Least Flycatcher Empidonax minimus is a small passerine migrant bird that passes through Arkansas in fall and spring migration. The birds are vocal during spring passage but relatively quiet and unobtrusive during fall migration, leading to many fewer reports by birdwatchers in fall than spring. We use eBird maps and data to present evidence to support this discrepancy between fall and spring observations. We also show that the species is under-reported in Arkansas during the fall compared to neighboring regions. This may be in part due to the reluctance of some birders to provide the minimal evidence required to substantiate their observations to satisfy eBird reviewers' queries.

26B. The Effect of Tallgrass Prairie Restorations on Soil Microbiomes- Bacterial diversity

Elham Hejaz, Le Nguyen, Jeff shaver*
Biology, University of Arkansas at Fort Smith

The decline of tallgrass prairies due to land development has highlighted the importance of restoration initiatives. Exploring the impact of restoration on soil microbiomes is essential, as these microbial communities play a fundamental role in maintaining the ecological integrity and functionality of prairie ecosystems. We will use 16S rRNA amplicon sequencing to characterize and compare bacterial diversity and abundance at 12 sites, including virgin, remnant, restored, and non-restored (turfgrass) tallgrass prairie. Soil samples were collected from these 12 sites, including four restored prairie sites in Ben Geren Park, one non-restored (turfgrass) site in Ben Geren Park, three remnant prairie sites in Ben Geren Park, and four nearby virgin prairie sites (Massard Prairie). Additional soil samples were also collected and will be analyzed from three other virgin prairies within Sebastian County, including Dillon, Long, and Walker Prairies. At each sampling location, soil was collected with a 2.5 cm diameter soil corer to a depth of 10 cm. For each sample, 250 mg of soil was transferred to 1.5 mL tubes with 500 µl of Zymo DNA/RNA Shield Solution and shipped to Zymo Research for 16S rRNA Amplicon Sequencing. Based on the sequencing results, we predict that non-restored (turfgrass) samples will be dominated by specific bacterial taxa adapted to turfgrass environments. In contrast, virgin tallgrass prairie samples are expected to host a distinct set of dominant taxa. Over time, restored prairie samples are likely to exhibit a gradual shift in dominant bacterial taxa, with an increase in those typically associated with native tallgrass prairie ecosystems. For example, we anticipate the enrichment of nitrogen-fixing bacterial taxa in restored prairie samples. This enrichment may promote soil fertility and the establishment of native plant species.

27A. Using Myxoma Virus to Understand the Intrinsic Immune Properties of SAMD9

Jennifer Chen, Jia Liu, mentor
Fulbright Honors College, University of Arkansas, Fayetteville

Poxviruses are useful for studying host species barrier and host immunity, due to their dependence on host machinery and ability to successfully inhibit and manipulate host pathways. Various members of the poxvirus family possess proteins that affect the mammalian protein, sterile alpha motif domain containing 9 (SAMD9), to establish cellular infection. SAMD9 is a conserved cytoplasmic protein in mammalian cells. Its deleterious mutation is associated with human diseases (NFTC, MIRAGE Syndrome, Myeloid Malignancies). SAMD9 is also known to present anti-poxvirus properties within host cells. Despite the diverse functions of SAMD9, its underlying molecular mechanisms are unknown. To unravel the mechanism in which it carries out its functions, a rabbit infecting poxvirus, Myxoma virus (MYXV), was utilized. MYXV consists of a M062 protein that encodes the sole inhibitor of human SAMD9. The aim of this study is to understand the mode of action of SAMD9 by exploiting the interaction between SAMD9 and MYXV M062 protein. To do this, the Liu lab generated a mutant MYXV, MAV-M062R, which will be compared to wildtype Lu-M062R virus. The mutation in MAV-M062R (I79T) prevents binding with the SAMD9 protein, resulting in defective protein expression. This defect in viral protein synthesis leads to attenuated infection. In this study, Western blot was utilized to further examine viral protein production that characterizes such effect. Five viral protein targets were used to analyze the expression of viral proteins, at different stages of the viral life cycle. By characterizing the absence or presence of these viral targets during different stages of infection, the stage of viral replication that is attenuated in MAV-M062R can be determined. Thus, by analyzing this relationship between the SAMD9 protein and the M062 protein of MYXV, we care able to gain a better understanding of how SAMD9 protein performs its antiviral effect in host cells.

27B. Unlocking the Secrets of NORAD and implications for Cancer Research and Treatment Using Zebrafish Models

Tatiyana Jennings is the presenter, Mentor Is Dr.Goodarzi
Biology, University of Arkansas at Little Rock

In the quest for advancing cancer prevention, early detection, and effective treatment strategies, an in-depth exploration of cancer mechanisms and the preservation of genomic stability in vertebrates emerges as a pivotal endeavor. Within this context, our research centers on the zebrafish, a well-established model organism renowned for its remarkable relevance to human biology. Our focus lies in understanding the pivotal role played by NORAD, a substantial long noncoding RNA (lncRNA), in maintaining genome stability within vertebrates. While NORAD's established function as a negative regulator of PUMILIO (PUM) proteins in the cytoplasm is well-documented and known to bolster genome stability, recent breakthroughs have unveiled its equally vital role in genome stability, this time through interactions with the nuclear RNA binding protein RBMX. Our ongoing research endeavors to untangle the intricate mechanisms governing NORAD's subcellular localization, with particular emphasis on its response to DNA damage—an imperative facet of cancer research. We are committed to deciphering the enigmatic processes underlying RNA nuclear export, with a specific focus on the efficient transport of intron less RNAs to the cytoplasm, an area of inquiry that has remained largely unexplored.

28A. The impact of toll-like receptor 8 (TLR8) on vesicular trafficking and foam cell formation

Aiiryel K. McCoy, Ahmed Tolba, Andrew Igbokidi, Ryan M. Allen
Chemistry, University of Arkansas at Little Rock

A third of all deaths in the United States are attributed to atherosclerotic cardiovascular disease (ASCVD), a chronic disease defined by progressive, lipid-rich plaque growth within arterial walls. Elevated levels of circulating cholesterol on low-density lipoprotein (LDL) are a primary risk factor for ASCVD due to LDL accumulation within the sub-endothelial space and LDL uptake by macrophages. The engorgement of the macrophages with LDL causes foam cell formation; a large, dysfunctional, lipid-loaded cell that often becomes necrotic and directly contributes to plaque growth. Treatment options that target foam cell formation to treat and prevent ASCVD are limited due to an incomplete understanding of why LDL uptake promotes macrophage dysfunction and foam cell biogenesis. Recently, our group reported that LDL transports small RNA and these non-traditional cargos trigger inflammatory polarization of macrophages by activating toll-like receptor 8 (TLR8), an endosomal sensor of single stranded RNA. Most intriguingly, antagonism of TLR8 reduced ASCVD in hyperlipidemic mice and blunted the formation of foam cells within developing plaques. With these recent discoveries, we hypothesize that TLR8 contributes to foam cell biogenesis by disrupting endosome-to-lysosome transport of internalized LDL particles. To test this hypothesis, we have developed fluorescent fusion proteins to track TLR8 containing vesicles and novel fluorescent viral-like particles that function as our molecular tools. We were able to successfully develop these tools and will use them to confirm the localization of TLR8 within the endo-lysosomal track, visualize the pinocytic uptake and transport via confocal microscopy, and assess how TLR8 could be contributing to LDL-induced foam cell dysfunction.

28B. Establishment of a Tick-Borne Pathogen Diagnostic Lab at University of Arkansas at Monticello

Sadie Whaley, Karissa McGuire, JC Adair, Jacob Courson, Keith Blount, Andrew Roser
Math and Science, University of Arkansas at Monticello

Tick-borne diseases are a serious public health concern in Arkansas because of the high density of various tick species located here. Several of the native tick species carry pathogens capable of infecting humans and are easily found in recreational and high foot trafficked areas. Little surveillance data for host-seeking infected ticks exists in Arkansas. Together with the Arkansas Department of Health (ADH) and the Centers for Disease Control (CDC), we are working to set up a diagnostic lab at the University of Arkansas at Monticello to screen ticks collected in Arkansas for various Rickettsia and Ehrlichia species (among others). Our first testing will be on ticks collected using flags through 100m transects in high trafficked areas of Cane Creek State Park located in Star City, Arkansas. Ticks were collected once weekly for over two years and includes tick species like Amblyomma americanum (lone-star tick) and Ixodes scapularis (deer tick/black-legged tick). Preliminary testing has focused on screening the ticks for Ehrlichia chaffeensis and Ehrlichia ewingii which cause ehrlichiosis. We used conventional nested PCR to detect the VLPT gene for E. chaffeensis and a segment of the 16S rRNA gene for E. ewingii. Future work includes screening for more tick-borne pathogens as well as begin screening ticks collected from dogs at veterinary offices and rescues. Through this surveillance project we hope to provide updates for both tick distribution and abundance as well as pathogen distribution data to help the ADH and CDC

reduce the impact of infectious vector-borne diseases in the state of Arkansas.

29A. Computational Study of CDC42 Inhibitors for Therapeutic Interventions in Triple Negative Breast Cancer

Ross Hunter, Emily Esquivel, Djamali Muhoza
Math and Science, University of Arkansas at Monticello

CDC42, a Rho GTPase, has been involved in various cellular processes, including cell morphology, migration, and division. Its dysregulation has been associated with various cancers, including triple negative breast cancer (TNBC), where it contributes to aggressive tumor behavior and metastasis. The present study used computational techniques to discover potential inhibitors that can modulate CDC42 activity in TNBC. Leveraging molecular docking and dynamic simulations, we analyzed a compound library of 10,000 small molecules for interactions with the CDC42 wild type and mutant. The most promising compounds, identified based on binding affinities, were further subjected to in silico pharmacokinetic and toxicity evaluations. Three standout compounds were identified that exhibited not only high binding affinities to CDC42 but also favorable drug-like properties with minimal predicted adverse effects. These compounds represent potential therapeutic agents for targeting CDC42-driven pathways in TNBC. Such interventions could attenuate the aggressive phenotypes associated with TNBC and enhance patient prognosis. Rigorous in vitro and in vivo validations are essential for these identified compounds. If substantiated in further studies, our findings could pave the way for novel therapeutic strategies targeting CDC42 in TNBC.

29B. In vitro establishment and micropropagation of *Ipomoea batatas* an Arkansas relevant crop to use as a sustainable educational model of molecular techniques for undergraduate students at UAM.

Alexandra Barnett, Pricila Tinajero, Michael Wilson, Edwin Martinez, Dr. Arturo Quintero Ferrer
Biology/Biochemistry, University of Arkansas at Monticello

An unknown cultivar of Sweet potato (Ipomea batata) was established in vitro and added to the UAM germplasm collection. Through this project, students have learned about concepts such as media preparation, aseptic techniques, pathogen identification and tissue culture techniques in a lab environment. After gaining an understanding of these techniques, our group created a goal: to establish molecular techniques using sweet potato as a model at the plant biotech lab. These techniques include whole genome nucleic acid extraction and serological detection of pathogens. Both techniques will use the micropropagated material from our germplasm collection of sweet potatoes. The extraction protocols presented are based on a nucleic acid extraction kit and nucleic acid CTAB extraction technique. The serological techniques presented in this work will test for the following sweet potato viruses: Sweet Potato Feathery Mottle Virus (SPFMV), Sweet Potato Virus G (SPVG), C (SPVGC) and 2 (SPVG2). All of these viruses belong to the Potyvirus genus. Our team will use the Potyvirus specific immunostrips to test the material for the presence of pathogens. This project allows students to gain an understanding of molecular techniques while striving to learn about and improve the quality of the sweet potato plant.

30A. Phylogenetic study of Heartland virus variants in the United States

Edwin Martinez, Dr. Arturo Quintero Ferrer, and Dr. Phillip Williams, Dr. Keith Blount
School of Math and Natural Sciences, University of Arkansas at Monticello

Identified in Missouri in 2014, the Heartland virus (HRTV) is a tickborne virus with fewer than 100 documented cases. It is closely related to severe fever with thrombocytopenia syndrome virus (SFTSV). Belonging to the Phlebovirus group, HRTV has very similar symptoms to SFTSV, which is exclusive to most of Asia. However, HRTV variants have been detected in multiple states throughout the United States. HRTV presents severe symptoms, though the mortality rate is low, still can be confused with STSV, which can causes misdiagnosis in patients. Through our project, we intend to use bioinformatics tools to characterize the variants and uncover their phylogeny. Which will enable us in the future to create effective molecular analytical tools to not only distinguish between the SFTSV and HRTV, but to also detect the HRTV variants within the United States. As a new uncommon virus, awareness and prevention for any virus is never an invalid option.

30B. In vitro establishment and micropropagation of Ipomoea batatas an Arkansas relevant crop to use as a sustainable educational model of molecular techniques for undergraduate students at UAM.

Alexandra Barnett, Pricila Tinajero, Macie Carter, Michael Wilson, Edwin Martinez, Dr. Arturo Quintero Ferrer
Biology, University of Arkansas at Monticello

In vitro establishment and micropropagation of Ipomoea batatas an Arkansas relevant crop to use as a sustainable educational model of molecular techniques for undergraduate students at UAM. Alexandra Barnett, Pricila Tinajero, Macie Carter, Michael Wilson, Edwin Martinez, Mentor: Dr. Arturo Quintero Ferrer.An unknown cultivar of Sweet potato (Ipomea batata) was established in vitro and added to the UAM germplasm collection. Through this project, students have learned about concepts such as media preparation, aseptic techniques, pathogen identification and tissue culture techniques in a lab environment. After gaining an understanding of these techniques, our group created a goal: to establish molecular techniques using sweet potato as a model at the plant biotech lab. These techniques include whole genome nucleic acid extraction and serological detection of pathogens. Both techniques will use the micropropagated material from our germplasm collection of sweet potatoes. The extraction protocols presented are based on a nucleic acid extraction kit and nucleic acid CTAB extraction technique. The serological techniques presented in this work will test for the following sweet potato viruses: Sweet Potato Feathery Mottle Virus (SPFMV), Sweet Potato Virus G (SPVG), C (SPVGC) and 2 (SPVG2). All of these viruses belong to the Potyvirus genus. Our team will use the Potyvirus specific immunostrips to test the material for the presence of pathogens. This project allows students to gain an understanding of molecular techniques while striving to learn about and improve the quality of the sweet potato plant.

31A. The influence of sodium chloride supplementation during heat activation on germination of Bacillus anthracis spores.

