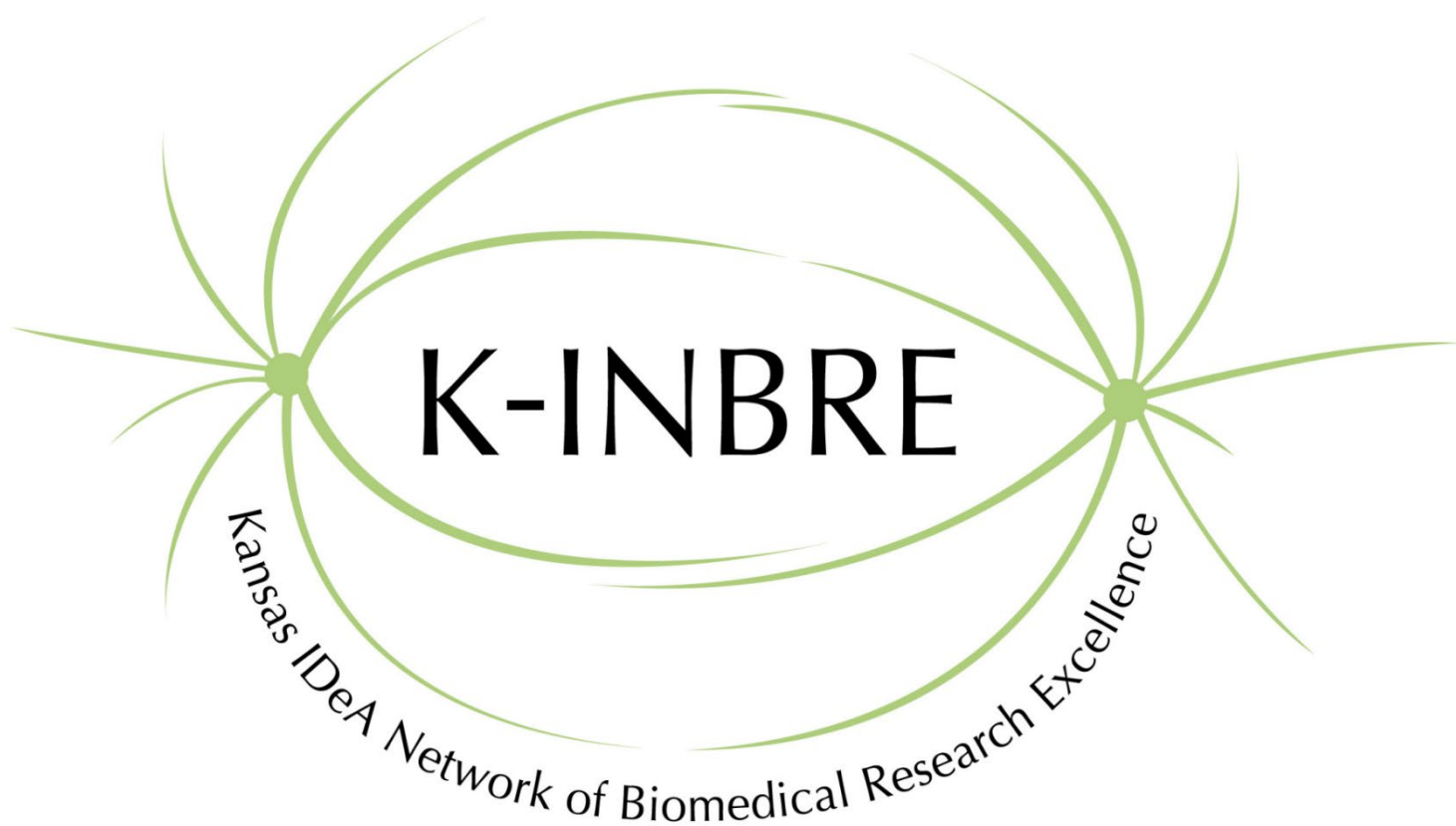


The 24th Annual Kansas-IDeA Network of Biomedical Research Excellence Symposium



**January 16-18, 2026
Sheraton Hotel
Overland Park, KS**

This program was made possible by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH) under grant number P20 GM103418. Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the NIH.

Overland Park Sheraton Floor Plan

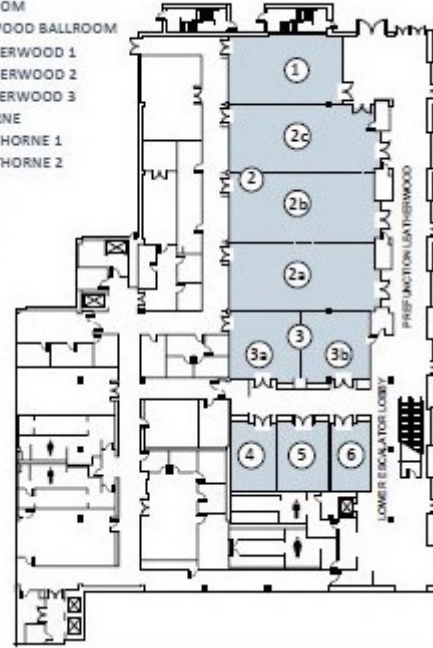
LOBBY LEVEL

1. SHERATON FITNESS
2. BIRCH ROOM
3. WILLOW ROOM
4. SHERATON LINK CAFE
5. COTTONWOOD BALLROOM
 - 5a. COTTONWOOD 1
 - 5b. COTTONWOOD 2
 - 5c. COTTONWOOD 3



LOWER LEVEL

1. MAPLE ROOM
2. LEATHERWOOD BALLROOM
 - 2a. LEATHERWOOD 1
 - 2b. LEATHERWOOD 2
 - 2c. LEATHERWOOD 3
3. HAWTHORNE
 - 3a. HAWTHORNE 1
 - 3b. HAWTHORNE 2
4. LINDEN
5. REDSUD
6. JUNIPER



LOCATION OF EVENTS:

- | | |
|-----------------------------|-------------------------------|
| • Registration: | Cottonwood Foyer |
| • Friday Night Dinner: | Cottonwood Ballroom |
| • Breakfast: | Cottonwood Ballroom |
| • General Session: | Cottonwood Ballroom |
| • Breaks: | Cottonwood Foyer |
| • Lunch: | Cottonwood Ballroom and Foyer |
| • Poster Session/Reception: | Leatherwood Ballroom |
| • Saturday Night Dinner: | Cottonwood Ballroom |
| • Boxed Lunches: | Cottonwood Foyer |

K-INBRE 2026 Symposium Table of Contents

Program Schedule.....	Page 2
Oral Presentation Abstracts.....	Page 4
DSC Oral Presentation Abstracts.....	Page 6
Poster Presentations.....	Page 7
Poster Presentation Abstracts.....	Page 19
Symposium Participants.....	Page 61
Notes.....	Page 72

Poster Presentations

Saturday, January 17th, 2026

(3:30-4:30 PM) Poster Session A

(4:30-5:30 PM) Poster Session B

(5:30-6:30 PM) Poster Session C

SUNDAY (9:50-10:30 AM) Poster Session D

SUNDAY (10:30-11:10 AM) Poster Session E

See Poster Presentation Schedule for details

IMPORTANT:

Please ensure that all publications resulting from INBRE funds follow the NIH Public Access Policy. Future awards from NIH will be delayed until evidence of compliance has been demonstrated. For more information on the Public Access policy, please visit this link: <http://publicaccess.nih.gov/policy.htm>

Note: A 2024 update to the NIH Public Access Policy now requires Author Accepted Manuscripts accepted for publication in a journal, on or after July 1, 2025, to be submitted to PubMed Central upon acceptance for publication, for public availability without embargo upon the Official Date of Publication.

When K-INBRE funds have supported your research, please remember to acknowledge this support by including the grant number P20 GM103418, regardless of the time between receipt of funding and the publication or presentation.

K-INBRE 2026 Symposium

Program Schedule

Sheraton Hotel
Overland Park, KS

Friday, January 16, 2026

3:00 PM	Early Registration Open Poster practice (until 6:30pm)	Cottonwood Foyer Leatherwood Ballroom
4:30 PM	Early Registration Closes	
6:30 PM	Friday Night Dinner	Cottonwood Ballroom and Foyer
7:30 PM	Dinner Ends	

Saturday, January 17, 2026

7:15 AM	Breakfast Buffet	Cottonwood Ballroom and Foyer
	Registration	Ballroom Foyer
8:15 AM	General Session	Cottonwood Ballroom
	<i>Doug Wright, Ph.D., K-INBRE Principal Investigator, University of Kansas Medical Center</i> Opening Remarks	
8:35 AM	<i>Dr. Hubert Tse, Ph.D., Associate Vice Chancellor for Research, University of Kansas Medical Center</i> Welcome from University of Kansas Medical Center	
8:45 AM	<i>Heather Wilkins, Ph.D., Associate Professor, University of Kansas Medical Center</i> Title: The Role of K-INBRE in My Career in Alzheimer's Research <i>Michael Gruenstaeudl, Ph.D., Assistant Professor, Fort Hays State University</i> Moderator: Trainee Presentations	
9:15 AM	<i>Juliane Simmons, Langston University, Langston, OK</i> Title: Exploring the Connection Between NUAK and 14-3-3zeta in Muscle Tissue	
9:30 AM	<i>Madison Craig, University of Kansas Medical Center, Kansas City, KS</i> Title: Methylglyoxal Drives Axon Degeneration and Metabolic Changes in Dorsal Root Ganglion	
9:45 AM	<i>Patryk Hupert, University of Kansas, Lawrence, KS</i> Title: Differential Gene Expression in Astrocytes, Microglia, and Neurons in an Accessible Triculture Model as Compared to Monoculture	
10:00 AM	<i>Yara Abdine, Wichita State University, Wichita, KS</i> Title: Evaluation of FSH glycoform ratios in female serum by ELISA	
10:15 AM	Break	Ballroom Foyer
	University Photos	Maple Room Foyer
10:20 AM	University of Kansas Medical Center Photo	
10:25 AM	Fort Hays State University Photo	
10:30 AM	Haskell Indian Nations University Photo	
10:35 AM	Wichita State University Photo	
10:40 AM	Langston University Photo	
10:45 AM	General Session	Cottonwood Ballroom
	<i>Dr. Maz Gashti, Ph.D., Assistant Professor, Pittsburg State University</i> Moderator: Trainee Presentations	
10:50 AM	<i>August Weishaar-Wilson, Washburn University, Topeka, KS</i> Title: Characterizing the achromatic visual acuity of <i>Terrapene ornata</i> across populations using the optokinetic response.	
11:05 AM	<i>Hazel Frans, Fort Hays State University, Hays, KS</i> Title: Impact of one nucleotide on organ enumeration and phyllotaxy in <i>Arabidopsis thaliana</i>	
11:20 AM	<i>Amelia Koehn, Kansas State University, Manhattan, KS</i> Title: Real-time gene expression mapping in a tissue-engineered microvessel to study Alzheimer's Disease	
11:35 AM	<i>Noah Freiburger, Pittsburg State University, Pittsburg, KS</i> Title: Infusing Zinc Hydroxide/Biotin/Gelatin Composite Particles in Sorghum Fibers for Biomedical Applications	
11:50 AM	Brief Legislative Update from Jessica Molesworth	Cottonwood Ballroom
12:00 PM	Lunch	Cottonwood Ballroom and Foyer

1:15 PM	Breakout Sessions	
	<i>Undergraduate Career Panel</i>	Cottonwood Ballroom 3
	Panelists – Dr. Carolyn Hovde Bohach (moderator), Dr. Maz Gashti, Joel Sydzyk, Dr. Riley Mittendorf, Dr. Tara Phelps-Durr	
	<i>Faculty Debate</i>	Cottonwood Ballroom
	Panelists – Dr. Doug Wright (moderator), Dr. Sue Lunte, Dr. Olivia Veatch, Dr. Hubert Tse, Dr. Robin Orozco, Dr. Ann Wozniak	
2:30 PM	Breakout sessions conclude/Break	Ballroom Foyer
	University Photos	Maple Room Foyer
2:45 PM	Pittsburg State University Photo	
2:50 PM	Washburn University Photo	
2:55 PM	Emporia State University Photo	
3:00 PM	Kansas State University Photo	
3:05 PM	University of Kansas, Lawrence Photo	
3:15 PM	Poster/Oral Judge Meeting	Hawthorne 2
3:30 PM	Reception/Poster Session A	Leatherwood Ballroom
4:30 PM	Reception/Poster Session B	Leatherwood Ballroom
5:30 PM	Reception/Poster Session C	Leatherwood Ballroom
6:30 PM	Poster Sessions End	
	Dinner	Cottonwood Ballroom
7:00 PM	Award Presentations	Cottonwood Ballroom
	<i>John Stanford, Ph.D., K-INBRE Program Coordinator, University of Kansas Medical Center</i>	
	<i>Virginia Rider, Ph.D., K-INBRE Icon, Retired from Pittsburg State University</i>	
7:30 PM	<i>Doug Wright, Ph.D., K-INBRE Principal Investigator, University of Kansas Medical Center</i>	
	Closing Remarks	
Sunday, January 18, 2026		
7:30 AM	Breakfast Buffet	Cottonwood Ballroom and Foyer
8:15 AM	General Session	Cottonwood Ballroom
	<i>John Stanford, Ph.D., Program Coordinator, University of Kansas Medical Center</i>	
	Opening Remarks	
8:20 AM	Data Science Core Session	
8:30 AM	<i>Bryce Steffan, Fort Hays State University, Hays, KS</i>	
	Title: Using de novo hybrid genome assembly approaches to characterize a new cyanobacterial strain in western Kansas	
8:50 AM	<i>Olivia Delmas, University of Kansas Medical Center, Kansas City, KS</i>	
	Title: Identification of Monitoring and Response Biomarkers for ADPKD Using Bulk RNA Sequencing in Mouse Models	
9:10 AM	<i>Carter Gray, University of Kansas, Lawrence, KS</i>	
	Title: On the Evolution of the SARS-CoV-2 Mpro and its Substrate	
9:30 AM	<i>Md Saiful Islam Saif, University of Kansas Medical Center, Kansas City, KS</i>	
	Title: From Design to Deployment: Optimizing Bridge Samples for Robust Batch-effect Correction in Olink Proteomic Data	
9:50 AM	Poster Session D	Leatherwood Ballroom
10:30 AM	Poster Session E	Leatherwood Ballroom
11:10 AM	Poster Session E ends	
11:15 AM	General Session	Cottonwood Ballroom
	<i>Robin Orozco, Assistant Professor, University of Kansas, Lawrence</i>	
	Title: Risk and Reward: Understanding the context-dependent consequences of the disease-associated <i>PTPN22</i> allele	
11:45 AM	<i>John Stanford, Ph.D., Program Coordinator, University of Kansas Medical Center</i>	
	<i>Oral Presentation Awards and Closing Remarks</i>	
12:00 PM	Boxed lunches available for pickup	Ballroom Foyer

K-INBRE 2026 Symposium Oral Presentation Abstracts

Saturday, January 17, 2026

Exploring the Connection Between NUAK and 14-3-3zeta in Muscle Tissue

Juliane Simmons¹, Emma Peters², Dr. Erika Geisbrecht²

¹Department of Biology, Langston University, Langston, Oklahoma

²Department of Biochemistry & Molecular Biophysics, Kansas State University, Manhattan, Kansas

Fruit flies (*Drosophila melanogaster*) serve as a valuable model for studying human muscle disease. Work from the Geisbrecht lab has shown that the serine/threonine kinase NUAK is essential for maintaining muscle integrity by regulating protein degradation and intracellular trafficking. To better understand this process, we aimed to identify proteins phosphorylated by NUAK that contribute to normal muscle function. Preliminary data indicate that NUAK phosphorylates the signaling protein 14-3-3 ζ at threonine 235. To investigate the role of this modification, I examined muscles expressing wild-type 14-3-3 ζ (WT), a non-phosphorylatable mutant (T235A), and a phosphomimetic mutant (T235E) using the Gal4/UAS system. Genetic crosses between males carrying each 14-3-3 ζ variant and Mef2-Gal4 females allowed for muscle-specific expression at 25 °C and 30 °C to determine optimal conditions. Larvae were dissected and stained to visualize muscle structure (F-actin), DNA (Hoechst), ubiquitinated material (p62), and endocytic trafficking (Rab7), followed by confocal imaging. Both T235A and T235E mutants showed increased p62 puncta, suggesting impaired protein turnover. Additionally, the overexpression of WT and T235A forms resulted in enlarged Rab7 structures, indicating altered trafficking. These findings support the notion that phosphorylation at T235 is crucial for 14-3-3 ζ function and that NUAK influences muscle health by regulating protein turnover and trafficking. Ongoing studies will examine larval movement and genetic interactions with NUAK to further define this pathway.

Methylglyoxal Drives Axon Degeneration and Metabolic Changes in Dorsal Root Ganglion

Madison Craig, Gentry Totta-Griese, Janelle Ryals, Douglas Wright

Department of Anesthesiology, University of Kansas Medical Center, Kansas City, KS

Diabetic peripheral neuropathy (DPN) affects nearly 60% of individuals with diabetes and is the leading cause of non-traumatic amputations in the United States. Methylglyoxal (MGO), a reactive byproduct of glycolysis elevated under hyperglycemia, has been linked to sensory fiber loss and pain. This project investigated how MGO alters cellular metabolism in dorsal root ganglia (DRG), the sensory neurons most impacted in neuropathy. Using extracellular acidification rate (ECAR) assays, we observed that MGO treatment significantly increased basal glycolysis in DRG at both day 1 and day 7. Seahorse assays confirmed elevated glycolytic activity ($p=0.0329$), while glycolysis inhibition with 2-deoxyglucose (2DG) prevented MGO-induced axon degeneration ($p=0.0636$). To further probe this metabolic shift, we tested whether MGO upregulates Hif-1 α , a transcription factor associated with glycolytic reliance, using immunohistochemistry (IHC). Technical challenges with antibody specificity limited quantitative analysis, but highlighted the importance of protocol optimization in visualizing metabolic markers. In vivo, MGO exposure also altered expression of metabolic stress markers GLUT1 and GLUT3, consistent with increased glycolytic demand. Importantly, complementary studies in the Wright Lab show that SARM1 knockout mice, which lack a key axon degeneration pathway, do not develop pain in response to MGO, underscoring the role of metabolic stress and reactive oxygen species (ROS) in neuropathy progression. Together, these findings support a model in which MGO drives metabolic reprogramming and ROS-mediated axon injury in DRG. By clarifying the metabolic mechanisms underlying neuropathy, this work advances understanding of DPN development and informs future therapeutic strategies.

Differential Gene Expression in Astrocytes, Microglia, and Neurons in an Accessible Triculture Model as Compared to Monoculture

Patryk Hupert^{1,2}, Jay Sibbitts^{1,3}, Andrea Graziani⁴, Giuseppe Caruso⁵, Brian Sanderson², Carlo Barnaba⁴, Susan M. Lunte^{1,4,6}

¹Department of Chemistry, University of Kansas; ²Department of Molecular Biosciences, University of Kansas; ³Department of Chemistry, Truman State University; ⁴Department of Pharmaceutical Chemistry, University of Kansas; ⁵Department of Medicine, Saint Camillus International University of Health Sciences Rome, Italy and IRCCS San Camillo Hospital, Venice, Italy; ⁶Adams Institute for Bioanalytical Chemistry, University of Kansas

Alzheimer's disease (AD) affects over 50 million people worldwide, yet therapeutic strategies targeting amyloid- β plaques have repeatedly failed, highlighting the need to explore alternative mechanisms. Growing evidence suggests that crosstalk between neurons and glial cells drives neuroinflammation and accelerates AD progression. Traditional monoculture models fail to replicate this complex environment, and existing mixed-culture systems often require specialized, costly platforms. In addition, downstream proteomic or transcriptomic analyses typically rely on cell sorting, which can alter phenotypes and lengthen the time between harvest and analysis.

To address these gaps, we developed an accessible triculture brain model using commercially available human microglia (HMC3), astrocytes (HA), and neurons (SH-SY5Y) that share the same extracellular medium while remaining physically separated. Microglia and astrocytes are seeded on opposite sides of a porous TranswellTM membrane, and differentiated neurons are seeded in the luminal compartment, at a 2:1:8 ratio. This configuration supports each cell type in its own compartment while allowing communication through a common medium, enabling cell-type-specific responses to be resolved without sorting. Viability in mono- and triculture was assessed by cell counting and calcein AM/ethidium homodimer staining. RNA-sequencing was performed under two conditions: (i) universal versus cell type-specific medium in monoculture, and (ii) triculture versus monoculture for each cell type. Initial analyses reveal robust differential gene expression associated with triculture. Metabolomic analyses of this system are underway. To our knowledge, this is the first comprehensive transcriptomic dataset for this specific triculture, providing insights into how these human cell lines model key brain functions.

Evaluation of FSH glycoform ratios in female serum by ELISA

Yara H. Abdine, Alan R. Brown, Viktor Y. Butnev, William K. White, Jeffrey V. May and George R. Bousfield

Department of Biological Sciences, Wichita State University, Wichita, Kansas, 67260 USA

Follicle-stimulating hormone (FSH) is essential for female reproductive function, regulating follicle growth and maturation in coordination with luteinizing hormone (LH). As a glycoprotein hormone composed of a shared α -subunit and a unique β -subunit, FSH exists in multiple glycoforms that differ in N-linked glycosylation. The three main variants: FSH₁₈, FSH₂₁, and FSH₂₄ vary in the number of attached N-glycans, influencing receptor affinity and biological activity. Hypoglycosylated forms, FSH₁₈ and FSH₂₁, demonstrate greater bioactivity, and age- or cycle-related changes in their abundance may influence fertility outcomes. However, current clinical assays measure only total FSH and cannot distinguish between its functionally distinct glycoforms. Our project aims to quantify FSH glycoform ratios in female serum and urine samples using a glycoform-specific enzyme-linked immunosorbent assay (ELISA). A potential FSH₁₈-selective ELISA was developed and demonstrated strong binding affinity for FSH₁₈ compared to FSH₂₁ and FSH₂₄. The assay's specificity and sensitivity were evaluated in both serum and urine to confirm its ability to differentiate among glycoforms. This preclinical validation supports the ELISA's potential as a tool for studying hormone regulation and reproductive aging. By enabling detection of specific FSH glycoforms, this work advances the development of diagnostic methods that could improve assessment of ovarian function and fertility potential in women.

K-INBRE 2026 Symposium Oral Presentation Abstracts

Characterizing the achromatic visual acuity of *Terrapene ornata* across populations using the optokinetic response.

Weishaar-Wilson, August,¹ and Reed, Benjamin¹

¹ Department of Biology, Washburn University, Topeka, KS

Terrapene ornata are known for fidelity to expansive home range areas over dense and rugged grassland terrain. This behavior necessitates strong navigational ability, the precise mechanisms of which have not been fully elucidated in the literature. Specifically, the visual capabilities of *Terrapene ornata* have not been quantified. We assessed the achromatic visual acuity of *Terrapene ornata* using the head movements of their optokinetic response. This method of assessing visual acuity in box turtles was first reported for *Terrapene triunguis*. *Terrapene ornata* has been observed to have high variation in physiological, behavioral, and morphological traits. We sampled from three wild populations of *Terrapene ornata* in northeastern Kansas and southwestern Nebraska to examine variation in visual acuity within and across populations. Our findings corroborated previous studies by showing high variation in visual acuity both within and across populations; with overall acuity lower than that of the *Terrapene triunguis*. This assessment of visual acuity serves to build a more robust physiological profile of this species without the need for invasive techniques.

K-INBRE grant P20 GM103418

Impact of one nucleotide on organ enumeration and phyllotaxy in *Arabidopsis thaliana*

Hazel Frans; Tara Phelps-Durr, PhD

Fort Hays State University Department of Biological Sciences

Arabidopsis thaliana is a model organism used by scientists to study plant genetics, development, and physiology. CRISPR-Cas9 is a biotechnology tool adapted from a bacterial defense mechanism to precisely edit DNA using a guide mRNA and a Cas9 protein. This project aims to create CRISPR-CAS9 mutations in the APETALA3 (AP3) gene of the model plant *Arabidopsis thaliana*. AP3 is a class B gene critical to the petal and stamen development of *Arabidopsis* flowers. The AP3 protein contains a MADS domain, which binds directly to DNA and may be responsible for the expression of the CaRG-box genes. AP3 works in conjunction with PISTILLATA, AGAMOUS, APETALA1, and SEPALLATA proteins to specify the development in the second and third whorls of the flower. While several alleles of AP3 already exist, these alleles are strong alleles that knockout gene function. The advantage of creating weak alleles is that they often reveal gene functions that knockout mutations mask due to their severity. Thus, examining the phenotypes caused by weak alleles allows researchers to fully characterize gene function. The CRISPR-CAS9 system can make a variety of mutations including small insertions, deletions, or substitutions. We will specifically choose and examine weak alleles for this project. T₃ plants have been identified as mutants through Sanger sequencing, where a single guanine nucleotide insert has induced a frame shift, leading to an early stop codon. Genotyping through an enzyme digest is used to identify mutants, whose flowers are imaged to characterize this phenotype.

Real-time gene expression mapping in a tissue-engineered microvessel to study Alzheimer's Disease

Authors: Amelia Koehn, Ava Hornung, Ninghao Zhu, Department of Electrical and Computer Engineering, Kansas State University

Microvessels play an important role in the exchange of nutrients and waste between blood and tissue. Microvessel abnormalities, especially in the brain, can be initiated from endothelium inflammation and atherosclerosis and lead to stroke or other neurological diseases. Therefore, efforts have been devoted to construct microvessel models in vitro to investigate human microvasculature in health and diseases. However, current microvessel models lack real-time gene expression monitoring methods. Current approaches, including qRT-PCR, RNA fluorescence in situ hybridization, and next generation sequencing require fixation or lysis of the cells, which limits their ability to detect gene expression in a living system. Here, we propose the integration of gold-nanorod based nanobiosensor into a tissue-engineered microvessel to allow the real-time gene expression in live cells. We first monitored the β -actin mRNA expression in the living tissue-engineered microvessel over five days. Then, we monitored the expression of GAD2 and NPTX2, the mRNAs responsible for cognitive decline in Alzheimer's Disease. The result is a living microvessel model with real-time gene expression capabilities. Next steps include siRNA treatments, permeability assays, and disease modeling in the microvessel. This platform is an unprecedented tool to monitor gene expression in a reliable human model, which will allow us to develop more accurate models of a wide range of diseases, paving the way for therapeutic development and treatments.

Infusing Zinc Hydroxide/Biotin/Gelatin Composite Particles in Sorghum Fibers for Biomedical Applications

Noah Freiburger^{1,2}, Mazeyar Parvinzadeh Gashti¹, Chris Ward², Anuradha Ghosh², Alessandro F. Martins¹.

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

This project develops multifunctional bio-based fibers by integrating Zinc Hydroxide/Biotin/Gelatin composite particles into sorghum-derived filaments using wet spinning. Sorghum flour provides a renewable, biodegradable platform, while the composite particles add antibacterial activity, biocompatibility, and drug-delivery potential to create fibers with intrinsic therapeutic function. These engineered fibers aim to support controlled release, improve local tissue environments, and reduce microbial contamination. Wet spinning allows controlled fiber morphology and optimized strength, flexibility, and particle distribution. By combining agricultural materials with biomedical engineering, this work offers an eco-friendly alternative to synthetic medical fibers and promotes value-added use of Kansas sorghum. The project also advances training in biomaterials, polymer science, and advanced fabrication.

References:

1. N. Freiburger, S. Henry, M. Parvinzadeh, C. Ward, A. Ghosh, A. F. Martins, The 23rd Annual Kansas-IDEA Network of Biomedical Research Excellence Symposium, InterContinental Hotel on the Plaza, Kansas City, MO. January 17-19, 2025.
2. Z. Noralian, M. Parvinzadeh, M.R. Moghaddam, H. Tayyeb, I. Erfanian, "Ultrasonically developed silver/iota carrageenan/cotton bionanocomposite as an efficient material for biomedical applications", International Journal of Biological Macromolecules, 180 (2021) 439-457.

K-INBRE 2026 Symposium
Data Science Core Oral Presentation Abstracts

Sunday, January 18, 2026

Using de novo hybrid genome assembly approaches to characterize a new cyanobacterial strain in western Kansas

Bryce Steffan¹, Louisa Acquah¹, and Michael Gruenstaedl¹

¹Department of Biological Sciences, Fort Hays State University

Cyanobacteria are photosynthetic prokaryotes found in aquatic environments; these organisms are prone to extremely fast reproduction, during this process, cyanotoxins are released into the environment. To identify these organisms and to access the genes necessary for cyanotoxin production from an uncharacterized cyanobacteria strain found last year in southwest Kansas we used a hybrid sequencing strategy. After cultivating the strain into an axenic culture, we conducted both short read skimming and long read sequencing via Illumina MiSeq and an Oxford Nanopore MinION, respectively. The hybrid assembly workflow was created using two independent bioinformatic pipelines: Bactopia and bacass. These yielded nearly identical results: each recovered three separate contigs corresponding to the complete bacterial genome, a plasmid, and a bacteriophage. Based on the results from these contigs, we used a variety of quality analyses. These all indicated reliable assembly results: K-mer spectrum analyses confirmed a single genomic source; assembly graph visualizations revealed no alternative structural configurations; contig-level quality assessments demonstrated strong contiguity and collinearity across both pipelines; and contamination screening did not identify any extraneous bacterial, archaeal, or viral sequences. Compared to the complete genome of a related cyanobacterial species, the assembled genome exhibited similar size and gene content but substantial genomic rearrangements, indicating that it likely represents a genetically distinct cyanobacterial strain.

Identification of Monitoring and Response Biomarkers for ADPKD Using Bulk RNA Sequencing in Mouse Models

Olivia Delmas¹, Rachel Griffard-Smith¹, Emily Schueddig¹, Stephen Parnell², Devin Koestler¹, Alan Yu³

¹Department of Biostatistics & Data Science, ²Department of Biochemistry and Molecular Biology, and ³Department of Nephrology, University of Kansas Medical Center

Autosomal dominant polycystic kidney disease (ADPKD) is a progressive genetic disorder and a leading cause of end-stage kidney disease. A key challenge in advancing ADPKD therapeutics is the lack of early-stage biomarkers to assess clinical efficacy in proof-of-concept (POC) trials. To address this gap, we employed a series of statistical and data science methodologies to analyze bulk RNA sequencing data from two ADPKD mouse models with distinct progression rates (e.g., moderate- and fast-progressing) to identify candidate monitoring biomarkers—genes consistently altered over the course of disease progression. Subsequently, mice from the moderate-progressing ADPKD model were treated with mozavaptan, rapamycin, or genetically re-expressed Pkd1 gene. Genes that were observed to change in response to treatment across all three interventions were designated response biomarkers and were compared with the monitoring set. Across approximately 15,000 kidney-expressed genes, only a single gene was identified as both a monitoring and response biomarker, highlighting its potential utility in tracking disease progression and therapeutic response. This study demonstrates how integrative data science approaches—including high-throughput sequencing, statistical modeling, and multi-condition comparison—can drive biomarker discovery and inform the development of a biomarker-driven clinical POC strategy in ADPKD.

On the Evolution of the SARS-CoV-2 Mpro and its Substrate

Carter J. Gray^{1,2}, Shwetha Sreenivasan¹, Liskin Swint-Kruse¹

¹Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS, ²Department of Electrical Engineering and Computer Science, University of Kansas, Lawrence, KS

Viral speciation involves genomic changes that lead to altered amino acid sequences in viral proteins. For example, changes in SARS-CoV-2 main protease (Mpro) alter its ability to cleave 11 endogenous substrates in the SARS-CoV-2 polyprotein. Predicting the functional effects of these substitutions can enhance our ability to predict future variants of concern. Unfortunately, attempts to predict substitution effects have been no better than random. Thus, we described a mutational framework that characterizes each position based on the distribution of mutational effects of every amino-acid. Using this framework in other protein families, we identified a characteristic phylogenetic signal at rheostat positions, that can tune the full range of functional outcomes. Here, we report this trend in the coronavirus-wide evolution of Mpro. To identify if this pattern persisted on a smaller evolutionary scale, we extracted ~8 million Mpro and substrate sequences from the SARS-CoV-2 genomes deposited in NCBI Virus. The two major variants of Mpro (Wuhan and P132H) were used as reference sequences. Between the two variants the sets of observed single mutations were compared against substitutions expected from random chance and to each other. Results lead to the hypothesis that P132H Mpro might cause wide-spread epistasis, rewiring the substitutional landscape of Mpro. Finally, we compared each Mpro variant with the co-evolving substitutions found in the endogenous Mpro substrates. Results showed (i) distinct sequence changes between the two Mpro variants (ii) distinct trends in a non-canonical substitution at the substrate P1 position, and (iii) that substitution frequencies between Wuhan P132H differ dramatically.

From Design to Deployment: Optimizing Bridge Samples for Robust Batch-effect Correction in Olink® Proteomic Data

Md Saiful Islam Saif¹, Rondi A Butler², Lucas A Salas³, Brock C Christensen^{3,4}, Annette M Molinaro⁵, John K Wiencke⁵, Karl T Kelsey², Devin C Koestler¹

[1] Department of Biostatistics & Data Science, University of Kansas Medical Center, Kansas City, KS, USA

[2] Department of Epidemiology, and Pathology, and Laboratory Medicine, Brown University School of Public Health, Providence, RI, USA

[3] Department of Epidemiology, Geisel School of Medicine at Dartmouth, Lebanon, NH, USA

[4] Department of Molecular and Systems Biology and Community and Family Medicine, Geisel School of Medicine at Dartmouth, Lebanon, NH, USA

[5] Department of Neurological Surgery, Weill Institute for Neurosciences, University of California, San Francisco, San Francisco, CA, USA

Olink® proteomics has become a leading platform for population-scale protein profiling, yet its measurements remain susceptible to batch effects. To reduce these artifacts, Olink recommends including technical replicates referred to as “bridge samples” across batches. Although guidelines exist for selecting and determining the number of bridge samples, systematic evaluations of their necessity, effectiveness, and optimal use remain limited. Using a simulation-driven framework grounded in real Olink datasets, we examined three questions: (1) Are bridge samples essential for batch-effect correction, or can established approaches such as ComBat, which do not require bridging, adequately mitigate batch effects? (2) If bridge samples are beneficial, what is the best strategy for selecting them? (3) How many bridge samples are needed for optimal performance of the Olink bridge-based method? We found that ComBat performs similarly to Olink’s bridge-based correction when case–control status is balanced across batches, but the Olink method is more effective under severe imbalance. Olink’s recommended bridge-sample selection strategy offered no clear advantage over random selection. Simulations further revealed that the optimal number of bridge samples depends on study design, batch size, and case–control balance: 2–8 samples are sufficient under balanced conditions, whereas 15–25 may be needed when imbalance is substantial. To support researchers in applying these insights, we developed an interactive Shiny application that provides study-specific guidance on the ideal number of bridge samples. Our simulation workflow and interactive tool enable researchers to optimize study design, improve data quality, and avoid unnecessary costs.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-1. Exercise from Afar: Progressing At-Risk Adults to Effective Independent Exercise for Dementia Risk Reduction

Erin Blocker¹, Luke Gleason¹, Kamon Haydock¹, Madison Newton¹, Natalie Alrid¹, Donovan Law¹
¹Health and Human Performance Department, Emporia State University

A-2. Incorporation of Chimeric Macrodomains into Murine Hepatitis Virus for Antiviral Testing of Multiple Coronaviruses in a Single System

Kendall A. Cranor, Anjali Singh, Nathan Quinton, Jessica J. Pfannenstiel, Anthony R. Fehr
Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

A-3. Identifying the deep intronic variant (missing heredity) in high-risk Latino families

King, Kara, Rains, Gracyn, Zweydoft, Rebekah, Weitzel, Jeffrey N and Pirani, Karim
University of Kansas Medical Center

A-4. Determine the impact of entomopathogenic fungi on *Aedes aegypti* mosquitoes transfected with *Wolbachia*

Ryan Thomas, David Hayes, and Kristin Michel

A-5. Effects of Voluntary Oral Consumption of Delta-Tetrahydrocannabinol on Home Cage Alcohol Drinking

Authors: Caden C. Blake, Dylan A. Laux, and Mary E. Cain. Department of Psychological Sciences at Kansas State University

A-6. Synthesis and Characterization of N-Quaternized Ammonium Pectin Derivatives for Tunable Antimicrobial Activity and Cytocompatibility

Christina Diab, Gabriel Tenório, Alessandro Francisco Martins, Department of Chemistry, Pittsburg State University

A-7. Nuclear shape dynamics drive collective cell migration through crowded tissue environments

Ben Lawrence, Rehan Khan, Jocelyn McDonald
Kansas State University Division of Biology

A-8. Evolution of cell number in migrating cell collectives

Kendra Visser¹, Gavin Rice¹, Jocelyn A. McDonald¹
¹Division of Biology, Kansas State University

A-9. Impact of Exposure to Simulated Galactic Cosmic Radiation on Ovarian Follicle Development in Mice

Lauren Higgins, Fereshteh Dalouchi, Joshua S. Alwood, April E. Ronca, V. Praveen Chakravarthi, Lane K. Christenson
Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, Kansas
Department of Human Factors and Behavioral Neurobiology, Embry-Riddle Aeronautical University, Daytona Beach, Florida
Space Biosciences Research Branch, NASA Ames Research Center, Moffett Field, California

A-10. Defining How Different Sulfation Patterns in the Extracellular Matrix Impact Myelin Repair in the Brain.

Corbin Fairchild¹, Jenna Williams, Matthew Zupan, Dr. Esther Holt, Jack Petersen, Dr. Meredith Hartley, Department of Chemistry, University of Kansas, Lawrence KS, United States of America.

A-11. Alternative Solvents to Dichloromethane for Ring Closing Metathesis of Azamacrocycles

Rebecca J. McCreight, Shaun E. Schmidt Department of Chemistry. Washburn University, Topeka, Kansas

A-12. Zein Protein-based Medical Pads with Antimicrobial Properties

Simon Wicks¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Chris Ward³
1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA
3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

A-13. A *Bacillus pumilus* Isolate With Promising Antimycobacterial Properties

Cody Pfaff, Eric T. Gillock
Department of Biological Sciences; Fort Hays State University

A-14. The role of RIC interneurons in longevity regulation in *Caenorhabditis elegans*

Moussa Gacko¹, Mingyi Liu¹, and Shijiao Huang¹
¹Biochemistry and Molecular Biophysics, Kansas State University

A-15. Immunohistochemical (IHC) Analysis of HNSCC/CAF Cells and Xenotransplants

McMillan, Riley. Wichita State University: Department of Biological Sciences

A-16. Investigate the Impact of CluH Silencing on Mitochondrial Distribution in Cancer Cell Lines

Jungjiao An, Sofia Steigner, Stephen Fields. Department of Biology in Emporia State University.

A-17. The autoimmunity-associated allele of *PTPN22* mediates macrophage production of pro-inflammatory cytokines

Tatum P. Aikin^{*}, Austin E. Eades, Tammy Cockerham, Nancy Schwarting, Robin C. Orozco^{**}
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-18. Improving Glycemic Control via Heat Therapy in Older Adults at Risk for Alzheimer's Disease

Elaine Gast,^{1,6} Anneka Blankenship,^{1,2} Riley Kemna,^{1,2} Paul Kueck,^{1,2} Casey John,^{1,2} Hana Mayfield,¹ Maggie Kroeger,¹ Jenae Pennington,¹ Rachel Reaves,¹ Raechel Camones,¹ Michelle Vitztum,³ Lauren Yoksh,⁴ Jonathan Mahnken,^{1,4,5} Eric Vidoni,^{1,2} Jill Morris,^{1,2} Paige Geiger^{1,6}

¹University of Kansas Alzheimer's Disease Research Center, University of Kansas Medical Center, Fairway, Kansas, United States.

²Department of Neurology, University of Kansas Medical Center, Kansas City, Kansas, United States.

³KU Diabetes Institute, Department of Internal Medicine, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁴Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁵Frontiers Clinical and Translational Science Institute, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁶Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, Kansas, United States.

A-19. CCR2-associated proteins alter metabolism in DCIS progression

Lillian O'Donnell¹, Wei Fang¹, Marcela Medrano¹, Michaella Rekowski², Zachary Clark, Macy Payne², Stefan Bossmann², Justin Douglas³, Laurie Harnad³, Philip Lorenz^{4,5}, Lin Tan^{4,5}, Brooke Fridley⁶, Chase Sakitis, Nikki Cheng^{1,2}

¹Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, ²Department of Cancer Biology, University of Kansas Medical Center, ³NMR Lab University of Kansas, ⁴Department of Bioinformatics and Computational Biology, MD Anderson, ⁵Metabolomics Facility MD Anderson, ⁶Biostatistics and Epidemiology Core, Children's Mercy Research Institute

A-20. Pay Equity Among Professors of Behavior Analysis in Rural and Urban Areas

Carter, K.¹, Boydston, P.¹, & Redner, R.²

Pittsburg State University, Department of Psychology and Counseling¹

Southern Illinois University- Carbondale, Department of Psychological and Behavioral Sciences²

A-21. Hepatic-Derived Extracellular Vesicles Enter the Brain *In Vivo* Regardless of Exercise or Sedentary Status but Have No Effect on Mitochondrial Respiration at a Low Dose

Authors: Bansal, Aanya^{1,3}; Salathe, Sebastian F.¹; Kugler, Benjamin A.¹; Boakye, Frederick B.¹; Franczak, Edziu¹; Busick, Zane¹; Allen, Julie¹; Hong, Xiaoman¹; Kelty, Taylor J.²; Meers, Grace M.²; Christenson, Lane¹; Wilkins, Heather¹; Booth, Frank W.²; Rector, R. Scott²; Thyfault, John P.¹

¹The University of Kansas Medical Center, ²The University of Missouri School of Medicine, ³The University of Southern California

A-22. A-22. ABC transporter localization in *C. elegans*

Gilmore, Caleb¹, Timmons, Lisa¹

¹Department of Molecular Biosciences, KU Lawrence

A-23. Exploring Ancestral Enzymes through Sequence Reconstruction and Stability Prediction

Jeyun Park¹ and Masakatsu Watanabe²

¹Academy of Mathematics and Science and ²Department of Chemistry Fort Hays State University, Hays, Kansas 67601, USA

A-24. Fabrication of Wheat Gluten based Films using Spray Jet Method

Asher Freiburger¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

A-25. Identifying Regulators of miRNA Strand Selection in *Caenorhabditis elegans*

Isabella Berndt¹, Jeff Medley¹, Sumire Kurosu¹, and Anna Zinovyeva¹

¹Division of Biology, Kansas State University, Manhattan, KS

A-26. Green Sodium Hypochlorite Oxidation of Primary Alcohols to Carboxylic Acids for the Undergraduate Organic Chemistry Laboratory

Avery Gutierrez,¹ Devi Steigner,¹ and Lucas McCormick¹

¹School of Science and Mathematics, Emporia State University

A-27. Interpopulation Phenotypic Variation in the Ornate Box Turtle (*Terrapene ornata*) Driven by Environmental Selective Pressures

Peterson, Grace, Peyton Samek, Brookelynn Powell, Caroline LeJuerne, Jady Falley, Bella Limback, Sage Dennis, August Wilson, Ash Van Dalsem, Erin Carter, Serena Schmitz, Kyra Jantzen, and Benjamin Reed
Department of Biology, Washburn University, Topeka, Kansas, USA.

A-28. Discovering the Signal-Detection Mechanism of *Chlamydia trachomatis*: Expression and Purification of the CtcB Sensor Domain

Yesem Hailemariam, Lexie Payton Cutter, Scott P. Hefty Ph.D.

Department of Molecular Sciences, University of Kansas

A-29. Developing a method to manipulate the immune system of mosquito larvae

Julia Chartier, David Hayes, and Kristin Michel,

Division of Biology, Kansas State University

A-30. Unique signatures of mitochondrial genomic evolution in threespine stickleback fish

Reed M Hodges, Emily A. Beck

Department of Molecular Biosciences, University of Kansas

A-31. Activated Maple Carbon as a Bio-Based Cathodic Material in Lithium-Sulfur Batteries for Electrochemical Energy Storage Applications

Alexandra Robinson², Anjali Gupta², Wang Lin¹ and Ram K. Gupta^{1,2*}

¹National Institute of Material Advancement, Pittsburg, KS 66762, USA

²Department of Chemistry, Pittsburg State University, Pittsburg, KS 66762, USA

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-32. WHAT'S LINKER GOT TO DO WITH IT? EXAMINING THE STRUCTURE AND STABILITY OF PALLADIN'S IG3-4 LINKER REGION

Lauren Hughes, Rachel Sargent, Nathan Ta, Colby Bradford, Dr. Moriah Beck
Department of Chemistry and Biochemistry, Wichita State University

A-33. A corticolimbic dopamine-glutamate pathway modulates partner seeking behavior during loss state in prairie voles (*Microtus ochrogaster*).

Guillen Saucedo, Nicolle^{1*}, Lowe, Camryn S.^{1*}, Taba, Amina H.², Vitale, Erika M.¹, Ahad, Nicole T.¹, Smith, Adam S.^{1,2}

¹Department of Pharmacology and Toxicology, School of Pharmacy, ²Program in Neuroscience, University of Kansas, Lawrence, KS, USA

*Contributed equally

A-34. The Effects of Supplemental Feeding on the Movement Ecology of the Ornate Box Turtle

Peyton Samek, Jadyne Falley, Brookelynn Powell, Grace Peterson, Caroline LeJuernne, Bella Limback, Sage Dennis, August Weishaar-Wilson, Ash Van Dalsem, Erin Carter, Benjamin Reed
Washburn Biology Department

A-35. Resistance to X chromosome meiotic drive in *Drosophila affinis*

Vincent Chan^{1*}, Anjali Gupta², Robert L. Unckless¹

¹Presenting author

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66045

²Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045

A-36. Transformation of *Chlamydia* by DNA-Transferrin Delivery

Sofía Chacón Araya, Dominique Jaramillo, Scott P. Hefty Ph.D.

Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

A-37. Genes regulating glucosinolate anticancer compounds in a plant model

Brynn R. Collier, Kathrin Schrick

Division of Biology, Kansas State University

A-38. Exploring Structure-Selective RNA-Targeting Compounds for Triple-Negative Breast Cancer Therapy

Maddox Johnson, James McAfee, Irene Zegar

Department of Chemistry, Pittsburg State University, Pittsburg, Kansas.

A-39. Cardiovascular health monitoring using multiple conformal photoplethysmography devices

Taylor Spinelli¹, Bryson Murphy¹ and Yongkuk Lee.¹

¹Department of Biomedical Engineering, Wichita State University.

A-40. Unoccupied

B-1. Chemotherapeutic 5-FU alters multifactor complex formation with oncogenic translation initiation factor 5MP1 and eIF proteins

Authors: Logan Glover, Susumu Ishiguro, Katsura Asano

Department of Biology, Kansas State University, Manhattan, KS, 66506

B-2. Gene engineering, cloning, and expression of the human CLPB variant, SAP

Eleanor Martin, Zachary Spaulding, and Michal Zolkiewski

Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, Kansas

B-3. Exploring the factors that are related to metabolic rate in Ornate Box Turtles (*Terrapene ornata*)

Authors: Ephraim Schlingensiepen, Tracy Wagner, Paul Wagner, Benjamin Reed

Washburn University Biology dept.

B-4. Floristic Summary of Bates County, Missouri

Mason, Rylan¹ and Neil Snow¹

¹Department of Biology, Pittsburg State University

B-5. Trastuzumab Utilization in Differential Selective Pressure Analysis: a Post-hoc Assessment of MSK-IMPACT 341 and TCGA-2015 in Clinical Outcomes

Authors: Auditya Jain, Marcus Yoakam, Maryam Nabavifard, Christopher Ward

Affiliations:

1- **Kansas City University:** 1750 Independence Avenue, Kansas City, MO 64106. Tel: (816) 654-7000

2-**Pittsburg State University Biology Department:** 101 Heckert-Wells Hall, 1701 S. Broadway, Pittsburg, KS 66762. Tel: (620) 235-4748.

B-6. Blazin' Brains: Reaction Time Training, Exercise and Cognition

Erin M. Blocker¹, Brynn McCormick¹, Savannah Stewart¹, and Abby Bachman¹

¹School of Applied Health Sciences, Emporia State University

B-7. Molecular test to differentiate between polymorphic Y chromosomes in *Drosophila affinis*

Kaylie Schroeder^{1*}, Anjali Gupta², Robert L. Unckless¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66046

²Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66046

¹Presenting author

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-8. Developmental origins of aberrant neurological trajectories in Down syndrome

Katherine I. McCarthy¹, Lexe M. West¹, Hayden C. Hawks¹, Sunita N. Varghese¹, Abhik Saha¹, Greta Foye¹, Luke Johnson¹, Keith P. Smith², Heather M. Wilkins², and Katherine A. Waugh¹
Departments of Cell Biology and Physiology¹ and Neurology², University of Kansas Medical Center, Kansas City, KS 66160

B-9. MicrobioME: A CURE for Staphylococcus aureus – Can our commensal bacteria help inhibit the formation of biofilms?

Darsh Lad, Rosana B.R. Ferreira, Eileen M. Hotze
Department of Molecular Biosciences, University of Kansas – Lawrence

B-10. Skin microbiomes transferred to clothing can be used in forensic identification of individuals

McGann, Alexa, Joselynn Hoff, Logan Shearer and Stephen Fields
Department of Biological Sciences, Emporia State University, Emporia, KS

B-11. DEVELOPING A WEARABLE FETAL HEART MONITOR: AN EVALUATION OF FETAL ELECTROCARDIOGRAM EXTRACTION ALGORITHMS

Emma Simmons, Dr. Yongkuk Lee
Department of Biomedical Engineering, College of Engineering

B-12. Watermelon Seed Protein-based Films for Wound Dressing Applications

Isaac Mountain¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³
1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA
3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

B-13. Loss of the Drosophila multispecific transporter, Malvolio, results in abnormal brain morphology and a defective developmental ionome.

List of Authors: Breanna Leach^{2*}, Divyankasri Padamati^{1*}, Prabriti Neupane¹, Justin Scott³, Puni Jeyasingh³, and Rajprasad Loganathan^{1,2}
Author Affiliations: 1) Department of Biological Sciences, Wichita State University; 2) Department of Biomedical Engineering, Wichita State University; 3) Department of Integrative Biology, Oklahoma State University.
*Co-presenting authors

B-14. Assessing genetic interactions between patient-derived alg-1 alleles and alg-2 knockout in Caenorhabditis elegans models of Argonate Syndromes

Rebecca Mitchell, Belén Gaete Humada, Anna Zinovyeva
Division of Biology, Kansas State University, Manhattan, Ks

B-15. Validation of a Pen-Side LAI and Deep Learning Tool for SARS-CoV-2 Surveillance in Animals.

Smith, M., Bakshi, A., Caragea, D., Gauderault, N.N., Richt, J., Trimpert, J., Panagonova, Y. and Bruning-Richardson, A., Miller, L.C.

B-16. Role of the GIR2 transcriptional adapter protein in controlling plant cell elongation

Kiaorie Stewart-Ricks^{1,2}, Lauren E. Apprill³ and Kathrin Schrick^{2,3}
¹Langston University; ²Division of Biology and ³Department of Biochemistry and Molecular Biophysics, Kansas State University

B-17. Volumetric Effects of Early Life Stress and Exercise on Brain Matter in Mice

Whitehouse, Katrina¹, Anna Ferkul¹, Tara McQuillan¹, Julie Christianson¹
¹Department of Cell Biology and Physiology, Neuroscience, University of Kansas Medical Center, Kansas City, Kansas

B-18. The Untold Truths of the Minds of Students' Mental Health and Academic Well-being

Lauren Moore¹ & Dr. Susan Abraham²
¹Department of Biology, School of Arts & Sciences and ²Department of Psychology, School of Education & Behavioral Sciences, Langston University**

B-19. Characterization of AT5G16120: A Putative Monoacylglycerol Lipase

America Zarate^{1,2}, Zolian S. Zoong Lwe^{1,3}, and Ruth Welti^{1,2}
¹Division of Biology, ²Kansas Lipidomics Research Center, ³Department of Biochemistry & Molecular Biophysics, Kansas State University, Manhattan, KS 66506

B-20. Comparative Study of Chitosan/Tripolyphosphate and Tanfloc/Tripolyphosphate Microparticles Prepared in a Pluronic-Stabilized Microemulsion

Caitlynn Tate, Kenny Kouadio, Alessandro Francisco Martins
Department of Chemistry, Pittsburg State University

B-21. Ultrasonic Vocalizations During Social Platform Mediated Active Avoidance in Male and Female Rats

Jasmine Wolf, Penylopi Zabzdyr, Maria Diehl
Department of Psychological Science, Kansas State University, Manhattan, Kansas, USA

B-22. Preliminary study focusing on the role of gut microbiota in the development visceral hypersensitivity

Colby Riddle¹, Erin Young², Kyle Baumbauer², Sree Chintapalli³, and Anuradha Ghosh¹
¹Biology Department, Pittsburg State University, Pittsburg, KS;
²Departments of Cell Biology and Physiology, and Anesthesiology, University of Kansas Medical Center, Kansas City, KS;
³Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-23. Benzimidazolium Salts from Renewable Sources for Antibacterial Applications

Kinsey Baldwin and Jody Neef
Pittsburg State University

B-24. Pumpkin Seed Protein-based Medical Pads for Wound Dressing Applications

Hannah Posterick¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³
1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA
3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

B-25. In-Silico Characterization of EGFR Signaling and Downstream Effectors in Breast Adenocarcinoma

AUTHORS: Sara Akhtar, Christopher Ward
AFFILIATIONS: Pittsburg State University

B-26. Comparing Lysholm Scores: Quadriceps, Hamstring, and Patellar Tendon Autografts in ACL Reconstruction

AUTHORS: Johnson, Riley¹; Barkley, Jayme¹; Rider, Kaylee¹; Henry, Sebastian¹, Sorell, Ryan MD²; Ward, Christopher MD¹
AFFILIATIONS: Pittsburg State University¹, Freeman Medical Center²

B-27. Molecular and Cellular Regulation of Microglia by Soy-Protein Nanofiber Scaffolds

Eliceo Caniza Velazquez, Kayla Cantu, and Li Yao
Department of Biological Sciences, Wichita State University

B-28. Fabrication of antimicrobial pads using materials from the nature

Braylon Brown¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³
1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA
3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

B-29. Structure-Guided Design of Potent Coronavirus Inhibitors with a 2-Pyrrolidone Scaffold

Zeeshan Azmi¹, Zoie Liska¹, Chamandi S. Dampalla¹, Yunjeong Kim², Alexandria Zabiegala², Dennis J. Howard¹, Harry Nhat Nguyen¹, Trent K. Madden¹, Hayden A. Thurman¹, Anne Cooper³, Lijun Liu³, Kevin P. Battaile⁴, Scott Lovell³, Kyeong-Ok Chang², and William C. Groutas¹
1 Department of Chemistry and Biochemistry, Wichita State University, Wichita, Kansas 67260, United States
2 Department of Diagnostic Medicine & Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506, United States
3 Protein Structure and X-ray Crystallography Laboratory, The University of Kansas, Lawrence, Kansas 66047, United States
4 NYX, New York Structural Biology Center, Upton, New York 11973, United States

B-30. Development of a Low-Cost Near-Infrared Reflectance System Using the AS7263 Spectral Sensor

Authors: Hannah Grace Rosario¹, Gao Yuanyuan²
¹ Department of Electrical Engineering, Wichita State University ² Department of Biomedical Engineering, Wichita State University

B-31. Development of dioxolenium ion crosslinking chemistry for molecules based on 2-bromo-3-hydroxypropionic acid

Vanessa Carey, Parisa Jahangiri, Coleen Pugh
Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS 67260-0004

B-32. Enhancing Anthrax Vaccine Efficacy: Protective Antigen-PP65 Conjugation Using SpyCatcher/SpyTag

Abby Bui & James G. Bann
Wichita State University Biochemistry and Chemistry Department

B-33. Redox Roots: Real-Time Tracking of Microbial Glutathione Production Under a Cysteine Gradient

Elijah Clark, Brooke Vogt, Sonny Lee
Kansas State University, Kansas State University Biology Department,
Langston University, K-INBRE, National Science Foundation

B-34. Examining Blood-Brain Barrier Permeability in a 3D Tissue-Engineered Micro vessel

Cassidy Huynh, Ninghao Zhu, Department of Electrical and Computer Engineering, Kansas State University

B-35. Gene-Metal-Microbe Interactions: The Effect of Genetic and Microbial Variation on Heavy Metal Response in Drosophila

Maggie Ridgway, Stuart J. Macdonald
University of Kansas, Lawrence
Department of Molecular Biosciences

B-36. Characterizing Genomic Alterations Associated with DCIS Progression

Ava Gartelos¹, Yan Hong¹, Carol Fabian², Andrew K. Godwin², Fariba Behbod², Ayantika Sen Gupta³, Jennifer Gerton³.
¹Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, Kansas City, KS 66160, ²Department of Medical Oncology, The University of Kansas Medical Center, Kansas City, KS, 66160, ³Stowers Institute for Medical Research, Kansas City, Missouri, 64110

B-37. Potential interactions of SIRT1, tirzepatide, and KRAS mutation in colorectal cancer

Magstadt, Alexa,¹ Anindita Mahanty,² Cara Wallingford,² Revan Hammontree,² Jennifer S. Davis^{2,3}
¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS, ²Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, ³University of Kansas Cancer Center, Kansas City, KS

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-38. Comparison of bacterial and human phosphoglycerate dehydrogenase

Ella P. Ruliffson and Kim T. Simons

School of Science and Mathematics, Emporia State University, Emporia, KS, USA

B-39. Investigation of Intrinsically Disordered Regions in the Drosophila Matrisome

Md Wasi Ul Kabir³, Tessa Nolen², Nazanin Kasirosafar^{1*}, Md Tamjidul Hoque³, and Rajprasad Loganathan^{1,2}

- 1) *Department of Biological Sciences, Wichita State University*
- 2) *Department of Biomedical Engineering, Wichita State University*
- 3) *Department of Computer Science, University of New Orleans*

*Co-presenting Authors

B-40. Unoccupied

C-1. Regulation of *cdeAB-oprM* efflux pump in *Chromobacterium subsugae* in response to antibiotics and quorum sensing

Leah I. Legleiter¹, Eryk Yarkosky¹, Josephine R. Chandler¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

C-2. A CURE for learning metagenomics

Matthias, Emily^{*}, Alexa McGann^{*} and Stephen Fields

Department of Biological Sciences, Emporia State University, Emporia, KS

C-3. Imidazolium Salts from Renewable Sources for Antibacterial Applications

Halle Finnerty and Jody Neef

Pittsburg State University

C-4. Watermelon Seed Oil based Coatings for Hospital Bedsheets

Savannah Grotheer¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

C-5. Clusterin (CLU) as a Modulator of Neuronal Excitatory/Inhibitory Balance

Vanessa Nguyen¹, Punam Rawal², Liqin Zhao^{2,3}

¹Molecular Biosciences Program, Department of Undergraduate Biology

²Department of Pharmacology and Toxicology, School of Pharmacy,

³Neuroscience Graduate Program, University of Kansas, Lawrence, KS 66045, USA

C-6. The impact of functional electrical signal on cellular process of neural cells

Amelie Zidarita, Li Yao

Department of Biological Sciences, Wichita State University

C-7. Advancing Genetic Engineering in Three Plant Lineages: *Mimulus*, *Antirrhinum*, and *Penstemon*

Krentzel, Jim T. and Lena C. Hileman

Department of Ecology and Evolutionary Biology, University of Kansas

C-8. Understanding Genomic Adaptation to High-Altitude Environments in the North American Deer Mouse (*Peromyscus maniculatus*)

Larissa Rockenbach¹ and Dr. Allie Graham^{1,2} University of Kansas¹, KU Center for Genomics²

C-9. Exploring the relationships between feeding behavior and personality traits in the Ornate Box Turtle (*Terrapene ornata*)

Powell, Brookelynn, Peyton Samek, Caroline LeJuerne, Jady Falley, Grace Peterson, Bella Limback, Sage Dennis, August Wilson, Ash Van Dalsem, Erin Carter, Serena Schmitz, Kyra Jantzen, and Benjamin Reed.

Department of Biology, Washburn University, Topeka, Kansas, USA.

C-10. Effects of neuromodulating drugs on *C. Elegans* Longevity

Ameerah Alfailakawi¹, Shelby Innes¹, Shijiao Haung¹

¹Department of Biochemistry and Molecular Biophysics, Kansas State University

C-11. Dual Function Inhibitors of Coronavirus 3CL Proteases and Cathepsin L

Zoie P. Liska⁴, Harry Nhat Nguyen¹, Pulini S. Ranasinghe¹, I. Kankanamge Ravindu S. Ilesinghe¹, Chamandi S. Dampalla¹, Athri D. Rathnayake¹, Abdul-Rahman M. Jesri¹, Zeeshan Azmi¹, Dustin E. Nenoven¹, Yunjeong Kim², Kevin P. Battaile³, Hayden A. Thurman¹, Egor Gusachenko¹, Scott Lovell⁴, Kyeong-Ok Chang², William C. Groutas¹. ¹Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS. ²Department of Diagnostic Medicine & Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS. ³NYX, New York Structural Biology Center, Upton, NY. ⁴Protein Structure Laboratory, The University of Kansas, Lawrence, KS.

C-12. Gene repression by a quorum-sensing transcription factor that normally functions as an activator.

Kristina Sim, Eryk Yarkosky, Josephine Chandler.

Department of Molecular Biosciences, University of Kansas

C-13. The study of activated astrocyte migration on nanofibers for neural regeneration

Lucas Seitz, Kayla Cantu, Li Yao

Department of Biological Sciences, Wichita State University

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-14. Leisure Interests and Barriers Among Adults with Intellectual and Developmental Disabilities

Kaitlyn Draper, Laura Covert Miller, Evelyn Smith, Kaeli Lynnes, Kinleigh Hall
Department of Health, Human Performance, and Recreation, Pittsburg State University, Pittsburg KS

C-15. Using molecular evolutionary analysis to detect novel function in a floral pigment pathway gene

Mays, Liz S., Haylee Coffman and Lena C. Hileman
Department of Ecology and Evolutionary Biology, University of Kansas

C-16. Destabilizing MALAT1: A Novel Approach to Lung Cancer Cell Migration and Invasion

Hannah Warner, Maddox Johnson and Dr. James McAfee, Dr. Irene Zegar
Chemistry, Pittsburg State University, Pittsburg, KS 66762

C-17. Spatial transcriptomics reveals misregulated extracellular matrix, transcriptional control and antioxidant genes in early ADPKD that is reversed by targeting metabolic sensor, Ogt

Gia Vo Luc^{1,5}, Matthew A. Kavanaugh^{1,5}, Saleem Ahmad^{1,5}, Darren P. Wallace^{2,5}, Stephen C. Parnell^{3,5}, Chad Slawson^{3,5}, Amrita Mitra⁴, Harsh Pathak⁴, Pamela V. Tran^{1,5}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

³Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁴Department of Pathology and Laboratory Medicine and the KU Cancer Center, University of Kansas Medical Center, Kansas City, KS

⁵The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

C-18. Expanding Transposon Library in *Chlamydia muridarum*

Komron Fardipour, Natalie Wagoner, Dominique Jaramillo, Scott Hefty, PhD
University of Kansas

C-19. Modifying the Synthesis Protocol of Graphene-based Quantum Dots to Adjust Emission Wavelengths

Miranda McCammon and Dr. Hoang Nguyen
Department of Chemistry, Washburn University

C-20. Analysis of Essential Oils Inhibiting Growth of Gram-Positive, Gram-Negative, and Fungal Pathogens

Maggie Peterson and Eric T. Gillock
Department of Biological Sciences at Fort Hays State University

C-21. Determining if PARP14 Impairs HSV-1 In A Strain-Specific Manner

Meghan Arias¹, Anna Ferkul¹, Anthony Fehr¹, David Davido^{1*}
¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66045

C-22. Analyzing the Therapeutic Potential of Naturopathic Compounds on Neuro-2a (N2a) cells modeling Alzheimer's Disease (AD)

Avani Gupta, Shelby, Fiegner, Shelby, Fletchall, and Duane A. Hinton
Department Of Biology, Washburn University

C-23. Identifying novel candidate genes contributing to differences in visceral pain sensitization between C57BL/6 substrains.

Sebastian Meriano¹, Morgan Ewald^{2,3}, Leena Kader^{2,3}, Audie Rodriguez^{2,3}, Kyle Baumbauer³, and Erin E. Young^{2,3,4}
¹University of Kansas, Lawrence, Kansas, United States
²Department of Anesthesiology, Pain, and Perioperative Medicine, KU Medical Center, Kansas City, KS, United States
³Neuroscience Graduate Program, KU Medical Center, Kansas City, KS, United States
⁴Department of Cell Biology and Physiology, KU Medical Center, Kansas City, KS, United States

C-24. Unoccupied

C-25. Gait Differences in ASD/Fragile X Rodent Models

Justin Berryhill¹, Bhavana Sivayokan², Dr. Bethany Plakke²,
¹Langston University Department of Biology
²Kansas State University Department of Psychology

C-26. Detection of Beta-Lactamase Antibiotic Resistance Genes in Rural Kansas Soils Across Agricultural Land-Use Types

Chloe Harmon¹, Ella Colson², Yaw Antwi², Bishnu Pangen², Claudia Da Silva Carvalho², PhD
¹Department of Chemistry, Fort Hays State University, Hays, KS, USA, ²Department of Biology, Fort Hays State University, Hays, KS, USA

C-27. Analysis of Nitrosamine Levels in Sandwich Meats Using GC-MS

Cortnie Morgan and Lindsay Davis, Ph.D.
Department of Chemistry and Physical Sciences, Langston University, Langston, OK 73050

C-28. PER-haps a Solution? Testing Phytocannabinoids Against Nicotinic Stress in Honey bees

P. Alex Swider¹, Joselyn Hoff¹, Jackson Arb¹, Oliver-Elias Hiszczynskyj¹ and Joanna C. Gress¹
¹ School of Science and Mathematics, Emporia State University

C-29. Small Molecules from Commensal Gut Bacteria affect Macrophage Activation

Berzansky, Marion¹, Tucker Folscroft¹, Sakshi Patel¹, Sophia Roccaro¹, Lauren Atkinson^{#,2}, Rayssa Durães Lima^{#,2}, Luis Caetano Martha Antunes^{#,2}, Dyan E. Morgan^{#,1}
¹Undergraduate Biology Program, ²Department of Molecular Biosciences, University of Kansas, ^{*,#,&} indicate equal contributions

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-30. Annotation of Protein Coding Genes in *D. willistoni* Contig18

Hinrichs, Kylie¹ and Takrima Sadikot¹

¹ Biology Department, Washburn University

C-31. Synthesis of Sterically Hindered Catechol Ligands for Hydrophobic Anti-Cancer Vanadium Complexes

Authors: Hannah Nimmo¹, Colson Browning¹, Jack Newman¹, Maggi Braasch-Turi*¹

¹Department of Chemistry, Fort Hays State University, Hays, KS.