Kinlee Baker, Taylor East, Allison Abney, and Andrew Roser, Ph.D.
Math and Science, University of Arkansas at Monticello

Bacillus anthracis is a gram-positive rod-shaped bacterium capable of forming dormant endospores in response to environmental stressors. Spores are the infective particles of anthrax disease which is

acquired via inhalation, ingestion, or injection of the endospores. Damage to hosts is caused after the spores transition into metabolically active cells through a process called germination. Germination can be stimulated artificially via molecules called germinants. In laboratory settings, spores are exposed to a sublethal heat treatment, called heat activation (HA), to increase the extent and rate of germination. The underlying mechanism of how a sublethal heat treatment primes spores to germinate is unclear. Manipulation of the ionic concentration during a germination assay has a similar impact on germination to HA for spores of other Bacillus species but has not been thoroughly studied in B. anthracis. Because NaCl supplementation is a physiologically relevant treatment and heat activation is not, we wanted to determine if supplementing NaCl during germination of unheated B. anthracis Sterne spores would have similar results to that of heat activated spores. Additionally, we wanted to determine if various sodium ion concentrations within the cortex of the spore would affect the mechanism of heat activation by showing a reduction in spore germination. Spore germination was measured via the loss of optical density at 580nm. We measured the germination of spores that were treated with varying concentrations of NaCl in water during heat activation at 65ºC for 30 minutes and samples that had NaCl supplementation during germination. Our results showed that supplementation of NaCl enhanced germination of B. anthracis spores as it has in other Bacillus species in both heated and unheated spore samples. However, NaCl supplementation during heat activation of the spores did not enhance nor reduce germination compared to the untreated spores. Our future experiments will explore the duration and temperature of heat activation with NaCl as well as testing different germinants pairs that would still be physiologically relevant. Understanding the impact of NaCl at concentrations that mimic those in the human body can shed light on how the spores interact with and germinate inside of macrophages while initiating infection.

31B. Macrophage markers CD206 and CD204 expression and role as prognostic indicators.

Carvis Campbell III, Ashley Allen, and Vinay Raj
Regulatory Science, University of Arkansas at Pine Bluff

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

prognostic indicators has to be evaluated further extensively.

32A. Peptidoglycan Hydrolase as an Alternative to Antibiotics to Treat Streptococcus

Jacqueline Twumwaah, Dr. Grace Ramena, Annik Segree
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Bacterial infections like Streptococcosis, caused by Streptococcus iniae, have exerted a significant economic impact on the global aquaculture industry. While antibiotics remain effective against many bacterial infections in fish, the growing resistance to antibiotics and their increased use in aquaculture raise concerns about severe environmental and human health consequences. Furthermore, multi-drug resistant strains have the potential to transfer antibiotic resistance from aquaculture farms to clinical settings. These potential complications have instigated intensive efforts to develop safer alternatives to traditional antibiotics. These novel antimicrobials, distinct from antibiotics, should exhibit resistance to the development of resistance themselves. Phage endolysins are peptidoglycan hydrolases (PGHs) that degrade bacterial cell walls, with peptidoglycan being a major structural component. Utilizing bioinformatic tools, we have identified ten PGHs with the potential to prevent and/or eradicate systemic and topical S. iniae infections in fish. We employed the pET21a (+) vector for the expression of PGHs with a 6x His tag in BL21 (DE3) E. coli, purified the resulting proteins, and subsequently tested them against S. iniae strains.

32B. Label Free Tracking of Cellular Metabolism in Glioblastoma Using Optical Metabolic Imaging in Response to Combined Chemo-Radiotherapy

Re'Nyah Vincent, Dr. Varsha Karunakaran, Dr. Narasimhan Rajaram
Biology, University of Arkansas at Pine Bluff

Glioblastoma is a type of glioma and the most aggressive form of cancer originating from the central nervous system (CNS). The common subtypes of glioblastoma are glioblastoma Isocitrate dehydrogenase (IDH) -wild type (IDHwt) and IDH-mutant (IDHm) type. Isocitrate dehydrogenase is a key enzyme involved in Krebs cycle, catalyzing the conversion of isocitrate to alpha-ketoglutarate using NAD+ as co-enzyme. IDH-m tumors are more responsive to chemoradiation therapy and have improved patient prognosis than IDH wild type. Thus, it is of great significance to detect, track, and elucidate, IDHm and IDHwt cell types and their response to therapy associated stress. Reduced nicotinamide adenine dinucleotide (NADH) and flavin adenine dinucleotide (FAD) are naturally fluorescent co-enzymes, which allows non-invasive imaging of cellular oxidation reduction reactions and metabolic activities of living cells and tissues via optical redox ratio (ORR) calculation and fluorescence lifetime imaging microscopy (FLIM) analysis. Hence, optical metabolic imaging of IDHwt and IDHm glioma cells can offer valuable insight into their distinction which will be beneficial for the clinicians for taking better treatment strategies for glioma patients. Herein, the primary aim of current research was to determine whether the ORR and FLIM measurements of the IDHwt and IDHm is capable to identify differences between them during radiation therapy, chemotherapy and combined chemoradiation therapy to allow for real time sensing of the phenotype of glioma stem cells undergoing mesenchymal transition (GSCMT). For radiation therapy, two groups of cells (Control group, and 10

Gy group), each containing IDHwt cells and IDHm cells, were imaged once every 24 hours over the course of two days in order to establish baseline changes in the ORR and FLIM. Even though there are some differences in ORR and FLIM between the two cell lines as well as different treatments and time points, the optical redox ratio appears to be very high at baseline, which is atypical for highly proliferating cells. Further studies with additional time points and associated statistical analysis are required to determine changes if any occurring during cellular metabolism in IDHwt cells and IDHm cells. IC50 of Temozolomide drug was determined for the chemotherapy part of the study which will be utilized to perform the multiphoton microscopy imaging of the chemotherapy and combined chemoradiation therapy. Current experimental design shows the potential of optical metabolic imaging for the utilization of this method in therapeutically targeting glioblastoma and developing precision medicine to improve health outcomes for glioblastoma patients.

33A. Exploring Underutilized Plant Leaves in Different Extracts for Health Benefits: Antimicrobial and Antioxidant Properties

Tasbida Sultana, Dr. Shahidul Islam
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In this study, we aimed to assess the presence of beneficial compounds and potential health benefits in leaf extracts from four different types of Cucurbitaceae plants, namely Bottle gourd (Lagenaria siceraria), Pumpkin (Cucurbita pepo), Bitter gourd (Momordica charantia L.), and snake gourd (Trichosanthes cucumerina). These commonly found vegetables have been utilized for their nutritional value and traditional medicinal uses. We looked at total phenolic and flavonoid levels, antioxidant properties, and their ability to combat microbes. We employed four different solvents—acetone, methanol, ethanol, and hexane—to extract the bioactive compounds present in these leaves. We put these extracts through a series of tests to check their natural properties. We used a method based on the Folin–Ciocalteu colorimetric approach to measure phenolic content. We employed the aluminum trichloride assay for flavonoids, while antioxidant capacity was determined using the 2,2-diphenyl-1-picrylhydrazyl radical scavenging assay. To measure antimicrobial activity, we used the disc diffusion method. Our findings showed that, on average, methanolic extracts have the highest yield. Among the different plant varieties, bottle gourd exhibited the highest levels of total phenolic content (458.16±1.34 mg tannic acid equivalent/g of dry plant extract), flavonoids content (74.81±0.60 mg quercetin equivalent/g of dry plant extract), and antioxidant capacity (IC50 value 86.93±5.25 of µg/mL). Our extracts also demonstrated bactericidal activity and antifungal effects. This suggests all tested extracts contain phenolic compounds and possess antioxidant and antimicrobial properties against Gram-positive and Gram-negative bacteria. The findings offered valuable insights into the prospective health advantages linked to the consumption of these leaves. Keywords: Antioxidant, Leaf Extract, Cucurbitaceae, Aluminum trichloride assay, IC50 value, Bactericidal activity.

33B. Intraspecies Variation in Adaptive Stress Response Regulation

Lily Pitts, Dr. Jeffrey Lewis, Carson Stacy
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Intraspecies Variation in Adaptive Stress Response Regulation Eukaryotes respond to environmental stresses by activating kinase signaling cascades. The highly conserved High Osmolarity Glycerol (HOG) pathway in Saccharomyces cerevisiae is traditionally characterized as a mitogen-activated kinase (MAPK) pathway that is activated solely by osmotic stress. The current understanding of the HOG pathway in

Saccharomyces cerevisiae is based on research centered around an artificially selected strain known as S288C, which has unusual phenotypic properties. It is currently unknown whether the HOG pathway's specificity to osmotic stress is an ancestral or derived phenotype in Saccharomyces cerevisiae. In this study, we examined the gene expression profiles of stress-exposed laboratory and wild-type Saccharomyces cerevisiae strains both with and without the Hog1 gene. As expected, the deletion of HOG1 in the laboratory strain resulted in zero differentially expressed genes in the response to ethanol and peroxide but did cause a change in gene expression when exposed to osmotic stress. However, in the HOG1 knockout wild strains, we saw significant differences in expression when exposed to peroxide and ethanol as well as osmotic stress. This indicates that the role of the MAPK Hog1p extends beyond the response to osmotic stress in tested wild strains. Further evidence for the non-representative nature of the laboratory strain's HOG pathway is the total number of genes differentially expressed in response to osmotic stress. In the laboratory strain, a total of 710 (12%) genes were differentially expressed, where 1621 (27%) and 2489 (41%) were differentially expressed in the vineyard and oak strains respectively. These results indicate a need to reconsider the breadth of functions of the canonical MAPK HOG pathway in S. cerevisiae to a set closer to that seen in higher order organisms, suggesting a new avenue for studying MAPK-related disorders using wild strains of S. cerevisiae as a reduced model system.

34A. Recruitment Patterns of HELB in the DNA Replication Stress Response

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DNA replication stress poses a significant challenge to cellular integrity. HELB, a DNA helicase, plays a vital role in cellular recovery from this stress. While its role in DNA repair is established, its involvement in replication and interactions with other proteins require further investigation. ATR, the master kinase regulating replication stress response, potentially links ATR-phosphorylated HELB to recruitment at single-stranded DNA sites, where it interacts with replication protein A (RPA). This study aims to examine ATR's influence on HELB recruitment during DNA replication stress. Wild-type cells were treated with hydroxyurea (HU) and HU plus ATR inhibitor AZD6738 to induce and prevent replication stress response activation, respectively. The experiment monitored Chk1 phosphorylation, a downstream ATR target, to establish an ATR control. Evaluating HELB's presence in different cellular fractions under varying treatment conditions aimed to elucidate recruitment patterns and explore ATR-HELB interplay during the replication stress response. GAPDH and histone H4 served as controls for soluble and chromatin fractions, ensuring precise fractionation techniques. Using this method, we found ATR-independent recruitment of HELB to chromatin upon HU treatment. In the subsequent stage, we investigated whether the catalytic activity of SMARCAL1 and ZRANB3 in replication fork reversal is crucial for HELB recruitment. Treating cells with siSMARCAL1 and siZRANB3 revealed that HELB recruitment to reversed fork structures occurs independently of these catalysts. Additionally, we aim to explore the requirement of HELB's interaction with RPA and/or ATPase activity in its chromatin localization process.

34B. Can the Genetic Programs be Reversed? Exploring and Understanding Dedifferentiation in Dictyostelium discoideum

Analise Black, Nelly Ortiz, Maria Salas, Elizabeth Willhite, Evan Wittig & Sandhya Baviskar
Biology, University of Arkansas at Fort Smith

Dedifferentiation is the process by which cells with specialized functions grow in reverse direction to become less differentiated. Understanding the process of dedifferentiation is a new focus in stem cell and regenerative medicine research because stem cells derived by dedifferentiation would pose no risk of genetic incompatibility or immune rejection. To understand dedifferentiation at a fundamental level, soil amoeba, Dictyostelium discoideum, is a suitable model as it readily transits back and forth between both unicellular and multicellular stages. During its developmental life cycle, Dictyostelium starving amoebae go through several stages to form a multicellular fruiting body which has a basal disc, stalk and spore at the top. Prior to the formation of a fruiting body, starving amoebae form a multicellular tubular structure called a slug. A slug looks relatively undifferentiated but contains several cell types such as anterior pre-stalk cells, posterior pre-spore cells, and in the posterior region, anterior-like cells. Can these differentiated cells of slug undergo dedifferentiation, that is, can these cells revert to their original form? To answer this question, Dictyostelium slugs were physically disaggregated. One group of disaggregated cells of slugs were maintained in HL5 nutrient medium and a second group was maintained in a non- nutrient development buffer. Cell morphology and behavior of both groups of disaggregated cells were observed and compared to normal Dictyostelium amoebae after 24 hours. We found that disaggregated slug cells in presence of nutrient medium dedifferentiate and look very similar to their original form.

35A. Citizen Science: Role of iNaturalist in Biodiversity Documentation and Education in Arkansas

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iNaturalist is a global online digital platform for documenting and fostering interest in biodiversity, with Research Grade (RG) entries being vetted and scientifically valid observations. Here we present a review of the role of approximately 16,000 Arkansans using the iNaturalist tool for recording 445,000 verifiable observations comprising 10,800 species, with 40 percent RG, and one third of observations still pending confirmation. Overall, plants lead in RG observations followed by invertebrates and birds. Within these groups, reptiles lead in proportion of RG observations, followed by birds and amphibians. Less charismatic or infrequently encountered organisms are less represented. Arkansas ranks about average in per capita number of RG observations relative to other states. We urge further usage of this tool to increase biota awareness and research within the state of Arkansas.

35B. Analyzing the Role of PCDH1 and GTPBP10 on Pronephric Development in X. laevis

Kolby Payne, Jasmeet Ghotra, Dr. 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 PCHD1 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.

36A. Validating proteomic findings in methionine-restricted colorectal tumors

Jeremiah Canady, Sarita Garg, Isabelle R. Miousse
Chemistry, University of Central Arkansas

Colorectal cancer is the fourth leading cause of death amongst cancer patients. This is true for both men and women, in the United States and for the state of Arkansas as well. Nearly half of colorectal cancer cases are associated with a mutation in the oncogene KRAS. Both chemotherapy and radiation therapy can be used, but patients with the KRAS-mutated (KRASmut) cancer cells do not usually respond well to the treatment. These activated-KRAS mutations make it difficult for any treatment to work properly, as the tumor cells display a high resistance. From previous research in our lab, existing literatures, and with the help of proteomics data collected here at UAMS, it is evident that KRAS mutated cancer cells are highly dependent on methionine, which is an essential amino acid. We also know that KRAS contributes to the metabolic pathway NRF2 and the PI3K/AKT signaling pathway. Our hypothesis is that reducing the intake of methionine would re-sensitize the KRAS mutant cells, and hence forth making them more susceptible to treatment. Therefore, the goal of our project is to confirm that the KRAS pathway is increased in the tumors from mice that were fed a diet low in methionine, while also looking at related proteins, and comparing them to the results from growing the same cancer cells in the lab in vitro.