*Corresponding Author: mmbraaschturi@fhsu.edu

C-32. Big Browns All the Way Down: DNA Identification of Bat Species Roosting at Fort Leavenworth

Alison K. Coykendall, Lorelei E. Patrick

Fort Hays State University Department of Biological Sciences

C-33. Metagenome analysis of poultry litter collected from farms across eastern region of Kansas with a focus on antibiotic resistant and foodborne pathogens

Owen Long, Debmalyo Rudra Sarma, and Anuradha Ghosh

Biology Department, Pittsburg State University, Pittsburg, Kansas

C-34. Role of asparagine synthetase and other transcription factor targets in epidermal morphogenesis

Jillian K. Rockley, Bibek Subedi, Bradley J.S.C. Olson, Aytuğ Ulutaş and Kathrin Schrick

Division of Biology, Kansas State University

C-35. Comparing the anatomy of 80-million-year-old conifer shoots from Antarctica with living southern cypresses

Jedidah Kapapula¹, Kelly C. Pfeiler^{1,2}, Brian Atkinson^{1,2}, Kelly Matsunaga^{1,2}

¹Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, Kansas 66045, USA

²Biodiversity Institute, University of Kansas, Lawrence, Kansas 66045, USA

C-36. What Makes Flies Sexy?

Janzen, Carly¹, Conway, Taylor², Unckless, L. Robert¹

¹Department of Molecular Biosciences, University of Kansas

²Department of Ecology and Evolutionary Biology, University of Kansas

C-37. Characterizing the translation accessory factor EF-G1B in *Pseudomonas aeruginosa* – biological function and role in antibiotic resistance.

Udita Shah¹, Vanessa M. Schmidt¹, Brielle M. Mckee¹, Josephine R. Chandler¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

C-38. (2026) Analysis of Cancer Mortality in the United States (2000-2023)

Aiyanna Davis and Sharon Lewis

Langston University, Chemistry Department

C-39. Glioblastoma U251 cells express opioid receptors

Emmalyn Greeves (1), Meena Kumari (1)

(1) Department of Anatomy and Physiology, College of Veterinary Medicine, Kansas State University

C-40. Unoccupied

D-1. Physical Therapy Patient Exercise Adherence Intervention: A HAPA-Based Behavioral Education Protocol

Authors: Montney, Justin¹, Carter Booe¹, Clark Dean¹, Ernesto Duenes¹, Eva Elder¹, Aiden Haworth¹, Nathan Jaeger¹, Gabe Tross¹, and Emery Wolfe¹

Affiliations: ¹Department of Health and Human Performance, Fort Hays State University

D-2. iCURE: a Course-Based Undergraduate Research Experience in Immunology

Dyan E. Morgan¹, Luis Caetano Martha Antunes², Lauren Atkinson^{#,2}, Rayssa Durães Lima^{#,2}¹Undergraduate Biology Program, ²Department of Molecular Biosciences, University of Kansas, # indicates equal contributions

D-3. Heterologous expression of *Aspergillus fumigatus* cryptic secondary metabolite biosynthetic gene clusters.

Todd, Richard B.¹ C. Elizabeth Oakley², Heather D. Forster¹ and Berl R. Oakley².

¹Department of Plant Pathology, Kansas State University;

²Department of Molecular Biosciences, University of Kansas.

D-4. Exploiting HPV-Induced DNA Repair Rewiring to Improve Cisplatin Efficacy in Cervical Cancer

Sebastian O. Wendel¹, Grant Brooke²

¹School of Health and Human Science, Kansas State University, Manhattan, KS, USA

²Division of Biology, Kansas State University, Manhattan, KS, USA

D-5. Genetic characterization and genome analysis of bloom-forming cyanobacteria in western Kansas

Louisa Acquah¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

D-6. Transcription and Regulation of the *mpt* PTS in *Enterococcus faecalis*

Tolulope I. Ade and Lynn E. Hancock

Department of Molecular Biosciences, University of Kansas, Lawrence, KS

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-7. Exploring the Link Between Soil Microbes, Land Use, and Antibiotic Resistance through a One Health Lens.

Yaw Agyapong Antwi¹, Alfred Kusi-Appiah¹, Chloe Harmon¹, Morgan Fischer¹, Jaime Arellanes¹, Claudia Da Silva Carvalho PhD¹

¹Department of Biological Sciences, Fort Hays State University

D-8. The role of Notch signaling in vascular integrity of Autosomal Dominant Polycystic Kidney Disease

^{1,2}Begum, Rahima; ^{1,2}McGonigle, Mercedes; ^{1,2} Wang, Wei; ^{1,2}Sommer, Nicole; ^{1,2}Placide, Sagine; ^{1,2}Wallace, Darren; ^{1,2}Sharma, Madhulika

¹Department of Cell Biology and Anatomy, University of Kansas Medical Center; ²The Jared Grantham Kidney Institute, Department of Internal Medicine, University of Kansas Medical Center, Kansas City, Kansas, United States

D-9. CCUSTR: A Phylogenetic Program for Automated Clade Splicing

David Bohorquez¹, Brandon Williams², Elijah McCullough³, Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

²Department of Computer Science, Fort Hays State University

³Department of Informatics, Fort Hays State University

D-10. Targeting HuR Mediated Regulation of CD147 on Extracellular Vesicles to Modulate Immune Response in Triple Negative Breast Cancer (TNBC)

Alfred Buabeng, Sunghae Kim, Qi Zhang, Xiaoqing Wu, and Liang Xu.

University of Kansas/ Department of Molecular Biosciences

D-11. Investigation of neuronal nanofiber interaction of glioblastoma

Cantu, Kayla, Li Yao

Department of Biological Sciences, Wichita State University

D-12. Metabolomic analysis reveals hyaluronic acid as a novel component of ADPKD pathobiology that links altered metabolism to extracellular mechanisms of cyst formation

Aakriti Chaturvedi^{1,5}, Chadve Ranganathan^{1,5}, Matthew A. Kavanaugh^{1,5}, Saleem Ahmad^{1,5}, Michele Pritchard^{2,5}, Madhulika Sharma^{3,5}, Darren P. Wallace^{3,5}, Stephen C. Parnell^{4,5}, Chad Slawson^{4,5}, Pamela V. Tran^{1,5}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Pharmacology and Toxicology, University of Kansas Medical Center, Kansas City, KS

³Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

⁴Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁵The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

D-13. Identification of a Genetic Suppressor of Antimorphic alg-1 Mutations

Heather Crawshaw, Jeff Medley, and Anna Zinovyeva

Division of Biology, Kansas State University

D-14. Targeting oxidative stress regulator Nrf2 to improve T-cell responses in inflammatory bowel disease and in colorectal cancers

Debolina Dasgupta¹, Aprajita Tripathi¹, Nadine Santana Magal¹, Rachel Griffard-Smith², Emily Burt¹, Jennifer S. Davis¹, and Kalyani Pyaram¹

¹Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, USA.

²Department of Biostatistics & Data Science, University of Kansas Medical Center, Kansas City, KS, USA.

D-15. Efficacy of Antibiotic Prophylaxis for Infective Endocarditis Recommended for Dental Patients

Gabriela C. Chianca^{1,2,3}, Helvécio C. C. Póvoa¹, Bruna A. Thurler^{1,2}, Raiane C. Chamon², Fábio F. da Mota⁴, Heidi Pauer³, Rosana B. R. Ferreira³, Natalia L. P. P. Iorio¹.

¹Department of Basic Sciences, Universidade Federal Fluminense (UFF), Nova Friburgo, Brazil, ²Department of Pathology, UFF, Niterói, Brazil,

³Department of Molecular Biosciences, University of Kansas and ⁴Department of Systems and Computational Biology, Instituto Oswaldo Cruz, Rio de Janeiro, Brazil.

D-16. Human *SPECC1L* mutation knock-in mouse model reveals the role of cytoskeletal regulation in palatogenesis

Iman Dilower¹, Brittany M Hufft-Martinez^{1,2}, An Tran¹, Dana Thalman¹, Michael Kuehn¹, Everett Hall¹, Jeremy Goering¹, Andras Czirok³, Irfan Saadi^{1,2}

¹Department of Cell Biology and Physiology, ²Institute of Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. ³Department of Biological Physics, Eotvos University, Budapest, Hungary.

D-17. Functional Characterization of Argonaute Syndromes Variants in *Caenorhabditis elegans*

Belén Gaete Humada¹, Rebecca Mitchell¹, Amélie Piton², Davor Lessel³, Hans-Jürgen Kreienkamp⁴, Victor Ambros⁵, Anna Zinovyeva¹

¹Division of Biology, Kansas State University, Manhattan, KS

²Department of Translational Medicine and Neurogenetics, Institute of Genetics and Molecular and Cellular Biology, Strasbourg University, Strasbourg, France

³Institute of Human Genetics, University of Regensburg, Regensburg, Germany

⁴Institute of Human Genetics, University Medical Center Hamburg-Eppendorf, Hamburg, Germany

⁵Program of Molecular Medicine, UMass Chan Medical School, Worcester, MA

D-18. Deep Learning Framework for Temporal Data Imputation in Longitudinal Electronic Health Records: Sequence-to-Sequence with Multi-Head Cross-Attention

Barsha Halder

Department of Biostatistics, University of Kansas Medical Center, Kansas

D-19. Scalable extraction, alignment, and annotation validation for thousands of plastid genomes through a novel bioinformatic software

Thanina Hamitouche¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-20. Interferon hypersensitivity in Down syndrome primes microglial dysfunction from development

Hayden C. Hawks¹, Lexie M. West¹, Katherine I. McCarthy¹, Sunita N. Varghese¹, Abhik Saha¹, Greta Foye¹, Luke Johnson¹, Keith P. Smith², Heather M. Wilkins², and Katherine A. Waugh¹

D-21. Identification and Optimization of Peptide Inhibitors of the Classical Complement Pathway

Author: Aprajita Jha¹, Shannon S. Allen², Hailee N. Nerber², Jon T. Skare², Brandon Garcia¹,

¹Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, KS

²Department of Microbial Pathogenesis and Immunology, College of Medicine, Texas A&M University, Bryan/College Station, TX

D-22. Profiling the NTMT1 Protein Network Using Spectrometry-based Proximity Labeling

Sahadev Khadka, Wei Wu, Ping Li

Kansas State University, Department of Chemistry, Manhattan, KS, USA

D-23. Coordinated collective cell invasion requires balanced levels of the stress response transcription factor ATF4

Rehan Khan¹, Emily Burghardt¹, Jocelyn McDonald¹

¹Division of Biology, Kansas State University, USA

D-24. Voltage-Gated Sodium Channels in Cancer Cells: Implications for Anesthetic Mechanisms and Clinical Sensitivity

Yousaf Khan¹, Will Krogman¹

¹Department of Anesthesiology, KU School of Medicine-Wichita

D-25. Novel truncation variants expand the role of *SPECC1L* in neurodevelopmental disorders

Michael Kuehn¹, Jeremy Goering¹, Luke Wenger¹, Yomna Badawi¹, Marta Stetsiv¹, Preethi Kunchala¹, An Tran¹, Brittany Martinez¹, Dana Thalman¹, Iman Dilower¹, Shubhangi Singh¹, Emily Farrow⁴, Olivia Veatch^{1,2}, Hiroshi Nishimune^{1,5}, Irfan Saadi^{1,3}

¹Department of Cell Biology and Physiology, ²Department of Psychiatry and Behavioral Sciences, ³Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. ⁴Genomic Medicine Center, Children's Mercy Hospital, Kansas City, MO. ⁵Department of Physical Medicine and Rehabilitation, University of Missouri, Columbia, MO.

D-26. The ABC transporter EF2223-EF2221 of *Enterococcus faecalis* imports high mannose glycans, and is dependent on a three-component signal transduction system

Abdulrahman M. Naeem¹, Tolulope I. Ade¹, Zakria H. Abdullahi¹, Rupa Addanki², Mark P. Farrell², Ana Flores-Mireles³, and Lynn E. Hancock¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS

²Department of Medicinal Chemistry, University of Kansas, Lawrence, KS

³Department of Biological Sciences, Notre Dame University, South Bend, IN

E-1. Up-Regulating the cGAS-STING Pathway via HuR Inhibition in Prostate Cancer

Ngoc Huan Nguyen¹, Sunghae Kim¹, Xiaqing Wu¹, and Liang Xu¹

¹Department of Molecular Biosciences, University of Kansas

E-2. Characterizing the HuR-ID1 Regulatory Network in Pancreatic Cancer

Candice Osagie¹, Xiaqing Wu¹, Liang Xu.¹ ¹Department of Molecular Biosciences, University of Kansas

Name of Institution to be credited - University of Kansas - Lawrence

E-3. Characterization of the Role of *BODYGUARD2* in the Formation of Cuticle in *Arabidopsis thaliana*

Zanri Pieterse^{1,2}, Yu Nj^{1,3}, Libin Yao^{1,3}, Zolian S. Zoong Lwe^{1,4}, and Ruth Welti^{1,3}

¹Kansas Lipidomics Research Center, ²Department of Anatomy and Physiology, ³Division of Biology, ⁴Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, KS 66506

E-4. Efforts Towards Enhancing Potency of PROTACs Specific to NTMT1

Arti Pujari, Chao Ann, Ping Li

Department of Chemistry, Kansas State University

E-5. Distinct behavioral phenotypes exhibit unique brain-wide neural activation patterns during observational avoidance learning.

Authors: Shannon Ruble, Helen Durrett, Cassidy Stecher, Cassandra Kramer, Lexie West, and Maria M. Diehl

Affiliation: Kansas State University, Department of Psychological Sciences

E-6. Unoccupied

E-7. Directed Evolution of Iridium-Containing TcDyP for Stereo-controlled Cyclopropanation for Drug Precursors

Tinky Sharma, Samiksha Khadka, Ping Li

Department of Chemistry, Kansas State University, Manhattan, Kansas, U.S.A.

E-8. Cognitive and behavioral impairment in *FMR1* knockout rats across the lifespan

Bhavana Sivayokan, Tsam Myu Shawng Maji, Bethany Plakke

Department of Psychological Sciences, Kansas State University

K-INBRE 2026 Symposium
Poster Presentation Abstracts

E-9. Disruption of the Blood–CSF Barrier by *Specc11* Deficiency Causes Embryonic Ventriculomegaly and Hydrocephalus

Dana Thalman¹, Brittany M. Hufft-Martinez^{1,2}, An Tran¹, Abigail Truong¹, Jeremy Goering¹, Luke Wenger¹, Zaid Umar¹, Benjamin Kelm¹, Sarah C. Wilson¹, Marta Stetsiv¹, Timothy C. Cox³, Erin E. Young^{1,4}, Irfan Saadi^{1,2}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS, ²Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS, ³Departments of Oral & Craniofacial Sciences, School of Dentistry, and Pediatrics, School of Medicine, University of Missouri-Kansas City, MO, ⁴Department of Anesthesiology, Pain, and Perioperative Medicine, KU Medical Center, Kansas City, KS

E-10. Assessment of GenBank-archived human mitochondrial genomes through modern quality filtering and reassembly

Buddha Thapa Magar¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

E-11. Nrf2 as a therapeutic target to improve T cell function in muscle invasive bladder cancer (MIBC)

Aprajita Tripathi, Nadine Santana-Magal, Jared Rack, Debolina Dasgupta, Benjamin L. Woolbright and Kalyani Pyaram

Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, USA

E-12. Interactions of PhoU in *Staphylococcus aureus*

Nikolas Yackovich, Stewart Gardner

School of Science and Mathematics, Emporia State University

E-13. Next Generation Sequencing at KU Genome Sequencing Core

Hackett, Jennifer^{1,2,3}, Kristen M. Cloud-Richardson^{1,2,3}, Erik A. Lundquist^{1,2,3}, Susan M. Lunte^{1,4,5}

¹Center for Molecular Analysis of Disease Pathways, ²Genome Sequencing Core, ³Department of Molecular Biosciences, ⁴Department of Chemistry, ⁵Department of Pharmaceutical Chemistry, University of Kansas, Lawrence KS, USA

E-14. The Synthetic Chemical Biology Core (SCB): A Resource for Research in Chemical Biology

Chamani Perera

Synthetic Chemical Biology Core Laboratory, University of Kansas, Lawrence, KS, USA

E-15. University of Kansas Nanofabrication Facility: Equipment and Capabilities

Ryan Grigsby^{1,2} and Susan M. Lunte^{2,3,4,5}

¹The KU Office of Research, The University of Kansas, Lawrence, KS, USA; ²The Center for Molecular Analysis of Disease Pathways, The University of Kansas, Lawrence, KS, USA; ³The Ralph N. Adams Institute for Bioanalytical Chemistry, The University of Kansas, Lawrence, KS, USA; ⁴Department of Pharmaceutical Chemistry, The University of Kansas, Lawrence, KS, USA; ⁵Department of Chemistry, University of Kansas, The University of Kansas, Lawrence, KS, USA

E-16. The Computational Chemical Biology and Molecular Modeling Core

David K. Johnson¹ (dkjohnson@ku.edu)

¹Computational Chemical Biology and Molecular Modeling Core, University of Kansas, Lawrence, KS, USA;

E-17. Spatial and temporal dynamics of darting behavior during platform-mediated active avoidance in rats.

Helen Durrett, Karissa Payne, Halle Ness, Shannon Ruble, and Maria M. Diehl.

Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA.

E-18. Cadmium-Induced Circadian Dysregulation Drives Epithelial to Mesenchymal Transition and Apoptosis in Alveolar Type 2 Cells

Stefanie Cravens¹, Chandrashekar Prasad², Santhosh Kumar Suraisamy², Issac Sundar²

¹Kansas City University, College of Osteopathic Medicine

²Department of Internal Medicine, University of Kansas Medical Center

E-19. Identification of interneurons in stress resistance and longevity

Mingyi Liu¹, Shelby Innes¹, Lizzie Vetter¹, Sophia Mccune¹, Moussa Gacko¹, and Shijiao Huang¹

¹ Biochemistry and Molecular Biophysics, Kansas State University

E-20. Primary ciliary homeostasis and the metabolic sensor, O-GlcNAc, are interconnected

Chadhve Ranganathan^{1,6}, Matthew A. Kavanaugh^{1,6}, Saleem Ahmad^{1,6}, Brittany M. Hufft-Martinez¹, Brenda Magenheimer^{2,6}, Madhulika Sharma^{3,6}, Stephen C. Parnell^{4,6}, Chad Slawson^{4,6}, Darren P. Wallace^{3,6}, Mihaela E. Sardi⁵, Robin L. Maser^{2,6}, Pamela V. Tran^{1,6}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Clinical Laboratory Sciences, University of Kansas Medical Center, Kansas City, KS

³Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

⁴Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁵Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS

⁶The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

E-21. Exploring Non-Invasive Biomarkers of ADPKD Progression

Singh, Siraj¹, Placide, Sagine¹, Sommer, Nicole¹, Chakraborty, Anubhav¹, Vanamamaly, Krishi¹, Wallace, Darren¹, Yu, Alan¹, and Sharma, Madhulika¹.

¹University of Kansas Medical Center, Department of Internal Medicine, Kansas City KS 66160.

E-22. Using auxin-inducible degron to investigate the loss of glycosylation genes in adult *Drosophila melanogaster*

Authors: Viet Hoang Le, Hans Dalton

Department of Molecular Biosciences, The University of Kansas, Lawrence, Kansas.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

E-23. University of Kansas High Throughput Screening/ Infectious Disease Assay Development Laboratory

Anuradha Roy, University of Kansas, Lawrence, KS
IDAD-HTS Laboratory, University of Kansas, Lawrence, KS, USA

E-24. Flow Cytometry Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory

Peter R. McDonald¹, Robin C. Orozco^{1,2}, and P. Scott Hefty^{1,2}.

¹ Flow Cytometry Core, Chemical Biology of Infectious Disease, The University of Kansas, Lawrence, KS, USA; ² Department of Molecular Biosciences, The University of Kansas, Lawrence, KS, USA

E-25. $G\alpha_q$ Subunits Engage Targets in the Nucleus

Joseph F. Loomis¹, Naincy R. Chandan², Michael Burroughs², Saji Abraham², Gregory G. Tall², Rongxi Zhang² and Alan V. Smrcka²

¹University of Michigan Program in Chemical Biology, ²Department of Pharmacology, University of Michigan Medical School, Ann Arbor, Michigan 48109

E-26. 3' Nucleotide Asymmetry Directs miRNA Strand Selection

Jeffrey C. Medley¹, Sumire Kurosu Moriya¹, Huiwu Ouyang², Heather Crawshaw¹, Sarah Y. Zhang¹, Ganesh Panzade^{1,3}, Will J. Sydzyik¹, Joel T. Sydzyik^{1,4}, Mira Bhandari^{1,5}, Christopher M. Hammell² and Anna Zinovyeva¹

¹ Division of Biology, Kansas State University, Manhattan, KS.

² Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

³ Laboratory of Human Retrovirology and Immunoinformatics, Frederick National Laboratory for Cancer Research, Frederick, MD.

⁴ University of Kansas School of Medicine, Kansas City, KS.

⁵ Department of Molecular Genetics and Cell Biology, University of Chicago, Chicago, IL.

E-27. Uncovering common molecular pathways of kidney-brain dysfunction in chronic kidney disease using spatial transcriptomics

Wei Wang¹, Henrietta Ehirim¹, Nicole Sommer¹, Sumedha Gunewardena², Aditi Gupta¹ and Madhulika Sharma^{1,2}

¹Nephrology and Hypertension, Department of Internal Medicine, University of Kansas Medical Center; ²Department of Cell Biology and Physiology, University of Kansas Medical Center

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-1. Exercise from Afar: Progressing At-Risk Adults to Effective Independent Exercise for Dementia Risk Reduction

Erin Blocker¹, Luke Gleason¹, Kamon Haydock¹, Madison Newton¹, Natalie Alrid¹, Donovan Law¹
¹Health and Human Performance Department, Emporia State University

Introduction: The purpose of this study was to determine the efficacy of a technology-driven exercise program on exercise adherence and health outcomes associated with dementia risk. **Methods:** Fifty (50) adults from the rural Midwest, between the ages of 36 and 72 years participated in this study. Participants either completed a 16-week exercise intervention delivered via a smart phone application (EXP) or were given no intervention (CON). EXP participants were encouraged to complete three workouts weekly for 16 weeks. All participants completed the Barriers to Being Active (BBAQ) survey, Exercise Self-Efficacy survey (SEE), muscular strength and cardiovascular fitness assessments at baseline and again after 16 weeks. Cholesterol and fasting blood glucose were also measured at baseline and follow-up. Exercise adherence was tracked via the app. **Results:** EXP participants completed an average of 23.48 exercise sessions; nearly 50% exercise adherence. The exercise intervention resulted in significant improvements in high density lipoproteins (HDL), triglycerides, cardiovascular performance (1 mile time) and muscular strength ($p < .05$). Barriers to exercise were significantly reduced following the 16-week intervention. **Conclusion:** Technology-driven exercise was effective at improving muscular strength and cardiovascular performance and reducing barriers to exercise in previously sedentary adults. In addition, HDL and triglycerides improved. This technology-driven exercise program may be effective for initiating exercise and reducing personal risk factors for dementia.

A-2. Incorporation of Chimeric Macrodmain into Murine Hepatitis Virus for Antiviral Testing of Multiple Coronaviruses in a Single System

Kendall A. Cranor, Anjali Singh, Nathan Quinton, Jessica J. Pfannenstiel, Anthony R. Fehr
Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

The Macrodmain 1 (Mac1) protein is a critical virulence factor of coronaviruses (CoVs) that promotes viral replication, suppresses the host immune response, and is required for disease in animal models. Mac1 binds and enzymatically removes ADP-ribose, a post-translational modification, from target proteins, which allows the virus to evade the host innate immune response. Deletion of Mac1 from the CoV genome leads to a significant replication defect and rescues host immune activity, indicating that Mac1 inhibitors could be effective against CoVs. To characterize the genetic variation of Mac1 proteins, we will insert the Mac1 genes of diverse CoVs into murine hepatitis virus (MHV), in place of the native MHV Mac1 protein. To do this, we will clone Mac1 genes into the MHV genome in *E. coli* by Lambda Red Recombination, a genetic engineering technique that uses bacteriophage lambda proteins to facilitate homologous recombination. We replaced the Mac1 gene of MHV, a β -CoV, with Mac1 from severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), another β -CoV. This virus replicates just like the original MHV, indicating a close evolutionary relationship of their Mac1 proteins. This system will be applied to the Mac1 genes from another β -CoV, Middle East respiratory syndrome virus (MERS-CoV), an α -CoV, porcine epidemic diarrhea virus (PEDV), a γ -CoV, infectious bronchitis virus (IBV), and a δ -CoV, porcine delta coronavirus (PD-CoV). This could provide insight on the genetic diversity and evolution of Mac1 proteins across the CoV genera and facilitate the testing of antivirals targeting Mac1 of multiple CoVs.

A-3. Identifying the deep intronic variant (missing heredity) in high-risk Latino families

King, Kara, Rains, Gracyn, Zweydooff, Rebekah, Weitzel, Jeffrey N and Pirani, Karim
University of Kansas Medical Center

Rare non-coding intronic variants can disrupt RNA processing by causing pseudo-exons to be incorrectly incorporated into mature mRNA, potentially contributing to hereditary disease. Pathogenic variants (PV) in *BRCA1* increase breast and ovarian cancer risk, yet standard clinical testing focuses on coding exons and short splice-adjacent regions, leaving deep intronic areas unexamined. These regions may contribute to "missing heredity" in high-risk families with uninformative genetic testing. Prior work identified recurrent *BRCA1* PVs among Latino populations in the United States and Mexico, including *BRCA1* c.4358-473T>G in intron 13 observed in two unrelated Mexican families. To investigate this possible contributor to hereditary cancer, we examined Mexican patients (N=700) with personal or family cancer histories but unknown genetic cause. DNA isolated from blood was tested using a PCR assay targeting intron 13 of *BRCA1*, followed by restriction digestion with NSP1, which cuts the wt allele, and BSL1, which cuts the allele containing the PV. All samples from Mexico City displayed digestion patterns consistent with the wt NSP1 cut, while only the control sample showed the expected pattern for the pathogenic allele, confirming assay accuracy and the absence of *BRCA1* c.4358-473T>G. Although this variant was not detected, the PCR-restriction digest method proved to be low-cost and effective for screening intronic regions and may support future efforts to identify hidden hereditary cancer variants as the cohort expands.

A-4. Determine the impact of entomopathogenic fungi on *Aedes aegypti* mosquitoes transinfected with *Wolbachia*

Ryan Thomas, David Hayes, and Kristin Michel

The yellow fever mosquito, *Aedes aegypti*, inflicts severe human illness and economic burden, because it vectors many important arboviruses. Arboviruses cannot infect *Ae. aegypti* mosquitoes that are infected with the bacterial endosymbiont *Wolbachia*. Whether *Wolbachia* also causes broad resistance to opportunistic mosquito pathogens is largely unknown. For *Wolbachia*-based control strategies to be effective, *Wolbachia*-infected mosquitoes must outcompete uninfected mosquitoes. Programs releasing *Wolbachia*-infected mosquitoes do so under current vector control strategies, which increasingly include entomopathogenic fungi (EPF). Entomopathogenic fungi are important mosquito pathogens, especially in the larval stage, and contribute to natural mosquito population control. We hypothesize that *Wolbachia*-infected mosquitoes will be more resistant to EPF exposure because *Wolbachia* infection confers resistance to other mosquito pathogens. To test this hypothesis, we plan to expose *Wolbachia*-infected mosquitoes and antibiotic-cleared control mosquitoes to stage-specific mosquito EPFs and assess and compare (1) survival and (2) sub-lethal fitness costs. Larvae will be exposed to *Culicinomyces clavosporus* using a previously established 24-well plate exposure assay. Larval survival and sublethal effects including development time, adult body size and adult sex ratio will be observed following larval exposure. Adult female and male mosquitoes will be exposed to *Beauveria bassiana* using a modified WHO susceptibility test and assessed daily for survival until all mosquitoes have died. Data collected from this study will provide the first assessment of *Wolbachia*'s ability to protect mosquito larvae from opportunistic infections, which could help *Wolbachia*-carrying mosquitoes to outcompete their *Wolbachia*-free counterparts.

K-INBRE 2026 Symposium Poster Presentation Abstracts

A-5. Effects of Voluntary Oral Consumption of Delta-Tetrahydrocannabinol on Home Cage Alcohol Drinking

Authors: Caden C. Blake, Dylan A. Laux, and Mary E. Cain. Department of Psychological Sciences at Kansas State University

Cannabis is the most widely used illicit drug in the United States with many studies showing a link between cannabis use and alcohol consumption, as the main psychoactive component Delta-Tetrahydrocannabinol (THC) can alter the incentive salience and hedonic value of alcohol. There have been recent efforts to develop translation models of oral consumption of THC in rats as the pharmacokinetics of THC are altered, including onset and duration of effects, depending on route of administration (oral, injected, inhaled, etc.) The current project is the use of a translational model of voluntary oral consumption of THC and its effects on home cage alcohol consumption in male rats. High (0.5 mg/kg) and low (0.05 mg/kg) doses of oral THC were given every other day to voluntarily consume, with rats having free access to alcohol with increasing concentration over 14 days, starting at 2% to a final 10%. We found that low doses of THC significantly increased alcohol consumption and preference above 2%, even on non-drug days, while high doses did not significantly alter consumption at any concentration compared to the control. We also plan to test brain region-specific Cannaboid-1 receptor (CB1) expression through western blotting. Altered consumption of alcohol could have implications for the development of alcohol use disorders (AUDs) and comorbidity with cannabis use disorders (CUDs).

A-6. Synthesis and Characterization of N-Quaternized Ammonium Pectin Derivatives for Tunable Antimicrobial Activity and Cytocompatibility

Christina Diab, Gabriel Tenório, Alessandro Francisco Martins, Department of Chemistry, Pittsburg State University

Pectin, a plant-derived polysaccharide structurally similar to hyaluronic acid, was chemically modified to produce N-quaternized ammonium derivatives with tunable antimicrobial and cytocompatibility properties. Pectin quaternization reactions were carried out in water, DMF, and water/DMF mixtures under basic conditions to minimize hydrolysis of the quaternizing agents Quat-188 and glycidyltrimethylammonium chloride (GTMAC). Modification of pectin with Quat-188 resulted in a degree of substitution of approximately 24%, as determined by ¹H NMR spectroscopy. Both the native and modified polymers were further characterized by FTIR to confirm structural changes associated with quaternization. The degree of quaternization of the GTMAC-modified pectin derivatives will be determined. Antimicrobial assays and cytotoxicity studies will also be performed to assess the biological performance of the quaternized pectin derivatives. This study aims to expand the application of plant-based polysaccharides in biomedical materials with controlled biological activities.

A-7. Nuclear shape dynamics drive collective cell migration through crowded tissue environments

Ben Lawrence, Rehan Khan, Jocelyn McDonald
Kansas State University Division of Biology

Cells move collectively during development and in diseases like cancer, but the mechanisms underlying this process are poorly understood. The nucleus, the largest cellular organelle, poses a physical constraint on collective cell migration. *Drosophila* border cells represent an excellent model for investigating how cell collectives migrate in vivo. In the ovary, 6-10 follicle cells form the border cell cluster, which moves collectively towards the oocyte. While migrating, the border cell cluster must squeeze through narrow spaces between the large nurse cells without falling apart or slowing down. Similarly, cancer cells can invade as collectives. While migrating, the nuclei of cancer cells also need to pass through tiny spaces, which can cause DNA damage and drive tumor progression. Here, we hypothesize that the shape and deformability of the nucleus plays a major role in how cell collectives migrate inside crowded tissues. To better understand the relationship between nuclear shape and collective cell migration, we analyzed nuclei in well-characterized genetic mutants in which border cell migration, cell shape, and/or nuclear membranes are altered compared to control. We quantified various nuclear shape parameters. Both area and perimeter were chiefly impacted when the nuclear lamina and cell shape were altered. Ongoing analyses focus on the correlation of cell and cluster shape with nuclear shape. By integrating precise quantifications of nuclear shape with defined genetic changes, our study aims to reveal how nuclear morphology facilitates efficient collective migration. These results will clarify the role of nuclear shape and collective invasion in development and cancer.

A-8. Evolution of cell number in migrating cell collectives

Kendra Visser¹, Gavin Rice¹, Jocelyn A. McDonald¹
¹Division of Biology, Kansas State University

Cell movement is critical for embryonic development and for the progression of cancer, including metastasis. While some cells move (migrate) as single cells, other cells migrate in small to large collectives. Our understanding of the molecular and cellular mechanisms that drive collective cell migration is incomplete due to the complexity of in vivo environments. A powerful model to study the migration of cell collectives is *Drosophila melanogaster*. During oogenesis, the border cell cluster, which is composed of 2 inner polar cells surrounded by 4-to-8 outer migratory cells, moves towards the oocyte through a crowded tissue. The stereotypical collective migration is amenable to live imaging, genetic manipulation, and sophisticated cellular analyses. Previous work has suggested that the number of cells recruited to form the border cell cluster varies, but that an optimal number of cells facilitates their movement inside the ovary. However, little is known about the natural variation in border cell cluster size in other *Drosophila* species. In preliminary studies, we found that *D. virilis* border cell clusters have more cells, whereas *D. erecta* has fewer cells. We are currently quantifying the number of border cells in multiple *Drosophila* species. This research will provide a better understanding of how optimal cell numbers help clusters gain the ability to move collectively, which can be applied to understand how cancerous cells become metastatic and how other cells shape organs and tissues in development.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-9. Impact of Exposure to Simulated Galactic Cosmic Radiation on Ovarian Follicle Development in Mice

Lauren Higgins, Fereshteh Dalouchi, Joshua S. Alwood, April E. Ronca, V. Praveen Chakravarthi, Lane K. Christenson
Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, Kansas
Department of Human Factors and Behavioral Neurobiology, Embry-Riddle Aeronautical University, Daytona Beach, Florida
Space Biosciences Research Branch, NASA Ames Research Center, Moffett Field, California
Grant Support: P20 GM103418 K-INBRE grant, NASA-80NSSC24M0072, and NASA-80JSC018N0001 NASA HRP VNSCOR grant

The impact of galactic cosmic radiation (GCR) exposure during exploration missions is a critical concern for female astronauts reproductive and general health. Ovarian follicular steroid hormone and oocyte production are critically important for normal organ/tissue support and for fertility. This study examined the dose response of simulated GCR on murine follicular development. Four groups (n=12/group) of 26-week-old female BL6 mice received sham (control) or 5, 15, or 50 cGy of 5-ion radiation and were euthanized either 14 days (IR+14) or 124 days (IR+124) post-exposure. Ovaries were fixed, paraffin-embedded, serially sectioned, and H&E-stained for microscopic analysis. Follicles were quantified by developmental stage: primordial, primary, secondary, tertiary, early antral, and antral as were corpora lutea. Serum anti-Müllerian hormone (AMH) was measured, and DNA damage was assessed by TUNEL staining. At IR+14, AMH levels did not differ between groups, while, at IR+124, AMH levels decreased in 15 and 50 cGy ($41.7 \text{ ng/ml} \pm 4.4$, 1.3 ± 0.3 , respectively) compared to control (73.8 ± 8.6) and 5 cGy (67.4 ± 12.3) groups. Mice exposed to 15 cGy had fewer primordial follicles, but no other follicle counts were different versus control. In contrast, 50 cGy completely blocked follicle development beyond the primary stage, and ovaries were smaller. TUNEL staining (%) was elevated in 15 and 50 cGy groups, indicating increased DNA damage. In conclusion, GCR-exposure impaired ovarian follicle development and health, causing premature depletion of the follicular reserve and shortening reproductive health span.

A-10. Defining How Different Sulfation Patterns in the Extracellular Matrix Impact Myelin Repair in the Brain.

Corbin Fairchild¹, Jenna Williams, Matthew Zupan, Dr. Esther Holt, Jack Petersen, Dr. Meredith Hartley, Department of Chemistry, University of Kansas, Lawrence KS, United States of America.

Multiple sclerosis is a neurodegenerative disease characterized by autoimmune degradation of myelin, known as demyelination. Myelin is a lipid-rich sheath produced by oligodendrocytes, which coats the axons of nerve cells and allows action potentials to travel effectively. For successful myelination to occur, oligodendrocyte progenitor cells (OPCs) must differentiate into mature oligodendrocytes. This process can be affected by many factors; previous studies have shown that chondroitin sulfate proteoglycans (CSPGs), a major constituent of the extracellular matrix, play an important role in the development of nerve cells and maintenance of the nervous system.

CSPGs contain a protein core with chondroitin sulfate (CS) glycosaminoglycan (GAG) disaccharide chains. Different sulfonation patterns of the GAG chains influence their function. Our lab has previously demonstrated that the CS-E motif can inhibit OPC differentiation and remyelination. To study how CS-E impacts demyelination and remyelination, we will induce demyelination in a global knockout of carbohydrate sulfotransferase 15 (Chst15), the enzyme that converts CS-A to CS-E. We will administer cuprizone-compounded chow to induce demyelination and study the effect of myelination, oligodendrocytes, and OPCs. Our goal is to elucidate the function of Chst15 in OPC differentiation by quantifying the number of new oligodendrocytes and OPCs in our model. To quantify the number of new oligodendrocytes and OPCs, EdU will be administered to mice in their drinking water to label newly forming cells. We predict that mice lacking CS-E will have improved remyelination and increased OPC differentiation.

A-11. Alternative Solvents to Dichloromethane for Ring Closing Metathesis of Azamacrocycles

Rebecca J. McCreight, Shaun E. Schmidt Department of Chemistry. Washburn University, Topeka, Kansas

Research on macrocycles shows strong potential for treating diseases such as bladder cancer, bacterial infections and autoimmune diseases. Using ring-closing metathesis (RCM), azamacrocycles can be synthesized from chains of 12 or more atoms that terminate in carbon-carbon double bonds. Dichloromethane has traditionally been used as the solvent in RCM reactions; however, due to OSHA standard 1910.1052.: monitoring dichloromethane exposure can make the use cost prohibitive. In this study, 1,2-dichloroethane, diethyl ether, and acetic acid were evaluated as potential substitutes for dichloromethane. Thin layer chromatography and ¹H nuclear magnetic resonance spectroscopy (NMR) indicates that 1,2-dichloroethane is a potential alternative to dichloromethane. Future work will explore initial or incremental catalyst loading; thermal excitation through either sonication or heating; and, additional solvents such as 4-methyltetrahydropyran.

A-12. Zein Protein-based Medical Pads with Antimicrobial Properties

Simon Wicks¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

Email: mparvinzadehgashti@pittstate.edu

We develop zein protein-based films incorporating silicone-based crosslinkers to enhance their structural integrity and functional performance. Zein, a renewable corn-derived protein, offers excellent film-forming properties but suffers from brittleness and poor moisture resistance. By introducing silicone crosslinkers, we will improve the flexibility, hydrophobicity, and durability of the films, making them more suitable for biomedical and packaging applications. The crosslinking also results in a denser film network, which contributed to improved barrier properties. Additionally, it is expected that the modified films exhibit notable antimicrobial activity against common pathogens such as *E. coli* and *S. aureus*, attributed to both the inherent properties of zein and the surface-modifying effects of the silicone agents. These antimicrobial characteristics make the films promising for use in wound dressings or food packaging. Characterization techniques such as FTIR, and antimicrobial assays confirmed the successful integration of crosslinkers and their functional benefits. Overall, this approach highlights a sustainable pathway toward multifunctional bio-based films.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-13. A *Bacillus pumilus* Isolate With Promising Antimycobacterial Properties

Cody Pfaff, Eric T. Gillock

Department of Biological Sciences; Fort Hays State University

The emergence of multidrug-resistant bacterial pathogens, particularly *Mycobacterium tuberculosis*, highlights the urgent need for new antimicrobial agents. Tuberculosis remains one of the world's deadliest infectious diseases, claiming over a million lives annually and posing increasing challenges due to the thick, lipid-rich, acid-fast cell wall of *Mycobacterium* species that renders them naturally resistant to many antibiotics. In this study, a soil sample collected from the Campus of Fort Hays State University yielded a bacterial isolate exhibiting strong antimicrobial activity. Initial screening against *Escherichia coli* MM294 showed a 10 mm inhibition zone, and subsequent testing identified the isolate as *Bacillus pumilus* via 16S rRNA gene sequencing (534 bp, 99.8% identity). When tested against multiple microbial targets, the isolate demonstrated moderate inhibition of *Serratia marcescens*, no inhibition of *Candida albicans*, and a pronounced 15 mm inhibition zone against *Mycobacterium smegmatis* ATCC 700084; a nonpathogenic model organism for *M. tuberculosis*. These findings suggest that *B. pumilus* produces a compound capable of penetrating or disrupting acid-fast cell walls, an uncommon property among naturally derived antibiotics. Ongoing work is focused on isolating and characterizing the active compound through solvent extraction, HPLC, and mass spectrometry to determine its chemical nature and mechanism of action. This research highlights the potential of environmental *Bacillus* isolates as a source of novel antimycobacterial compounds and future therapeutics.

A-14. The role of RIC interneurons in longevity regulation in *Caenorhabditis elegans*

Moussa Gacko¹, Mingyi Liu¹, and Shijiao Huang¹

¹Biochemistry and Molecular Biophysics, Kansas State University

Aging is accompanied by progressive loss of physiological function, and the nervous system plays a key role in coordinating organismal responses that influence lifespan. The nematode *Caenorhabditis elegans* is a powerful model for aging research because it is transparent, has a rapid 3-day life cycle at 20 °C, a short 20–30-day lifespan, large brood size, and is easy and inexpensive to maintain. Interneurons occupy a central position in the nervous system, integrating sensory inputs to regulate behavior and physiology. We focus on RIC neurons, a pair of head interneurons that release the neuromodulator octopamine and function in the locomotion circuit, as candidate regulators of longevity. To investigate their role, we used cell-specific expression of caspase-3 to ablate RIC neurons and then asked whether these neurons are required for normal lifespan and for established longevity pathways, including dietary restriction, reduced mitochondrial activity, increased hypoxic response, and neuronal activation of the endoplasmic reticulum unfolded protein response. Our preliminary data show that RIC-ablated worms live shorter than control animals, suggesting that RIC neurons contribute positively to normal lifespan regulation. However, RIC neurons are not necessary for lifespan extension induced by dietary restriction or by reduced mitochondrial function, indicating that some longevity pathways can bypass these interneurons. Ongoing experiments will test whether hypoxic response and ER stress-induced longevity also act independently of RIC neurons. This work will advance our understanding of how specific interneurons in the nervous system modulate aging.

A-15. Immunohistochemical (IHC) Analysis of HNSCC/CAF Cells and Xenotransplants

McMillan, Riley. Wichita State University: Department of Biological Sciences

Head and Neck Squamous Cell Carcinomas (HNSCCs) are the sixth most prevalent cancer worldwide, with carcinomas taking root in areas of the upper digestive/respiratory tracts. The study was created with a focus on immunohistochemical (IHC) analysis of two types of HNSCC cell lines and xenotransplants derived from them. Different antibodies were tested against the cells and xenotransplants to determine effectiveness, in hopes of laying a foundation for future cancer research. Xenotransplants of carcinomas were grown within the immunologically privileged hamster cheek pouch before being harvested and fixed to histology slides for the established IHC procedure. Cancer-associated fibroblasts (CAFs) were derived from a patient to aid in tumor cell extracellular matrix formation, while the two cell lines were chosen by the study's collaborators from epithelial cells of carcinomas from two patients. One goal of the study was to determine a more effective xenotransplantation procedure: whether it was more effective to co-transplant CAFs and the cell line organoids that were grown in separate dishes or to co-culture and transplant the CAFs and cell line organoids. Although many antibodies were used throughout the research study, two antibodies of interest will be discussed here: Cortactin and PRMT5. From the results, it was determined that both antibodies chosen bound to their target proteins in cells and transplants, and that expression in the co-culture and transplant procedures yielded more dramatic results than in the co-transplant procedure.

A-16. Investigate the Impact of CluH Silencing on Mitochondrial Distribution in Cancer Cell Lines

Junqiao An, Sofia Steigner, Stephen Fields. Department of Biology in Emporia State University.

This study investigates how the CluH protein influences mitochondrial distribution in PC3 and HeLa cells. Cancer cell lines were selected because emerging evidence suggests that cancer cells rely on mitochondrial dynamics to support rapid proliferation. Previous findings show that loss of CluH causes mitochondria to cluster around the nucleus, indicating a potential role in maintaining their proper intracellular localization. In this project, the CluH gene was silenced using siRNA, and mitochondria were visualized with MitoTracker Green staining. The resulting mitochondrial distribution patterns were assessed both qualitatively and quantitatively using fluorescence microscopy and ImageJ analysis. Overall, this research aims to characterize differences in mitochondrial organization in the presence and absence of CluH, without addressing specific underlying molecular mechanisms.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-17. The autoimmunity-associated allele of *PTPN22* mediates macrophage production of pro-inflammatory cytokines

Tatum P. Aikin*, Austin E. Eades, Tammy Cockerham, Nancy Schwarting, Robin C. Orozco**
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

Protein Tyrosine Phosphatase Non-Receptor Type 22 (*Ptpn22*) is an immune gene encoding the phosphatase Lyp (PEP in mice), which is expressed exclusively in all immune cells. Through its tyrosine phosphatase activity, Lyp regulates immune cell function and signaling. An alternative allele, 1858C>T, is present in 5-15% of the North American population and has been linked to a higher risk of autoimmunity. Previously, our group showed that mice carrying the equivalent of the autoimmunity-associated allele (PEP-R619W) exhibited an enhanced anti-viral and anti-tumor immune response relative to the major (wild-type) allele. However, the molecular mechanisms responsible for this enhanced response are incompletely defined. During these diseases, an immune cell called the macrophage can control disease pathology through inflammation and activation of other immune cells. Yet, a significant gap remains in understanding how PEP-R619W affects macrophage specific function. We hypothesize that PEP-R619W promotes activation and increased pro-inflammatory secretion in bone marrow-derived macrophages (BMMs). To test this, we use M-CSF differentiated BMMs from wild-type (PEP-WT) and PEP-R619W mice. LPS-treated PEP-R619W BMMs showed increased production of IL-1 β , TNF- α , and IL-6, and showed increased CCL8 in a sex dependent manner. Flow cytometry analysis revealed no difference between genotypes in expression of surface activation markers CD86, PD-L1, and CD40. These results suggest that PEP-R619W enhances macrophage pro-inflammatory cytokine production independent of expression of activating markers and provides insight into the molecular mechanisms behind the protective effects of this pro-autoimmune allele.

A-18. Improving Glycemic Control via Heat Therapy in Older Adults at Risk for Alzheimer's Disease

Elaine Gast^{1,6}, Anneka Blankenship^{1,2}, Riley Kemna^{1,2}, Paul Kueck^{1,2}, Casey John^{1,2}, Hana Mayfield¹, Maggie Kroeger¹, Jenae Pennington¹, Rachel Reaves¹, Raechel Camones¹, Michelle Vitztum³, Lauren Yoksh⁴, Jonathan Mahnken^{1,4,5}, Eric Vidoni^{1,2}, Jill Morris^{1,2}, Paige Geiger^{1,6}

¹University of Kansas Alzheimer's Disease Research Center, University of Kansas Medical Center, Fairway, Kansas, United States.

²Department of Neurology, University of Kansas Medical Center, Kansas City, Kansas, United States.

³KU Diabetes Institute, Department of Internal Medicine, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁴Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁵Frontiers Clinical and Translational Science Institute, University of Kansas Medical Center, Kansas City, Kansas, United States.

⁶Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, Kansas, United States.

Alzheimer's Disease (AD) is the most common type of dementia with 6.7 million American being affected by the disease. Impaired glycemic control increases risk for type 2 diabetes (T2D) and AD. Heat therapy (HT), via hot water immersion (HWI), has shown promise in improving blood glucose regulation, insulin sensitivity, and inflammation, but it has not been studied in the context of AD. This pilot study tested the feasibility of HT via HWI in cognitively healthy older adults with metabolic risk for AD. Eighteen participants (mean age: 71.1 \pm 3.9 yr) completed a 4-week HT intervention (three 45-minute visits/week) with cognitive testing, glucose tolerance, sleep assessments, and MRI scans pre- and post-intervention. Adherence was 96% with one mild adverse event. Post-intervention survey revealed that participants did not find the study to be a burden on their schedule. Despite a relatively short intervention, HT significantly improved mean arterial pressure, diastolic blood pressure, and cerebral blood flow ($P < 0.05$), and a trend towards improved body mass index was shown. These findings demonstrate HT's potential as an effective intervention to mitigate metabolic risk factors for AD.

The trial has progressed to phase two, incorporating a thermoneutral control group and expanding the trial to a ten-week intervention with 60 participants. Pre- and post- FDG PET has been included to investigate changes in cerebral glucose metabolism.

Funding:

R01 AG081304 Geiger and Morris (MPI) 05/01/2023 – 04/30/2028 Title: Feasibility of improving glycemia with heat therapy to prevent Alzheimer's Disease
P20 GM103418 K-INBRE Translational Research Scholar

A-19. CCR2- associated proteins alter metabolism in DCIS progression

Lillian O'Donnell¹, Wei Fang¹, Marcela Medrano¹, Michaella Rekowski², Zachary Clark, Macy Payne², Stefan Bossmann², Justin Douglas³, Laurie Harnad³, Philip Lorenzi^{4,5}, Lin Tan^{4,5}, Brooke Fridley⁶, Chase Sakitis, Nikki Cheng^{1,2}

¹Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, ²Department of Cancer Biology, University of Kansas Medical Center, ³NMR Lab University of Kansas, ⁴Department of Bioinformatics and Computational Biology, MD Anderson, ⁵Metabolomics Facility MD Anderson, ⁶Biostatistics and Epidemiology Core, Children's Mercy Research Institute

Breast cancer accounts for nearly 30% of all female cancer diagnoses in the United States, with about 1 in 5 of new cases identified as ductal carcinoma in situ (DCIS), a pre-invasive form of the disease. Because molecular precursors of DCIS progression are poorly understood, standard treatment measures are often inadequate or excessive. Recent studies show that the chemokine CCL2 and its receptor CCR2, involved in inflammation, augment progression into IDC. The application of a multi-omics approach will allow for development of expression profiles which help clinicians to better tailor treatments. Through corroborating metabolomic and proteomic data of DCIS and IDC tissue samples, investigators aimed to discern effects of CCR2 expression on metabolic changes associated with DCIS progression. Meta-analyses allowed for the identification of differentially expressed metabolites and proteins. Metabolite and pathway analyses revealed metabolite sets and pathways enriched in the presence of CCR2. From these results, increased CCR2 levels in DCIS were associated with changes in amino acid anabolism and catabolism and pathways that promote cancer cell proliferation and migration. Researchers concluded that progression of DCIS to IDC, as mediated by CCR2, is linked to altered cell metabolism, enabling cancer cells to propagate irregular division, chemotaxis, and proliferation.

A-20. Pay Equity Among Professors of Behavior Analysis in Rural and Urban Areas

Carter, K.¹, Boydston, P.¹, & Redner, R.²

Pittsburg State University, Department of Psychology and Counseling¹

Southern Illinois University- Carbondale, Department of Psychological and Behavioral Sciences²

Wage disparities amongst behavioral practitioners and faculty have been identified consistently in recent literature (e.g., Baires et al., 2023; Li et al., 2025), with individuals in urban areas making consistently higher wages than those in rural areas. Additional variables impacting pay disparities require identification for a variety of reasons, including to assist in increasing recruitment and retention of qualified practitioners and academics in underserved areas of the country. The purpose of the present study is to continue to explore differences in compensation across several variables, specifically for faculty working in accredited and/or recognized behavior analysis training programs. Public, state universities based in the United States that house such programs will be reviewed (via publicly available salary data) for individual faculty salary in conjunction with university-wide average salaries per faculty rank for each reviewed university. Wages will then be evaluated against variables such as university location, university research designation, and so on. Results of the study will be used to inform future research on structural changes that may ameliorate or eliminate wage disparities.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-21. Hepatic-Derived Extracellular Vesicles Enter the Brain *In Vivo* Regardless of Exercise or Sedentary Status but Have No Effect on Mitochondrial Respiration at a Low Dose

Authors: Bansal, Aanya^{1,3}; Salathe, Sebastian F.¹; Kugler, Benjamin A.¹; Boakye, Frederick B.¹; Franczak, Edziu¹; Busick, Zane¹; Allen, Julie¹; Hong, Xiaoman¹; Kelly, Taylor J.²; Meers, Grace M.²; Christenson, Lane¹; Wilkins, Heather¹; Booth, Frank W.²; Rector, R. Scott²; Thyfault, John P.¹

¹The University of Kansas Medical Center, ²The University of Missouri School of Medicine, ³The University of Southern California

Exercise supports healthy aging in the brain and stimulates the release of extracellular vesicles (EVs) that may modulate systemic benefits. The liver is central to exercise-induced adaptations and liver-derived EVs are a critical mechanism by which exercise could benefit brain health. However, whether EVs released by the liver reach the brain *in vivo* and affect mitochondrial respiration remains unknown. 12-14 week old male and female (n=8/9) Exomap1 mice received an i.p. AAV8.TBG.PI.Cre.rBG injection. After 4 weeks, mice were randomly assigned to sedentary or exercise (1-hour treadmill) conditions. Immediately after intervention, mice were anesthetized and the brain and liver excised. Whole-brain and liver homogenates were processed for western blotting. Next, male and female (n=10) 6-month old Fisher rats underwent sedentary or exercise (30-minute treadmill) intervention. Immediately after exercise, the common hepatic vein was cannulated and EVs isolated via serial ultracentrifugation. Rat primary cortical neurons were cultured from isolated embryonic cortices and treated with pooled sedentary or exercised, male or female, EVs for 4 hours at 2.5ug/mL (n=7). Mitochondrial respiration was measured using a Seahorse XF. Hepatic-labelled EVs in Exomap1 mice were detected in the brain with no effect of exercise in either male or female mice. In rat primary cortical neurons, neither male nor female exercise-induced hepatic-derived EVs increased mitochondrial respiration. These data therefore suggested the liver may mediate effects on the brain through EVs, however we saw no effect on mitochondrial respiration at a dose of 2.5ug/mL.

Funding: K-INBRE P20 GM103418, 5T32DK128770

A-22. ABC transporter localization in *C. elegans*

Gilmore, Caleb¹, Timmons, Lisa¹

¹Department of Molecular Biosciences, KU Lawrence

ABC transporters constitute one of the largest protein superfamilies across biology and are present in nearly all cellular membranes. However, they are rarely detected at the nuclear envelope. A notable exception occurs in highly metastatic cancer cells, in which ABC transporters exhibit an altered localization pattern, accumulating at the nuclear periphery. This phenomenon is thought to contribute to drug resistance in cancer cells and correlates with poor patient outcomes. Despite the longstanding nature of this observation, there have been no systematic studies that reveal the conditions that lead to the change in subcellular location or the mechanisms that allow this change in membrane localization pattern.

We have previously studied the ABC transporter, HAF-6, using *Caenorhabditis elegans*. Although HAF-6 typically localizes to the endoplasmic reticulum, we have occasionally observed strong relocalization at the nuclear envelope in both antibody-stained fixed tissues and live animals expressing a GFP reporter. Because these animals are wild type and were not exposed to mutagens, we can exclude genetic background variation as a contributing factor and are investigating dietary and other environmental influences. Using *C. elegans*, we can interrogate both the environmental conditions, the protein sequence requirements, and the molecular mechanisms that govern HAF-6 localization. Our goal is to define the features of the nuclear envelope that promote HAF-6 relocalization and identify the cellular conditions and mechanisms underlying this process.

A-23. Exploring Ancestral Enzymes through Sequence Reconstruction and Stability Prediction

Jeyun Park¹ and Masakatsu Watanabe²

¹Academy of Mathematics and Science and ²Department of Chemistry
Fort Hays State University, Hays, Kansas 67601, USA

Understanding how ancient proteins evolved helps reveal the molecular principles underlying the structure, stability, and function of enzymes. In this work, we developed a new computational workflow for ancestral sequence reconstruction (ASR) as an extension of AncFlow, aiming to improve accuracy and structural evaluation. Using β -lactamase and β -glucosidase as model systems, we reconstructed ancestral proteins to trace their evolutionary history. Modern sequences were gathered from publicly available databases and aligned using BLAST and MAFFT to identify conserved and variable regions. IQ-TREE was then used to build phylogenetic trees and infer ancestral nodes. The reconstructed ancestral sequences were modeled into three-dimensional structures using AlphaFold, a deep learning tool recognized for its high structural accuracy. FoldX was subsequently applied to calculate folding energies and assess the theoretical stability of these models. Our workflow integrates sequence analysis, structure prediction, and stability evaluation within a single reproducible pipeline. Importantly, results from this method were compared with those obtained from the Molecular Evolutionary Genetic Analysis (MEGA) program to evaluate consistency. The comparison revealed that, while both approaches generated similar evolutionary patterns, our AncFlow-based workflow provided enhanced structural validation and achieved higher stability prediction than MEGA. By combining advanced computational approaches within an extended AncFlow framework, this study demonstrates a powerful and accessible method for investigating ancestral enzymes, providing new insight into how sequence changes influence protein evolution, stability, and function.

A-24. Fabrication of Wheat Gluten based Films using Spray Jet Method

Asher Freiburger¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

Email: mparvinzadehgashti@pittstate.edu

The increasing demand for sustainable and functional packaging materials has driven research into biodegradable films with enhanced protective properties. This project focuses on the development of gluten-based films incorporated with antimicrobial agents to improve shelf life. Gluten, a protein-rich byproduct of cereal processing, offers excellent film-forming ability, mechanical strength, and biodegradability, making it a promising alternative to synthetic plastics. By integrating natural or synthetic antimicrobial compounds into the gluten matrix, the resulting films are expected to inhibit microbial growth on food surfaces, thereby reducing spoilage and contamination risks. The study will investigate film preparation methods, optimize antimicrobial loading, and evaluate key properties such as tensile strength, barrier performance, and antimicrobial efficacy. The anticipated outcome is a novel, eco-friendly packaging material that combines sustainability with active protection, contributing to advancements in food preservation and reducing reliance on non-biodegradable plastics.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-25. Identifying Regulators of miRNA Strand Selection in *Caenorhabditis elegans*

Isabella Berndt¹, Jeff Medley¹, Sumire Kurosu¹, and Anna Zinovyeva¹

¹Division of Biology, Kansas State University, Manhattan, KS

MicroRNAs (miRNAs) are small non-coding RNAs that regulate gene expression by binding to specific sequences within target messenger RNAs (mRNAs). During miRNA biogenesis, double-stranded precursors undergo a process called strand selection in which one strand is incorporated into the Argonaute protein (ALG-1 in *C. elegans*) to form the miRNA-induced silencing complex (miRISC), while the other strand is degraded. Improper strand choice has been linked to developmental disorders, highlighting the importance of proper strand choice. However, the regulatory mechanism of this process remains poorly understood. In *C. elegans*, *mir-58* is a highly abundant miRNA essential for normal body size, and loss of *mir-58* results in a significant reduction in body length. To identify regulators of strand selection, we performed RNAi knockdowns of ALG-1-interacting proteins previously identified by mass spectrometry (Zinovyeva et al, 2015) in a genetic background where *mir-58* switches strand selection. We hypothesize that knockdown of these ALG-1-interacting proteins will alter body length of *mir-58* strand-switching mutants if these factors regulate *mir-58* strand selection. Thus, body length serves as an indirect readout for miRNA strand selection. Several candidates, including *cey-3*, *hrg-11.1*, and *lin-67* increased the body length of *mir-58* strand-switching mutants. Notably, *lin-67* knockdown restored body length to wild-type levels, suggesting it may play a role in the ALG-1 miRISC and influence strand selection. We are currently testing whether these factors directly regulate strand selection by measuring *mir-58* miRNA levels using TaqMan-based absolute quantification. These results should provide new insights into the mechanisms regulating miRNA strand selection.

A-26. Green Sodium Hypochlorite Oxidation of Primary Alcohols to Carboxylic Acids for the Undergraduate Organic Chemistry Laboratory

Avery Gutierrez,¹ Devi Steigner,¹ and Lucas McCormick¹

¹School of Science and Mathematics, Emporia State University

Traditional alcohol oxidation often relies on chromium salts that generate hazardous waste byproducts, prompting interest in greener alternatives such as sodium hypochlorite (household bleach), which has been shown to effectively oxidize secondary alcohols to ketones. However, primary alcohols represent a greater challenge due to the added difficulty of selective oxidation to either an aldehyde or carboxylic acid. Existing literature precedent for application of the greener hypochlorite method to primary alcohols is limited, inconsistent, and difficult to reproduce. This project aims to develop a reliable and environmentally friendly undergraduate laboratory protocol for oxidation of primary alcohols to carboxylic acid using sodium hypochlorite. The optimized procedure employs ethyl acetate solvent, tetrabutylammonium bromide phase-transfer catalyst, and a reaction time of 40 minutes at 45 °C. Following acid-base extraction and vacuum filtration, carboxylic acid products were obtained in 20-97% yields and characterized by melting point and IR spectroscopy. The method was successfully applied to both saturated and unsaturated alcohols, with cinnamyl alcohol affording the highest yield. This work demonstrates the use of sodium hypochlorite as a safe, efficient, and sustainable alternative to chromium-based oxidation of primary alcohols, suitable for implementation in an undergraduate organic chemistry laboratory setting. Future efforts will focus on resolving the lower yielding reactions, expanding the substrate scope, and functional-group tolerance testing.

A-27. Interpopulation Phenotypic Variation in the Ornate Box Turtle (*Terrapene ornata*) Driven by Environmental Selective Pressures

Peterson, Grace, Peyton Samek, Brookelynn Powell, Caroline LeJuerrne, Jacyn Falley, Bella Limback, Sage Dennis, August Wilson, Ash Van Dalsem, Erin Carter, Serena Schmitz, Kyra Jantzen, and Benjamin Reed

Department of Biology, Washburn University, Topeka, Kansas, USA.

Natural selection plays a profound role in driving differences in phenotypic traits between different populations of species. Body condition, body size, personality, and ranging activity, are all major contributors that affect an individual's overall fitness within their environment, often selected for differently between different populations. For example, given different selective pressures it may be advantageous to have a bolder personality in one population compared to a shyer personality in another. The Ornate Box Turtle (*Terrapene ornata*) provides an ideal model for studying interpopulation phenotypic variation, presenting a wide variety of behavior, personality, and innate traits. The objective of this poster/study is to compare populations of turtles inhabiting different environmental conditions and determine which traits are similar and different between the different populations. Within the time period of the study (2025), we collected data on body mass, body condition (residual of shell measurements on mass), personality traits, and ranging activity for a minimum of 40 turtles in three different populations, all with different environmental types. Our findings reveal significant intra and interpopulation variation within the Ornate Box Turtle populations. These findings are important as they show the Ornate Box turtles' interaction with their environment is much more complex than originally assumed and proper management/conservation efforts would likely need to be population dependent to be the most effective for this specific species.

A-28. Discovering the Signal-Detection Mechanism of *Chlamydia trachomatis*: Expression and Purification of the CtcB Sensor Domain

Yesem Haillemariam, Lexie Payton Cutter, Scott P. Hefty Ph.D.

Department of Molecular Sciences, University of Kansas

Bacterial pathogens rely on specialized signaling systems to sense and adapt to their environments, which is essential for infection and survival within a host. The signal that initiates the two-component system that *Chlamydia trachomatis* utilizes to control its developmental cycle involves the histidine kinase CtcB. Purifying the CtcB sensor domain to investigate its function in signaling is the goal of this study. Western blot analysis will be used after short-term induction to assess protein expression in *Escherichia coli* BL21 (DE3). Large-scale purification employing SDS-PAGE analysis and immobilized metal affinity chromatography (IMAC) will follow confirmed expression. Gaining insight into the regulation of CtcB may help identify novel treatment targets to break the infection cycle of *C. trachomatis* and prevent the progression of illness.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-29. Developing a method to manipulate the immune system of mosquito larvae

Julia Chartier, David Hayes, and Kristin Michel,
Division of Biology, Kansas State University

Vector competence, the ability of mosquitoes to transmit human pathogens, is dependent on the mosquito immune system. Research has primarily focused on immune factors that limit human pathogen transmission; however, the mosquito immune system is influenced by potentially lethal encounters made early in their lives as aquatic larvae occupying habitats full of opportunistic microbial pathogens. The overall goal of this study is to determine key immune factors that protect mosquito larvae from fungal and bacterial infections. Our current goal is to establish a protocol that induces gene-specific RNAi in larvae of the African malaria mosquito, *Anopheles gambiae*. We used a 24-well plate assay to expose individual larvae to three different yeasts: a negative control containing nutritional yeast, a positive control yeast strain containing a short hairpin (sh)RNA loop interfering with the essential *shaker* gene and a negative RNAi control containing a scrambled shRNA sequence. For each yeast type we exposed 72 larvae that either remained in the same well until pupation or were moved to a fresh water well after 3 days to resemble existing infection protocols. Larvae were assessed daily for mortality and development to pupation and adulthood. All larvae exposed to sh*Shaker* yeast died within 24 hours of exposure. Over 80% of larvae exposed to nutritional yeast or scrambled shRNA yeast developed to pupae independent of whether they were moved to fresh water. Therefore, this protocol is effective in using shRNA yeast to induce RNAi in *An. gambiae* larvae and allows for experimental infection.

A-30. Unique signatures of mitochondrial genomic evolution in threespine stickleback fish

Reed M Hodges, Emily A. Beck
Department of Molecular Biosciences, University of Kansas

Mitochondria are essential organelles that perform many functions in cellular physiology including energy production and regulation of the cell cycle, cell death, lipid biosynthesis, calcium homeostasis, and redox optimized reactive oxygen species (ROS) balance. They also help cells respond to stress and help organisms adapt to new environments. Mitochondria perform these multifaceted roles in part using their own genomes (mitogenomes). These small genomes typically encode 13 protein coding genes which must interact with the much larger mito-proteome mostly encoded by the nuclear genome. Nuclear and mitogenomes evolve at different rates, with mitogenomes evolving 5-10 times faster than the nuclear genome. They are also inherited differently, with mitogenomes typically inherited only maternally as opposed to the nuclear genome which is inherited biparentally. A major question in biology is how these different genomes coevolve to maintain mito-nuclear compatibility and function. The threespine stickleback fish (*Gasterosteus aculeatus*) provides an excellent system to understand these dynamics. Stickleback have evolved extreme intraspecific divergence in their mitogenomes due to a gene flow event during the last glacial maximum. Today, there are stickleback of two mitogenomic haplotypes (mitotypes) existing in admixture in hundreds of populations. My project explores how these two mitotypes are segregating in various populations and how mitogenomes may be evolving to maintain compatibility with the nuclear genome.