36B. Plate-Based SP4 and Other Plate-Based Sample Prep Methods for Proteomic Analysis

Natalie Stocks Dennis Province
Chemistry, University of Central Arkansas

Global proteomics is the study of proteins and the proteome. The analysis method used for this type of experiment is mass-spectrometry of the peptides after separation by reverse phase liquid chromatography. For a sample's peptides to be analyzed in the mass-spectrometer, it must undergo sample preparation to extract the proteins which are then digested into tryptic peptides. In this experiment, the focus is the sample preparation that extracts the proteins from the other cellular material. There are a multitude of different sample preparation protocols specialized for specific samples and desired data. At the IDeA National Resource for Quantitative Proteomics the most preferred method for tissue and

cells is chloroform-methanol extraction (CME). This is a reliable method that yields high peptide counts but works best with 100ug protein. It is a labor-intensive protocol that requires samples to be processed individually. In addition to this, a primary concern at the National Resource is high-throughput. A filter plate-based method to extract proteins is more desirable because this method would be compatible with positive pressure and liquid handling robotics, which can cut time, allow 96 samples to be processed at once, and increase reproducibility. A newly developed method that only requires 10ug of sample and has potential to be adapted into a plate-based method, is solvent precipitation single-pot, solid-phase-enhanced sample preparation, also called SP4.

37A. Volumetric Parcellation of the Brain of the Nine-Banded Armadillo

Student authors: Olivia Farnsworth, Zechariah Johnson, Martin Ugarte Faculty mentor: Dr. Jeffrey Padberg Will be presenting the poster with Martin Ugarte.
College of Natural Sciences and Mathematics, University of Central Arkansas

Members of the mammalian superorder Xenarthra (sloths, anteaters, and armadillos) present a wide range of morphological variations, both in external physical appearance and brain structure. The similarities and differences between the neuroanatomical makeup of xenarthran brains have been lightly studied; however, recent studies have described functional properties in the visual cortex of armadillos (Scholl et al., 2017). Another avenue of study is to examine the thalamus of armadillos compared to those of other mammals. The mammalian thalamus is loosely described as a "relay station" for sensory information and is composed of many nuclei that contribute to both sensory and motor function. The thalamic nuclei project afferent signals to other structures including cortex, which continues the process. To date, the specific neuroanatomical organization of armadillo thalami is not fully understood. For our project, using Nikon software and the confocal microscope in CCCS, we worked towards generating a volumetric analysis of the nine-banded armadillo (Dasypus novemcinctus) brain, by outlining boundaries so we can determine volumes of the different brain subdivisions. The data collected includes the volume of the entire brain, left and right hemispheres, as well as cortical and olfactory volumes where applicable. Whereas rats and some other mammals have a neuroanatomical atlas (e.g., Paxinos and Watson, 2013) for use in neuroanatomical analysis, armadillos do not. In our research, we hope to create an atlas complete with various histochemical and immunohistochemical stains which will provide an aid for further research on the topic. With this information, we will hopefully gain more understanding about the role of armadillo thalami in behavior and processing.

37B. Volumetric parcellation of the Brain of Nine-Banded Armadillo

Olivia Farnsworth, Zechariah Johnson, Martin Ugarte, Dr. Jeffrey Padberg
Biology, University of Central Arkansas

Members of the mammalian superorder Xenarthra (sloths, anteaters, and armadillos) present a wide range of morphological variations, both in external physical appearance and brain structure. The similarities and differences between the neuroanatomical makeup of xenarthran brains have been lightly studied; however, recent studies have described functional properties in the visual cortex of armadillos (Scholl et al., 2017). Another avenue of study is to examine the thalamus of armadillos compared to those of other mammals. The mammalian thalamus is loosely described as a "relay station" for sensory information and is composed of many nuclei that contribute to both sensory and motor function. The thalamic nuclei project afferent

signals to other structures including cortex, which continues the process. To date, the specific neuroanatomical organization of armadillo thalami is not fully understood. For our project, using Nikon software and the confocal microscope in CCCS, we worked towards generating a volumetric analysis of the nine-banded armadillo (Dasypus novemcinctus) brain, by outlining boundaries so we can determine volumes of the different brain subdivisions. The data collected includes the volume of the entire brain, left and right hemispheres, as well as cortical and olfactory volumes where applicable. Whereas rats and some other mammals have a neuroanatomical atlas (e.g., Paxinos and Watson, 2013) for use in neuroanatomical analysis, armadillos do not. In our research, we hope to create an atlas complete with various histochemical and immunohistochemical stains which will provide an aid for further research on the topic. With this information, we will hopefully gain more understanding about the role of armadillo thalami in behavior and processing.

38A. The prevalence of Chlamydiae symbionts in natural populations of social amoebas in Arkansas

Alyssa Nolan, Alexis Villalobos, Kira Gibbs, Mackenzie Hoogshagen, James Gabe DuBose, Tamara Haselkorn
Biology, University of Central Arkansas

Chlamydiae is a diverse bacterial phylum with over one thousand different families. Some of these families are part of what is known as environmental Chlamydiae; bacteria that have been found by metagenomic sequencing, although their hosts are only beginning to be discovered. So far, these environmental Chlamydiae have recently been found to live intracellularly in an increasingly wide range of hosts, including amoebae. Novel Chlamydiae lineages have been found in a particular species of social amoeba, Dictyostelium discoideum, which is a commonly used model organism to study host-symbiont interactions. The prevalence and diversity of Chlamydiae in other species of social amoebas, however, is unknown. To elucidate this potential symbiotic relationship between social amoebas and Chlamydiae, we are exploring how the Chlamydiae prevalence varies by location, species, and other environmental factors. We collected 11 different social amoebae species in damp soils across 11 parks in Arkansas. We then extracted their DNA and performed PCR using Chlamydiae-specific primers to detect infection. We found that the average Chlamydiae prevalence in social amoebae in various parks in Arkansas ranges from 10-72% with social amoebae hosts D. discoideum and D. giganteum having the highest infection. Chlamydiae prevalence was highest in logs and during the warmer months. Studying these novel symbiotic interactions between social amoebae and their Chlamydiae symbionts will help to understand their significance in the natural environment.

38B. The Relationship Between the Presence of the Cytoskeleton and Mitochondrial Fission and Fusion

Cameron Heslip, Dr. Kari Naylor
Biology, University of Central Arkansas

Mitochondria play vital roles in the cell, including production of ATP and influencing apoptosis. There are detrimental consequences to mitochondrial dysfunction, which is suspected to be the cause of many human diseases. Alteration of mitochondrial dynamics of fission and fusion significantly contribute to mitochondrial dysfunction, and thus disease. Through this research, the relationship between mitochondrial dynamics and the cytoskeleton is examined, which may reveal a correlation between the presence of the cytoskeleton and human disease. To accomplish this goal, in early experiments, we visualized actin with a LimEΔCC-GFP construct expressed by Dictyostelium discoideum and determined the distance of

mitochondrial fission and fusion events from the actin cytoskeleton. Early results showed that 60.56% of individual mitochondria were localized farther than 1 μm from an actin filament. In terms of fission and fusion, most events occurred 1-2 μm from an actin filament. These results suggest that mitochondria do not interact with actin filaments, and that mitochondria do not need direct interaction with actin for fission and fusion in our system. To ensure these results were specific to the actin cytoskeletal filament, we repeated the experiment after destabilizing actin with Lat-B. Here we present our results from the analysis of LimEΔCC-GFP cells treated with Lat-B and EtOH, as a control. As expected, in the strain treated with Lat-B, most mitochondria were found greater than 2 μm from visible actin filaments, and correspondingly, most fission and fusion events occurred 2 μm or more away from a filament. In the future, we will repeat this experiment with GFP-tubulin Lat-B and EtOH treated cells.

39A. The Effects of DJ-1 Protein Mutants on Mitochondrial Dynamics in Dictyostelium discoideum

Hyoju Kim, Kari Naylor
Biology, University of Central Arkansas

Mitochondrial dysfunction plays a role in the progression of Parkinson's Disease (PD), thus understanding mitochondrial dysfunction is one of the important keys to finding PD treatment. Mitochondrial dysfunction is directly linked to mitochondrial structure. Our lab studies the processes that establish mitochondrial structure, including mitochondrial fission, fusion, and motility. We have shown that in our model, Dictyostelium discoideum, 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 trying to understand the role DJ-1 plays in these processes. DJ-1 is a protein linked to PD and mitochondria, yet its function is poorly understood. Thus we are determining the rates of fission, fusion, and motility when DJ-1 is overexpressed or under-expressed in D. discoideum. Our results will help clarify its function and the relationship between DJ-1, dynamics, and mitochondrial dysfunction. Thus far we have analyzed seven DJ-1 mutant strains and calculated the average number of fission and fusion events/min/cell in 30 cells. Our preliminary data suggest that overexpression of DJ-1 has little effect on the rates of fission and fusion compared to wild-type cells (AX2), while loss of DJ-1 increases fission. These results suggest that DJ-1 is an inhibitor of fission with little effect on fusion. Our future work includes an analysis of mitochondrial motility. Ultimately, this work will contribute to a better understanding of the DJ-1 function and pathogenesis of PD.

39B. Investigate the effects of diffusible signals from plant growth-promoting bacterium, Azospirillum brasilense, on rice.

Presenter: Samuel Hoggard Mentor: Dr. Arijit Mukherjee Other authors: Matthew Calhoun, Mary Galloway, Hunter Price, Carli Wattigney
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. To identify the transcriptomic changes in rice plants during the microbial signal-induced growth promotion, we extracted RNA samples from rice for RNA sequencing. The RNA samples passed the integrity tests and will be sequenced soon. 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 future, we plan to identify the chemical nature of these microbial signals, which can have important implications for improving agriculture sustainably.

40A. The diversity and stability of Chlamydiae bacterial symbionts in different species of social amoebas

Lulu Quebedeaux, Johnna Hollis, Donovan Clark, and Tamara Haselkorn
Biology, University of Central Arkansas

While Chlamydiae bacteria are most well known as obligate intracellular parasites of many organisms, including humans, recent metagenomic sequencing has uncovered an even larger diversity of lineages within this bacterial phylum. In many cases, the hosts of these novel lineages are unknown, making it difficult to study the ecology, evolution, and function of these new Chlamydiae. Some species of amoebae have been known to host particular Chlamydiae lineages, and recent studies of natural populations of a group of amoebae known as social amoebae have shown that they are potential hosts for some of these novel lineages of Chlamydiae. We have sampled 11 different species of social amoebae from soils in 10 different areas of Arkansas. We extracted DNA from over 800 individual amoeba isolates, using Chlamydiae-specific PCR primers to screen for the presence of Chlamydiae symbionts. So far we have found over 40 different Chlamydiae haplotypes in our social amoeba species. To determine the stability of these relationships we isolated individuals from 6 different amoebae species with 10 unique Chlamydiae haplotypes, propagating them in the lab for 10 generations. Each of these Chlamydiae haplotypes persisted in its host, suggesting that these are stable symbioses in natural populations and providing new opportunities to study these symbioses in the lab.

40B. Exploring the Relationship Between the Cytoskeleton and Mitochondrial Dynamics in Dictyostelium discoideum: by disrupting microtubules and determining the localization of dynamic events

Sophia Rushing, Kari Naylor
Biology, University of Central Arkansas

Mitochondria are dynamic organelles that divide, fuse, and move around the cell. Mitochondrial dynamics are known to be influenced by the presence of the cytoskeleton, particularly microtubules and actin filaments. This relationship is not clearly understood in our model organism, Dictyostelium discoideum. D. discoideum is an amoeba that is widely used for studying many eukaryotic cellular processes, such as development and mitochondrial dynamics. In order to analyze the relationship between the cytoskeleton and mitochondrial dynamics, D.discoideum cells were treated with nocodazole, a drug which inhibits the polymerization

of microtubules. Confocal microscopy and time-lapse images were used to assess morphology, examine the distance of mitochondria from cytoskeletal filaments, and quantify the distances between remaining cytoskeletal filaments and any fission and fusion events that occurred. Preliminary results suggest that fission and fusion events may be more likely to occur at further distances away from actin filaments in D. discoideum, even if microtubules are disrupted. Understanding the relationship between the cytoskeleton and mitochondrial dynamics will help us to understand how mitochondrial dynamics in eukaryotes evolved from cell division in prokaryotes. Additionally, researching this topic may contribute to an understanding of the mechanism of mitochondrial diseases.

41A. Azospirillum brasilense improves rice growth under salt stress by regulating the expression of key genes involved in salt-stress response, abscisic acid signaling, and nutrient transport.

Matthew Calhoun, Dr. Arijit Mukherjee Other authors: Seth Dixon, Zach Degon, Samuel Hoggard, Mary Galloway, Sophia Gulutzo, Hunter Price.
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. This study shows that total and root plant mass is improved in A. brasilense-inoculated rice plants compared to the uninoculated plants grown under high salt concentrations (100 mM and 200 mM NaCl). We observed this growth improvement at seven- and fourteen days post-treatment (dpt). Next, using RNA sequencing we identified the transcriptomic changes in rice plants during A. brasilense-mediated salt stress tolerance. Overall, our transcriptomic data indicate that A. brasilense improves rice growth under salt stress by regulating the expression of key genes involved in defense and stress response, abscisic acid and jasmonic acid signaling, and ion and nutrient transport, among others. Our findings will provide essential insights into salt stress mitigation in rice by A. brasilense.

41B. The armadillo's shell shows pregnancy and lactation osteopenia

Reese Ramirez, Rayli Ruby, Dr. Frank Knight
Biology, University of the Ozarks

All women lose minerals from their endochondral bones during pregnancy and lactation. Though rare, bone loss during reproduction may be severe, resulting in debilitating osteoporosis. Altering nutrition does not prevent pregnancy and lactation associated bone loss. To support shell mineralization of their neonates, lactating armadillos produce milk with a higher calcium concentration than any other mammal. It follows that armadillo mothers should display substantial osteopenia, or osteoporosis. Our hypothesis is that the adult shell acts as an additional reservoir of calcium, protecting the skeleton from excessive bone loss during pregnancy lactation. We predict the armadillo shell will contain a lower calcium concentration during lactation than during pregnancy. To test our prediction, we measured calcium concentration in the shell, serum, urine, and

feces of wild-caught, pregnant armadillos (n=9). We repeated these measurements after the armadillos gave birth (n=7). Shell calcium concentration was lower during lactation than during pregnancy (paired T-test, $p<0.05$). Serum calcium remained the same, while urine and fecal calcium concentration increased. These results are evidence that armadillos mobilize calcium from the intramembranous bone of the shell to support their developing offspring even when dietary calcium is more than that which is necessary for serum calcium regulation.