A-31. Activated Maple Carbon as a Bio-Based Cathodic Material in Lithium-Sulfur Batteries for Electrochemical Energy Storage Applications

Alexandra Robinson², Anjali Gupta², Wang Lin¹ and Ram K. Gupta^{1,2*}

¹National Institute of Material Advancement, Pittsburg, KS 66762, USA

²Department of Chemistry, Pittsburg State University, Pittsburg, KS 66762, USA

As scientists search for alternative forms of producing and harnessing clean energy, much research has been focused on electrochemical energy storage devices, such as the Lithium-Sulfur Battery (LSB), to mitigate the current energy crisis with sustainable and economic materials. Of these, LSBs are primarily favorable for their high theoretical energy density of 500 Wh/kg, thanks to their unique mechanism. The conversion mechanism of LSBs is more intricate than other devices, and it increases efficiency by interconverting sulfur and sulfide via 16-step oxidation-reduction reactions during charge and discharge cycles. Impediments such as the shuttle effect, dendrite formation, and volume expansion (due to (de)lithiation) are the reason LSBs are not currently commercialized, despite electrochemically outperforming the current lithium-ion batteries severalfold. To combat these, a high surface area carbon material was synthesized using maple leaves to facilitate incremental conductivity in the presence of structural pores, which allow space for sulfur expansion. Different ratios of the activating agent (KOH) to the bio-based maple carbon were used to fabricate LSBs and tested through using cyclic voltammetry, electrochemical impedance spectroscopy, galvanostatic charge-discharge measurements, and cyclic stability at different C-ratings. The MC-KOH (1:1) performed the best, with a specific capacitance of 641 mAh/g at 1C. Next, similar methods will be employed to test different percentages of sulfur content within the cathodes.

A-32. WHAT'S LINKER GOT TO DO WITH IT? EXAMINING THE STRUCTURE AND STABILITY OF PALLADIN'S IG3-4 LINKER REGION

Lauren Hughes, Rachel Sargent, Nathan Ta, Colby Bradford, Dr. Moriah Beck
Department of Chemistry and Biochemistry, Wichita State University

Actin is the most abundant protein within all eukaryotic cells and is essential for motility, structure, and cellular division. Actin participates in more protein-protein interactions than any other known protein, and one such relationship involves palladin. Palladin is a lesser-known protein that is typically only expressed during embryonic development. However, recent work has proven that palladin is expressed in metastatic cancer cells.

To understand the role palladin plays in cancer metastasis, we must first understand its structure. Palladin is comprised of five immunoglobulin-like domains (Ig), each connected via an unstructured linker region. Our research focuses on the Ig3-4 linker region. The Ig3-4 linker consists of forty-one amino acids and is predicted to be intrinsically disordered. Previous research has shown that Ig3 is the minimal actin-binding domain; however, the binding affinity is significantly increased when the Ig3-4 linker domain is present. Current research seeks to determine the Ig3-4 linker region's effect on palladin and actin's interactions. To determine the structure and function of the Ig3-4 domain, we introduced several mutations to the linker. The most prominent mutation is RLinkerA, a conversion of the domain's ten arginines into alanines, which completely disrupted the binding ability of both actin and palladin. All the mutated and wild-type linker regions were subjected to circular dichroism spectroscopy to determine structure, as well as chemical and thermal denaturation tests to determine stability. Analysis of these results indicates no alteration in the structure or stability of the Ig3 domain or its linker, despite the obstruction of actin binding.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

A-33. A corticolimbic dopamine-glutamate pathway modulates partner seeking behavior during loss state in prairie voles (*Microtus ochrogaster*).

Guillen Sauceda, Nicolle¹, Lowe, Camryn S.¹, Tbara, Amina H.², Vitale, Erika M.¹, Ahad, Nicole T.¹, Smith, Adam S.^{1,2}

¹Department of Pharmacology and Toxicology, School of Pharmacy, ²Program in Neuroscience, University of Kansas, Lawrence, KS, USA

*Contributed equally

When we experience grief, we often seek reminders of a lost loved one—photos, places, or personal belongings. A similar pattern appears in the socially monogamous prairie voles (*Microtus ochrogaster*) when they are separated from their pair-bonded partners. This behavior has been linked to a feedback circuit between the ventral tegmental area (VTA) and anterior cingulate cortex (ACC). To further explore this hypothesis, we combined behavioral testing with pharmacological manipulation to examine how partner cues affect stress responses during loss. Voles were paired with an opposite-sex, genetically compatible partner for one week. Bond formation was evaluated through a partner preference test (PPT). Voles who were pair-bonded were separated for one week. On the day of behavioral testing, voles received bilateral, site-specific infusions of a nonspecific dopamine antagonist or a glutamate receptor agonist in the VTA and were immediately exposed to an odor preference test (OPT). Pair-bonded loss animals spent more time investigating partner odors than non-bonded loss animals and pair-bonded controls. Blocking dopamine receptors in the ACC or activating glutamate receptors in the VTA each reduced partner-odor investigation in pair-bonded loss voles. This study provides the first evidence that corticolimbic signaling directly drives increased partner-cue seeking during partner loss, though further work is needed to define the molecular mechanisms underlying this dopamine circuit.

A-34. The Effects of Supplemental Feeding on the Movement Ecology of the Ornate Box Turtle

Peyton Samek, Jady Falley, Brookelynn Powell, Grace Peterson, Caroline LeJuermne, Bella Limback, Sage Dennis, August Weishaar-Wilson, Ash Van Dalsem, Erin Carter, Benjamin Reed
Washburn Biology Department

The home-range size an animal uses can be influenced by a multitude of factors including habitat quality, resource distribution, energy costs associated with moving throughout various terrain types, and the individual's overall body condition. One factor that unifies these diverse factors is the individual's overall access to food within their home range. In this study we specifically asked whether well-fed animals move more (rich get richer mentality) or move less (reduce risk, avoid unnecessarily leaving shelter if fed)? To investigate the influence of food access on ranging behavior, we manipulated the fed-state of radio telemetered Ornate Box Turtles (*Terrapene ornata*) to experimentally examine how access to additional food would influence home range size and use. For this study, radio tracked 48 turtles split into four diet-specific treatments (unfed but still handled control group, sugar diet, protein diet, sugar and protein diet). Turtles were tracked three times weekly for nearly twelve weeks in the summer of 2025 and were handled/fed twice weekly for the last six weeks of this study. Our analyses found variation across our study turtles in their likelihood of eating supplemental food and their ranging behavior, yet no direct link could be made between treatment and home-range size as we originally expected. These findings suggest that other physiological or ecological factors may be driving our observed variation in home range areas, prompting further investigation into other variables.

A-35. Resistance to X chromosome meiotic drive in *Drosophila affinis*

Vincent Chan¹, Anjali Gupta², Robert L. Unckless¹

¹Presenting author

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66045

²Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66045

Under Mendelian inheritance, homologous chromosomes have an equal probability of transmission, giving “XY” males equal probabilities of producing male or female offspring. However, selfish genetic elements can violate these rules. One such example is sex-ratio meiotic drive, where X-linked drivers kill Y-bearing sperm, resulting in female-biased offspring sex ratios. While this benefits the X chromosome, it can threaten population survival. Suppressors can evolve on autosomes or Y chromosomes to restore balance.

In *Drosophila affinis*, two distinct X-linked meiotic drivers and their suppressors coexist in the wild, providing a powerful system to study this evolutionary arms race. To examine suppression variation, we established laboratory drive strains from wild-collected flies to capture genetic diversity in the population. I crossed females carrying the driving X chromosomes to the wild-derived strains, then tested their sons for the sex ratio they sired.

To test autosomal suppression, I screened multiple iso-female strains for each driving X. Driving X females were crossed to males from different iso-female strains, and offspring sex ratios were recorded. Strains producing balanced ratios were inferred to carry suppressors. We found resistance for each of the two distinct X-linked meiotic drivers.

For Y-linked suppression, I generated Y-chromosome replacement strains by backcrossing wild-caught males or sons of wild females to virgin females from a lab strain. After ≥6 generations of backcrossing, Y-replacement males were crossed to driving X females. Offspring sex ratios revealed variation in Y-linked suppression.

A-36. Transformation of *Chlamydia* by DNA-Transferrin Delivery

Sofía Chacón Araya, Dominique Jaramillo, Scott P. Hefty Ph.D.

Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

The transformation of *Chlamydia* is an important tool in identifying genes essential to infection. As an obligate intracellular organism, in order to transform *Chlamydia* it has to be inside the host cell causing it to be highly inefficient process. Based on previous publications there might be a way to optimize those transformations by using transferrin as a DNA carrier.

K-INBRE 2026 Symposium Poster Presentation Abstracts

A-37. Genes regulating glucosinolate anticancer compounds in a plant model

Brynn R. Collier, Kathrin Schrick
Division of Biology, Kansas State University

Glucosinolates are sulfur- and nitrogen-containing glycosides produced in *Arabidopsis* and other Brassicaceae species that include broccoli, cabbage, and mustard. When hydrolyzed, glucosinolates generate indoles and isothiocyanates with anti-inflammatory and antioxidant properties. These glucosinolate derivatives have demonstrated potential in cancer prevention when consumed in the human diet. RNA-sequencing data from our laboratory showed that the adaptor protein GIR1 negatively regulates genes in the glucosinolate biosynthesis pathway, including the transcription factor genes *MYB28* and *MYB29*. These two transcription factors act redundantly to activate multiple genes of the glucosinolate biosynthesis pathway. Accordingly, the *myb28;myb29* double mutants fail to accumulate aliphatic glucosinolates. Loss-of-function *gir1* mutants display excess giant cells in sepals, suggesting a possible relationship between glucosinolate metabolism and epidermal cell expansion. Our hypothesis is that glucosinolates contribute to giant cell formation, and that GIR1 represses giant cells partly by limiting glucosinolate production. To test this, we are generating *gir1;myb28;myb29* triple mutants using two approaches. First, CRISPR-Cas9 constructs targeting *GIR1* were transformed into *myb28;myb29* double mutants. T1 progeny are being screened using DsRed fluorescence, segregation patterns, PCR genotyping, and microscopy. Second, we are pursuing traditional genetic crosses, although this is challenging because *GIR1* and *MYB29* are closely linked on chromosome 5. By analyzing mutant combinations for glucosinolate levels and giant cell phenotypes, we aim to determine whether glucosinolate deficiency suppresses giant cell expansion. These results will clarify how glucosinolate metabolism interacts with epidermal growth pathways.

This project is supported by the Kansas INBRE (P20 GM103418) and USDA-NIFA (KS00-0009-NC1203).

A-38. Exploring Structure-Selective RNA-Targeting Compounds for Triple-Negative Breast Cancer Therapy

Maddox Johnson, James McAfee, Irene Zegar
Department of Chemistry, Pittsburg State University, Pittsburg, Kansas.

Triple-negative breast cancer (TNBC) is an aggressive subtype that lacks hormone receptor and HER2 expression, making it difficult to treat using targeted therapies. Long noncoding RNAs (lncRNAs) such as metastasis-associated lung adenocarcinoma transcript 1 (MALAT1) have been linked to cancer progression and may serve as novel therapeutic targets. This project examines MALAT1 expression and function in TNBC cells (MDA-MB-468) compared with nonmalignant breast epithelial cells (MCF-12A). Quantitative real-time PCR (RT-qPCR) will be used to measure MALAT1 transcript levels in both cell lines. Cytotoxicity assays will evaluate the effects of unique small molecules that bind to the 3' end of MALAT1 and cause its destabilization. Serial dilutions and multiple replicates will be performed to establish dose-response relationships and assess selectivity between cancer and healthy cells. Migration and invasion assays will determine whether compound treatment reduces the motility of TNBC cells. Fluorescence in situ hybridization (FISH) may also be used to visualize MALAT1 localization within intact cells, as time permits. Together, these studies aim to clarify the role of MALAT1 in TNBC cell behavior and explore RNA structure-based regulation as a possible therapeutic avenue. The results will contribute to a better understanding of noncoding RNA biology in aggressive breast cancers and provide early validation for a new class of structure-selective anticancer agents.

A-39. Cardiovascular health monitoring using multiple conformal photoplethysmography devices

Taylor Spinelli¹, Bryson Murphy¹ and Yongkuk Lee.¹
¹Department of Biomedical Engineering, Wichita State University.

Astronauts' physiological systems are often disturbed by several stressors including microgravity, fluid shifts, and space radiation exposure. Current monitoring of cardiovascular health for astronauts is carried out by electrocardiogram (ECG), ultrasound imaging, blood sampling, and blood pressure screening during routine health checks. These devices appear to provide reliable measurements of various physiological signals; however, those systems are often invasive and bulky so they may not be suitable for continuous ambulatory monitoring in space. Wearable health monitoring systems are relevant in medical applications because of their small form factor and abilities for non-invasive continuous quantification of physiological information. Photoplethysmography (PPG) is an optical, non-invasive measuring technique and uses a light source and a photodetector to monitor regional blood volume changes near the skin. It can be utilized to extract valuable information such as blood pressure, cardiac outputs, autonomic functions, and various cardiovascular-related diseases. PPG has great potential for providing a simple and versatile diagnostic tool as an alternative to traditional cardiovascular health monitoring. Yet, studies which incorporate multi-site PPG monitoring are limited. In this work, conformal PPG devices are placed on the forehead, wrist, and ankle to monitor PPG signals synchronously. Along with these devices, a small, fabricated ECG device is laminated on the skin near the heart. Our findings demonstrate the feasibility of our paired PPG and ECG device network as an accurate, low-profile, and low-resource monitoring system for cardiovascular health.

A-40. Unoccupied

B-1. Chemotherapeutic 5-FU alters multifactor complex formation with oncogenic translation initiation factor 5MP1 and eIF proteins

Authors: Logan Glover, Susumu Ishiguro, Katsura Asano
Department of Biology, Kansas State University, Manhattan, KS, 66506

Translational control is a crucial driving force in tumorigenesis or tumor progression. It has been observed that a translation initiation regulatory factor 5MP1 is frequently over expressed in colorectal cancer (CRC) and is associated with metastasis and poor survival of CRC patients. The amplification of this 5MP1 reprograms the ratio of CUG to AUG start codon usage, thus increasing the oncogenic AUG-initiated C-Myc isoform. However, 5MP1 cannot function without first creating a multifactor complex (MFC) with eukaryotic translation initiation factors 2 and 3 (eIF2/3). In this study, we characterized how the MFC is affected by a chemotherapeutic drug 5-FU, which alters DNA metabolism. The interactions of this protein complex were studied using Bio-Layer Interferometry (BLI) with a GST tagged 5MP1 wild-type as well as common oncogenic mutants (E413K, H386R, P327L and E316K). The optical responses measured from the BLI assays were compared to a known concentration of the binding partner, eIF2/3, and the dissociation constant was calculated in the absence or presence of 5-FU. The binding between 5MP1 wild-type/mutants and eIF2 were increased by 5-FU. This discovery indicates that 5-FU enhances the oncogenicity of 5MP1, which may reduce the efficacy of 5-FU's anticancer properties. Thus, it is postulated that 5MP1 may be a possible mode of chemotherapy resistance. By further characterizing the MFC and its interactions with chemotherapeutics as well as different oncogenic point mutations in 5MP1, a better understanding of how this complex leads to worse outcomes in CRC patients may be achieved.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-2. Gene engineering, cloning, and expression of the human CLPB variant, SAP

Eleanor Martin, Zachary Spaulding, and Michal Zolkiewski

Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, Kansas

Our laboratory explores protein structure and functions. We currently focus on several members of the diverse protein superfamily of AAA+ ATPases that use energy from ATP hydrolysis to maintain protein homeostasis. This project is focused on a mitochondrial member of the AAA+ family called CLPB (also known as SKD3). Mutations within the CLPB gene are known to cause congenital neutropenia, and 3-methylglutaconic aciduria. Yet, there is lacking information regarding the protein function and mechanism. A related bacterial protein, ClpA associates with the protease ClpP to form the ClpP complex, which is capable of degrading misfolded bacterial proteins threatening proteostasis. This complex is formed by stabilization of contact through the loops in ClpA containing the hydrophobic IGL motif. Gene engineering to add the bacterial ClpA loops to the human CLPB protein will provide an opportunity to discover how the substrate interacts with CLPB and will be used to determine the mechanism of reactions supported by CLPB. The engineered protein is referred to as SAP (SKD3, which like ClpA binds to ClpP). Based on the published structure of CLPB, we selected a site for insertion of the polypeptide fragment containing the IGL motif. We engineered the DNA construct for SAP and expressed the protein in *Escherichia coli*. Preliminary experiments failed to detect interaction of SAP with ClpP. We hypothesize that the ClpP access to the engineered IGL motif in SAP might be limited by the mobile ankyrin domain in SAP, as suggested by the latest X-ray crystallography data.

B-3. Exploring the factors that are related to metabolic rate in Ornate Box Turtles (*Terrapene ornata*)

Authors: Ephraim Schlingensiepen, Tracy Wagner, Paul Wagner, Benjamin Reed

Washburn University Biology dept.

The metabolic theory of ecology is based on the relationship between an organism's energy expenditure, its body size, and its temperature; smaller organisms or those with warmer core temperatures generally have higher mass-specific metabolic rates than larger or cooler-bodied organisms. Metabolic rate is an important factor influencing many fitness-related traits, including growth rate, reproductive output, and lifespan. In this study, we examined several factors expected to influence metabolic rates in individual animals. To address this objective, we recorded oxygen consumption and carbon dioxide production as proxies for metabolic rate in Ornate Box Turtles (*Terrapene ornata*) across seasons and populations. We found variations in metabolic measures across age classes, seasons, and populations. Documenting these metabolic patterns will help us better understand the current energy needs of this species in a changing environment.

B-4. Floristic Summary of Bates County, Missouri

Mason, Rylan,¹ and Neil Snow¹

¹Department of Biology, Pittsburg State University

Many counties across the USA are incompletely surveyed for their native and non-native vascular plant diversity, such as Georgia, South Dakota, Tennessee, and Texas. Data from the two online digital databases SEINet and BONAP suggested in 2023 that Bates County in western Missouri was less surveyed than many surrounding counties. Our null hypothesis that the county was incompletely surveyed was corroborated after the first full field season. Presently (Fall 2025), 68 of the first 1,023 collections (6.7%) represent county records. Among the non-native first reports are Amur honeysuckle, Autumn olive and Musk thistle. First documentations for native species include Mayapple, Buffalograss and Common arrowhead. Our annual surveying involves seven or more day-long collecting trips, mostly to areas managed by the Missouri Department of Conservation with their permission. Current botanical knowledge on the land is important because the geographical range and local abundance of species frequently change and shifting averages in annual temperatures and precipitation may contribute to these shifts. In addition, non-native taxa can greatly decrease productivity on farms and ranches and are costly to mitigate. The current emphasis is data retrieval from online sources to determine the dates of first documented occurrences for approximately 909 plant species and subspecies. The goals of the project are to further update knowledge of vascular plants in Bates County, provide baseline data for future ecological comparisons of flowering times, document the presence of non-native species, and monitor species of conservation concern.

B-5. Trastuzumab Utilization in Differential Selective Pressure Analysis: a Post-hoc Assessment of MSK-IMPACT 341 and TCGA-2015 in Clinical Outcomes

Authors: Auditya Jain, Marcus Yoakam, Maryam Nabavifard, Christopher Ward

Affiliations:

1- **Kansas City University:** 1750 Independence Avenue, Kansas City, MO 64106. Tel: (816) 654-7000

2- **Pittsburg State University Biology Department:** 101 Heckert-Wells Hall, 1701 S. Broadway, Pittsburg, KS 66762. Tel: (620) 235-4748.

In this study we compared via post-hoc analysis of MSK-IMPACT 341 and TCGA-2015. This was done with respect to trastuzumab use. Trastuzumab is a HER2-targeted monoclonal antibody that has significantly improved outcomes in HER2-positive breast cancers. While its efficacy is clear, many effect sizes and the interplay between selective pressure on tumor evolution remains underexplored. Deidentified data was collected from cbiportal and Genomic Data Commons. Heatmaps were generated and data plotted in aggregate through cbiportal. Time to event analysis using R studio was conducted to collect Kaplan Maier Statistics, Cox Proportional Hazard Model, and General Demographics were analyzed using epitools and various survival packages. It was shown that, in MSK-IMPACT 341 population, 1212[18.9%] of the population received Trastuzumab or a conjugate whereas only 8[5.8%] received it in the TCGA 2015 cohort. The cox model showed after adjusting for multiple covariates that hazard ratio to overall survival for use of trastuzumab was 0.86[95%CI 0.75-0.97] while adjusting for sex, race, histology, and HER2 Status. Differential Gene Expression showed upregulation in mTOR and PI3K/AKT pathway activity post treatment. Differences in shoenfeld test results suggests that the efficacy of trastuzumab is highly time sensitive in promoting overall survival, but differs in the outcomes between these trials. This suggests significant utilization of trastuzumab in early HER2 positive cancers.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-6. Blazin' Brains: Reaction Time Training, Exercise and Cognition

Erin M. Blocker¹, Brynn McCormick¹, Savannah Stewart¹, and Abby Bachman¹
¹School of Applied Health Sciences, Emporia State University

Research suggests that exercise is beneficial for the aging brain. Although a variety of "brain-training" devices exist, research regarding their effectiveness remains limited. This pilot study investigated the impact of reaction time training on cognitive function in older, already-active women. Participants first completed baseline cognitive assessments via a smartphone application (Sway app, Sway Medical, Tulsa, OK), including inspection time, reaction time, impulse control, and memory evaluations. Following baseline testing, participants engaged in an 8-week, twice-weekly group exercise program. Each session incorporated traditional fitness components along with a minimum of 10 minutes of reaction time training using Blaze Pod® (Version 4.61). Attendance was encouraged but not strictly regulated to enhance real-world applicability. Upon completion of the 8-week program, participants repeated all cognitive assessments. Fourteen women (ages 55-89 years) completed baseline assessments and participated in the program, with 11 completing post-testing. No significant changes were found in any measured cognitive parameters ($p < .05$). The lack of statistically significant findings was likely influenced by the small sample size and short duration of the study. Although cognitive gains were not observed, incorporating Blaze Pod® training provided a novel and enjoyable exercise modality for older women. Future research should examine reaction time training among untrained older adults over longer durations to better determine potential cognitive benefits.

B-7. Molecular test to differentiate between polymorphic Y chromosomes in *Drosophila affinis*

Kaylie Schroeder¹, Anjali Gupta², Robert L. Unckless¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66046

²Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS 66046

¹Presenting author

Chromosome configurations turn over rapidly among sex chromosomes. Miller and Stone, 1961 showed that polymorphic Y chromosomes varying in shape and size segregate in the wild in populations of the fruitfly, *Drosophila affinis*. *D. affinis* has 5 different Y chromosome morphs that segregate in natural populations with 3-fold variation in size and a complete lack of a Y in some individuals. Even today, in order to identify the Y chromosome karyotype in this species, we have to examine metaphase chromosome karyotypes using larval brain squashes (similar to Miller & Stone 1961), which are cumbersome and less feasible for karyotyping large sample sizes.

Hence, our goal is to develop a polymerase chain reaction (PCR) test to easily differentiate between the different morphs of the Y chromosome. To do this, we designed primers specific to a few genes present only on a single Y chromosome morph type. We tested these primers using ~100 strains of *D. affinis* established from single wild-collected males, where we identified the Y chromosome morph type by examining metaphase chromosomes using larval brain squashes. This easy PCR test confirmation to differentiate Y chromosome morphs, becomes very useful for us to screen thousands of wild-collected *D. affinis* males without culturing them in the lab, and screening each strain through larval brain squashes.

B-8. Developmental origins of aberrant neurological trajectories in Down syndrome

Katherine I. McCarthy¹, Lexe M. West¹, Hayden C. Hawks¹, Sunita N. Varghese¹, Abhik Saha¹, Greta Foye¹, Luke Johnson¹, Keith P. Smith², Heather M. Wilkins², and Katherine A. Waugh¹
Departments of Cell Biology and Physiology¹ and Neurology², University of Kansas Medical Center, Kansas City, KS 66160

Key inflammatory pathways are conserved across neurodevelopmental and degenerative conditions, such as autism spectrum disorder (ASD), Alzheimer's disease (AD), and Down syndrome caused by trisomy 21 (T21). T21 represents the most common genetic cause of intellectual and developmental disability, and severity ranges from mild to severe. ASD is reported in up to one third of children with T21, and adults with T21 exhibit completely penetrant AD neuropathology by age 40, though disease progression follows highly variable timelines through largely unknown mechanisms. These findings highlight heterogeneity in neurodevelopmental and neurodegenerative outcomes among individuals with T21. Emerging evidence suggests overlapping immunomodulatory networks shape lifelong neurocognitive profiles through microglial mediators, with T21-associated hyperactivation detectable by the second trimester. We hypothesize environmental inflammatory exposures at neurodevelopmental timepoints further amplify these nodes and confer lasting impacts on neurodiversity among genetically hypersensitive individuals with T21. I initiated development of a novel pipeline to dissect inflammatory mechanisms contributing to the developmental origins of aberrant neurological trajectories heterogeneously experienced by people with T21. We used both T21 and control disomic (D21) human induced pluripotent stem cells (hiPSCs), differentiated them into yolk sac progenitors of microglia for exposure to titrated levels of interferon cytokines for assessment of karyotype-specific impacts by flow cytometry, then sequentially into microglia for future study. We anticipate long-term functional consequences of human microglia after programming of progenitors derived from individuals with T21 who are genetically hypersensitive to interferon stimulation. Overall, we aim to define immunomodulatory mechanisms underlying T21-associated neurodiversity, providing a foundation for personalized interventions.

B-9. MicrobioME: A CURE for Staphylococcus aureus – Can our commensal bacteria help inhibit the formation of biofilms?

Darsh Lad, Rosana B.R. Ferriera, Eileen M. Hotze

Department of Molecular Biosciences, University of Kansas – Lawrence

The human skin microbiome is a complex community of bacteria that plays a vital role in maintaining skin health and protecting against pathogenic organisms. Among its many functions, commensal bacteria are thought to contribute to host defense by inhibiting the formation of pathogenic biofilms. In the Bacterial Infectious Disease Laboratory course, students participated in a Course-based Undergraduate Teaching Experience (CURE) which explored the potential of commensal skin bacteria to inhibit the formation of *Staphylococcus aureus* biofilms, a common cause of skin infections. Two bacterial isolates were identified through MALDI-TOF and biochemical tests: *S. aureus* (C11.1) and *S. capitis* (C11.2). *S. aureus*, a commensal species commonly found on human skin, was further investigated for its ability to influence pathogenic *S. aureus* biofilm formation in vitro. Biofilm assays revealed that *S. aureus* C11.1 was able to reduce biofilm formation by another *S. aureus* strain, suggesting an inhibitory interaction between the two possible strains. These findings suggest that commensal bacteria, such as *S. aureus*, may play a protective role on the skin by limiting the growth and persistence of harmful pathogens. This study underscores the importance of understanding the dynamic interactions between commensal and pathogenic bacteria on the skin, particularly in the context of biofilm-related infections.

K-INBRE 2026 Symposium Poster Presentation Abstracts

B-10. Skin microbiomes transferred to clothing can be used in forensic identification of individuals

McGann, Alexa, Joselynn Hoff, Logan Shearer and Stephen Fields
Department of Biological Sciences, Emporia State University, Emporia, KS

Skin microbiomes are influenced by many genetic and environmental factors as well as geographic location. The skin microbiome is therefore unique to a person, which makes it a potentially useful tool for forensic science. Both transient and residential skin microbiomes can be transferred to various surfaces, including the clothing a person is wearing. This pilot project tests if clothing can be matched to a person that had been wearing it based solely on the corresponding microbiomes. In a blinded study, we characterized skin microbiomes of three of the authors along with the microbiomes contained on cloths exposed to their skin. The skin and cloth samples were analyzed to determine whose skin the cloth pieces came from. We were able to look at quantified, stacked graphs of the most abundant microbes and accurately match the cloth microbiome to the skin microbiome. The results show that transferred skin microbiome analyses may be developed as a potential tool in forensic science when human DNA is not present or in the case of identical twins.

B-11. DEVELOPING A WEARABLE FETAL HEART MONITOR: AN EVALUATION OF FETAL ELECTROCARDIOGRAM EXTRACTION ALGORITHMS

Emma Simmons, Dr. Yongkuk Lee
Department of Biomedical Engineering, College of Engineering

Congenital heart defects (CHDs) are the leading cause of infant mortality. Early detection of CHDs enables healthcare providers to intervene timely, reducing fetal and infant death rates. The current gold standards for fetal observation include Doppler sound and invasive fetal electrocardiogram (I-fECG). However, these techniques are either too imprecise for effective CHD detection or pose significant risks to the mother and fetus. The non-invasive fetal electrocardiogram (NI-fECG) offers a safer alternative for detecting the fetal QRS (fQRS). This technique utilizes a configuration of electrodes on the maternal abdomen to capture fetal signals. However, it also captures maternal signals and noise, making the fQRS difficult to analyze. Therefore, developing an accurate extraction algorithm is essential to enable reliable, non-invasive, and ambulatory fetal heart monitoring. In this study, we analyzed simulated and practical abdominal ECG (aECG) data. For the simulated data, an open-source database (FECGSYN) was utilized to synthesize 1 minute-long, 160 samples of aECG recordings containing fetal signals, maternal signals, and noise. For the practical data, aECG signals were collected from 20 participants for comparison. Each sample was analyzed with three main extraction algorithms (BSS, TS, and AFM) along with various electrode configurations. Average F1 values were used for statistical analysis. Our findings indicate that BSS provides the most consistent results, but low F1 values. In contrast, AFM produced higher F1 values but more variable outcomes. TS compromised with higher F1 values than BSS and more consistent results than AFM. These trends were consistent across both simulated and practical data sets.

B-12. Watermelon Seed Protein-based Films for Wound Dressing Applications

Isaac Mountain¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³
1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA
3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA
Email: mparvinzadehgashti@pittstate.edu

We developed watermelon seed protein-based films incorporating different crosslinkers to enhance their structural integrity and functional performance. Watermelon seed protein exhibits excellent film-forming properties. By introducing various crosslinkers, we will improve the flexibility, hydrophobicity, and durability of the films, making them more suitable for biomedical and packaging applications. The crosslinking also results in a denser film network, which contributed to improved barrier properties. Additionally, it is expected that the modified films will exhibit notable antimicrobial activity against common pathogens such as *E. coli* and *S. aureus*, attributed to both the inherent properties of watermelon seed protein and the surface-modifying effects of crosslinking agents. These antimicrobial characteristics make the films promising for use in wound dressings. Characterization techniques such as FTIR, and antimicrobial assays will confirm the successful integration of crosslinkers and their functional benefits.

B-13. Loss of the Drosophila multispecific transporter, Malvolio, results in abnormal brain morphology and a defective developmental ionome.

List of Authors: Breanna Leach², Divyankasri Padamati¹, Prabriti Neupane¹, Justin Scott³, Puni Jeyasingh³, and Rajprasad Loganathan^{1,2}
Author Affiliations: 1) Department of Biological Sciences, Wichita State University; 2) Department of Biomedical Engineering, Wichita State University; 3) Department of Integrative Biology, Oklahoma State University.
*Co-presenting authors

Malvolio (*Mvl*) is the *Drosophila* ortholog of the mammalian Solute Carrier Protein Slc11a2, which transports divalent metal cations, including iron. The function of *Mvl* in the developing *Drosophila* brain is unclear and the developmental anomalies of the brain in *Mvl* mutant, if any, have not been investigated. As the first documented *Mvl* mutant allele showed taste behavioral defects, our objective in evaluating the developmental trajectory of the mutant was to investigate potential neural developmental defects in the L3 larval stage. Ferritin 1 heavy chain homolog protein trap GFP levels were recorded as an indicator of cellular iron levels in the *Mvl* loss-of-function mutant, *Mvl*^{exc1}. After confirming that the loss of *Mvl* results in a lack of iron storage in the larval midgut iron cells, we investigated the brain tissue. Contrary to our expectation, we observed differential and sharply contrasting regions of Ferritin expression in the *Mvl* mutant brain compared to control. Relative to the central brain lobe, the optic lobes localized high levels of Ferritin in the *Mvl* mutant. The finding that the *Mvl* mutant optic lobe has high Ferritin expression implies one or more of the following testable scenarios: (i) Despite the loss of *Mvl*, brain tissue can access iron, via non-*Mvl* dependent cellular metal import mechanisms, and/or (ii) Ferritin expression in the brain tissue is uncoupled from the status of cellular iron levels. Quantification of elemental levels, moreover, revealed an abnormal developmental ionome in the *Mvl* mutant compared with the control. Together, these results suggest a critical role for *Mvl* in directing developmental brain growth and maintaining ionome homeostasis.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-14. Assessing genetic interactions between patient-derived *alg-1* alleles and *alg-2* knockout in *Caenorhabditis elegans* models of Argonaute Syndromes

Rebecca Mitchell, Belén Gaete Humada, Anna Zinovyeva
Division of Biology, Kansas State University, Manhattan, Ks

Gene expression regulation enables diversified cellular functions and is crucial for animal development. One way gene regulation occurs is through microRNAs (miRNAs), small non-coding RNAs, which work with Argonaute (AGO) proteins to silence genes post-transcriptionally. Due to their importance in gene regulation, altered miRNA or AGO activity disrupts development. Recently, coding variants in human AGO genes were implicated in developmental disorders termed Argonaute Syndromes (AS). Our goal is to determine how these clinical variants affect AGO function in miRNA-dependent gene regulation. We use the nematode *Caenorhabditis elegans* to model AS variants and characterize their genetic and molecular behavior. Using genome editing, we previously modeled a subset of human AGO1/2 AS variants in the *C. elegans* homolog *alg-1*. Initial genetic analysis revealed that while some *alg-1* AS alleles cause severe phenotypes, others have relatively mild effects. Currently, we are examining the effects of mild *alg-1* AS variants in the absence of a related gene *alg-2*. Because ALG-1 and ALG-2 proteins play partially overlapping roles, we hypothesized that removing *alg-2* would enhance developmental defects of *alg-1* AS strains. To test this, we generated select *alg-2*(null); *alg-1* AS double mutants and assessed their developmental phenotypes; however, we did not observe significant enhancement of phenotypic severity compared to the single mutants. In the future, we will examine the effects of temperature on double-mutant phenotypic severity. Our efforts will help better classify AS variants and could clarify genotype-phenotype causalities.