Chemistry

100A. Docking Studies of Novel Antibacterials Against Fabk and Bccp Proteins

Siam Chowdhury, Mohammad Abrar Alam, Shailesh Budhathoki, Subrata Roy
Computer Science, Arkansas State

A group of thiazole derivatives are synthesized and screened for antimicrobial activity. Several of these derivatives demonstrated potent antimicrobial activity against Streptococcus mutans, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, and other gram-positive bacterial strains. To investigate the mechanism of action of our compounds, we screened a potent compound against a library of about 200 S. mutans strains with essential genes repressed via an inducible CRISPRi system. CRISPRi utilizes a Cas9 Smu protein modified to eliminate endonuclease activity (dCas9). A customized sgRNA allows for localization of dCas9 to the genetic target. dCas9 sterically hinders RNA polymerase binding, interfering with the expression of target genes. In the screening of HTM-18 against CRISPRi model, several genes related to transcriptional proteins and fatty acid synthesis are observed as gene hits. On confirmation of gene hits based on growth curve analysis, fatty acid synthesis genes Fab K and bccp are strongly inhibited followed by transcriptional factors genes rs5 and alaS. We will present the molecular docking studies of the lead compounds against these genes.

100B. Novel screen-printed electrodes use enzymes from corn to detect glucose levels.

Anahita Izadyar, Nathaniel Lamb
Chemistry, Arkansas State University

Diabetes is a chronic disease that affects about 150 million people worldwide and is one of the leading causes of death and disability. Diagnosis of diabetes requires close monitoring of blood glucose levels for millions of people with diabetes, making glucose the most common analyte tested. The polyaniline (PANI) - gold nanoparticles (GNPs)- glucose oxidase (GOX)- plant-produced manganese peroxidase (PPMP)/ screen-printed electrodes composition showed excellent square Wave Voltammetry (SWV) response for the selective and sensitive enzymatic detection of glucose. Keywords: Plant-produced manganese peroxidase from corn, Enzyme-Based Biosensors, Glucose, Square Wave Voltammetry (SWV).

101A. Metabolic Approach to Comparing the Chemical Space of Medicinal Plant Extracts Using LC-MS

Elizabeth T. Martin, Chiraz-Soumia M. Amrine
Physical and Earth Sciences, Arkansas Tech University

New treatments for cancer and bacterial infections are needed, especially because most patients acquire resistance to conventional first-line treatments. Many natural product metabolites exhibit potent activity. Sambucus sp., or elderberry, and Salvia sp., or sage, are both well-known shrubs for their therapeutic benefits. This study aims to analyze how anthocyanins are extracted from the native American Elderberry, Sambucus canadensis, and Sage, Salvia officinalis. It also aims to investigate the process of vinegar baking of the Elderberries and sage to enhance the chemical space and increase the biological properties. Frozen elderberries baked in vinegar and non-vinegar baked elderberries were utilized to test this theory. The same was done with dried sage. A Soxhlet extractor was used to extract anthocyanins. For many liquid-liquid extraction steps, a rotary evaporator and a separatory funnel were required. The samples are subjected to

Liquid chromatography coupled to a mass spectroscopy LC-MS in the hope of identifying secondary metabolites. Our preliminary results show an improvement in the antibacterial activity of both the elderberries and sage baked in vinegar extract compared to the raw organic extract.

101B. Investigating the Chemical Profile of Different Salvia officinalis Extracts Using GC-MS

Caitlin Drake, Allison Norton, Elizabeth Martin, Chiraz Soumia M. Amrine
Physical and Earth Sciences, Arkansas Tech University

The continual search for new drugs for different diseases is of vital importance since most patients develop resistance to traditional first-line treatments. Natural product's metabolites proved their potency. Salvia sp., also known as sage, is a well-known shrub for its medicinal properties. The purpose of this research is to investigate the volatile secondary metabolites isolated from Salvia officinalis. It also intends to research the process of vinegar baking in order to boost the chemical space and biological properties. Separately, dried sage leaves and dried sage leaves baked in vinegar were extracted using a Soxhlet. Many liquid-liquid extraction processes were done. To identify the secondary metabolites present, the organic extracts were filtered and then subjected to gas chromatography linked to mass spectrometry (GC-MS). Samples from the extracts were used to test the antibacterial activity.

102A. Chemistry of Bixa orellana's Berries Using GC-MS and their Antibacterial Activity

Allison Norton, Caitlin Drake, Yasmin Garcia, and Chiraz Soumia M. Amrine
Physical and Earth Sciences, Arkansas Tech University

Bixa orellana is a flowering plant that flourishes in tropical climates and has a multitude of purposes for the people native to where it grows. The research found B. orellana to have anticonvulsant, antiprotozoal, and antibiotic effects. B. Orellana berries were found to be alexipharmic which aids the body in its natural defenses against intrusive substances. In this experiment, we investigated the chemical and biological aspects of the berries. The dried berries were extracted using a Soxhlet followed by three steps of liquid-liquid extraction. The final extract was subjected to gas chromatography linked to mass spectrometry (GC-MS) to identify the secondary metabolites present. Different concentrations of the organic extract were used to test the antibacterial activity against E. coli.

102B. Meta-Stable State Photoacid Proton Release Under Blue and Green Light

Trevor Martin, Dr. Rajib Choudhury, Jocelyn Dong
Biology, Arkansas Tech University

The use of metastable-state photoacids to generate a large amount of proton (H+) in solution allows for their potential use in many critical acid-catalyzed chemical and biochemical reactions. In order to be an effective candidate, a photoacid must present a sustainable change in pH and efficient timing of forward and reverse reactions. These concepts were tested on a newly developed photoacid which released a proton under blue and green LED light irradiation. The photo-generated proton was reversibly transferred to a suitable proton acceptor. Evidence of proton transfer was obtained from UV-

vis and fluorescence spectroscopic studies. In the latter technique, a colorless proton acceptor, such as amino acids, can be used. Photo-controlled proton generation and acid-base reactions can be monitored by the photoacid fluorescence signature. Overall, the results demonstrated that this new generation of photoacids will be a good candidate for use as a metastable-state photoacid in manipulating biochemical reactions.

103A. Manipulating Biochemical Reactions Using Metastable Photoacids

Jocelyn Dong, Trevor Martin, and Rajib Choudhury (instructor/ mentor)
Physical Sciences (Chemistry), Arkansas Tech University

The use of metastable-state photoacids to generate a large amount of proton (H+) in solution allows for their potential use in many critical acid-catalyzed chemical and biochemical reactions. In order to be an effective candidate, a photoacid must present a sustainable change in pH and efficient timing of forward and reverse reactions. These concepts were tested on a newly developed photoacid which released a proton under blue and green LED light irradiation. The photogenerated proton was reversibly transferred to a suitable proton acceptor. Evidence of proton transfer was obtained from UV-vis and fluorescence spectroscopic studies. In the latter technique, a colorless proton acceptor, such as amino acids, can be used. Photo-controlled proton generation and acid-base reactions can be monitored by the photoacid fluorescence signature. Overall, the results demonstrated that this new generation of photoacids will be a good candidate for use as a metastable-state photoacid in manipulating biochemical reactions.

103B. ZnO Nanostructures by Hot Water Treatment for Photocatalytic Bacterial Disinfection

Carson Stewart, Bennett Lowry, Cindy White
Chemistry and Biochemistry, Harding University

On the international space station, bacteria is invading the water tubing and creating biofilm, making it difficult to sterilize while also contaminating the water supply. An effective and efficient solution for this problem is photocatalysis: using a light source coupled with a photocatalyst to create electron-hole pairs to produce reactive oxygen species to destroy bacterial cell walls and erode their biofilm network. In this experiment, we are partnering with UA Little Rock to assist NASA in using hot water treated ZnO nanostructures in order to prevent biofilm accumulation on the ISS. This work centers around optimizing this procedure so as to obtain the best prevention for biofilm growth. Various experimental techniques such as altering the distance between the UV light source and bacteria as well as the optimal time the UV light is exposed to the biofilm have been shown to improve the efficacy of the method.

104A. Development of a Noncovalent Fluorophore Conjugation Method for Histidine Tagged Proteins

Sydney Greene, Dr. Julie E. C. Gunderson, and Dr. William A. Gunderson
Chemistry, Hendrix College

Fluorescence-based assays are powerful experimental tools for studying molecular mechanisms of protein action in biomedical research. Many fluorescence-based methods require fluorescent dyes to be attached to proteins in a stoichiometrically defined, site specific, and stable manner. Covalent attachment of fluorophores to proteins is site specific and stable, but to achieve

single-site specificity, protein mutations or peptide ligations are often required. To date, there has not been widespread use of non-covalent labeling strategies. Because many proteins are purified using a histidine tag, non-covalent labeling strategies that target histidine tags could find widespread use. We have identified an RNA aptamer from the literature that has picomolar affinity for histidine tagged proteins. We hypothesize that this RNA aptamer can be used for labeling histidine tagged proteins with a fluorophore. Here, we characterize the interaction between the RNA aptamer and histidine tagged proteins and demonstrate the utility of this fluorophore labeling scheme with proof-of-principle fluorescence experiments. The universality of the histidine tag as a purification method makes this labeling strategy particularly appealing. In addition, the aptamers can be readily obtained commercially conjugated to a large selection of labels.

104B. The effect of dielectric environment on protein denaturation

Regina Delgadillo Galaviz, Isabel M Jara, Bhavya Lenin, David A. Hales
Chemistry, Hendrix College

Protein folding and misfolding are at the root of many diseases, so the circumstances under which proteins unfold from their native states are of interest. Here, denaturation of bovine Cytochrome c is studied as a function of dielectric environment (solvent composition). The results are monitored by electrospray ionization – ion trap mass spectrometry (ESI-ITMS). As a protein is denatured, any newly exposed basic sites can become protonated in the ESI process. The resulting shift in charge state distribution allows us to monitor the change in conformation in the mass spectrum. The lower the dielectric constant of the non-aqueous component of the solvent, the less is required for denaturation.

105A. Chemical Manipulations of Rifamycin Core Providing New Solutions to an Old Problem: Multidrug-Resistant Tuberculosis

Braden Glenn[(1),] Wyatt Treadway[(1)], Lola Beeser[(1)], Clara Nikkel[(1)], Ryan Holdiness[(1)], Jake Smith[(1)] Daniel Armstrong[(1),] Jessie Parchman[(1),] Marissa Fullerton[(2)], Amanda Dragan[(2)] , Daniel Voth[(2),] Irosha N. Nawarathne[(1)] (PI)
Chemistry, Lyon College

In 1999, the World Health Organization estimated that one-third of the population had latent tuberculosis (TB) infection. This has since been updated to one-fourth of the world. The danger of TB is amplified by mutations which can result in antibiotic resistance. Long term use or misuse of an antibiotic acts as a selection force for bacteria that are drug resistant, which necessitates the development of new drugs. Rifamycin, particularly rifampicin, has been a mainstay of TB treatment since the 1960's; it binds the beta subunit of the MBT RNA polymerase (RNAP) and blocks RNA synthesis. 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. 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 and triazole functionalities, the

innovative products of coupling complex rifamycin chemistry and simple click chemistry.

105B. The Synthesis of Tautomerically Ambiguous Nucleosides

Allison DeMuth Vincent Dunlap
Division of Science and Mathematics, McKendree University

Human Immunodeficiency Virus (HIV) is an infection that uses the replication mechanisms of the host against itself. While there are compounds used to treat HIV, the host is frequently negatively affected by the treatments. Reverse transcriptase, the enzyme responsible for viral genome duplication experiences a high degree of mutation and is the main reason that treatment progression for HIV is slow. The high degree of mutation causes a high error load that will be taken advantage of in this study. By developing cytosine-based nucleosides, it is hypothesized that they will undergo tautomerization resulting in the scrambling of the hydrogen bonding faces causing greater mispairing. It is believed that the HIV genome operates near an "error threshold", thus introduction of the ambiguously hydrogen bonding tautomer will lead to an "error catastrophe" in the replication process. This results in destabilization of the replicated duplex and thus jettisoning the virally infected cells. The design and synthesis of the bicyclic cytosine analogs will be discussed as well as the oligonucleotide integration.

106A. Synthesis of 1,4-disubstituted triazoles as potential glutamate receptor antagonists.

Jared McMaster, Dr. James Donelson; Sean Sluder, Walee Baig, Rayhan Shaikh
Chemical and Physical Sciences, Missouri Southern State University

Glutamate, the brain's main excitatory neurotransmitter, serves as the primary facilitator of sensory information, motor coordination, emotional reaction, and cognition. Glutamate levels have been found to be elevated among individuals with autism spectrum disorder (ASD). To possibly mitigate the impact of the elevated glutamate levels, metabotropic glutamate receptor 5 (mGluR5) inhibitors are of interest. Using a known mGluR5 allosteric antagonist Dipraglurant as a model, two series of 1,4-disubstituted triazoles were designed and synthesized. The first set consists of 4-aryloxymethyl-1-arylmethyltriazoles. The aryl propargylic ethers were synthesized via SN2 reaction from the corresponding phenol and propargyl bromide. The second set consists of 4-arylmethyl-1-arylmethyltriazoles. The aryloxymethyl-substituted triazoles were synthesized from various aryl propargylic ethers and either aryl or benzyl azides. Synthesis of the benzyl-substituted azide reagents were obtained by substituting a variety of benzyl bromide species and sodium azide. The final 1,4-disubstituted triazole compounds were synthesized using a [3+2] cycloaddition between the various substituted azides and substituted propargylic ethers or arylalkynes. The cycloadditions were carried out using a CuSO4 catalyst with L-ascorbic acid. Using this 3-step combinatorial sequence, a small library of 1,4-disubstitutedtriazoles were synthesized.

106B. Analysis of BPA Leaching from Feminine Hygiene Products using Fluorescence Spectrophotometry

Maryann Rettig, Sara E. Hubbard, Ph.D.
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. 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 leaching of BPA from menstrual pads was analyzed over a six-hour time period in both the 1:1 methanol/water and simulated vaginal fluid; 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 for both the 1:1 methanol/water solvent and simulated vaginal fluid methods.

107A. Detection of BPA in Clothing using Fluorescence Spectrophotometry

Isabella Rushing, Dr. Sara E. Hubbard, Ph.D.
Chemistry, Ouachita Baptist University

Bisphenol-A (BPA) is a carcinogenic compound found in many plastic-containing products due to its ability to add rigidity and strength to the plastic. However, BPA has been found in a wide variety of products not traditionally thought of as "plastic," including feminine hygiene products, printer receipts, and even clothing containing a polyester/spandex blend. BPA in clothing indicates possible dermal exposure to BPA—which is traditionally excluded from human BPA exposure analysis—as well as environmental exposure through clothing discarded in landfills. BPA is a fluorescent compound, with an excitation wavelength of 278 nm and an emission wavelength of 304 nm. Using fluorescence spectrophotometry, the presence of BPA in polyester/spandex blended clothing was determined by monitoring the leaching of BPA from the fabric over time. Strips of clothing containing polyester/spandex blends were submerged in a 1:1 methanol/water solution for varying amounts of time, ranging from 0 minutes to 6 hours, allowing BPA to seep out of the material. Using the standard addition method to control for other compounds that could also possibly be leaching out of the material, the sample solution (5 mL) and varying amounts of stock solution (0 mL, 2 mL, 5 mL, 7 mL, 10 mL) were added to 25- mL volumetric flasks for each time point and diluted to the line with 1:1 methanol/water solution. The concentration of BPA that leached from the material was then determined by using the Edinburgh Instruments FS-5 to measure the fluorescence emission intensity. Statistical analysis was performed on the results, including linear range, limit of detection, and limit of quantitation.