B-15. Validation of a Pen-Side LAI and Deep Learning Tool for SARS-CoV-2 Surveillance in Animals.

Smith, M., Bakshi, A., Caragea, D., Gauderault, N.N., Richt, J., Trimpert, J., Panagonova, Y. and Bruning-Richardson, A., Miller, L.C.

Rapid and reliable surveillance is needed to prevent outbreaks of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), a zoonotic RNA virus. Previously, we developed a simple and cost-effective pen-side latex agglutination immunoassay (LAI) for the detection of SARS-CoV-2 in animals. The main objective of this study was to validate an AI algorithm for automated positive and negative results for the pen-side test. To test the accuracy of the AI, known positive and negative serum samples from deer, cat, and mouse were tested by LAI at 1:10 and 1:100. Photos of the LAIs were taken up to 15 minutes after mixing with a commercial cell phone. Automated results were compared to known antibody positivity in the serum. The percentage of correct results was calculated. At the time of submitting this writing, the result calculations are still being collected. The development of this LAI test in combination with automated AI resulting will improve diagnostic testing by offering portable, cost-effective tools for pen-side and field surveillance of SARS-CoV-2 and potentially other infectious diseases in the future.

B-16. Role of the GIR2 transcriptional adapter protein in controlling plant cell elongation

Kiaorie Stewart-Ricks^{1,2} Lauren E. Apprill³ and Kathrin Schrick^{2,3}

¹Langston University; ²Division of Biology and ³Department of Biochemistry and Molecular Biophysics, Kansas State University

Plant cell elongation is a fundamental process that determines organ size, sepal morphology, flower shape, and overall plant growth. In *Arabidopsis thaliana*, the small adaptor proteins GIR1 and GIR2 physically interact with class IV homeodomain leucine-zipper (HD-zip IV) transcription factors to regulate epidermal cell growth. Although GIR1 and GIR2 share 71% amino acid similarity, their specific functional relationship is still unclear. The *gir1* mutants showed giant cell phenotypes, with approximately 70-80% of the sepal epidermal cells enlarged compared to the wild-type plants. In contrast, *gir2* mutants displayed a significant reduction or absence of giant cells. This study investigated whether GIR2 can compensate for the loss of GIR1 function in controlling plant cell elongation. Using *gir1* and *gir2* mutant lines, as well as EGFP:GIR2 overexpression constructs, we analyzed plant morphology and enhanced green fluorescent protein (EGFP) expression patterns under controlled conditions. Overexpression of GIR2 in the *gir1* background partially rescued the giant cell phenotype, reducing the number of enlarged cells by nearly half. The fluorescence microscopy has shown that EGFP:GIR2 localization in trichome nuclei, supporting its role in transcriptional regulation aside from HD-zip IV factors. These findings suggest that GIR2 may functionally overlap with GIR1 in the regulation of epidermal cell elongation. Future PCR confirmations of transgene insertion and expression levels will verify transgene integrity and further clarify the relationship between GIR2 expression and the amount of phenotypic rescued we have seen in the plants.

B-17. Volumetric Effects of Early Life Stress and Exercise on Brain Matter in Mice

Whitehouse, Katrina¹, Anna Ferkul¹, Tara McQuillan¹, Julie Christianson¹

¹Department of Cell Biology and Physiology, Neuroscience, University of Kansas Medical Center, Kansas City, Kansas

Early life stress (ELS) is known to have significant and lasting effects on brain matter while exercise is known to have many clinical benefits on stress outcomes. Neonatal maternal separation (NMS) is an ELS rodent model used to investigate these effects. We tested whether sex, NMS, and exercise influence brain volumes in mice. Male and female C57Bl/6 mice were assigned to naïve or NMS rearing followed by access to a wheel in their cage for exercise conditions, or no access to a wheel for sedentary conditions. Magnetic resonance imaging (MRI) of the brain matter was collected and volumetrically analyzed via Voxel-Based Morphometry (VBM). Data were interpreted as an aggregate of significant volume changes ($p < 0.01$, $k > 0 \text{ mm}^3$), and exact locations of significant volume change ($p < 0.01$, $k > 0.06 \text{ mm}^3$). Significant cluster aggregations revealed more extreme results in female mice than in male mice. Both NMS and naïve females showed increases in brain matter for sedentary mice over exercised mice. The most abundant locations of change were observed as left hemispheric increases in white matter for sedentary compared to exercised naïve females. This pattern implies that female brain structure may be especially sensitive to activity level, with sedentary conditions supporting greater white matter volume than exercise conditions. Further work is necessary to determine whether these volumetric changes reflect effects of exercise modalities and/or duration, or are stress related alterations in neurodevelopment, or effects of exercise modalities and/or duration.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-18. The Untold Truths of the Minds of Students' Mental Health and Academic Well-being

Lauren Moore¹ & Dr. Susan Abraham²

¹Department of Biology, School of Arts & Sciences and ²Department of Psychology, School of Education & Behavioral Sciences, Langston University**

The purpose of this study is to examine the relationship between mental health indicators and academic performance among college students. Specifically, this study investigates how depression, stress, and anxiety affect academic well-being among Langston University students, a historically Black university in Oklahoma. Recent studies indicate growing levels of psychological challenges and distress experienced on college campuses which directly impact student retention, persistence, and graduation. Hence, there is a critical need to understand these challenges at historically Black institutions within culturally meaningful context. This study is grounded in the Theory of Self-Determination (Ryan & Deci, 2002) and Bronfenbrenner's Ecological Systems Theory. These developmental frameworks provide a basis for understanding how these psychological indicators influence the college students' academic well-being within a culturally affirming historically Black institution. A survey was administered to a random sample of students enrolled during Fall 2025 at Langston University, to measure depression, anxiety, stress, and academic well-being. Data were collected from 208 students to test the null hypothesis that mental health challenges and academic well-being among students attending a historically Black university are not related. Preliminary correlational analysis revealed significant relationship between mental health indicators of depression, anxiety, stress and students' subjective sense of well-being. Planned analyses include analysis of variance (ANOVA) to examine group differences across varying levels of demographic variables of academic classification and gender. In addition, regression analysis will be conducted to understand the predictability of depression, anxiety and stress on academic well-being among students attending a historically Black university.

B-19. Characterization of AT5G16120: A Putative Monoacylglycerol Lipase

America Zarate^{1,2}, Zolian S. Zoong Lwe^{1,3}, and Ruth Welti^{1,2}

¹Division of Biology, ²Kansas Lipidomics Research Center, ³Department of Biochemistry & Molecular Biophysics, Kansas State University, Manhattan, KS 66506

Lipases are enzymes that hydrolyze lipids. The substrates and products of these enzymes are diverse; the biological functions of lipases are just as varied. They are involved in processes ranging from seed oil composition remodeling to the breakdown of fats in food for nutrient absorption in the intestine. The gene product of AT5G16120 has been annotated as a monoacylglycerol (MAG) lipase (Kim et al., 2017, Plant J., 85, 758). The authors first identified the AT5G16120 protein as likely having MAG-lipase activity because the modeled protein structure is similar to that of a known MAG lipase, and they named the protein AtMAG15. Heterologous expression of AtMAG15 in *E. coli* demonstrated MAG lipase activity for the enzyme. Furthermore, the authors determined, using confocal microscopy, that AT5G16120 localizes to the cytosol in tobacco leaves. Lipid profiles of two independent T-DNA insertion mutants in AT5G16120 indicated that lack of functional AT5G16120 protein results not only in buildup of MAG but also of digalactosylmonoacylglycerol (DGMG), suggesting that DGMG may also be an AtMAG15 substrate. We are currently characterizing the effect of the T-DNA insertions on AT5G16120 mRNA levels in the mutants. We will also create complementation lines in the mutant lines to further validate that the mutations in AT5G16120 are responsible for the lipid phenotypes we observed. Because the gene expression level of AT5G16120 is highly upregulated under osmotic stress, we hypothesize that AT5G16120 is involved in the osmotic-stress response and that the mutants will not adjust to the stress as well as the wild type plants. We also plan to test this hypothesis.

B-20. Comparative Study of Chitosan/Tripolyphosphate and Tanfloc/Tripolyphosphate Microparticles Prepared in a Pluronic-Stabilized Microemulsion

Caitlynn Tate, Kenny Kouadio, Alessandro Francisco Martins

Department of Chemistry, Pittsburg State University

This work reports the preparation of chitosan/tripolyphosphate (CS/TPP) and tanfloc/TPP (TN/TPP) microparticles using a microemulsion system composed of water and sunflower oil stabilized by Pluronic F-127. The morphology of the resulting microparticles was examined by scanning electron microscopy (SEM), and their chemical structures were characterized by Fourier-transform infrared spectroscopy (FTIR). To the best of our knowledge, this is the first time that TN/TPP microparticles have been produced, and their properties were compared with those of the well-established CHT/TPP system. Controlled-release studies using a model drug will be conducted in simulated physiological fluids.

B-21.

Ultrasonic Vocalizations During Social Platform Mediated Active Avoidance in Male and Female Rats

Jasmine Wolf, Penylopi Zabzdyr, Maria Diehl

Department of Psychological Science, Kansas State University, Manhattan, Kansas, USA

Every year, ~18% of Americans experience anxiety, and 3.5% suffer from post-traumatic stress disorder (PTSD) (Kessler et al., 2005). Animal models have advanced understanding of fear and avoidance learning. Our lab utilizes the platform-mediated active avoidance (PMA) task, in which rats learn that a tone-signaled footshock can be avoided by stepping onto a safe platform across 10 days of training (Bravo-Rivera, et al., 2014; Diehl, et al., 2018). We recently modified the task to include a social aspect, in which a rat undergoes PMA in the presence of another rat (Ruble et al., 2025). We recorded ultrasonic vocalizations (USVs) during each training day to determine whether USVs correlate to the learning process of social PMA training, specifically, if USVs are used as social signals to enhance learning or if they are more prevalent during specific behaviors during the task. To achieve this task, we quantified the number of aversive (22kHz) and appetitive (50kHz) USVs that each rat pair emitted during early (Day 1) and late (Day 10) stages of the task. Our preliminary data show that most rat pairs emit more appetitive USVs during early compared to late stages whereas the number of aversive USVs appear to remain the same across training stages. Ongoing analyses will examine whether there are any sex differences in USVs during the PMA task and if USVs are correlated with freezing or avoidance during PMA training. This work will help us better understand how social signals are used to avoid danger.

K-INBRE 2026 Symposium Poster Presentation Abstracts

B-22. Preliminary study focusing on the role of gut microbiota in the development visceral hypersensitivity

Colby Riddle¹, Erin Young², Kyle Baumbauer², Sree Chintapalli³, and Anuradha Ghosh¹

¹Biology Department, Pittsburg State University, Pittsburg, KS;

²Departments of Cell Biology and Physiology, and Anesthesiology, University of Kansas Medical Center, Kansas City, KS;

³Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR

Increased sensitivity to bowel distention, termed visceral hypersensitivity (VH), is a primary driver of chronic abdominal pain. Differences in microbial colonization are associated with disease, but how bacteria drive pain and the potential therapeutic targets remain poorly understood. This study aims to investigate how the gut microbiome evolves temporally when VH is induced in both male and female mice. For this, a group of 5 male and 5 female mice were divided into two treatment groups: zymosan and saline. One subset of the study collected mice fecal samples from baseline, day 7 and 21 post treatment with each of neomycin, rifaxmin, and vancomycin. A total of 90 male and 90 female individual fecal samples were obtained and DNA was extracted. These samples were combined into 6 pools (5 mice with same treatment) for male and female in equal proportion, quantitated using nanodrop, and then used as a template for 16S rRNA gene amplification and will be further processed for Illumina sequencing for 16S metagenomic analysis. Another part of the study treated a mice population with 20mg/kg/day of spermidine. With similar treatment groups as above a total of 100 male and 100 female individual fecal samples were collected from baseline, day 1, 7, 14, and 21 post spermidine administration and will be processed similarly for metagenomics. The ultimate goal of this research project is to systematically assess the impact of altered microbial colonization on the host and examine novel therapeutic approaches to restoration/stabilization of the microbial response.

B-23. Benzimidazolium Salts from Renewable Sources for Antibacterial Applications

Kinsey Baldwin and Jody Neef

Pittsburg State University

Bacterial infections and bacterial contamination of food is a growing concern with the rise of antibiotic resistance bacteria. Several approaches such as antimicrobial peptides, silver nanoparticles, or carbohydrate polymers have shown promise in combating bacteria. Another approach which has received considerable attention is the use of imidazolium salts.¹ Imidazolium salts are known to disrupt the cell wall of the bacteria causing death. Here, we report the synthesis of benzimidazolium salts from epoxidized soybean oil (ESBO) as a potential antibacterial agent. ESBO is made from a renewable resource, in addition to being inexpensive and readily available.³ The synthesis of these materials was a straightforward two-step process. ESBO was reacted with benzimidazole in refluxing IPA overnight. The resulting benzimidazole containing ESBO was then reacted with an alkyl halide (pentyl, octyl, or undecyl). These benzimidazolium containing materials were characterized by IR and H-NMR spectroscopy. Subsequent research with these materials will include antibacterial properties with gram-positive and gram-negative bacteria and use as a plasticizer.

1. M. Hassanpour, S.M. Torabi, D. Afshar, M.H. Kowsari, A.A. Meratan, and N. Nikfarjam, ACS Appl. Bio Mater. 2024, 7, 1558–1568

2. R. Turco, S. Mallardo, D. Zannini, A. Moieni, M. Di Serio, R. Tesser, P. Cerruti, and G. Santagata, Giant, 20, 2024, 100328

B-24. Pumpkin Seed Protein-based Medical Pads for Wound Dressing Applications

Hannah Posterick¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

Email: mparvinzadehgashti@pittstate.edu

Wound closure pads produced from natural materials have seen a growing interest in medical materials. Cotton or polyester are generally used for this purpose. The aim of this project is to integrate quercetin into pumpkin seed protein for developing wound dressing pads with antimicrobial properties and biocompatibility. Jet spray method, a versatile and cost-effective method, was employed to transform pumpkin seed protein as renewable material into sustainable, functional pad that enhances wound healing and supports regional agricultural industries.

Using other potential agricultural sources such as pumpkin seed protein can be particularly valuable in reducing wound healing complications, enhancing tissue regeneration, and aligning with eco-friendly medical practices. It is worth noting that US' abundant agricultural resources provide a robust foundation for developing various innovative biomedical products including operational pads.

For this purpose, we loaded quercetin onto pumpkin seed protein and evaluated the chemical structure of the composite pads through Fourier-transform infrared spectroscopy (FTIR). Additionally, we measured the antimicrobial activity of pads against Staphylococcus aureus, and Escherichia coli. The composite pads demonstrated excellent antimicrobial properties against Staphylococcus aureus. Our work is ongoing to study the cytotoxicity of these pads.

B-25. In-Silico Characterization of EGFR Signaling and Downstream Effectors in Breast Adenocarcinoma

AUTHORS: Sara Akhtar, Christopher Ward

AFFILIATIONS: Pittsburg State University

Background: EGFR and its isoforms play important roles in regulating cell growth and survival, yet their clinical usefulness as cancer biomarkers has been inconsistent. Variability in reported EGFR levels across studies suggests that isoform-specific expression, rather than total abundance, may better distinguish malignant cellular behavior. We performed an in-silico comparison of the MCF7 breast adenocarcinoma cell line and normal breast epithelium, focusing on both EGFR isoforms and key downstream signaling components. **Research Question:** Which downstream pathway proteins show altered expression in MCF7 cells compared to normal breast epithelium, and how do these patterns relate to EGFR signaling activity? **Methods:** Publicly available RNA-Seq datasets were processed using a transcript-level expression pipeline. Raw reads were quality-checked and aligned using HISAT2, followed by transcript reconstruction and isoform quantification with StringTie. Differential expressions were assessed with edgeR. Visualizations and comparative analyses were generated using ggplot2 and ComplexHeatmap. **Results:** MCF7 cells displayed expression shifts in multiple downstream effectors, despite only modest changes in overall EGFR expression. Notably, STAT3 and JUN showed marked upregulation. CDH1 exhibited pronounced downregulation. Isoform-level analysis revealed variation among EGFR transcript variants. **Discussion:** Our findings show that while total EGFR levels may not distinguish malignant from normal breast tissue, isoform-specific expression patterns and downstream pathway dysregulation provide clearer biological signals. The strong activation of MAPK and PI3K/AKT-related genes suggests a shift toward growth-promoting and anti-apoptotic states. These results support the idea that targeting specific EGFR isoforms or downstream signaling nodes may offer improved diagnostic and therapeutic strategies compared to relying on EGFR expression alone.

K-INBRE 2026 Symposium Poster Presentation Abstracts

B-26. Comparing Lysholm Scores: Quadriceps, Hamstring, and Patellar Tendon Autografts in ACL Reconstruction

AUTHORS: Johnson, Riley¹; Barkley, Jayme¹; Rider, Kaylee¹; Henry, Sebastian¹; Sorell, Ryan MD²; Ward, Christopher MD¹
AFFILIATIONS: Pittsburg State University¹, Freeman Medical Center²

Background: Anterior cruciate ligament (ACL) injuries are common among athletes and active individuals. Following ACL reconstruction with an autograft tendon, functional outcomes are often assessed using a Lysholm Score, an inventory of patient function. **Purpose:** This study compares autograft tendons—quadriceps tendon (QT), hamstring tendon (HT), and patellar tendon (PT). This is to determine the relationship between the tendon donor site and average Lysholm scores. **Methods:** A meta-analysis was conducted on studies involving individuals aged 18 and older who underwent ACL reconstruction with HT, QT, or PT. A Logit transformation of semi-quantitative outcomes was applied using generic inverse variance in both common and random effects models. Chi-squared analyses for intergroup and intragroup comparisons was used. Heterogeneity and tau statistics were generated using the common effects model. **Results:** Based on the common effect model, HT scored 90% [88%;92%], QT 92% [91%;93%], and PT 91% [91%;92%]. **Discussion:** These findings suggest there may be a modest benefit to using the quadriceps tendon as a donor site. They all appear to be relatively comparable across at the 24-month follow-up period. This leads to a conclusion that at 2 years, the symptomatic outcomes do not appear to depend heavily on tendon donor site. This suggests that outcomes of other metrics should dictate the surgeon's choice of tendon autograft.

B-27. Molecular and Cellular Regulation of Microglia by Soy-Protein Nanofiber Scaffolds

Eliceo Caniza Velazquez, Kayla Cantu, and Li Yao

Department of Biological Sciences, Wichita State University

Microglia are the primary immune cells of the central nervous system, responsible for regulating inflammation during neurodegeneration and neural injury. Studying microglial mobility and activation in settings that resemble injured neural tissue is made possible by nanofiber scaffolds. Since soy protein isolate (SPI) is biocompatible, naturally degrades, and has been shown to promote cell adhesion and perhaps impact inflammatory signaling, it is a material of interest for nanofibers. Additionally, the SPI was reported to have an immune regulation function, and the function was observed in wound healing studies. In this project, we study the effects of soy-protein isolate (SPI) nanofibers on immunological activation, microglial motility, and proliferation.

Nanofibers were fabricated by SPI, collagen, and polycaprolactone (PCL) using electrospinning. The composition of the nanofiber components was characterized by Fourier Transform Infrared (FTIR). Rat primary microglia were seeded in both aligned and random orientations on nanofiber scaffolds that included SPI, collagen, and PCL. The cells were cultured on the fibrous matrix. The cells were labeled with wheat germ agglutinin (WGA) with Alexa Fluor to study the cell attachment and migration. The cell migration was recorded by time-lapse recording imaging using a fluorescent microscope. The cell migration pattern and velocity are analyzed by ImageJ software. Ongoing studies will concentrate on carrying out assays for proliferation and measuring chemokine expression to assess the inflammatory response. The significance of SPI as an immunoregulatory scaffold for upcoming neuro-injury models is potentially implicated by these studies.

B-28. Fabrication of antimicrobial pads using materials from the nature

Braylon Brown¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

Email: mparvinzadehgashti@pittstate.edu

For the first time, this study will present a novel approach for fabricating naturally available-antimicrobial pads using spray-jet technique. The anti-inflammatory and antimicrobial properties of fabricated pads will be studied. The physicochemical properties of the composite pads will be characterized by Fourier Transform Infrared Spectroscopy (FTIR), and optical microscopy. Antimicrobial efficacy will be evaluated against *Escherichia coli* and *Staphylococcus aureus* using the disk diffusion method. The chemical interactions between various active ingredients will also be confirmed by FTIR spectroscopy. Our cost-effective, biocompatible fabrication method will provide promising prospects for developing functional biomedical pads with sustained drug delivery potential, particularly in wound healing applications.

B-29. Structure-Guided Design of Potent Coronavirus Inhibitors with a 2-Pyrrolidone Scaffold

Zeeshan Azmi¹, Zoie Liska¹, Chamandi S. Dampalla¹, Yunjeong Kim², Alexandria Zabiegala², Dennis J. Howard¹, Harry Nhat Nguyen¹, Trent K. Madden¹, Hayden A. Thurman¹, Anne Cooper³, Lijun Liu³, Kevin P. Battaile⁴, Scott Lovell³, Kyeong-Ok Chang³, and William C. Groutas¹

1 Department of Chemistry and Biochemistry, Wichita State University, Wichita, Kansas 67260, United States

2 Department of Diagnostic Medicine & Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506, United States

3 Protein Structure and X-ray Crystallography Laboratory, The University of Kansas, Lawrence, Kansas 66047, United States

4 NYX, New York Structural Biology Center, Upton, New York 11973, United States

Zoonotic coronaviruses, including SARS-CoV-2 and MERS-CoV, continue to cause substantial morbidity and mortality and are likely to give rise to future outbreaks. Their 3C-like protease (3CLpro) is essential for viral replication and is a validated antiviral target that is conserved across diverse coronaviruses. In this work, we applied a structure-guided design strategy to develop a series of coronavirus 3CLpro inhibitors incorporating an N-substituted 2-pyrrolidone scaffold linked to a Leu-Gln P2-P1 recognition motif. This design was intended to optimize interactions with the S3-S4 subsites and exploit stereochemical and conformational control around the 2-pyrrolidone ring.

The resulting aldehyde and bisulfite adduct inhibitors were evaluated in biochemical assays against SARS-CoV-2 and MERS-CoV 3CLpro, in cytotoxicity assays, and in cell-based antiviral assays. Multiple analogues exhibited nanomolar inhibitory activity against both proteases and potent antiviral effects in infected cells, while maintaining minimal cytotoxicity. High-resolution cocrystal structures of selected inhibitors bound to SARS-CoV-2 and MERS-CoV 3CLpro revealed key interactions within the S1-S4 subsites, clarified the contributions of the N-substituted 2-pyrrolidone scaffold, and confirmed a reversible covalent mechanism involving nucleophilic addition of the catalytic cysteine to the inhibitor warhead.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-30. Development of a Low-Cost Near-Infrared Reflectance System Using the AS7263 Spectral Sensor

Authors: Hannah Grace Rosario¹, Gao Yuanyuan²

¹ Department of Electrical Engineering, Wichita State University ² Department of Biomedical Engineering, Wichita State University

Near-infrared (NIR) reflectance techniques are widely used in both material analysis and biological research due to their sensitivity to absorption and scattering properties. While medical-grade functional near-infrared spectroscopy (fNIRS) systems are expensive and complex, low-cost multispectral sensors such as the AS7263 offer a potential platform for educational and prototype-level investigations. This study evaluates the AS7263 six-channel NIR sensor as a low-cost tool for measuring reflectance from tissue and tissue-like materials in the 610–870 nm range.

A custom measurement setup was developed to examine how sensor-to-sample distance, ambient conditions, and surface properties influence spectral readings. The sensor was tested on fingertip tissue and on controlled materials with known reflectance characteristics to compare biological and non-biological optical responses. Results show that decreasing the source–detector distance leads to increased reflectance intensity, consistent with expected reductions in scattering losses. When placed against the fingertip, the sensor detected higher diffuse reflectance compared to open-air measurements, demonstrating its sensitivity to biological tissue optical behavior.

Although the AS7263 cannot quantify hemoglobin species or provide clinical fNIRS data, it reliably captures relative changes in NIR reflectance, supporting its suitability for low-cost optical studies, prototype instrumentation, and engineering education. Ongoing work includes optimizing a custom PCB with improved optical isolation and validating the system against standard NIR measurement equipment.

B-31. Development of dioxolenium ion crosslinking chemistry for molecules based on 2-bromo-3-hydroxypropionic acid

Vanessa Carey, Parisa Jahangiri, Coleen Pugh

Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS 67260-0004

Aromatic polymers are useful for biomaterials applications that require high mechanical strength. However, they have the drawbacks of difficult material processing and manufacturing. An option to mitigate these issues is to use a thermal crosslinker with aromatic polymers to strengthen and stabilize while avoiding byproducts. To investigate the mechanism of such a crosslinker, we studied the rearrangement of the model compound, methyl-3-acetoxy-2-bromopropionate (Acetoxy-BrH), via a dioxolenium ion and its subsequent reaction with anisole through electrophilic aromatic substitution. Nuclear magnetic resonance (NMR) spectroscopy was used to confirm the substitution. Additionally, we synthesized the proposed crosslinker, 1,6-hexanediol-bis(2-bromo-3-acetoxypropanoate) (Acetoxy-BrH-dimer), and performed thin-layer chromatography (TLC) to determine the optimal solvent system for column chromatography, which will be used to purify the crosslinker.

B-32. Enhancing Anthrax Vaccine Efficacy: Protective Antigen–PP65 Conjugation Using SpyCatcher/SpyTag

Abby Bui & James G. Bann

Wichita State University Biochemistry and Chemistry Department

Vaccines remain the most effective defense against infectious diseases, yet development remains challenging for pathogens such as malaria, tuberculosis, and HIV. Strengthening antigen-specific T-cell responses represents one strategy to improve vaccine performance. Protective antigen (PA), a component of the *Bacillus anthracis* toxin, naturally binds dendritic cells with high affinity through its receptor CMG2 and has been shown to inhibit cytokine release and T-cell activation as part of its pathogenic mechanism. Since PA is efficiently internalized by dendritic cells, conjugating an antigen to PA may enhance antigen uptake and allow processing through both CD4 and CD8 pathways.

Previous work using a PA-Spy0469 conjugate supported this concept but exhibited stability concerns and reduced CMG2 affinity. PP65, an immunodominant cytomegalovirus antigen that elicits strong human memory T-cell responses, provides a promising alternative antigen for conjugation. Our objective is to develop a stable PA-PP65 conjugate using the SpyCatcher/SpyTag system, which forms a spontaneous covalent bond and minimizes structural disruption. We have generated purified PA and SpyCatcher fragments through PCR and protein purification and will covalently link PP65 following plasmid transformation. Future evaluation will determine whether PA-PP65 maintains key PA attributes, including CMG2 binding and pore-forming capability, while enabling efficient antigen presentation. If successful, this platform could enhance CD8-biased immune responses and contribute to vaccine strategies against intracellular pathogens.

B-33. Redox Roots: Real-Time Tracking of Microbial Glutathione Production Under a Cysteine Gradient

Elijah Clark, Brooke Vogt, Sonny Lee

Kansas State University, Kansas State University Biology Department,
Langston University, K-INBRE, National Science Foundation

Glutathione (GSH) is a tripeptide antioxidant made up of glutamine, cysteine, and glycine. GSH is essential for maintaining redox balance throughout and detoxifying reactive oxygen species (ROS) in both plants and microbes, reducing the stress levels within the cells. In bacteria, GSH is synthesized through two ATP-dependent enzymes: glutamate–cysteine ligase (GCL) and glutathione synthetase (GS), with cysteine serving as the rate-limiting precursor. With a complete GSH biosynthesis pathway, this experiment monitors GSH production in a consortium of drought-adapted rhizosphere bacteria. To investigate the impact of extracellular cysteine levels on microbial glutathione (GSH) production, the consortium will be grown under varying cysteine concentrations (0, 10, 100, 500, and 1000 μM) to determine if there is a correlation between GSH output and cysteine concentration. The OD will be retrieved on an hourly basis over a 24-hour duration. GSH concentrations will be analyzed carefully using a colorimetric GSH assay comparing the zero and 24-hour timepoints. This experiment aims to investigate how microbial antioxidant production responds to changes in cysteine availability, with particular relevance to plant-microbe interactions in arid environments. By monitoring microbially produced glutathione (GSH) in real-time, our research provides valuable insights into how rhizosphere microbes may enhance plant stress resilience by regulating redox processes and mitigating reactive oxygen species (ROS).

B-34. Examining Blood-Brain Barrier Permeability in a 3D Tissue-Engineered Micro vessel

Cassidy Huynh, Ninghao Zhu, Department of Electrical and Computer Engineering, Kansas State University

The blood-brain barrier (BBB) is composed of brain microvascular endothelial cells (BMECs) and numerous other supporting cells. These cells are tightly connected by tight junctions, which help regulate the transport of nutrients between blood and the brain. The main purpose of the BBB is to maintain an internal environment that is stable. This ensures protection of the neural tissue from harmful substances in the bloodstream. The BBB plays a key role in the progression of neurodegenerative diseases. Due to this, we want to find the permeability of the BBB using in vitro 3D tissue engineered micro vessels. We introduced fluorescent dye to the micro vessel, and the transport of the dye into the surrounding extracellular matrix (ECM) was measured over time to observe the permeability of the micro vessel. This approach will help provide a relevant model of the BBB and may support future studies on neurodegenerative disease mechanisms and drug deliveries.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-35. Gene-Metal-Microbe Interactions: The Effect of Genetic and Microbial Variation on Heavy Metal Response in *Drosophila*

Maggie Ridgway, Stuart J. Macdonald
University of Kansas, Lawrence
Department of Molecular Biosciences

Heavy metals such as iron, copper, and zinc are essential for many biological processes in humans. However, elevated levels of these metals, or the presence of non-essential metals (e.g. lead), can cause severe toxicity. As metal levels in the environment increase, it is critical that we understand the genetic mechanisms that maintain metal homeostasis in humans and other organisms. Absorption and metabolism of heavy metals occur in the intestines, where the gut microbiome plays a critical regulatory role. Heavy metals can disrupt microbial communities and induce dysbiosis, while the microbiome can influence metal uptake by forming physical barriers, sequestering metals, and detoxifying them. To investigate these interactions, I am using *Drosophila melanogaster*, a genetically tractable model that shares conserved metal-response pathways with vertebrates. My project focuses on Metallothionein C (MtnC), a metal-binding protein upregulated during metal exposure. Using a Gal4-UAS system, I am knocking down MtnC expression specifically in the gut using two independent transgenic strains, and assessing organismal survival across four metals. These assays will be conducted under both conventional and microbe-free conditions to evaluate whether the microbiome influences heavy metal resistance. Current progress includes establishing Gal4-UAS crosses, determining metal concentrations for survival assays, optimizing egg collection, developing an axenic fly protocol, conducting preliminary axenic trials, and verifying sterility using LB plating and 16S PCR. Overall, this work aims to clarify how host genetics and the microbiome jointly regulate metal homeostasis and toxicity.

B-36. Characterizing Genomic Alterations Associated with DCIS Progression

Ava Gartelos¹, Yan Hong¹, Carol Fabian², Andrew K. Godwin², Fariba Behbod², Ayantika Sen Gupta³, Jennifer Gerton³.

¹Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, Kansas City, KS 66160, ²Department of Medical Oncology, The University of Kansas Medical Center, Kansas City, KS, 66160, ³Stowers Institute for Medical Research, Kansas City, Missouri, 64110

Ductal Carcinoma in Situ (DCIS) is the most common form of non-invasive breast cancer, yet less than 50% of untreated cases will progress to invasive ductal carcinoma (IDC), leading many patients to undergo unnecessary aggressive treatment. Chromosomal and centromeric instability are hallmarks of breast cancer. Identifying aneuploidies that predict DCIS progression could help reduce overtreatment and promote more patient-centered clinical decision making. To study human breast cancer progression, the Behbod Laboratory developed the Mouse-INtraDuctal (MIND) model. This involves the intraductal injection of patient-derived DCIS cells into the mammary ducts of immunocompromised mice, where they display a course similar to the evolution of human breast cancer. Mammary glands were collected as Formalin-Fixed, Paraffin-Embedded (FFPE) samples. Fluorescence in-situ hybridization (FISH) was performed using probes that target specific centromeres on paired patient and MIND-progressed DCIS samples. Semi-automated image segmentation using ImageJ quantified the number and sizes of centromere signals within each nucleus. In the patient DCIS sample, centromere 7 foci ranged from 1–5 per nucleus, with a modal number of 2 foci per nucleus, indicating largely diploid cells with minimal aneuploidy. In the MIND-progressed sample, ~30% of cells lacked detectable chromosome 7 signals, and the modal population exhibited 1, indicating the loss of chromosome 7. Some cells also displayed large-scale triploidy of chromosome 7. We have optimized FISH methodologies to detect centromere number and size in paired patient and MIND samples. Ongoing work aims to expand the panel of FISH probes and samples to detect common chromosome instability signatures.