107B. Monitoring Per- and Polyfluoroalkyl Substances in Central Arkansas Surface Waters

Alexander Treadway, Jack Nolen, and Gunnar Boysen.
Chemistry, Ouachita Baptist University

Per- and Polyfluoroalkyl Substances (PFAS) constitute a class of highly stable and enduring chemical compounds. Their pervasive presence in the environment stems from extensive employment in commercial, consumer, and industrial applications. PFAS garnered substantial public attention in the United States following a recent report by the Agency for Toxic Substances and Disease Registry (ATSDR), which highlighted adverse health effects associated with PFAS exposure (ATSDR 2021). Presently, there exists no monitoring or regulation pertaining to PFAS in Arkansas' surface water. This deficiency raises concerns about public health due to the Central Arkansas region's population of approximately 750,000 individuals. Consequently, this study aims to assess surface water in Central Arkansas, collecting preliminary data concerning PFAS contamination in the state. To achieve this goal, we established a liquid chromatography-mass spectrometry (LC-MS) approach in accordance with the EPA Draft Method 1633. Sample collection was conducted at Saline River, Rock Creek, and Fourche River. Notably, Saline River exhibited an absence of detectable PFAS. In contrast, Rock Creek revealed the presence of 2 detectable PFAS compounds, while Fourche Creek exhibited 6 identifiable PFAS compounds. Our initial findings, derived from distinct surface water sources, offer valuable insights into the detection of PFAS. Such insights hold the potential to enhance public health measures and augment the overall environmental quality for the state of Arkansas.

108A. Pollution in Urban Areas within Northern Britain

Luke Lawson, Dr.Clear, Dr. Creevy, Dr. Halsall
Biology, Ouachita Baptist University

Within the experiment the different levels of pollution in areas around Liverpool were tested. These areas were Stanley Park, Lunt Meadows, and Woolton Road. At Stanley Park one of two transects had a geochemical analysis as well as magnetic measurements run to investigate source attribution within the urban environment resulting in data showing high variability in soil properties among the transect. Having data supporting evidence of diamagnetic, paramagnetic, and ferromagnetic properties in soil along the same transect. At Lunt Meadows, through the use of XRF for soil samples and nitrate and phosphate testing for water samples, it was found that there was an abnormally high amount of iron within the first two centimeters of the soil, a trend also seen in Ca, Mn, and Sr. Additionally, strong positive correlations between presence of the element and depth were found in Al, Si, P, and Ti and negative correlations were present in S and Cl. The nitrate and phosphate water test found high amounts of nitrate and low amounts of phosphate. At Woolton Road, low Xfd% values as well as negligible XRF data proposed the insignificant levels of pollution within the soil.

108B. Hemp Seed Oil-based Highly Flame-Retardant Rigid Polyurethane Foams

Sagar Jariwala, Yash Desai, Ram K Gupta
Polymer Chemistry, Pittsburg State University

In today's world, the idea is to synthesize bio-based polyurethane goods, which reduces reliance on petroleum-based products. As a result, we produced polyol from hemp seed oil (HSO) and evaluated it using FTIR, hydroxyl value, and acid value. We discovered that the peaks of the polyol produced

were comparable to those of other bio-based polyols. Polyol is successfully synthesized and combined with additional ingredients such as catalysts, blowing agents, hardeners, and flame-retardant chemicals to produce stiff polyurethane foams. The focus of the group was to synthesize high-quality flame-retardant rigid polyurethane foams (RPUF) through the addition of several flame retardants to the foaming mixture under increasing concentrations. Within this line, the majority of the RPUF presented a closed-cell content greater than 65%. Also, a considerable improvement in flame retardancy was observed as the neat HSO-based RPUF had a burning time of 110 s and a weight loss of 82%. Yet, the addition of 10 wt% of TEP reduced to 19 s and 5% respectively. The other two flame retardants are dimethyl methyl phosphate (DMMP) and expandable graphite (EG) which showed similar trends with flame retardancy and mechanical properties. As a result, our research on the manufacture of biobased RPUFs was successful. Furthermore, additional research may be conducted to improve the qualities of the HSO foams created, which can be used commercially.

109A. Bio-based Polyurethane Wood Adhesive with Additional Crosslinker Providing Enhanced Thermal and Mechanical Properties.

Yash Desai, Ram K Gupta
Polymer Chemistry, Pittsburg State University

Polyurethanes (PU) have been promising polymeric materials with a wide range of applications including adhesives. Projecting an estimated revenue from 42.8 billion $ in 2021 to 61.5 billion $ by 2026. However, many PU adhesives are sourced from petroleum products. Therefore, to lower the dependence on non-renewable resources and to provide sustainable as well as affordable alternatives. In this work, we synthesized bio-based adhesives of polyurethane from modified castor oil-based polyol. Generally, polyurethane reaction depends on the properties of polyol and isocyanates. The most important aspect of these reactions is the OH number of the polyol which is responsible for the crosslinking and bonding strength of the adhesives. Therefore, to increase the OH value and provide a better reaction platform an external bio-based crosslinker in the form of tannic acid is to be incorporated and characterize the improvement in the chemical, thermal, and mechanical properties of the adhesives. The adhesive gave out 6.09 MPa of tensile strength with 10 wt% of tannic acid followed by a higher Tg as compared to conventional polyurethane adhesives at 3.47MPa. Through this research, we found some better bio-based adhesives with extensive properties that work sustainably and clearly.

109B. Synthesis of 6-Bromo Substituted Catechols to Investigate L-DOPA Dioxygenase Function

Joseph C. Hane, Emma G. Gruss, Gabriella A. Krisanic, Kudzai L. Nyamkondiwa, Keri L. Colabroy, Larryn W. Peterson
Chemistry, Rhodes College

The linearization of catechol aromatic rings by dioxygenase enzymes showcases exciting and powerful chemistry, yet the substrate tolerance of the enzymes remains to be fully realized. L-DOPA-2,3-dioxygenase is an enzyme of particular interest as it cleaves the aromatic ring of L-DOPA in a number of pathways that produce antitumor and antibacterial compounds. To further investigate this chemistry, a variety of catechol substrates are needed. We report the synthesis of substituted catechols, including 6-bromodopamine, 6-bromo-3,4-dihydroxyhydrocinnamic acid (6-bromoDHHCA) and 6-bromo-L-DOPA, and determination of their physical properties. These catechols will be used in an effort to broaden the understanding of dioxygenases and other enzymes and provide important insight into the potential of dioxygenases

in bioremediation and semi-enzymatic synthesis of novel, bioactive compounds.

110A. An In Silico Analysis of Potential Inhibitors of LpxC

Maria F. Alvaro, Trinity L. Liaw, Gabriella A. Krisanic, Jacob D. Greenberg, Emma J. Chow, Eleanor A. Fontana, Larryn W. Peterson
Chemistry, Rhodes College

While the synthesis of novel compounds with broad-spectrum antibacterial properties has experienced a notable decline, the challenge of combating highly resistant Gram-negative bacteria continues to grow. Compounds based on propargylglycine and featuring an alkyl biphenyl appendage have displayed antibacterial effectiveness against Escherichia coli. However, this efficacy was limited to compounds where the TolC-mediated efflux system, responsible for expelling potentially harmful molecules from the cell, had been rendered inactive. Several analogs were meticulously designed with heightened hydrophilicity to enhance their binding affinity within both the polar region of the LpxC active site and the enzyme's hydrophobic pocket, aimed at circumventing the efflux mechanism. Compounds incorporating indole rings and polar side chains were the primary focus of computational molecular docking assessments utilizing AutoDock Vina. These tests facilitated the identification of crucial interactions within the LpxC active site through docking scores. Notably, compounds featuring a heterocyclic side chain exhibited more robust interactions and improved binding within the LpxC active site, contrasting with their simpler alcohol-derived counterparts.

110B. Synthesis of catecholamine derivatives to probe dioxygenase activity

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Dioxygenase enzymes are essential protein catalysts involved in various bioremediation pathways and implicated in the creation of antibiotic molecules. Specifically, the enzyme L-3,4-dihydroxyphenylalanine (L-DOPA) catalyzes the breakdown of aromatic and catecholic rings, structural components of plant woody tissue, in a mechanism that is not fully understood. This work focuses on the synthesis, redox potentials, and pKa values of dopamine, DHHCA, and L-DOPA derivatives that are substituted at the 6-position, and their characterization as substrates of L-DOPA dioxygenase. The addition of different substituents to the 6-position of the catechol core has been found to alter the properties of the molecule that are crucial to the overall reactivity of the compound. Expanding this toolkit of derivatives provides access to better understand the enzyme, its mechanism, and its applications.

111A. Characterization of catechols using UV-vis spectroscopy and HPLC

Leah Grace Borders, Gisela Xhafkollari, Emma Gruss, Keri L. Colabroy, Larryn W. Peterson
Chemistry, Rhodes College

Catecholamines in the human body serve as a blueprint for various important synthetic drugs, and they function as substrates for enzymes such as L-DOPA dioxygenase, catechol-O-methyltransferase and cytosolic sulfotransferases. We have successfully synthesized several novel derivatives of dopamine and related catechols with different substituents on the aromatic ring. An understanding

of the properties and behavior of the compounds is critical before biological testing; therefore, the stabilities of the catecholamines at various pHs were studied using HPLC and the pKa values of each derivative were determined to comprehend their reactivity and gain insight into their predicted behavior. The pKa values and the stabilities of each derivative will be further discussed.

111B. Toxicity of Antimicrobial Peptide Analogs from Fish P. punctata Venom

Chinmayi Alli, Darsani Patel, Roberto de la Salud Bea
Chemistry, Rhodes College

Due to the increase of resistance by pathogenic organisms to traditional drugs, there is an interest to find new active compounds with novel modes of activity for the treatment of diseases. Currently there is also a new interest for natural products as a source of potential drugs. Animal and plant venoms contain a variety of active molecules with useful and potential medicinal applications. The venom of Pogonoperca punctate, also known as “soap fish” contain short peptides with antimicrobial properties. One of these is Grammistin Pp2a, a 13 amino acids peptide with a reported broad spectrum of antimicrobial activity against Gram positive and Gram negative bacteria. In our group we have designed and synthesized a library of 14 analogs, including the original, of the peptide Pp2a. This design includes modifications on specific positons of the amino acid sequences and, for a second library of peptides, the addition of a fatty acid chain (Myristic acid) on each peptide to increase hydrophobicity and an expected increase in antimicrobial activity. We plan to test these analogs for antibacterial, antifungal, insecticide properties and for toxicity.In this work, we will present the first results of this project, which includes the synthesis of all the analogs and the toxicity results against human red blood cells.

112A. A Comparative Study of Nobel Prizes in Chemistry, Physics and Physiology or Medicine Over One Hundred Twenty Years

Jordan Smith and Ganna Lyubartseva
Agriculture, Southern Arkansas University

The pool of Nobel Prize winners in science consists primarily of older men. Being aware of this fact, we aimed to analyze demographic data to identify possible trends. In the current study we analyzed 638 Nobel Prize winners in three fields: Chemistry, Physics and Physiology or Medicine with respect to gender and age of laureates. With the first Nobel prize awarded in 1901, the time period covers over one hundred and twenty years of demographic data. We compared data from the twentieth century (one hundred years) and the beginning of the twenty-first century (twenty-two years) to identify historical and current trends in gender of laureates and their age during the year of their Nobel Prize award. In addition, we compared numbers from these three different fields to examine women representation, age of men vs. women and age of all laureates in a field over the course of two centuries. Based on our findings, despite disproportionately small numbers of women in all three areas, the Nobel Prize in Physiology or Medicine has the highest number of women, followed by the Nobel Prize in Chemistry. Physics Nobel Prize has the least percentage of women winners, not surprisingly, perhaps due to physics being the most math-intensive field. However, all three categories show the trend of increasing women’s presence among Nobel Prize laureates over time. In her 2016 article, 2022 Chemistry Nobel Prize winner Carolyn Bertozzi wrote in regards to chemistry professoriate “I think we can, in my lifetime, increase the proportion of women”. This seems to be true about the fields of Chemistry, Physics and Physiology or Medicine Nobel Prize as well when comparing demographic data of laureates at the beginning of the twenty-first century to the data from the twentieth century.

During age analysis we observed a curious fact: on average women were awarded the Nobel Prize in Chemistry and Physics at a younger age compared to men. From the previous century to the current one, most Nobel prize winners appear to "age" on average across all groups, except women laureates in Physiology or Medicine for whom the average age decreases. We are hopeful that our study will inspire more women to choose research in science and more educators and administrators to move beyond historical issues and address current ones to increase women's representation in chemistry, physics and various biomedical fields.

112B. Microwave-assisted Synthesis of Pyrazole and Imidazole Derivatives

Joshua Pack, MaryGrace McAfee, Brian L. Walker
Chemistry, University of Arkansas at Little Rock

Literature precedent supports that microwave-assisted organic synthesis can afford fast, high-yield, and efficient synthetic pathways, often comparable to or better than traditional heating methods. Building on this, our work utilizes microwave-assisted synthesis for the epoxide ring opening of phenyl glycidyl ether through nucleophilic addition, aiming to create both pyrazole and imidazole derivatives. These heterocyclic azole compounds have shown to be important due to their presence in many natural products, as well as their biological and pharmacological activities. We are exploring the use of microwave irradiation under neat (solvent-free) conditions, focused on a streamlined approach to minimize time, energy consumption, and solvent waste en route to these molecules. The synthesized products are isolated and purified by conventional analytical techniques such as preparative thin-layer chromatography (TLC) and column chromatography. Characterization is conducted through standard 1H-NMR and 13C-NMR spectrometric techniques. Our hypothesis posits that microwave-assisted synthesis will yield higher efficiencies and sustainability compared to traditional methods.

113A. Synthesis and evaluation of unnatural prodigiosin analogs as anti-cancer drugs

Joseph Alley, Brian Walker
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Title: Synthesis and evaluation of unnatural prodigiosin analogs as anti-cancer drugs The naturally occurring prodigiosins (PGs) compounds are a major metabolite of the gram-negative bacteria, Serratia marcescens and are known to produce brilliant red colors. Many of these natural products have shown anti-cancer, immunosuppressive, and antimicrobial actions, amongst other biological activities. However, early studies indicated that natural PGs are too cytotoxic for normal cells and, therefore, their potential as anti- cancer drug candidates has been limited. The goal of this work is to optimize the potency and physiochemical properties of naturally occurring PGs by designing synthetic analogs for anti-cancer activity. We propose to build upon previously discovered evidence of the therapeutic efficacy and the structural profile of these natural and unnatural chemotherapeutic drugs. We will incorporate functional diversity into the core structure of PG by known synthetic chemistry. Bioanalysis of the compounds made during the study may prove potent and will guide further elaboration of the therapeutic targets. Our hypothesis is to use a straightforward chemical synthesis to incorporate benzothiazole and benzothiazole derivatives at the C-ring of the PG framework, which can improve the drug-like properties, and to test the compounds against cancer cells. The core A and B ring fragment will come from a commercially available substrate, common in the PG family. It will be condensed by microwave-assisted synthesis with 2- aminothiophenols to form benzothiazoles derivatives, which are also quite common heteroaromatic motifs in medicinal

chemistry. The cell viability and efficacy in cancer cells will be tested for the compounds.