B-37. Potential interactions of SIRT1, tirzepatide, and KRAS mutation in colorectal cancer

Magstadt, Alexa,¹ Anindita Mahanty,² Cara Wallingford,² Revan Hammontree,² Jennifer S. Davis^{2,3}

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS, ²Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, ³University of Kansas Cancer Center, Kansas City, KS

In the United States, colorectal cancer (CRC) is the third-most diagnosed and second-most lethal cancer among men and women combined. In 2019, 20% of CRC diagnoses were in patients under age 55. As this is double the percentage in 1995, there is a clear need to understand the lifestyle and environmental factors contributing to the rising incidence of early-onset CRC. A recent study by Wei et al. (2023) implicated the NAD⁺-dependent deacetylase Sirtuin 1 (SIRT1) as a promoter of CRC metabolic flexibility. In the presence of glucose deprivation or oxidative stress, SIRT1 upregulation enabled HCT116 and DLD-1 CRC cell lines to switch from glycolysis to fatty-acid oxidation. Interestingly, incretin mimetics exert many of their effects through upregulation of SIRT1 expression and activity. The use of these agents for weight loss and glucose control has risen dramatically, with 1 in 8 Americans reporting usage. However, the impact of incretin mimetics on CRC development and progression is currently unclear. The first aim of this work is to establish how various nutrient availability conditions, including high- and low-glucose and adipose conditioned medium, impact CRC cell viability, measured by MTT assay, and SIRT1 activity, measured by fluorometric assay. The second aim is to assess how treatment with incretin mimetic tirzepatide, a dual GIP/GLP-1 agonist, impacts cellular phenotype, SIRT1 expression and activity, and metabolic flexibility. Differences in these results based on KRAS status, a commonly mutated GTPase in CRC, will also be explored. Together, these studies may provide mechanistic insight into how incretin mimetics influence CRC progression across metabolic contexts.

B-38. Comparison of bacterial and human phosphoglycerate dehydrogenase

Ella P. Ruliffson and Kim T. Simons

School of Science and Mathematics, Emporia State University, Emporia, KS, USA

In the first step of the production of L-serine, phosphoglycerate dehydrogenase (PHGDH) catalyzes the conversion of 3-phosphoglycerate (3PG) into 3-phosphopyruvate (PHP). PHP is then transaminated and dephosphorylated in the following steps to produce L-serine. The PHGDH gene is often overexpressed in tumor cells. *E. coli* PHGDH catalyzes the oxidation of other substrates and is feedback inhibited by L-serine, while *H. sapiens* PHGDH is specific to 3PG and is not feedback-regulated by L-serine. To better understand the enzyme specificity and regulation of both species, the structure of *E. coli* and *H. sapiens* active sites were analyzed, with several amino acid differences within 10 angstroms of the active site noted. Site-directed mutagenesis was used to change several of the *E. coli* PHGDH positions into *H. sapiens* sequence. The wild-type and mutant enzymes were purified, and enzyme activities were monitored using the cofactor NADH. To date, the substrates α -ketoglutarate (α KG) and oxaloacetate (OAA) have been used as substitutes for 3PG. Preliminary results indicate decreased enzymatic activity in mutants as compared to the wild-type *E. coli* PHGDH, indicating decreased specificity for substrates α KG and OAA. Continued mutagenesis is being used to identify critical positions in the sequence that confer specificity.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

B-39. Investigation of Intrinsically Disordered Regions in the Drosophila Matrisome

Md Wasi Ul Kabir³, Tessa Nolen², Nazanin Kasirosafar^{1*}, Md Tamjidul Hoque³, and Rajprasad Loganathan^{1,2}

- 1) Department of Biological Sciences, Wichita State University
- 2) Department of Biomedical Engineering, Wichita State University
- 3) Department of Computer Science, University of New Orleans

*Co-presenting Authors

Organ formation is associated with large-scale motion dynamics within the embryo. The protein network that supports cells—Extracellular Matrix (ECM)—has been studied as a passive substrate that functions exclusively to support cell motion and tissue organization. To form tissues and organs, however, embryos need to transport the ECM along with cells as a tissue composite. Although some studies have shown motile ECM in the context of embryogenesis, the material properties that confer ECM with these dynamic roles are poorly understood. We test the hypothesis that certain components of the embryonic ECM have fluid-like material properties and may show the potential to form biocondensates consequent to their structural properties. As a starting point for testing our hypothesis, we systematically screened the Drosophila matrisome using a computational framework to rank proteins containing intrinsically disordered regions (IDRs). Our computational screening identified at least 30 Drosophila matrisome components with high-confidence IDRs, some of which show robust embryonic expression. Ongoing studies examine the biological roles of Fondue, one of these ECM components that exhibit robust IDRs.

B-40. Unoccupied

C-1. Regulation of *cdeAB-oprM* efflux pump in *Chromobacterium subtsugae* in response to antibiotics and quorum sensing

Leah I. Legleiter¹, Eryk Yarkosky¹, Josephine R. Chandler¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

Chromobacterium subtsugae is a nonpathogenic soil bacterium that relies on both antibiotic production and antibiotic resistance to compete with other microbes in its environment. One mechanism of resistance is the CdeAB-OprM efflux pump involved in extruding a variety of antibiotics from the cell. Prior studies showed that the *cdeAB-oprM* genes are activated by a population density-dependent quorum-sensing system and repressed by an antibiotic-responsive transcription repressor, CdeR. In this study, we sought to elucidate how the *cdeAB-oprM* genes are coordinately regulated by quorum sensing and CdeR. Our results suggest the quorum-sensing system does not directly interact with the upstream promoter of these genes (the *cdeA* promoter) and is likely through another regulator. However, our results are consistent with the idea that CdeR directly represses *cdeA* transcription. We observed CdeR-dependent repression of transcription from the *cdeA* promoter in a heterologous host, and we were able to abolish repression by altering a putative CdeR binding site in the promoter. These results clarify how *C. subtsugae* regulates antibiotic resistance through the CdeAB-OprM efflux pump, providing new insight into how bacteria integrate environmental cues to optimize competitive strategies.

C-2. A CURE for learning metagenomics

Matthias, Emily*, Alexa McGann* and Stephen Fields

Department of Biological Sciences, Emporia State University, Emporia, KS

Course-based Undergraduate Research Experiences (CUREs) are concentrated forms of active learning that reduce student failure rates and enhance student performance when compared to more traditional classroom settings. Undergraduates that have participated in CUREs are more likely to remain in their chosen STEM fields and/or complete post-baccalaureate programs. We utilized the CURE format to teach a metagenomics methods course to eight undergraduates at Emporia State University during the Spring 2025 semester. The first several weeks of the course involved lectures on DNA sequencing and metagenomic analyses, along with an introductory project that contrasted soil microbiomes from cultivated and undisturbed plots. During this initial period, students learned how to isolate DNA, perform 16S rDNA PCR, prepare libraries, and sequence DNA with the Oxford Nanopore Minion sequencer. Finally, students were introduced to the online Galaxy platform for analysis of their sequence data. After completing the analysis, student groups were asked to develop a mini-metagenomics research project that could be completed by the end of the semester. Details of the projects will be presented in the body of the poster along with strategies for tracking student success beyond graduation.

*These authors contributed equally to the poster

C-3. Imidazolium Salts from Renewable Sources for Antibacterial Applications

Halle Finnerty and Jody Neef

Pittsburg State University

Bacterial infections and bacterial contamination of food is a growing concern with the rise of antibiotic resistance bacteria. Several approaches such as antimicrobial peptides, silver nanoparticles, or carbohydrate polymers have shown promise in combating bacteria. Another approach which has received considerable attention is the use of imidazolium salts.¹ Imidazolium salts are known to disrupt the cell wall of the bacteria causing death. Here, we report the incorporation of imidazolium salts into epoxidized soybean oil (ESBO). ESBO is made from a renewable resource, in addition to being inexpensive and readily available.²

The synthesis of these materials was a straightforward two-step process. ESBO was reacted with imidazole in refluxing IPA overnight. The resulting imidazole containing ESBO was then reacted with an alkyl halide (pentyl, octyl, or undecyl). These benzimidazolium containing materials were characterized by IR and H-NMR spectroscopy. Subsequent research with these materials will include antibacterial properties with gram-positive and gram-negative bacteria and use as a plasticizer.

1. M. Hassanpour, S.M. Torabi, D. Afshar, M.H. Kowsari, A.A. Meratan, and N. Nikfarjam, ACS Appl. Bio Mater. 2024, 7, 1558–1568

2. R. Turco, S. Mallardo, D. Zannini, A. Moeini, M. Di Serio, R. Tesser, P. Cerruti, and G. Santagata, Giant, 20, 2024, 100328

K-INBRE 2026 Symposium Poster Presentation Abstracts

C-4. Watermelon Seed Oil based Coatings for Hospital Bedsheets

Savannah Grotheer¹, Mazeyar Parvinzadeh Gashti^{1,2*}, Irene Zegar¹, Chris Ward³

1- Department of Chemistry, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

2- National Institute for Materials Advancement, Pittsburg State University, Pittsburg, KS, 66762, USA

3- Department of Biology, Pittsburg State University, 1701 South Broadway Street, Pittsburg, KS, 66762, USA

Email: mparvinzadehgashti@pittstate.edu

The Global Water Repellent for Textile Market was valued at USD 736.1 Million in 2023 and is anticipated to reach USD 1153.4 Million by 2030. Current liquid repellent products in the healthcare textiles are largely based on toxic chemicals called per- and polyfluoroalkyl substances (PFAS), often referred to as "forever chemicals" due to their persistence in the environment and potential for serious health concerns. Plant oil derivatives have garnered attention as sustainable and eco-friendly alternatives for various biobased chemical processes, particularly in imparting biobased foam products.

This project will validate embedding watermelon seed oil for application on medical bedsheets as a safe water repellent. Also, initial studies showed that watermelon seed oil has a good water repellent property on textiles due to existence of fatty acid in oil.

Our group applied chemical crosslinkers on medical sheets followed by watermelon seed treatment. The water contact angle of samples will be reported as tests are currently ongoing. We will also perform the chemical properties of textiles by FT-IR analytical tool.

C-5. Clusterin (CLU) as a Modulator of Neuronal Excitatory/Inhibitory Balance

Vanessa Nguyen¹, Punam Rawal², Liqin Zhao^{2,3}

¹Molecular Biosciences Program, Department of Undergraduate Biology

²Department of Pharmacology and Toxicology, School of Pharmacy,

³Neuroscience Graduate Program, University of Kansas, Lawrence, KS 66045, USA

Clusterin (CLU), also known as apolipoprotein J, is the third major genetic risk factor for Alzheimer's disease (AD). While CLU is well-characterized for its role in modulating amyloid- β (A β) aggregation, clearance, and transport—key processes in plaque formation and neuroinflammation—emerging evidence highlights broader neuroprotective functions. We investigate the impact of CLU deficiency on neuronal integrity and excitatory/inhibitory (E/I) synaptic balance in the adult mouse brain. Using 15-month-old wild-type (WT), CLU knockout (CLU^{-/-}) mice, employing immunohistochemistry, Western blotting, and single-nucleus RNA sequencing (snRNA-seq) to examine structural and transcriptional changes. Immunostaining for MAP2 revealed significant neuronal disorganization and reduced neuronal density in CLU^{-/-} mice. Additionally, expression levels of synaptic markers VGAT (inhibitory), VGLUT1 (excitatory) showed alterations, indicating disrupted E/I balance. These findings were validated by Western blot analysis. snRNA-seq profiling of cortical tissue from male CLU^{-/-} mice further revealed transcriptional signatures indicating hypo-excitability, including a significantly decreased ratio of the percentage of excitatory versus inhibitory neurons in the total cell counts. These data suggest CLU plays a critical role in maintaining neuronal homeostasis and network stability. Ongoing studies using Acridine orange assays aim to functionally quantify synaptic activity, bridging structural and molecular changes with physiological outcomes. Collectively, our findings demonstrate that CLU loss can lead to changes in neuronal structure and composition, contributing to synaptic and cognitive deficits. This study expands the understanding of CLU's role in AD pathogenesis beyond A β handling, pointing to its importance in synaptic integrity and identifying potential therapeutic targets for neurodegeneration intervention.

C-6. The impact of functional electrical signal on cellular process of neural cells

Amelie Zidarita, Li Yao

Department of Biological Sciences, Wichita State University

In a developing nervous system, endogenous electric signals affect embryonic growth. Electrical activity has been recognized as a guidance cue that regulates the axonal pathfinding. It was reported that the axonal growth of cultured neurons can be guided by electric fields. In a cornea wound healing model, endogenous electric field was detected in the wound and it can guide the nerve extension direction toward the tissue closure. Numerous studies have been performed to investigate the effect of electric stimulation on cell migration including neural cells. We recently reported that the migration of cultured primary glial cells and, neural stem cells can be guided by an applied direct current EF. However, few studies reported the impact of electrical stimulation on cell proliferation and cell damage. In this study, we applied electric fields stimulation to the cultured PC12 cells. The cell migration was recorded with time-lapse microscopy. We quantified the cell migration directedness and migration velocity under the stimulation of different electric field strengths. The outcomes showed that the electrical stimulation can guide the cell migration direction. Flowcytometry assay was performed to investigate how electrical stimulation can affect the cell cycle change and cell apoptosis. We observed that the stimulation did not affect cell cycle compared with the control cells on different cell cycle phases. Our work also explored the influence of the field stimulation on cell apoptosis process. The study implicates that the potential application of the electric fields in neural repair without significant damage on neural cells viability.

C-7. Advancing Genetic Engineering in Three Plant Lineages: *Mimulus*, *Antirrhinum*, and *Penstemon*

Krentzel, Jim T. and Lena C. Hileman

Department of Ecology and Evolutionary Biology, University of Kansas

The ability to engineer plant genomes can expand our understanding of the biochemical and developmental mechanisms contributing to flower morphology, pigmentation, and nectar reward. Yet, many plant systems still lack efficient tools for genetic manipulation, limiting our ability to test gene function. In the Hileman Lab, we study the genetics of floral trait development in *Mimulus*, *Antirrhinum*, and *Penstemon*, three closely related genera of flowering plants. Our goal is to adopt genetic modification tools that will allow us to dissect the contribution of specific genes to floral trait development. To accomplish this, we utilize *Agrobacterium*-mediated stable transformation techniques along with monomeric Enhanced Green Fluorescent Protein (mEGFP) as an easily observable marker for successful gene transfer. We employ a recently developed *Agrobacterium* strain carrying a helper plasmid that dampens the plant immune response, increasing transformation efficiency (GoldBio). We use mEGFP, which is derived from EGFP by an A206K substitution that prevents dimerization while preserving fluorescence, facilitating rapid identification of transformed tissues. In *Mimulus*, we are testing direct *Agrobacterium* delivery to ovules by injection to generate transgenic seeds, with initial success. In *Antirrhinum* and *Penstemon*, we are testing a tissue culture-based stable transformation protocol. In *Antirrhinum*, we have successfully regenerated whole plants from tissue culture. These ongoing efforts will establish reliable transformation platforms across *Mimulus*, *Antirrhinum*, and *Penstemon*. This will expand molecular tools in established model systems like *Mimulus* and *Antirrhinum*, and enable functional genetic analyses in *Penstemon*, supporting functional dissection of the genetic basis of floral trait development.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-8. Understanding Genomic Adaptation to High-Altitude Environments in the North American Deer Mouse (*Peromyscus maniculatus*)

Larissa Rockenbach¹ and Dr. Allie Graham^{1,2} University of Kansas¹, KU Center for Genomics²

High-altitude environments impose many physiological challenges, including reduced oxygen availability, aridity, and increased UV exposure. Understanding how mammals adapt to these conditions is central to evolutionary biology and offers greater insight into the genetic basis of survival in extreme habitats. The North American deer mouse (*Peromyscus maniculatus*) is a widespread and ecologically adaptive species and offers a powerful model for investigating genomic adaptation across altitudinal gradients. Earlier studies of high-altitude adaptation in mammals have emphasized changes in hemoglobin function and ventilatory control. However, the broader genomic architecture underlying these adaptations are still incompletely characterized. The general question addressed in this study is whether *P. maniculatus* populations living at high elevation show consistent signatures of selection in genes associated with hypoxia tolerance. In this project, I examined whole-genome sequencing data from 50 individuals from two populations - low (122 m) and high altitude (1585 m). Using the genetic variation from this data, I have performed outlier analyses to find whether there are specific variants in genes that are statistically associated with high-altitude; thus, suggesting they are important in adaptation to this harsh environment. Identifying variation will provide a foundation for understanding how selective pressures act on multiple physiological systems in response to high-altitude stressors. More broadly, this study will highlight the deer mouse as a model for looking at the genetic basis of environmental adaptation. By focusing on candidate genes linked to hypoxia tolerance, the project contributes to a wider perspective on how selective pressures shape genomic diversity and resilience across taxa.

C-9. Exploring the relationships between feeding behavior and personality traits in the Ornate Box Turtle (*Terrapene ornata*)

Powell, Brookelynn, Peyton Samek, Caroline LeJuerne, Jadyn Falley, Grace Peterson, Bella Limback, Sage Dennis, August Wilson, Ash Van Dalsem, Erin Carter, Serena Schmitz, Kyra Jantzen, and Benjamin Reed.
Department of Biology, Washburn University, Topeka, Kansas, USA.

Understanding the behavior of wildlife is essential for identifying individual needs, patterns of energy use, and factors that influence fitness and long-term population trends. For many species, especially ectotherms, behavioral tendencies and their links to body condition remain poorly understood. The goal of this research was to examine how individual tendencies (personality traits) of Ornate Box Turtles (*Terrapene ornata*) influence feeding behavior during a controlled food-supplementation study. Over a 10-week study period, we established a new study population of 48 turtles and assigned individuals to one of four supplemental treatments: unfed, supplemental protein, supplemental sugar, and supplemental protein and sugar. We also conducted personality assays during the first two weeks of the study and subsequently offered turtles food twice weekly for six weeks, recording whether each individual ate during the trial period as well as pre and post-feeding body mass. We also handled and weighed unfed turtles to serve as control for disturbance and condition-related change. Using these data determined whether body condition covaries with behavioral traits, whether personality influences the likelihood of a turtle eating during feeding trials, and how these factors might mediate energy investment in daily or seasonal activities. This study contributes to a broader understanding of how individual behavioral variation shapes ecological patterns and energy allocation in a historically understudied species. Our research may also guide future work examining why certain individuals have greater foraging success or energy reserves than others, potentially relating to differences in movement patterns, reproductive effort, or overall health.

C-10. Effects of neuromodulating drugs on *C. Elegans* Longevity

Ameerah Alfaiakawi¹, Shelby Innes¹, Shijiao Haung¹

¹Department of Biochemistry and Molecular Biophysics, Kansas State University

Neurodegenerative diseases are closely linked to aging, yet therapeutic strategies remain limited. The overall goal of this research will be to identify common mechanisms between aging and neurodegenerative diseases. Neuromodulatory pathways regulate conserved stress and metabolic responses, we tested whether clinically used neuromodulators influence longevity in *Caenorhabditis elegans*. *C. elegans* are small nematode roundworms with simple biology, short lifespans, and easily modifiable genomes. These characteristics make them an ideal model organism for studying aging and neural pathways. We found that serotonin and dopamine antagonists both showed extensions in lifespan and healthspan in the *C. elegans*. Current work is now focused on determining possible mechanisms for the lifespan and healthspan benefits. We are currently investigating the role of fatty acid metabolism and transport genes through RNAi knockdown experiments. Together, these studies provide insight into how neuromodulatory signaling intersects with conserved pathways to influence aging and healthspan in *C. elegans*. Future experiments could look into how the drugs affect brood sizes and behavioral crawling artifacts.

C-11. Dual Function Inhibitors of Coronavirus 3CL Proteases and Cathepsin L

Zoie P. Liska¹, Harry Nhat Nguyen¹, Pulini S. Ranasinghe¹, I. Kankanamge Ravindu S. Ilesinghe¹, Chamandi S. Dampalla¹, Athri D. Rathnayake¹, Abdul-Rahman M. Jesri¹, Zeeshan Azmi¹, Dustin E. Nenoven¹, Yunjeong Kim², Kevin P. Battaile³, Hayden A. Thurman¹, Egor Gusachenko¹, Scott Lovell⁴, Kyeong-Ok Chang², William C. Groutas¹. ¹Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS. ²Department of Diagnostic Medicine & Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS. ³NYX, New York Structural Biology Center, Upton, NY. ⁴Protein Structure Laboratory, The University of Kansas, Lawrence, KS.

Periodic transmissions of β -coronaviruses (SARS-CoV, MERS-CoV, and SARS-CoV-2) from animals to humans underscore the need to devise rapid response strategies to minimize the harmful impacts on global health. These novel human β -coronaviruses with high virulence belong to the Merbecovirus and Sarbecovirus subgenera, and members of these groups are considered to have a high zoonotic potential. The cysteine protease active site topographies of β -coronaviruses are largely conserved and are not found in human proteases. However, a broad-spectrum antiviral treatment remains elusive, and numerous β -coronaviruses lack established therapeutics. Further, SARS-CoV-2 can enter host cells via two pathways: the cell surface pathway and the endosomal pathway. Following clathrin-mediated endocytosis of viral particles via the endosomal pathway, host Cathepsin L (CatL) cleaves the viral Spike-protein (S-protein) enhancing virion release into the cell. Certain SARS-CoV-2 variants have been shown to prefer the endosomal pathway due to S-protein mutations, which has led CatL to become an attractive target for viral inhibition. Our research aims to use a structure-guided approach to design a dual-function antiviral therapeutic and prophylactic for β -coronaviruses that acts by inhibiting both CatL, as well as the 3CL protease, an enzyme essential for coronavirus replication.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-12. Gene repression by a quorum-sensing transcription factor that normally functions as an activator.

Kristina Sim, Eryk Yarkosky, Josephine Chandler.

Department of Molecular Biosciences, University of Kansas

Quorum sensing is a type of cell-cell communication used by many bacteria to regulate changes in gene transcription when they reach a critical population density or “quorum.” Quorum sensing relies on diffusible small molecules that accumulate with increasing cell density. These molecules are produced by a signal synthase enzyme and detected by a cytoplasmic transcription regulator, which is a DNA-binding protein. Signal binding causes the regulator to change conformation and bind DNA upstream of the target promoter, thereby activating its gene expression. Some of these signal-binding transcription activators can become repressors when their DNA recognition site is synthetically moved to a different position; however, few studies have examined the potential for these activators to function as repressors in their native host. In a prior study of the quorum-sensing regulon of *Chromobacterium substugae*, we identified genes that were strongly repressed by adding quorum-sensing signals, suggesting there may be transcription repression by the quorum sensing transcription factor. In this study, we evaluate four of these repressed genes using fluorescent reporters and a CviR-expressing heterologous host. The results provide new information regarding the timing and level of gene repression in response to quorum-sensing signals. These findings will provide new insights into bacterial gene regulation and how bacteria use quorum sensing to elicit complex transcriptional changes.

C-13. The study of activated astrocyte migration on nanofibers for neural regeneration

Lucas Seitz, Kayla Cantu, Li Yao

Department of Biological Sciences, Wichita State University

After neural tissue injury, astrocytes are activated from a quiescent state and migrate to the lesion where they have multiple functions in neural repair. The cell migration is a crucial process in neural regeneration. The reactive astrocytes proliferate to form a glial scar, and the ECM secreted by astrocytes generates fibrous scar tissue. This scar tissue fills the lesion and produces a dense barrier around the cavity, thereby inhibiting axonal growth. The cytokines and chemokines produced by astrocytes activate and recruit immune cells that help clean the damaged tissue. Nanofibers have been broadly investigated for tissue regeneration as the fibrous structure mimics the tissue extracellular matrix. The oriented migration of activated astrocytes on nanofibers may promote neural repair. However, the cellular reaction to the fibrous structure has not been reported yet. In this study, we fabricated nanofiber matrices that are formed by collagen (CO) and polycaprolactone (PCL) or hyaluronan (HA) and PCL. The fibers were generated by electrospinning. The fiber components were characterized by Fourier-Transform Infrared (FTIR), and wettability test. Human adult astrocytes were activated by IL1 α and TNF α . The activated and non-activated astrocytes were cultured on the nanofiber matrices and labeled with Wheat Germ Agglutinin (WGA). Time-lapse recording was performed to record the cell migration on the CO/PCL and HA/PCL fibers. The cell migration velocity and distance were quantified. The cells showed oriented migration on aligned fibers. The study demonstrated the potential of nanofiber for the application in neural regeneration.

C-14. Leisure Interests and Barriers Among Adults with Intellectual and Developmental Disabilities

Kaitlyn Draper, Laura Covert Miller, Evelyn Smith, Kaeli Lynnes, Kinleigh Hall

Department of Health, Human Performance, and Recreation, Pittsburg State University, Pittsburg KS

People with intellectual and developmental disabilities (IDD) often face functional challenges which can put them at a higher risk for chronic health issues and early physical decline. This population can experience barriers to leisure participation, including limited transportation, lack of inclusive programs, and reduced support. Research indicates that participating in meaningful leisure activities, such as physical exercise, creative programs, or social groups, can improve overall wellbeing by boosting fitness levels, reducing stress, and building social connections. These findings highlight the importance of continuing to better understand leisure interests and barriers in the IDD population. Adults with IDD from local day services were recruited to participate in this study. This research project was approved by Pittsburg State University's Institutional Review Board. Informed consent and assent forms were required to participate. Eligible participants were to be over the age of 18 and be able to communicate verbally or nonverbally with researchers. Leisure interests and barriers were gathered using the Leisure Assessment Inventory, a tool designed to identify preferred activities and factors that limit participation. Scores were collected on general leisure interests, levels of participation, and barriers limiting participation in activities. Data collection is currently in progress. Based on previous research it is predicted that participants' leisure participation will be influenced by the amount and type of barriers the participants experience. Individuals that report higher levels of environmental, social, or personal barriers are expected to show lower levels of engagement in meaningful leisure activities compared to those with lower identified barriers.

C-15. Using molecular evolutionary analysis to detect novel function in a floral pigment pathway gene

Mays, Liz S., Haylee Coffman and Lena C. Hileman

Department of Ecology and Evolutionary Biology, University of Kansas

The flowering plant genus, *Penstemon*, displays an amazing diversity in flower color and form. Most striking are multiple evolutionary shifts from blue to red flowers associated with transitions from bee to hummingbird pollination, respectively. Anthocyanins are a class of pigment molecules responsible for variation in flower color, including the blue-red color differences seen in *Penstemon*. A key gene in the anthocyanin pathway is *Flavonoid 3',5'-hydroxylase* (*F3'5'H*), which catalyzes the addition of hydroxyl groups on the carbon ring that comprises the final delphinidin (blue) pigment molecule. Many independent transitions across *Penstemon* to red pigment result from loss of function mutations in *F3'5'H*. We recently isolated the *F3'5'H* coding sequence from the newly sequenced genome of red-flowered *P. kunthii*. Unlike other red-flowered *Penstemon* species, the *F3'5'H* gene in *P. kunthii* does not exhibit clear loss of function mutations and is in fact expressed at higher levels in *P. kunthii* than in a closely related *Penstemon* species with blue flowers. Based on these results, we hypothesize that *F3'5'H* in *P. kunthii* has evolved a novel function. As an initial test for potential new function, we are employing a molecular evolutionary statistical framework to determine if *P. kunthii* *F3'5'H* has experienced a history of positive selection consistent with the evolution of new function. Alternatively, if *P. kunthii* *F3'5'H* has lost function similar to other red-flowered *Penstemon* species, our results will be consistent with a history of neutral evolution, i.e., no selection acting to conserve a role for *P. kunthii* *F3'5'H* in pigment production.

K-INBRE 2026 Symposium Poster Presentation Abstracts

C-16. Destabilizing MALAT1: A Novel Approach to Lung Cancer Cell Migration and Invasion

Hannah Warner, Maddox Johnson and Dr. James McAfee, Dr. Irene Zegar
Chemistry, Pittsburg State University, Pittsburg, KS 66762

Long non-coding RNAs (lncRNAs), which constitute 98% of the noncoding transcriptome, play crucial roles in gene regulation, including oncogenic and tumor-suppressive pathways. MALAT1, a highly abundant nuclear lncRNA, also regulates metastasis-associated gene expression and exhibits extraordinary thermal stability, largely due to its unique triple-stranded 3'-end structure.

Previous work carried out in this lab, began with virtual docking studies aimed to identify a set of small molecules that bind strongly to the triple-stranded region of MALAT1. Five of 350,000 molecules were chosen based on their virtual binding constants (4×10^8 - 5×10^{10}). This is typical among strong binding ligands that are known to cause cell toxicity more so than the moderate binders resulting in prominent perturbation in the function of MALAT1.

Experimental validation through UV-absorption and fluorescence spectroscopy confirmed binding affinities that align with the theoretical predictions. Furthermore RNA-melting assays, showed that, the five molecules significantly destabilized the MALAT1 triple-helix structure, highlighting their potentials as therapeutic agents.

In this work, we assess the cytotoxic effects of these five molecules on lung cancer. To achieve this, a cell viability assay was conducted using the lung cancer cell line, A549-CCL-185, in the presence and absence of the chosen molecules. Control healthy Chinese hamster cells were also used. In viable cells, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT), a pale-yellow color, undergoes reduction by the enzyme mitochondrial succinate dehydrogenase to a violet color compound called formazan. However, in dead cells, MTT remains unreduced, maintaining a pale-yellow color.

C-17. Spatial transcriptomics reveals misregulated extracellular matrix, transcriptional control and antioxidant genes in early ADPKD that is reversed by targeting metabolic sensor, *Ogt*

Gia Vo Luc^{1,5}, Matthew A. Kavanaugh^{1,5}, Saleem Ahmad^{1,5}, Darren P. Wallace^{2,5}, Stephen C. Parnell^{3,5}, Chad Slawson^{3,5}, Amrita Mitra⁴, Harsh Pathak⁴, Pamela V. Tran^{1,5}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

³Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁴Department of Pathology and Laboratory Medicine and the KU Cancer Center, University of Kansas Medical Center, Kansas City, KS

⁵The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

Autosomal Dominant Polycystic Kidney Disease (ADPKD) causes the progressive growth of fluid-filled kidney cysts and is the 4th leading cause of renal failure worldwide. There is one approved therapy, Tolvaptan, but which has variable effectiveness, underscoring the need to elucidate pathogenic mechanisms to develop novel therapies. Therapies that target cyst-initiating mechanisms are likely to be the most effective. However, cyst-initiating mechanisms remain a major knowledge gap. We have reported that the metabolically regulated post-translational modification, O-GlcNAcylation, is increased in cyst-lining cells of human and mouse ADPKD kidneys. Importantly, deleting O-GlcNAc transferase (*Ogt*) in ADPKD mice restrained O-GlcNAcylation and reduced renal cystogenesis, inflammation, and fibrosis. Remarkably, *Ogt* deletion in juvenile ADPKD mice increased survival from postnatal day 21 to over a year. This indicates *Ogt* is a critical node in ADPKD pathogenesis, and possibly, in early ADPKD. To identify early transcriptional changes that map to cyst-lining epithelia during cyst initiation, we implemented GeoMx Digital Spatial Profiling. Relative to control and *Pkd1;Ogt* double knockout collecting duct cells, from which the largest cysts derive, extracellular matrix genes, *Tacsdt2*, *Fbln5*, and *Col4*, were increased in *Pkd1* conditional knockout cells. In proximal tubule cells, which are susceptible to injury, chromatin and nuclear morphology regulators, *Smc3*, *Speer2* and *Speer4b*, were increased, while antioxidant genes, *Selenop*, *Gpx1* and *Px12a*, were decreased in *Pkd1* conditional knockout cells. These findings identify dysregulated extracellular matrix, transcriptional control and antioxidant activity as early cell type-specific ADPKD drivers. Further, targeting *Ogt* mitigates these alterations, indicating its immense therapeutic potential.

C-18. Expanding Transposon Library in *Chlamydia muridarum*

Komron Fardipour, Natalie Wagoner, Dominique Jaramillo, Scott Hefty, PhD
University of Kansas

Chlamydia is an obligate, intracellular, gram-negative bacterium with heavy medical implications as one of the most common sexually transmitted infections, the leading cause of preventable blindness, and with no approved vaccine. However, due to its intracellular nature and biphasic life cycle, few genetic tools exist to manipulate its genome. To address that limitation, this research looks to expand the current *C. muridarum* transposon library by inducing mutations with the plasmid pCMA. This plasmid uses the Himar C9 transposon system to integrate beta-lactam resistance between an AT site, a trait that enables antibiotic selection for isolation of mutated colonies for whole-genome sequencing. Following isolation, Oxford Nanopore sequencing and subsequent analysis through the bioinformatics program GENEIOUS have identified 20 mutations to date. Notably, genome conservation among surviving mutants ranges from 20 to 100%. Additionally, no plasmid mutations and a single double mutation have been observed. Building on these findings, isogenic *hctB*, *glgC*, and *ytfF* mutants have been selected for further *in vivo* study to evaluate their impact on ATP/ADP production and amino acid transport when disrupted. These genes were prioritized because of their previously demonstrated importance in *Chlamydia*'s developmental cycle and cellular function. Ultimately, by expanding the mutant library through the addition of transposon mutants and usable plasmids, *C. muridarum* can be further optimized as a model organism for *C. trachomatis*. With a stronger model, understanding of the human strain can advance through continued research in the mouse system.