113B. Combination Therapy Approach for Multi-Drug Resistant Bacteria

Armin Mortazi, Noureen Siraj, Amanda Jalihal
Chemistry, University of Arkansas at Little Rock

The overarching purpose of this work is to discover a simple and concise method to combine two distinct killing mechanisms in a single compound. Bacteria have long been developing resistance to the drugs designed to eliminate them. Unfortunately, this has led to the emergence of infections that cannot be treated by conventional medications. According to the Centers for Disease Control, approximately 2.8 million people are infected with resistant pathogenic bacteria. Of these infections, 35,000 cases result in death. Due to these staggering statistics, there is an urgency to discover a treatment that circumvents the resistance of the bacteria while preventing others to develop. One such method is to combine two distinct killing mechanisms in one drug. This type of combination drug enhances the potential to kill susceptible bacteria but also contains an alternate mechanism to kill any resistant cells present. In this work, we seek to combine a commercial antibiotic with a near-infrared dye to acquire a chemical killing mechanism with a photoactive killing mechanism.

114A. Revealing Nanoconfinement Induced Catalytic Selectivity at Single Molecule Level

Darby Heffer, Bin Dong, Ph.D.
Chemistry, University of Arkansas

Utilizing nanoconfinement within defined linear nanopores of a core-shell catalyst, it is possible to create a well-defined procedure to investigate variable mass transport and kinetic behaviors for a catalytic process in nanoscale space. As such, the catalytic oxidation of amplex red by platinum nanoparticles (PtNPs) has been quantitatively studied using optical microscopy imaging techniques at single molecule level. Here, we studied the reduction of resazurin by PtNPs confined in a mesoporous silica shell at both single-molecule and ensemble levels. In agreement with previous study of the oxidation of amplex-red, the reduction results also indicated confinement-enhanced activity when the PtNPs were confined in nanopores. This enhancement depends on both the pore length and diameters. However, new experimental results indicate that the stability of PtNPs for reduction reactions also increased under nanoconfinement. These confinement effects reveal phenomena regarding this reduction mechanism that have previously gone unstudied; therefore, providing useful information for the future design of more specialized, high-performance catalysts.

114B. Identifying the Effects of Antimicrobial Agents Coupled with Chelating Agents against E. coli through Antimicrobial Assays

Lidia Belete, Dr. Susanne Striegler
Chemistry and Biochemistry, University of Arkansas

As the surge of antimicrobial compounds emerge in the world of health, researchers and pharmaceutical companies continue to look for the next effective antibiotic. In this research, various antimicrobials such as polymerized microgels are tested against Escherichia coli BL21(DE3). The microgels are composed of ethylene glycol dimethacrylate (EGDMA), butyl acrylate, and a metal-coordinating ligand. To disrupt the outer cell membrane and penetrate the cell, various additional chelating agents are used to determine whether the antimicrobial-chelating agent suspensions exhibit bacteriostatic or bactericidal properties. EDTA concentrations between 25 and 35 mM coupled with different antimicrobial agents show bacteriostatic effects mandating further efforts. The results provide

nevertheless valuable information within the investigation of the antimicrobial properties of microgels against common gram-negative bacteria.

115A. Synthesizing Center-Modified Polymethine Dyes

Alex Van Horn, Seth Lewman, Shang Jia
Chemistry and Biochemistry, University of Arkansas at Fayetteville

The near-infrared (NIR, 700 – 1000 nm) and shortwave infrared (SWIR, 1000 – 2000 nm) domains have garnered significant attention for their potential in optical imaging, particularly in disease diagnosis, surgical guidance, and therapy response assessment. While polymethine dyes are esteemed for their proficiency in NIR and SWIR imaging, they grapple with challenges of limited solubility and stability under physiological conditions. In contrast, xanthene dyes, effective in the visible region, offer superior solubility, improved stability, and versatile modulation options. This project endeavors to amalgamate the strengths of xanthene dyes with polymethine scaffolds through a center-substitution technique, drawing inspiration from pre-established xanthene dye synthesis methods. This new approach is poised to yield water-soluble, photo- and kinetically-stable polymethine dyes, thus enriching the repertoire of NIR and SWIR fluorophores. The aim of this initial project will be on developing a synthetic method for center-modified polymethine scaffolds, showcasing enhanced water solubility and stability, all without compromising the essential optical properties of the dyes.

115B. Design of FGF21 Variant(s) with Increased Stability

Jason Hoang, Dr. Suresh Thallapuranam
Chemistry and Biochemistry, University of Arkansas at Fayetteville

Fibroblast Growth Factor 21 (FGF21) is a protein present in the human body that acts similarly to hormones and affects metabolism. Its influence on metabolism, most importantly fatty acid and glucose metabolism, is what makes it a potential candidate for pharmaceutical use to treat metabolic diseases such as diabetes and obesity. However, FGF21 is relatively unstable and thus would not be biologically functional long enough for practical pharmaceutical use. A more stable version of FGF21 may be created by identifying and replacing amino acids, the fundamental building blocks of proteins, contributing to the instability of FGF21. A more stable FGF21 with equal or increased biological function may make it possible for pharmaceutical use to treat diabetes and obesity, diseases that affect many people worldwide. The purpose of this project is to identify amino acid residues that may contribute to FGF21's relatively high instability and construct more stable variants via direct mutagenesis. Native FGF21 is unstable, making it impractical for clinical use due to its relatively short half-life. Key components of the FGF21 signaling pathway are the C-terminus and N-terminus of FGF21, the mandatory co-receptor β-Klotho, and FGF Receptors (FGFRs). The C-terminus of FGF21 serves as an anchor for β-Klotho binding while the N-terminus interacts with the FGFR. β-Klotho serves as a required co-receptor for FGF21 to interact with FGFRs and induce signaling. Due to the protein instability, an FGF21 variant will be created that still retains the original function while possessing a higher level of stability. The goal is to create a significantly more stable FGF21 recombinant that retains its therapeutic properties, making it more practical for clinical use.

116A. Purification and Characterization of the Ribosomal Protection Protein Tet(Q)

Benjamin Haddinger, Dylan Girodat, Ph.D.
Chemistry and Biochemistry, University of Arkansas at Fayetteville

Through the indiscriminate and inappropriate use of antibiotics, many pathogenic microorganisms are evolving antimicrobial resistance to some of our most implemented antibiotics. This is growing into a global concern as in 2019 there were more than 1.29 million deaths due to antimicrobial resistance, and that number is expected to grow to more than 10 million by 2050. A successful strategy in antimicrobial resistance for pathogenic bacteria has been the evolution of ribosomal protection proteins that are effective at providing resistance against tetracycline antibiotics. These proteins work to remove tetracyclines bound to ribosome in a GTP-hydrolysis dependent manner. The mechanism by which they catalyze tetracycline dissociation and the role of nucleotide binding or GTP hydrolysis in their function is currently unclear. Tet(Q) is a previously uncharacterized protein from B. faecalis, a microorganism known to cause endocarditis, that has been classified as a ribosomal protection protein based on sequence conservation. This research project entails the first purifications of Tet(Q) and a previously characterized ribosomal protection protein Tet(M) for control. Using Ni2+ immobilized metal affinity chromatography Tet(Q) was purified from E. coli cells for the first time. The purified protein is inherently unstable and denatured rapidly into fragments. Therefore, Tet(M) was used for pre-steady state measurements of ribosome protection protein nucleotide exchange assays. By performing fluorescence resonance energy transfer (FRET) based assays the kinetics of GDP and GTP dissociation from Tet(M) were determined to be 1.7 x 10-3 ± 0.4 x 10-3 s-1 and 2.4 x 10-3 ± 0.2 x 10-3 s-1, respectively. These slow dissociation constants indicate the ribosome protection proteins do not turnover nucleotide rapidly inside cellular conditions. Given that these proteins compete with the ribosomal binding site for essential translational auxiliary factors, slow nucleotide dissociation may regulate the GTP dependent binding of RPPs to the ribosome.

116B. Synthesis and Characterization of Hydrogels

Muhammad Rayaan, Noureen Siraj, Mujeebat Bashiru
Chemistry, University of Arkansas at Little Rock

Devices for drug delivery have been a substantial topic in recent years. A desirable device should be able to keep a drug isolated from environmental interference and maintain biocompatibility with its recipient. It must also respond to environmental stimuli and be inexpensive to manufacture. The TRIS/NaDC (sodium deoxycholate) hydrogel accomplishes all of these tasks. Thus, we aim to synthesize and characterize various different concentrations of TRIS/NaDC hydrogels to better understand their capabilities and potential as drug delivery devices. In sum, our findings indicate hydrogels composed of lower TRIS concentrations correspond to higher drug encapsulation properties. However, decreasing TRIS compromises the hydrogel's structural maintenance.

117A. Mono-substituted cationic porphyrin synthesis and characterization as a potential photosensitizing agent for photodynamic therapy (PDT)

Sarbjot Singh, Noureen Siraj, Ph.D.
Biology/Chemistry, University of Arkansas at Little Rock

Purpose Cancer has been known to be one of the leading causes of death in the world. Chemotherapy has been widely used in treating cancer, but it has extreme side effects on patients. Research works are

focused on developing new therapies which are non-invasive and among them is photodynamic therapy (PDT). PDT involves the use of a photosensizing agent (PS), light and oxygen. Porphyrins have been widely used as PS, but they easily aggregate. One way to improve the photophysical properties of porphyrin as PDT is to replace the small counter ion with a bulky ion to prevent face aggregation. Most of the porphyrins used have tetra-substituted ion. The goal of this project is to synthesize a mono-substituted cationic porphyrin (5-(4-N, N, N-Trimethylaminophenyl)-5,10,15-triphenyl porphyrin, replace the counter ion (Iodine) with a bulky anion (IR783 and BETI), perform photophysical studies to evaluate its potential use in PDT. Materials & Methods Mono-substituted cationic amine porphyrin will be synthesized through a four-step reaction. The final products and all intermediates will be confirmed with NMR and mass spectrometry. Ionic compound through ion-exchange reaction of the cationic porphyrin and two other anions (Lithium BETI and IR783) will be synthesized. Mass spec and NMR will be used to confirm the successful synthesis of the ionic materials (IMs). Finally, we will characterize the IMs (absorption, emission, fluorescence, lifetime, and phosphorescence) to evaluate their potential use as drug for cancer treatment.

117B. 3D Hollow Nanobeads and Drug Delivery

Fidaus Razak, Zach McGowan, Shenyang Li, Alexei Basnakian, Qinglong Jiang
Chemistry and Physics, University of Arkansas at Pine Bluff

3D hollow nanobeads are small nanoparticles, usuallybetween 50 nm to 500 nm in diameter. They can only bevisualizes using Scanning Electron Microscope (SEM). The 3D hollow nanobead are hollow inside because the polystyrene (PS)in the middle of the metal oxide bead is burned out at high temperature. Potentially, 3D hollow nanobead nanobeads can be used for drug delivery due to the hollow structure, in which medicines can be releasedslowly for long lasting comparing with traditional pill and currrent nanoparticles as drug delivery system. However, prior to the development of this new drug delivery approach, the absence of toxicity in the nanobeads must be established. For this, we preprared SnO2 based 3D hollow nanobead and exposed normal rat kidney tubular epithelial NRE-52E cells with varying concentrations of the nanobeads and applied TUNEL assay for DNA fragmentation to quantify the cell death.Our study established that SnO2 3D hollow nanobeads have low but statistically significant toxicity toward NRK-52E cells.Therefore, prior to using these nanobeads for drug delivery,additional purification will need to be applied to remove this residual toxicity.

118A. Unlocking the Potential: Sulforaphane vs. TNBC

Endia Douglas, Dr. Zeeshan Habeeb
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Triple-negative breast cancer (TNBC) remains a formidable challenge in oncology due to its aggressive nature and limited treatment options. However, a natural compound derived from cruciferous vegetables, sulforaphane, has demonstrated anti-cancer properties. We use this information to assess the bioactivity of the encapsulated sulforaphane-peptide construct and its potential as a treatment for TNBC. Our approach involved the synthesis of the sulforaphane-peptide construct and its subsequent evaluation in a toxicity study using the 4T1 cell line, which demonstrated promising outcomes.

118B. The Synthesis of 2-Bromoprydine and Benzolmedizole to Create the Ligand "Bimpy" as a Precursor for Potential Fuel

Imani Mbong, Dr.Marsha Massey, Noah K. Taylor, Haley R. Cox, Elisabeth B. Hicklin
University of Central Arkansas
Chemistry/Biochemistry, University of Central Arkansas

The Synthesis of 2-Bromoprydine and Benzolmedizole to Create the Ligand "Bimpy" as a Precursor for Potential Fuel With the increasing growth of the human population, the need for everyday resources like sustainable energy increases. Today's method of accessing energy sources releases a great amount of CO2 that causes an increase in today's average temperatures. Because of this, we are currently suffering the consequences of the change of our earth's current climate. To make use of the excess amount of CO2 in the atmosphere, our goal is to use the ligand 1-(2-pyridinyl)-1H-benzimidazole, also known as "bimpy", to create another sustainable fuel source. This method will require the use of a microwave, which will make this process 5-10 minutes with a 1-hour workup time. To allow for the CO2 to be reduced to CO, the ligand will be attached to a metal complex like Manganese (Mn(CO)5Br), which will form a catalyst to help produce another form of fuel.

119A. Bromination of Phenylalanine via Organic Electrosynthesis

Robert Winzerling, Josh Beeler, and Dr. Henry White
Chemistry, University of Central Arkansas

The bromination of amino acids is a common practice in the pharmaceutical industry. However, traditional bromination methods require the use of environmentally-unfriendly chlorinated solvents and harsh organic oxidants. In our research, an electrochemical synthetic method called "reductive oxidation," which is based on prior work from the White lab, is being investigated as a method for bromination. Reductive oxidation is performed in an aqueous solution and uses an inorganic electrocatalyst to generate a strong oxidizing radical. The radical then activates and oxidizes the amino acid, allowing for the bromination to follow. In this work, reductive oxidation is used to generate a sulfate radical anion (SO4-·), which abstracts a hydrogen atom from phenylalanine. In the presence of carbon tetrabromide, the phenylalanine radical is brominated. Cyclic voltammetry indicates that hydrogen atom abstraction from phenylalanine occurs as the results are consistent with prior experiments. Based on the results of this experiment, this method may prove as an acceptable and environmentally-friendly substitute for the bromination of amino acids.

119B. Synthesis of Copper Complexes Supported by a Binucleating Amide Ligand and Investigation of CO2 Reactivity

Nathan Taylor (presenter), Olivia Benefield, Lei Yang Ph.D. (mentor)
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 CO 2 activation

studies. In addition to its ideal chemical properties, copper has a relatively low toxicity and cost, making it an ideal catalyst for 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.

120A. Microenvironment-specific Variations in the Conformational Ensemble of PEP-19

William Anderson, Dr. Victoria Dunlap
Chemistry and Biochemistry, University of Central Arkansas

PEP-19 is a 6.7 kDa intrinsically-disordered protein that indirectly regulates the cellular response to calcium ion influx via non-covalent interactions with Ca2+ binding protein calmodulin (CaM). Upon binding to CaM, PEP-19 increases both the association and dissociation rate constants of Ca2+ binding to the C-lobe of CaM, effectively speeding up the cellular response to Ca2+ influx in cells that express PEP-19. Because PEP-19 is intrinsically disordered, its conformational ensemble is likely to vary depending on the microenvironment, which in turn could fine-tune the response of CaM in different subcellular conditions. In this work, variations in the conformational ensemble of PEP-19 in the presence of various chaotropic agents and macromolecular crowders were examined. This was accomplished by incorporating a tryptophan containing 5-fluoroindole into the amino acid sequence of PEP-19 at the N-terminal end during expression and observing the change in signal from the fluorine atom via 19F NMR spectroscopy. The chemical shift of the 19F signal was influenced by the addition of chaotropes or macromolecular crowders, suggesting that the interaction PEP-19 with CaM may be regulated by the microenvironment.

120B. PCP-4 Purification Processes

Charles Williams, Dr. Tori Dunlap
Chemistry, University of Central Arkansas

Intrinsically disordered proteins(IDP) are unique in that they are naturally unstructured. These proteins can take part in an array of mechanisms that have various effects. Purkinje cell protein 4(PCP-4), for example, is an IDP that binds to calmodulin, the primary translator of calcium signals, and impacts its ability to bind target proteins. PCP-4 levels have correlation with patients who have various brain diseases. PCP-4 levels are increased in brain areas spared in Alzheimer's disease and are overall lower in Parkinson's disease. Research studies pertaining to IDPs usually have a more difficult time in production and purification of the protein; which can have a hindrance on research results. Their difficulty in investigating is possibly because of their disordered nature and because of IDPs being newer investigations, techniques developed for purifying ordered proteins are not the most optimal. Here we will focus on multiple purification techniques of PCP-4 to analyze the production and purity of each technique for IDPs.

121A. Neglected Tropical Diseases: Drug Research for Schistosomiasis

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

Schistosomiasis, or snail fever, is a neglected tropical disease that affects millions of people with only one approved treatment option, praziquantel (PZQ). This

creates the problem of drug immunity that will eventually cause PZQ to be 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 different diarylureas using varying aniline and isocyanate compounds, since these types of compounds have been shown to have antischistosomal properties. Currently, we are exploring the use of chloroisocyanates and (trifluoromethyl)isocyanates as building blocks for our drug targets. The compounds are then analyzed using either proton and carbon-13 nuclear magnetic resonance (NMR), infrared spectroscopy (IR), or mass spectrometry or a combination of these techniques. Thus far, I have synthesized four potential drug candidates with percent yields ranging from 30.6% to 86.4%. In future research, I plan to move on to synthesizing thioureas as well as diureas.

121B. The Synthesis and Polymerization of Paramagnetic Metal-Metal Pyrazolide Dimers

Yesenia Perez, Patrick J. Desrochers
Chemistry and Biochemistry, University of Central Arkansas

Molecular magnets can have important applications in nanotechnology. A molecular magnet was synthesized in our lab using K[pyrazolide] with NiCl2 in dry DMF, giving K[Cl-Ni(-pz*)3Ni-Cl] as a purple solid (nickel dimer), pz* is 3,5 dimethyl pyrazolide. The dimer synthesis was reproducible and confirmed with IR, UV-vis spectroscopy, and single-crystal x-ray crystallography. The dimer synthesis was optimized using a minimal amount of DMF and mild heating at about 100°C for 10 minutes. Similar results were also seen with CoCl2 which gave the corresponding cobalt dimer, but MALDI suggests it is not the same structure. Assembling the nickel dimer into a larger polymer structure could allow for greater magnetism. Inspired by previous research, our lab set out to see if our nickel dimer could yield a similar polymer, following a method adopted from CJC 1998. We found our nickel dimer an effective precursor to the oligomer represented in that paper. Electronic spectroscopy (diffuse reflectance) confirmed a 4-coordinate nickel environment in the oligomer. MALDI also confirmed the formation of the oligomer consisting of about 4 Ni(pz*)2 units. Preliminary results show that the transformation of our nickel dimer into a polymer can potentially lead to tailored control of the magnetic properties of this class of paramagnetic materials. A. Storr; D.A. Summers; R.C. Thompson. Canadian Journal of Chemistry. 1998, 76, 1130-1137.

122A. Photochemical Amino Acid Radical Generation

Cassidy Jones, Dr. Nolan Carter
Chemistry, University of Central Arkansas

Proteins play essential roles throughout the body. The unique structure of each protein is crucial for its function. Like all biomolecules, proteins are susceptible to attack by radicals, which results in oxidative stress. This process is complex and involves the formation of many different protein radicals and damage products derived from them. To understand these complex reactions, we will study one amino acid radical that will serve as a model for formation of similar radicals within the amino acid chain of a protein. Photochemical radical generation via UV irradiation of an aryl selenide precursor will be the strategy used for producing the radical. The synthetic route to this radical precursor involves NBS bromination followed by zinc mediated carbon-selenium bond formation. A challenging aspect of the synthesis is achieving bromination at the benzylic position rather than the alpha position. The reaction temperature was lowered to 00C to improve selectivity for the beta position. Preliminary results of this reaction indicate a mixture of bromination and elimination products.

122B. Investigating the impact of PEP-19 on calmodulin target binding

Rachel Harmon, Victoria B. Dunlap
Chemistry and Biochemistry, University of Central Arkansas

Investigating the impact of PEP-19 on calmodulin target binding Rachel Harmon, Victoria B. Dunlap Department of Chemistry and Biochemistry, University of Central Arkansas, 201 Donaghey Ave. Conway, AR 72035 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.

Physics

200. Ordering-Disordering of GeSn films using RAMAN Spectroscopy

Kennedy Abanihe, Joel Ruzindana, Wisdom Ariagbofo, Manoj K. Shah*, and Mansour Mortazavi.*
Chemistry and Physics, University of Arkansas at Pine Bluff

We studied the atomistic configuration of Gen films through an investigation on the order-disorder analysis via Raman spectroscopy. The Raman measurement from Ge0.95S0.5 to Ge0.831Sn0.169 films grown on the silicon substrate was performed over the temperature range of 90 to 450 K using 785 nm and 532 mm lasers. The measured spectra were fitted for the Ge-Ge order, Ge-Ge disorder, Ge-Sn, a-Sn, and B-Sn modes. The main Ge-Ge peak shifts left from 300 cm-1 showing incorporation of Sn in the Ge lattice. The shift induced by temperature is larger than the S incorporation, which is mainly attributed by phonon-phonon coupling and thermal expansion.

201. Temperature-dependent speed of sound in formalin and phosphate buffered saline

Emily E. Bingham, Grace I. Nehring, Ann M. Viano, Brent K. Hoffmeister
Physics, Rhodes College

Tissue specimens are commonly stored in phosphate buffered saline (PBS) solution and formalin solution. Ultrasonic measurements of tissues may be performed in these same solutions. The goal of the present study was to measure the speed of sound of ultrasonic pulses in these fluids over a typical range of room temperature. A 7.5 MHz ultrasonic transducer was mechanically moved to scan an aluminum block with a precisely machined 0.500-in. step. The block was placed in a 1 L specimen tank containing the fluid of interest. The specimen tank was then placed in an 8 L water bath where the temperature of the fluid of interest was controlled using a thermostatically controlled heater and ice packs. Measurements were performed in 0.5 °C intervals from 15.0 °C to 25.0 °C. The time difference between echoes received from either side of the step was used to calculate the speed of sound in the fluid at each temperature. The speed of sound was found to increase monotonically with temperature for both fluids, with ranges of 1484 m/s - 1512 m/s for PBS and 1509 m/s - 1532 m/s for formalin.

202. Single-molecule fluorescence studies of translesion DNA synthesis

Jack Carroll, Julie Gunderson
Physics, Hendrix College

Translesion synthesis (TLS) is a highly conserved means of tolerating DNA damage and bypassing natural fork barriers such as four-stranded G-quadruplex (G4) structures. Rev1 is a TLS polymerase (pol) that plays an active role in G4 replication. Rev1 promotes G4 TLS by preferentially catalyzing dCMP insertion regardless of the identity of the template base and through recruitment of other pols that are able to perform processive DNA synthesis across lesions, but the mechanistic details of Rev1-mediated TLS are still not clearly defined. In this study, we use single-molecule fluorescence techniques to explore the mechanism of action of Rev1 on G4 substrates.

203. Effect of transducer angle on ultrasonic parameters in bone simulating material

Kate Hazelwood, Brent Hoffmeister
Physics, Rhodes College

There is interest in developing ultrasonic techniques for diagnosing osteoporosis. Many techniques perform measurements at skeletal sites such as the heel, hip and spine where the bone tissue consists of a non-porous outer layer of cortical bone that surrounds a porous interior region of cancellous bone. The goal of the present study was to develop a bone model that simulates this tissue configuration. A block of polymer open cell rigid foam (OCRF) was partially embedded in a thin layer of clear epoxy casting resin to create the specimen. The resulting specimen were 40 mm × 40 mm × 20 mm with one 40 mm × 40 mm face embedded in ~3 mm of resin. Backscatter measurements were then performed to investigate how non-normal incidence of an ultrasonic wave on the bone cortex produces errors in these measurements. The effect of transducer angle on these measurements was also investigated. When comparing the cortical and the OCRF as the incident surface, AIB had percent differences of 28.01 %, 26.75%, 25.31%, 30.29%, 31.65%, 38.83% and 18.08% for angles ranging from 0 to 30, respectively. This indicates that AIB is somewhat resistant to changes due to the cortical layer and transducer angle.

204. The Fluorino Version 2: An Open-Source, Arduino-Controlled Fluorometer

Jacie Hill, Harry Lance, Julie Schwartz, William A. Gunderson, and Julie E. C. Gunderson
Physics/Math, Hendrix College

Fluorometers, used for measuring fluorescence intensities and spectra, are commonly used in chemistry, biochemistry, and biophysics educational curricula and research. However, the high cost of purchasing and maintaining research-grade fluorometers restricts their implementation in education and research laboratories. We propose an open-source, Arduino-controlled fluorometer, which we call the Fluorino Version 2 (V2), to provide an affordable and functional alternative to commercial fluorometers. The Fluorino V2 can be easily built using 3D printable optomechanical components, inexpensive optical and electrical hardware, an Arduino Mega 2560 microcontroller, and open-source computer software. This instrument is built from open-source, 3D printable optomechanical components. Our instrument is controlled by our provided Arduino IDE and processing code and software. To test the device, we performed fluorescence measurements on both the Fluorino V2 and a commercial fluorometer to compare the measurements of the spectroscopic intensities of various fluorescein concentrations among both devices. Demonstrated by the functionality and accessibility of the Fluorino V2, this instrument can be easily implemented into educational curricula—granting students both a functional and "under the hood" understanding of fluorescence instrumentation.

205. Effect of Space Radiation on Normal Rat Leg Bones

Kayla M. Reynolds, Leslie Palmer Rahul Mehta (Mentor) Brent Hill (Mentor)
Physics, University of Central Arkansas

This study utilizes a ground-based rat model of hind limb unloading to simulate weightlessness and examine the effects of 0.3 Gy radiation dose given every other day for a 10-day period and look for changing biomarkers that may be affected by radiation. The variables in this research are the control group and irradiated (IR) group. The bones were subjected to bending techniques to measure the stress, strain, and elastic modulus. The bending method fixes the bones at one end (cantilever method)

or both ends (3-point bending) while a known force is applied perpendicular to the bone. Each leg bone (tibia and femur) is bent with a force prod acting on either posterior or medial or lateral or anterior points of the center of the bone. After the bending experiments, the bones were cut in a thin cross-section with a diamond tip saw. Then, the bone cross-sections were imaged using a Leica MZ6 microscope (IL, USA) equipped with an OptixCam digital camera. The image analysis program, ImageJ (NIH, USA), is used to measure the cortical and cavity areas. The pixel area was converted to mm square for each respective area. Next step was to sputter coat bone samples with gold for analysis using SEM (Scanning Electron Microscope). An energy dispersive analysis (EDX) quantifies the relative percentages of carbon, oxygen, phosphorus, and calcium present. Preliminary data is summarized using graphs and the validity of data is ascertained using statistical analysis. The stiffness and flexture force showed no change between irradiated and control at all 4 points (posterior or medial or lateral or anterior points of the center of the bone). The elemental compositional ratios of calcium (Ca) to phosphorus (P) revealed increases between control versus irradiated rats on the tibia at Lateral and Anterior points and no change at Posterior and medial points. The chemical analysis of bone suggests that there must be some change in the hydroxyl or phosphate group of the main component of bone structure, due to the increased level of radiation. A statistically significant decrease in elastic Young's modulus (Y) was found for irradiated rats compared to control on the tibia. The decrease in Y on tibia was much less on the lateral side then on the Posterior side. The anterior side of tibia showed a much greater decrease in Y for irradiated rats over the control rats. Acknowledgment: Arkansas Space Grant Consortium (ASGC), INBRE manuscript grant and the assistance of Hypatia Mereviglia, Manling Cheng and Parimal Chowdhury.

206. 3D Printable Library of Optomechanical Components: An Affordable Alternative to Commercial Optical Products

Harry Lance, Julie Schwartz, Jacie Hill, William A. Gunderson, and Julie E. C. Gunderson
Physics, Hendrix College

Over the last several decades, 3D printing, otherwise known as additive manufacturing, has become a standard in open-source hardware development. Fused Filament Fabrication (FFF) 3D printers, specifically, have provided many scientists and engineers with affordable alternatives to developing and customizing parts for experiments and prototypes. FFF is a type of 3D printing in which thermoplastic filament is extruded through a hot, mechanized nozzle and laid onto a platform in successive layers to eventually produce a desired object from an uploaded Computer Aided Design (CAD) file. Because many scientific applications require specialized parts that are oftentimes expensive to purchase or to maintain, being able to 3D print customized components for scientific instrumentation can potentially save time (commercial manufacturing and shipping) and money, as FFF 3D printing only requires one moderately priced 3D printer. And due especially to its affordability, 3D printing has become a practical means of scientific instrumentation. Thus, we present a library of 3D printable optomechanical components. These 3D printable components are near identical to as well as fully compatible with commercial optomechanical components; the library includes posts, post holders, bases, lens mounts, kinematic optics mounts, LED holders, and a breadboard holder. These components were tested for optical functionality and stability in entirely 3D printable optical systems, and we further compared the systems' performances with their commercial counterparts. Therefore, we expect this presented library of 3D printable optomechanical components

to be compatible in scientific research and educational laboratories.

207. Ultrasonic Attenuation Estimation and Parametric Imaging of Human Scalp Tissue

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

Transcranial ultrasonic techniques are being developed for biomedical applications with diagnostic and therapeutic uses. Ultrasonic waves propagate through three media: scalp, skull, and brain. While the ultrasonic properties of skull and brain have been studied extensively, the properties of scalp are relatively unknown. The goal of the study was to calculate the frequency-slope of attenuation (FSA) using the reference-phantom method and create cross-sectional parametric images of FSA for human scalp tissue to determine if parametric images revealed structures within the scalp tissue. Specimens were prepared from four human cadaveric donors with measurements taken with a 7.5 MHz transducer at 37 °C. FSA was calculated to be (2.00 + 0.34) dB/cm/MHz using the reference-phantom method. These results were then compared to the shadowed reflector method used in a previous study with a strong correlation ($R = 0.53$, $p < 0.05$) found between the two methods.

208. Effect of Formalin Fixation on Ultrasonic Properties of Bovine Brain Tissue

Phyu Sin M. Myat, Amalia M. Bay, Grant R. Jenson, Kate E. Hazelwood, Blake C. Lawler, Emily E. Bingham, Cecille Labuda, Brent K. Hoffmeister, and Ann Viano
Physics, Rhodes College

The goal of this study was to investigate the effect of formalin fixation on the ultrasonic properties of brain tissue. Two ultrasonic parameters were measured: speed of sound (SOS) and frequency slope of attenuation (FSA). Ultrasonic measurements were performed with a 5 MHz transducer on 1-cm thick slices of bovine brain in a tank of phosphate-buffered saline at room temperature. A total of 28 brain specimens from 9 brains were studied. Measurements were made for two different time points: within a few hours after harvesting (fresh) and after a year of fixation in formalin (year). Results were reported as mean ± standard deviation. SOS and FSA of fresh brain tissue were (1524 ± 4) m/s and (0.44 ± 0.06) dB/cm/MHz, respectively. SOS and FSA of brain tissue after a year of fixation were (1535 ± 9) m/s and (0.55 ± 0.11) dB/cm/MHz, respectively. Thus, formalin fixation produced a 0.7% increase in SOS and a 25% increase in FSA.

209. Modeling of III-V-on-Sapphire Waveguides for Sapphire-based Photonic Integrated Circuits Platform

Joel Ruzindana, Kennedy Abanihe, Wisdom Ariagbofo, Manoj K. Shah, and Mansour Mortazavi*
**Corresponding author*
Chemistry and Physics, University of Arkansas at Pine Bluff

Photonic integration 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 epitaxial film and substrate is the dominant factor responsible for the generation of large number of defects and eventually, device failure. From a material growth perspective and closely matching linear coefficient of thermal expansion of sapphire to that of GaAs and GaSb, sapphire is a favorable substrate for the growth of III-V materials. Thus, a sapphire-based platform has the potential to be used for large-scale integration platforms just like silicon-based photonic integrated platforms. Methods: We studied a

GaSb/AlSb-on-Sapphire waveguide for Sapphire-based photonic integrated circuit platform by finite-element-method (FEM) using commercial software Ansys. The materials GaSb, AlSb, 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 GaSb/AlSb-on-sapphire straight waveguides over a broad optical wavelength. Results: We presented the cut-off, single-mode and multi-mode operation conditions of rib and strip waveguides. The higher index contrast between core and substrate layer allowed us to design compact, low-loss waveguides in the mid-infrared regime. Conclusion: The presented low-loss, GaSb/AlSb-on-sapphire photonic integrated platform would enable a range of applications in defense systems, and numerous civilian applications such as big data machine learning, fiber optic communication, instrumentation, RF photonics, space exploration, and in nuclear applications. Keywords: Group III-V materials, optical waveguides, photonic integrated chips, finite-element-method.

210. Multi-pad Launch Controller for Low-, Mid-, and High-Power Model Rockets

Sean Thomas, David J. Thomas (P.I.)
Industrial Technology Department, University of Arkansas Community College at Batesville

The Thomas lab at Lyon College uses mid- and high-power model rockets to collect microorganisms from the atmosphere. Our current launch equipment consists of a five-channel low- and mid-power launch system (dubbed "Saturn 5") as well as two single-channel launch systems that can launch low- through high-power rockets. While these systems are functional, we wanted a single-unit, multi-channel launch system that can launch any type of model rocket. Here we present a six-channel, 12-volt, launch system (dubbed "ScotRocket") that can launch all power levels of model rockets, including those with clustered engines. Where the old five-channel system used individual two-conductor cables for each launch pad, the ScotRocket system uses a single, seven-conductor launch control cable for six launch pads. The launch control cable is 14.5 m long, is connected to the control box via a recreational vehicle trailer connector, and terminates in a power strip with six standard three-prong outlets. Individual two-meter AC power cords connect the power strip with each rocket's igniter wires. For high-power launches, which require greater distances between the launch system and launch pad, standard extension cords can be plugged into the power strip to achieve the necessary length. The system also includes a warning strobe that flashes while the system is powered, and a "heads-up" warning siren that can be activated from the launch system panel. This project was funded, in part, by a Student Intensive Training Grant from the Arkansas Space Grant Consortium, and by Lyon College.

211. Growth & Characterization of Layered Magnets

Taksh Patel, Laurent Bellaiche, Jin Hu ,Rabindra Basnet, Gokul Acharya
Physics, University of Arkansas at Fayetteville

MnPS3 and GdPS are being researched due to the recent insight into 2D magnetism. The ZrSiS family (the family of GdPS) can be used as topological materials through elemental substitution and strain application. On the other hand, MnPS3 belongs to the MPX3 family (M is a transition metal, and X is a chalcogen). Both crystals are synthesized through the Chemical Vapor Transport method. GdPS is heated till 975-1075℃ in a furnace for 1 week. On the other hand, MnPS3 is heated to 600-650 °C for 1 week. Then, the material composition and the crystal structure are determined through XRD (X-ray Diffraction) and EDS (Energy-Dispersive

Spectroscopy). Finally, the temperature dependence of the magnetic susceptibility (χ) is measured by putting both samples in the PPMS (Physical Property Measurement System). The susceptibility is measured by applying out-of-the-plane (H||c) and in-plane(H||ab) magnetic fields. Both materials exhibit a Néel temperature. For GdPS, the Néel temperature is around 7 K. For MnSP3, the temperature is around 78 K. However, MnPS3 could be doped with other elements. For example, Mn0.36Fe0.64PS3 has a Néel temperature of 48.4 K. Finally, the Manganese in MnPS3 could be replaced with other elements. For example, Ni0.82Co0.18PS3 has a Néel temperature of 146 K and FePS1.5Se1.5 a Néel temperature of 106 K. These new doped materials are more temperature resistant before losing a long-term magnetic order, making them more applicable.

212. Microbial Collection Via LADCAP

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

Model and high-power rocketry can be used to conduct scientific experiments. These experiments often make use of the payload section of the rocket, which can hold relevant technology or specimens. During the summer of 2023, we made progress in our research with LADCAP (Launchable Automatic Device for Collecting Airborne Particles). LADCAP is an airborne particle collection system used in model rockets. To date, we have used LADCAP in a scratch-built G-Lifter, a Loc Precision Hi-Tech, and Madcow Adventurer. LADCAP comprises a vacuum pump and filter which draws air through the side of the rocket using rubber tubing. The filter catches airborne microbes that can later be cultured. An onboard flight computer records altitude throughout launch and descent using barometric pressure. The flight computer signals to begin collecting samples after apogee for a duration of fifty seconds. LADCAP collects high-altitude microorganisms called extremophiles which can withstand harsh 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. Research with LADCAP system and rocketry is contained within the designation of "aeromicrobiology." This research is supported with grants from the Arkansas Space Grant Consortium.

213. 3db Measurement

Wisdom Ariagbofo, Joel Ruzindana, Kennedy Abanihe, Manoj Shah, Mansour Mortazavi
Physics, University of Arkansas at Pine Bluff

Integrated Microwave Photonics (IMWP) incorporates the functions of MWP components in monolithic or hybrid photonic circuits with the aim of meeting future needs. IMWP offers the promise of reduction of size-weight-and-power and low production cost. Recently, the intriguing properties of band gap and lattice constant tunability, true direct-band gap, wavelength coverage up to 12 μm and CMOS compatible process of Germanium-tin (GeSn) has drawn much attention in the photonic society. Over a decade, many GeSn based photodetectors have been reported with dramatic improvement in their performance. Here, we have demonstrated high-speed Si-based GeSn photodetector design with Sn % of 8% for the IMWP applications. The measured 3 dB bandwidth of the devices achieve nearly 2.5 MHz, however, showed discrepancy with the simulations, resulting due to the leakage. This result indicates GeSn high speed photodetectors have promising perspectives in next-generation mid infra-red optic communications.

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12A. Phuong D. Tran
107B. Alexander Treadway
18B. Barrett Troup
18A. Duncan Troup
32A. Jacqueline Twumwaah
37B. Martin Ugarte
1A. Jacqueline Romani Vargas-Ulloa
32B. Re'Nyah Vincent
9B. Eryn Wagoner
28B. Sadie Whaley
6B. Abby White
34B. Elizabeth Willhite
120B. Charles Williams
04:00 PM. William Winston
119A. Robert Winzerling

Arkansas INBRE
IDeA Network of Biomedical Research Excellence

2024 UPCOMING EVENTS

***Tentative dates May 13-16*: INBRE Sponsored Health Sciences Entrepreneurship Boot Camp.**

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

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

Arkansas INBRE
IDeA Network of Biomedical Research Excellence

2024 UPCOMING EVENTS

May 22nd: A one-day free workshop focusing on cardiovascular disease.

Spend a day with clinicians and scientists exploring what it takes to do cardiovascular research.

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

Arkansas INBRE
IDeA Network of Biomedical Research Excellence

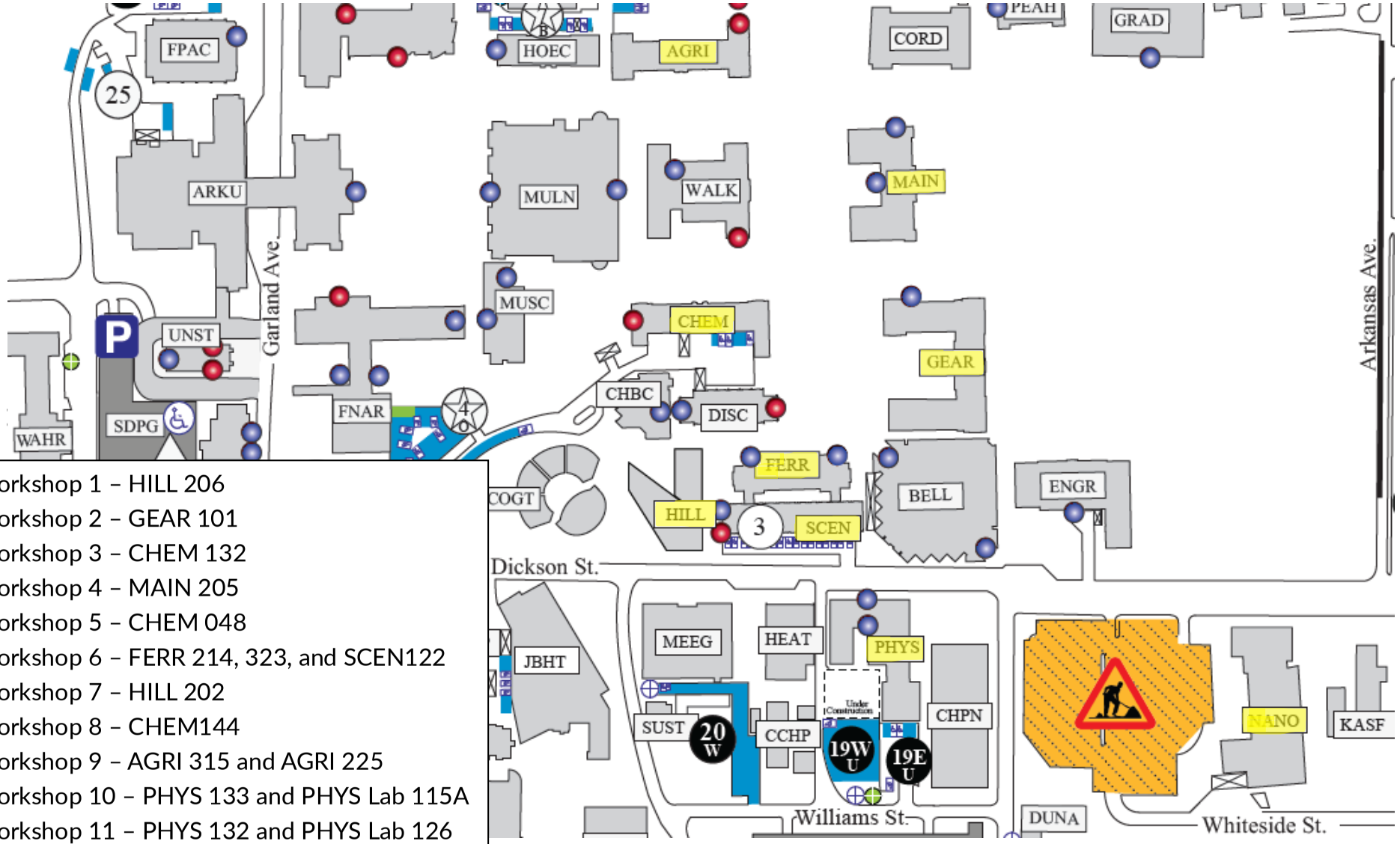
2024 UPCOMING EVENTS

May 20 – July 26: INBRE Undergraduate Summer Research Fellowship Program. Cancer Fellowships also available.

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

QR Code

INBRE Workshops: 10:30 – 11:30 a.m.



Workshop 1 – HILL 206
Workshop 2 – GEAR 101
Workshop 3 – CHEM 132
Workshop 4 – MAIN 205
Workshop 5 – CHEM 048
Workshop 6 – FERR 214, 323, and SCEN122
Workshop 7 – HILL 202
Workshop 8 – CHEM144
Workshop 9 – AGRI 315 and AGRI 225
Workshop 10 – PHYS 133 and PHYS Lab 115A
Workshop 11 – PHYS 132 and PHYS Lab 126
Workshop 12 – PHYS 134
Workshop 13 – NANO 105