C-19. Modifying the Synthesis Protocol of Graphene-based Quantum Dots to Adjust Emission Wavelengths

Miranda McCammon and Dr. Hoang Nguyen
Department of Chemistry, Washburn University

The goal of this research project is to control emission wavelengths and improve the overall stability of graphene-based quantum dots (GQDs). Two types of quantum dots—undoped GQDs and nitrogen-doped GQDs (N-GQDs)—were synthesized using citric acid precursors. N-GQDs were prepared with varying mass ratios of citric acid to urea (1:1 to 1:15) to explore the effect of nitrogen content on fluorescence emission of our synthesized quantum dots. Graphene oxide (GO) was synthesized separately and incorporated into selected samples of both GQD's and N-GQDs to test its role as a stabilizing material. The fluorescence of each sample was analyzed by measuring the emission wavelength peaks, intensity, and distribution of quantum dots, both with and without GO. Comparing these results helps identify how nitrogen doping and GO addition influence the emission and overall stability. Understanding these effects can guide the development of more stable, tunable graphene-based quantum dots for future applications in imaging, sensing, and electronic materials.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-20. Analysis of Essential Oils Inhibiting Growth of Gram-Positive, Gram-Negative, and Fungal Pathogens

Maggie Peterson and Eric T. Gillock

Department of Biological Sciences at Fort Hays State University

Due to the global rise in antibiotic resistance and the lack of development in new antibiotics, this research aimed to analyze the broad-spectrum antibiotic properties of various essential oils and explore their potential as therapeutic agents. This aims to identify new compounds that can inhibit microbial growth in a wide range of pathogens. To conduct this research, a modified Kirby-Bauer test was used, where a uniform lawn of surrogate for acid-fast pathogens (*M. smegmatis*), gram-negative pathogens (*S. marcescens*), or fungal pathogens (*C. albicans*) was split into four quadrants on each plate. Three quadrants contained a sterile disc impregnated with exactly 10 μ L of one of a variety of essential oils. The fourth quadrant was used as a negative control and contained a sterile disc saturated with 10 μ L of growth media broth. After incubation, zones of inhibition were collected as a unit of measurement for the effectiveness of each essential oil. With certain highly effective essential oils, a 1:10 dilution of essential oil in an organic solvent (DMSO) allowed for a measurable zone of inhibition that was recorded and denoted as a dilution. For the diluted plates, DMSO was used as the negative control to account for any effect it may have on the zones of inhibition. These results were compared to a variety of commonly used antibiotics to measure their potential effectiveness in medicine.

C-21. Determining If PARP14 Impairs HSV-1 In A Strain-Specific Manner

Meghan Arias¹, Anna Ferkul¹, Anthony Fehr¹, David Davido^{1*}

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66045

Herpes simplex virus 1 (HSV-1) is a ubiquitous human pathogen that can cause significant health complications in immunocompromised hosts. HSV-1 establishes a permanent infection in its host, lying dormant in sensory neurons and can reactivate from stimuli such as DNA damage and hormonal changes. As current treatments have limited efficacy, there is a need for new therapies that are suitable for long-term use. A family of host proteins called PARPs (Poly-adenosine diphosphate ribose polymerases) have garnered interest in recent decades due to their involvement in immune regulation, cancer progression, and host-pathogen interactions. PARPs can catalyze the addition of one or multiple ADP-ribose molecules on a target protein. PARP14, specifically, has been found to have antiviral effects against coronaviruses and one wildtype strain of HSV-1, although the mechanisms of its inhibitory activity are not well understood. Our study aimed to determine the extent that PARP14 inhibits HSV-1 replication. We performed plaque assays to examine the replication of HSV-1 on A549 (human lung) cells with and without functional PARP14. We specifically examined whether PARP14's inhibitory effects extend beyond wildtype HSV-1 Strain KOS to a more pathogenic strain of HSV-1, Strain 17. Recent data suggests that PARP14 restricts replication of both HSV-1 strains. Future experiments will elucidate the stage of the HSV-1 replication cycle in which PARP14 exerts its antiviral effects. Our research findings will contribute to understanding how PARP14 impairs HSV-1, potentially aiding in the development of novel treatments or therapeutics against HSV-1 diseases.

C-22. Analyzing the Therapeutic Potential of Naturopathic Compounds on Neuro-2a (N2a) cells modeling Alzheimer's Disease (AD)

Avani Gupta, Shelby, Fiegner, Shelby, Fletchall, and Duane A. Hinton

Department Of Biology, Washburn University

Alzheimer's Disease (AD) is a neurodegenerative disease characterized by the formation of Amyloid Beta (A β) plaques and aggregation of Tau proteins into neurofibrillary tangles (NFTs). The accumulation A β plaques and NFTs results in disruption of neuronal synapses and neuronal cell death leading to cerebral atrophy. Identification of a potential preventative measure or treatment for AD still remains a challenge. In this study, we assessed the neuroprotective effect of certain naturopathic compounds on Neuro-2a (N2a) cells modeled to show increased expression of A β and Tau protein. N2a cells were activated with platelet-activating factor C-16 (PAFC-16) to increase expression of Amyloid Precursor Protein (APP) and Betulinic Acid (Beta) to increase expression of Tau. The activated cells were treated with select concentrations of curcumin, indole-3-carbinol and sinigrin which are two types of glucosinolates, and lithium orotate. Levels of gene expression in N2a cells were assessed by Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR) and Gel Electrophoresis as well as Western Blotting. Preliminary analysis of results suggests the select naturopathic compounds may have an inhibitory effect on AD pathology in N2a cells. The current focus of the study is to establish an N2a cell line optimal for modeling AD. Meanwhile, activation, treatment, and analysis of cells remain ongoing. The aim of this study is to gain an insight into the role of integrative therapeutics in AD progression by developing an N2a cell line simulating AD pathology which can be modulated with naturopathic compounds.

C-23. Identifying novel candidate genes contributing to differences in visceral pain sensitization between C57BL/6 substrains.

Sebastian Meriano¹, Morgan Ewald^{2,3}, Leena Kader^{2,3}, Audie Rodriguez^{2,3}, Kyle Baumbauer³, and Erin E. Young^{2,3,4}

¹University of Kansas, Lawrence, Kansas, United States

²Department of Anesthesiology, Pain, and Perioperative Medicine, KU Medical Center, Kansas City, KS, United States

³Neuroscience Graduate Program, KU Medical Center, Kansas City, KS, United States

⁴Department of Cell Biology and Physiology, KU Medical Center, Kansas City, KS, United States

Funding: Kansas IDeA Network for Biomedical Network Research Excellence (K-INBRE)

Functional abdominal pain (FAP) is a detrimental symptom that affects the quality of life in patients with disorders of gut brain interactions (DGBIs), such as irritable bowel syndrome (IBS). A major factor that contributes to FAP is visceral hypersensitivity (VH), which refers to increased sensitivity to mechanical stimulation of visceral organs. VH is present in up to 90% of IBS patients, yet the etiology remains completely unknown. Therefore, understanding mechanisms underlying VH can reduce visceral pain and increase quality of life in IBS patients. In previous data collected in our lab, researchers found differences in visceral sensitization between two substrains of mice, C57BL/6J and C57BL/6NTac, even though they are similar. Researchers performed a mini systematic review to identify all genes associated with pain, nociception, and/or hypersensitivity between these groups through whole genome sequencing. In this study, we furthered our systematic review by creating and validating primers for genes that were identified from the review. We were able to measure primers at the distal colon and spinal cord level where we successfully identified primer sets with adequate efficiency for quantification of three and five candidate genes identified in the genomic comparisons respectively. Quantification of candidate gene expression within the spinal cord and distal colon are underway. Data from this ongoing study will provide evidence for subsequent follow up studies on the role of specific candidate genes in differential susceptibility to chronic abdominal pain as in IBS.

C-24. Unoccupied

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-25. Gait Differences in ASD/Fragile X Rodent Models

Justin Berryhill¹, Bhavana Sivayokan², Dr. Bethany Plakke²,
¹Langston University Department of Biology
²Kansas State University Department of Psychology

Fragile X Syndrome (FXS) is a neurodevelopmental disorder where individuals have problems with cognitive functioning, repetitive behavior, and altered social communication. FXS is a genetically inherited disorder caused by the repeat expansion of the codon CGG on the *Fmr1* gene, which results in low levels of FMR protein (FMRP). This protein plays a crucial role in brain development and neural plasticity. The loss of this protein can also lead to altered brain connectivity, cerebellar dysfunction, and impaired motor coordination. Individuals with FXS exhibit an altered walking gait due to these changes. This study uses *Fmr1* knock-out rats (wild-type (WT), heterozygous knockout (Het), and homozygous knockout (KO) Long-Evans) to model the phenotypes and examine gait differences. This was achieved using Footprint gait analysis, where paws were painted to collect footprints, and then stride length, stride width, and toe spread were measured. Data was collected at 1-month and ~7-month time periods by blind-to-condition researchers. It was hypothesized that *Fmr1* KO rats would exhibit increased stride length, width, and toe spread compared to the WT controls, while Het females would show deficits, but not as severe as those in the KO rats. Understanding the rodent phenotype over time is crucial to verifying that motor deficits are consistent throughout development. Future studies will examine cerebellar differences between KO and WT animals. Understanding these differences can contribute to a more comprehensive understanding of the neurobiological underpinnings of neurodevelopmental disorders.

C-26. Detection of Beta-Lactamase Antibiotic Resistance Genes in Rural Kansas Soils Across Agricultural Land-Use Types

Chloe Harmon¹, Ella Colson², Yaw Antwi², Bishnu Pangeni², Claudia Da Silva Carvalho², PhD
¹Department of Chemistry, Fort Hays State University, Hays, KS, USA, ²Department of Biology, Fort Hays State University, Hays, KS, USA

Antimicrobial resistance (AMR) is a growing global health threat driven by clinical antibiotic misuse and extensive agricultural application of antibiotics. Rural soils can serve as reservoirs for antibiotic resistance genes (ARGs), particularly in regions where livestock waste or agricultural runoff introduces antibiotic residues into the environment. This study aims to evaluate the presence and relative abundance of two clinically relevant beta-lactamase genes, *blaSHV* and *blaOXA*, in soils collected from rural Kansas sites representing different land-use types. We hypothesize that agricultural soils will exhibit higher frequencies of these ARGs compared to low-disturbance rural soils due to repeated exposure to antibiotic-contaminated inputs.

Soil samples from western Kansas agricultural and non-agricultural sites will undergo DNA extraction using a soil-optimized protocol, with purity assessed by NanoDrop ratios. Control strains with known resistance profiles (MRSA and *Klebsiella quasipneumoniae*) will be used to establish PCR optimization parameters and standard curves. Gene-specific primers for *blaSHV* and *blaOXA* will be used for PCR detection, and quantitative PCR will be performed to estimate relative gene abundance. Amplicons will be visualized via gel electrophoresis to confirm specificity.

We anticipate observing variation in ARG presence across land-use categories, with agricultural soils showing higher prevalence of beta-lactamase genes. Findings will contribute to understanding how land-use practices influence environmental AMR and will provide baseline data for future monitoring and development of strategies aimed at reducing environmental contributions to antibiotic resistance.

Acknowledgements: Supported by the Kansas INBRE, P20 GM103418

Bibliography: World Health Organization. (2025, October 13). *WHO warns of widespread resistance to common antibiotics worldwide*. <https://www.who.int/news/item/13-10-2025-who-warns-of-widespread-resistance-to-common-antibiotics-worldwide>

C-27. Analysis of Nitrosamine Levels in Sandwich Meats Using GC-MS

Cortnie Morgan and Lindsay Davis, Ph.D.
Department of Chemistry and Physical Sciences, Langston University, Langston, OK 73050

Nitrosamines are potentially carcinogenic compounds that occur in various foods such as cured meats, cheeses, processed fish, and alcoholic beverages. Chronic exposure to these compounds has been associated with an increased risk of liver, stomach, and esophageal cancers. Recent studies also suggest that dietary exposure to nitrosamines may contribute to autoimmune disorders by disrupting normal immune regulation and promoting chronic inflammation. Nitrosamines typically form through reactions between secondary amines and nitrosating agents during food processing or storage. This study aims to quantify nitrosamine concentrations in commercial sandwich meats using gas chromatography–mass spectrometry (GC-MS). By determining the levels of nitrosamines in commonly consumed meats, we hope to better understand potential links between diet, nitrosamine exposure, and the onset of autoimmune diseases. The findings may support efforts to improve food safety and reduce disease risks associated with processed meat consumption.

C-28. PER-haps a Solution? Testing Phytocannabinoids Against Neonicotinoid Stress in Honey bees

P. Alex Swider¹, Joselyn Hoff¹, Jackson Arb¹, Oliver-Elias Hiszczynskij¹ and Joanna C. Gress¹
¹ School of Science and Mathematics, Emporia State University

Honey bees are increasingly encountering pesticides in the environment which can introduce toxic residues to the colony and contribute to hive collapse. One group of pesticides they are increasingly encountering are neonicotinoids, particularly imidacloprid. Imidacloprid disrupts associative learning and memory in foraging-age bees and decreases their sensitivity to taste. Efficient foraging by bees depends on their ability to rapidly learn, remember and communicate the identity and location of flowers offering nectar and pollen rewards. Foraging bees exposed to imidacloprid exhibit alterations in waggle dance communication, orientation, and navigation after consuming imidacloprid residues through food. Phytocannabinoids including CBD and CBN have many documented potentially health-promoting properties. These cannabinoids including CBD are also reported to have a neuroprotective effect in a variety of organisms though they have not been evaluated in honeybees to date. We conducted in-lab trials looking at the effects of CBD on learning and memory using proboscis extension response (PER). Foragers fed CBD and CBN showed a significant increase in PER compared to those fed imidacloprid. This indicated phytocannabinoids may be beneficial to learning and memory.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-29. Small Molecules from Commensal Gut Bacteria affect Macrophage Activation

Berzansky, Marion¹, Tucker Folscroft¹, Sakshi Patel¹, Sophia Roccaro¹, Lauren Atkinson^{#,2}, Rayssa Durães Lima^{#,2}, Luis Caetano Martha Antunes^{&,2}, Dyan E. Morgan^{&,1}

¹Undergraduate Biology Program, ²Department of Molecular Biosciences, University of Kansas, ^{#,&} indicate equal contributions

While it is clear that the overall microbiome and its metabolites affect immune cell function, the details of these interactions need further elucidation. With these details, we can better understand host-microbiome interactions and identify new therapeutic strategies for inflammatory diseases. In our K-INBRE-funded CURE (Course-based Undergraduate Research Experience), we took three complementary approaches to investigate how organic extracts from commensal bacteria affect the activation of LPS-stimulated macrophages. First, we took a candidate approach with a focus on TNF- α as a major inflammatory cytokine. We measured TNF- α expression via ELISA and TNF- α activity via biological reporter assay. Second, we broadened our approach, using a flow cytometry-based multiplex immunoassay. This assay allowed us to characterize the effects of our bacterial extracts on LPS-stimulated macrophages by measuring 13 pro- or anti-inflammatory cytokines. Third, we sequenced and annotated the genomes of the bacterial strains we tested. As we compare experimental results across bacterial strains, we plan to compare these annotated genomes in hopes of identifying genes associated with biological activity. Our results to date are preliminary and further analyses will be reported at the meeting.

C-30. Annotation of Protein Coding Genes in *D. willistoni* Contig18

Hinrichs, Kylie¹ and Takrima Sadikot¹

¹ Biology Department, Washburn University

With the completion of the *Drosophila melanogaster* genome in 2000, new opportunities emerged for studying heterochromatic regions and exploring the genomes of other *Drosophila* species. The Genomics Education Partnership (GEP) contributes to this effort by annotating and analyzing *Drosophila* genomes to investigate specific genomic regions through the study of amino acids, nucleotide, and exon sequences. The primary objective is to improve genome annotations and gain insights into evolutionary patterns across different *Drosophila* species by identifying conserved elements and unusual genomic features. Such comparative genomic analysis contributes to a broader understanding of chromosome structure, function, and evolutionary conservation. In this project, contig18 a region on chromosomes 3R (E element) of *Drosophila willistoni* was analyzed. Comparative bioinformatics methods were used to study and annotate this genome, specifically to determine the number of genes present in this contig using *D. melanogaster* as a reference and utilizing the GEP's genome annotation tools. Initial predictions indicated that there were about 31 genes in this region, our results show that only 7 genes truly exist in contig18 and are homologous to genes found in *D. melanogaster*. These include Mekk1-PD, Mekk1-PB, ChAT-PA, ChAT-PB, VAcHT, CG7714, and CG7715.

C-31. Synthesis of Sterically Hindered Catechol Ligands for Hydrophobic Anti-Cancer Vanadium Complexes

Authors: Hannah Nimmo¹, Colson Browning¹, Jack Newman¹, Maggi Braasch-Turi^{*1}

¹Department of Chemistry, Fort Hays State University, Hays, KS.

*Corresponding Author: mmbraaschturi@fhsu.edu

Hydrophobic vanadium complexes have recently shown greater anti-cancer activities than cisplatin, the gold standard of cancer chemotherapy. In the cell, vanadium ions oxidize to form vanadate (VO₄³⁻), a known inhibitor of phosphatase enzymes. Vanadium complexes are used to treat diabetes to deliver vanadate into cells. Studies have shown that vanadium complexes must be sufficiently hydrophobic to prevent hydrolysis of the complex to ensure the release of vanadate within the cell. Recently, two vanadium complexes, [VO(HSHED)(cat)] and [VO(HSHED)(dtb)] ([Hshed= *N*-(salicylideneamino)-*N'*-(2-hydroxyethyl)-1,2-ethanediamine, cat= catechol, and dtb= 3,5-di(tert-butyl)catechol]) were evaluated against cisplatin for their anti-cancer activity. [VO(HSHED)(dtb)] demonstrated greater anti-cancer activity than both [VO(HSHED)(cat)] and cisplatin. The increased hydrophobic character of the (dtb) derivative is thought to be responsible for its increased anti-cancer activity. Thus, the hydrophobic properties of [VO(HSHED)(dtb)] have inspired the development of a library of hydrophobic ligands for vanadium complexes to evaluate their anti-cancer and physical properties. We aim to synthesize hydrophobic catecholate ligands as part of an international collaboration with the Crans/Lay team from Colorado State University and the University of Sydney, respectively. Specifically, our lab will prepare bulky catechol ligands through the alkylation of catechol with chiral terpene substituents and the synthesis of catechol-cycloalkane fused rings systems. Our approach and progress will be described.

C-32. Big Browns All the Way Down: DNA Identification of Bat Species Roosting at Fort Leavenworth

Alison K. Coykendall, Lorelei E. Patrick

Fort Hays State University Department of Biological Sciences

Previous reports have identified several bat species located at Fort Leavenworth, including big browns, eastern red bats, hoary bats, little browns, northern long-eared bats, and evening bats and tricolored bats. Bats are reported roosting in buildings on base periodically and presence of bats, including guano deposits and skeletal remains, have been found at several locations. To better understand the species of bats using human-made structures on base, guano was collected from 19 locations. Quantity and quality of guano varied substantially between locations. DNA was extracted from 3-30 individual guano pellets from each site and bat-specific mini-barcodes were used to amplify DNA. From 310 pellets over 19 sites, 55 samples were successfully amplified and 53 were Sanger sequenced. Of these 51 were identified as *Eptesicus fuscus*, or big brown bats.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-33. Metagenome analysis of poultry litter collected from farms across eastern region of Kansas with a focus on antibiotic resistant and foodborne pathogens

Owen Long, Debmalyo Rudra Sarma, and Anuradha Ghosh

Biology Department, Pittsburg State University, Pittsburg, Kansas

There is growing concern about the use of antibiotics in food animals and poultry. Efforts are in place to bring in a change to the usage of antibiotics in animal husbandry primarily addressing the negative impact on human health besides acknowledging other confounding factors. CDC data shows *Salmonella* causes about 1.35 million infections, 26,500 hospitalizations, and 420 deaths while more than 2.8 million antimicrobial-resistant infections occur annually in the U.S. This study aimed (i) to investigate the abundance of antibiotic-resistant enterococci and (ii) to determine the prevalence of pathogenic *Salmonella* serovars in poultry samples. Poultry litter was collected from 13 different farms around eastern region of Kansas using the collection kit that contained 5 collection tubes. One gram of each sample was diluted with phosphate-buffered saline and evenly distributed on Neogen Petrifilm® Rapid Aerobic Count plate and subsequently based on dilution count plated on mEnterococcus agar. A total of 65 putative enterococcal colonies were streaked on nutrient agar and confirmed at the genus level using esculin hydrolysis. All confirmed isolates will be characterized for antibiotic resistance and virulence profile. A fraction of each litter sample was processed for total DNA extraction using MagBeads FastDNA™ Kit for feces. DNA concentration was determined using agarose gel electrophoresis and nanodrop. Further experiments will focus on PCR amplification and metagenome sequence analysis. The data obtained from this research will not only address food safety issues but will actively contribute to potential risk mitigation strategies.

C-34. Role of asparagine synthetase and other transcription factor targets in epidermal morphogenesis

Jillian K. Rockley, Bibek Subedi, Bradley J.S.C. Olson, Aytuğ Ulutaş and Kathrin Schrick

Division of Biology, Kansas State University

Asparagine synthetase is an enzyme responsible for generating asparagine from aspartate and glutamine. This enzyme is tightly regulated in animal and plant tissues. Mutations in the human *ASNS* gene lead to asparagine synthetase deficiency, which causes severe neurological pathologies. Evidence also suggests a regulatory role in several cancers, as overexpression of *ASNS* has been shown to upregulate tumor cell proliferation. In the plant model *Arabidopsis*, asparagine synthetase controls nitrogen distribution throughout development. RNA-sequencing work in the lab led to the discovery that *ASPARAGINE SYNTHETASE1/ DARK INDUCIBLE6 (ASN1/DIN6)* and other amino acid metabolic genes are upregulated in leaves displaying an abnormal “curly-leaf” phenotype due to overexpression of *GLABRA2 (GL2)*, a homeodomain leucine-zipper (HD-Zip) transcription factor. A DAP-seq experiment performed with *PROTODERMAL FACTOR2 (PDF2)*, an HD-Zip protein needed for epidermal differentiation, showed DNA binding peaks within the promoter region of *ASN1*. This project investigates whether *ASN1* is a direct transcriptional target of *GL2* and/or *PDF2*. Bioinformatic and molecular genetic approaches, including evaluation of putative DNA binding sites and development of reporter gene constructs, are in progress. Analysis of the progeny of genetic crosses suggests that while *DIN1* is not required for the curly-leaf phenotype, *ASN1* may be required. This hypothesis is being analyzed further by phenotyping *asn1* plants that have been transformed with the *proGL2:YFP:GL2* construct, which induces leaf curling. Understanding the function of *ASN1* in plants may contribute to understanding similar amino acid metabolic genes in human biology.

This project is supported by the Kansas INBRE (P20 GM103418) and USDA-NIFA (KS00-0009-NC1203).

C-35. Comparing the anatomy of 80-million-year-old conifer shoots from Antarctica with living southern cypresses

Jedidah Kapapula¹, Kelly C. Pfeiler^{1,2}, Brian Atkinson^{1,2}, Kelly Matsunaga^{1,2}

¹Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, Kansas 66045, USA

²Biodiversity Institute, University of Kansas, Lawrence, Kansas 66045, USA

This study describes the cellular anatomy of two three-dimensionally preserved conifer shoots from the Late Cretaceous (~80 million years ago) of Antarctica. The fossil exhibits bifacially flattened shoots and dimorphic leaves, a characteristic shared by several members of the cypress family, Cupressaceae. Given the fossils' Southern Hemisphere origin, we hypothesize their affinity lies within the subfamily Callitroideae, the southern cypresses. Only three genera in Callitroideae, *Libocedrus*, *Papuacedrus*, and *Austrocedrus*, possess bifacial shoot morphology. To study these fossils, we sectioned them via the cellulose-acetate peel technique. Prior to sectioning, one specimen was imaged using X-ray microcomputed tomography. Images and measurements from the prepared slides were then compared with histological sections of living species. We were able to use the degree of flatness of shoots, and the positions and shape of facial and lateral leaves to characterize morphological and anatomical variation in the living and fossil species. One fossil specimen shows the greatest resemblance to the genus *Libocedrus*, and the second specimen with *Austrocedrus*. These specimens provide the earliest evidence of bifacially flattened foliage. Their presence in Late Cretaceous deposits demonstrates that these plants exhibited morphology and anatomy similar to modern southern cypresses as early as 80 Ma. This research will allow us to investigate evolutionary trends in shoot and leaf morphology within the cypress family, contributing to our broader understanding of ecological adaptations in Cupressaceae in deep time.

C-36. What Makes Flies Sexy?

Janzen, Carly¹, Conway, Taylor², Unckless, L. Robert¹

¹Department of Molecular Biosciences, University of Kansas

²Department of Ecology and Evolutionary Biology, University of Kansas

In *Drosophila*, it is known that most of the 1200 species have sterile XO males. *Drosophila affinis* is one exception, because XO males are fertile and can produce progeny. Past studies have shown that XY outcompetes XO in cages (Voelker and Kojima, 1971) previously done, which opened up the topic of components of fitness. Here we are testing female mate choice between XO and XY males to see if the female is choosing to mate with the XY male more than the XO Male. Under controlled laboratory conditions, virgin, 5 to 7 day old XO (dark) male, XY (M40) male, and a female were placed into a vial, and allowed to mate for two hours. The male that successfully was mated to the female was declared the “winner” and the other male is labeled as the “loser”. The winners and losers were then scored by eye color. The winning male then had genomic DNA extracted, and PCR amplification using the Y-specific primers to confirm the presence of the Y chromosome status. This data was compared using a chi-square test to assess deviation from the random mating expected ratio of 50:50. This data provides a framework for testing the female mate choice preference and successful mating between males containing a Y chromosome, and males that lack a Y chromosome. These results will show if a Y chromosome influences the female's preference for a mate, and if the Y chromosome makes the male fly more attractive.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

C-37. Characterizing the translation accessory factor EF-G1B in *Pseudomonas aeruginosa* – biological function and role in antibiotic resistance.

Udita Shah¹, Vanessa M. Schmidt¹, Brielle M. Mckee¹, Josephine R. Chandler¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

Pseudomonas aeruginosa is a multidrug-resistant pathogen that causes problems ranging from ear and urinary tract infections to life-threatening conditions in immunocompromised individuals, including cystic fibrosis patients. Antibiotic resistance in *P. aeruginosa* is often driven by adaptive mutations in translation machinery, particularly in the elongation factor EF-G encoded by *fusA1*. Certain *fusA1* mutations subtly alter translation, triggering stress responses such as production of the MexXY efflux system, which confer resistance to aminoglycosides like tobramycin through their extrusion. Interestingly, *P. aeruginosa* also encodes a second EF-G homolog, *FusA2*, whose role in translation and resistance remains unclear. Here, we focus on investigating the contribution of *FusA2* to antibiotic resistance and its interplay with *FusA1*. We hypothesize that *FusA2* provides translational resilience under ribosome stress, modulating resistance mechanisms. We showed that synthetically expressing *fusA2* in multiple *fusA1* mutants restored sensitivity to several classes of antibiotics. These results suggest *FusA1* and *FusA2* have functional redundancy. The results also provide evidence that increasing *fusA2* expression may have therapeutic potential by restoring antibiotic sensitivity in antibiotic-recalcitrant infections.

C-38. (2026) Analysis of Cancer Mortality in the United States (2000-2023)

Aiyanna Davis and Sharon Lewis

Langston University, Chemistry Department

The objective of this research was to investigate cancer mortality in the United States using data from the National Cancer Institute's (NCI) Surveillance, Epidemiology, and End Results (SEER) Explorer Cancer Statistics Network. Epidemiology involves the study and analysis of the distribution, patterns, and determinants of health and disease conditions within defined populations. The SEER dataset represents approximately 45.9% of the U.S. population, covering 39.6% of Whites, 43.5% of Black, 64.9% of Hispanics, and 69.9% of Asians/Pacific Islanders. This project analyzed mortality data for 26 types of cancer, including: anus, bladder, bones/joints, brain, breast, cervix/uteri, colon/rectum, esophagus, kidney/renal pelvis, larynx, leukemia, liver/bile duct, lung/bronchus, melanoma, myeloma, oral cavity/pharynx, non-Hodgkin lymphoma, ovary, pancreas, small intestine, soft tissue (including heart), stomach, thyroid, urinary bladder, vagina, and vulva. During the first specific aim we mined the SEER Explorer dataset for cancer mortality data spanning 2000–2022 across four racial and ethnic groups (white, black, Hispanic, and Asian/Pacific Islander). The second specific aim we expanded the dataset to include 2023, updated data. For the third specific aim, we generated Excel-based line graphs to visualize mortality in 26 cancers, 4 populations, male and female, ages (15–39 and 40–64). Our key results were as follows: brain, leukemia and soft tissue mortality was higher in Hispanic men, age 15-39, than black men. Also, Hispanic females, ages 15-39 had a higher leukemia, cervix uteri, and bone/joint mortality. What was interesting is that Hispanic, females, stomach mortality was higher than white and black.

C-39. Glioblastoma U251 cells express opioid receptors

Emmalyn Greeves (1), Meena Kumari (1)

(1) Department of Anatomy and Physiology, College of Veterinary Medicine, Kansas State University

Glioblastoma is a type of cancer that arises from glial cells. When in care, the patient who has glioblastoma will usually receive pain medications, such as oxycodone or morphine. Being originated from glial cells, glioblastoma cells may express opioid receptors and get activated. In the present study, we used U251 cells to determine expression of three types of opioid receptors, mu opioid receptors (MOR), delta opioid receptors (DOR), and kappa opioid receptors (KOR) at the mRNA level by RT-PCR and at the protein level by Western blotting. Since U251 cells are of human origin, we used primary cultures of human astrocytes as positive control. Results of this study will be presented at the meeting.

C-40. Unoccupied

D-1. Physical Therapy Patient Exercise Adherence Intervention: A HAPA-Based Behavioral Education Protocol

Authors: Montney, Justin,¹ Carter Booe,¹ Clark Dean,¹ Ernesto Duenez,¹ Eva Elder,¹ Aiden Haworth,¹ Nathan Jaeger,¹ Gabe Tross,¹ and Emery Wolfe¹

Affiliations: ¹Department of Health and Human Performance, Fort Hays State University

Non-adherence to prescribed home exercise programs significantly undermines the efficacy of physical therapy (PT), with research indicating only approximately 35% of patients fully adhere to regimens. This contributes to suboptimal recovery and places a substantial financial burden on the healthcare system. The primary objective of this study was to evaluate the effectiveness of a 14-week behavioral education intervention designed to improve patient exercise adherence outside the clinical setting. The intervention utilized the Health Action Process Approach (HAPA) model. PT staff implemented a protocol involving a motivational-volitional screener, and trained student aides delivered targeted Patient Education Tools to address adherence barriers. Data were collected at pre-intervention, post-intervention, and follow-up intervals using validated surveys on HAPA constructs, physical activity (IPAQ), pain ratings (NPRS), and quality of life. It was hypothesized that this program would lead to a marked increase in patient adherence and improved management of chronic conditions. By targeting behavioral determinants of adherence, this intervention aims to reduce disability rates. Future recommendations include expanding to multi-site trials and integrating wearable technology to reinforce behavioral education.

D-2. iCURE: a Course-Based Undergraduate Research Experience in Immunology

Dyan E. Morgan¹, Luis Caetano Martha Antunes², Lauren Atkinson^{#,2}, Rayssa Durães Lima^{#,2} ¹Undergraduate Biology Program, ²Department of Molecular Biosciences, University of Kansas, # indicates equal contributions

Undergraduate research is one of eleven high-impact practices known to promote student success in college. However, a recent survey of KU-Lawrence biology faculty found that only around 10% of our undergraduate students are conducting research with a faculty member. By converting the immunology laboratory to a course-based undergraduate research experience (CURE), we can increase participation in undergraduate research by 28%. With support from K-INBRE and in collaboration with the Antunes laboratory, students in the immunology lab course are exploring the effects of small molecules from commensal gut bacteria on macrophages, while also learning key techniques such as cell culture, ELISA, and flow cytometry among others. The gut microbiome clearly influences immune cells, and our CURE takes a step towards mapping the cellular and molecular details of these interactions (see our lab's poster: Berzansky et al). We implemented and evaluated the full CURE during Fall 2025. At the meeting, we plan to present data from the Fall 2025 semester with comparisons to Fall 2024 data including Laboratory Course Assessment Survey (LCAS) results and measurements of student learning.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-3. Heterologous expression of *Aspergillus fumigatus* cryptic secondary metabolite biosynthetic gene clusters.

Todd, Richard B.,¹ C. Elizabeth Oakley,² Heather D. Forster,¹ and Berl R. Oakley,²

¹Department of Plant Pathology, Kansas State University;

²Department of Molecular Biosciences, University of Kansas.

Aspergillus fumigatus is the most common species causing Invasive Aspergillosis, a devastating opportunistic fungal disease with a high mortality rate. One of the reasons *A. fumigatus* is a successful pathogen is its ability to produce secondary metabolites (SMs). SMs are compounds that are dispensable for viability but confer a selective advantage to the producing organism, often by inhibiting biologically important activities in other organisms. At least seven *A. fumigatus* SMs are known to contribute to virulence. In fungi, SM biosynthetic pathways are encoded by genes that are clustered in the genome. *A. fumigatus* genomes contain ~34 SM biosynthetic gene clusters (BGCs). Sixteen BGCs are cryptic (i.e., their products remain unknown) because most SM BGCs are not expressed in culture and *A. fumigatus* has a high background metabolite profile that makes the compounds difficult to detect even if the BGC genes are activated. This lack of knowledge impedes progress in fully understanding *A. fumigatus* virulence. Herein we work towards the elucidation of the *A. fumigatus* secondary metabolome by heterologous expression of two cryptic BGCs in an engineered *Aspergillus nidulans* host. The BGCs were reconstructed in *A. nidulans*, with their expression driven by upregulating a BGC-associated transcription factor gene that, in turn, drives expression of the remaining genes of the BGC. Expression of the BGCs was assessed using RNA-seq. This work will lay the foundation for identification of the SMs produced by these BGCs and the understanding of their roles in *A. fumigatus* pathogenesis. Supported by K-INBRE, P20 GM103418.

D-4. Exploiting HPV-Induced DNA Repair Rewiring to Improve Cisplatin Efficacy in Cervical Cancer

Sebastian O. Wendel¹, Grant Brooke²

¹School of Health and Human Science, Kansas State University, Manhattan, KS, USA

²Division of Biology, Kansas State University, Manhattan, KS, USA

Cervical cancer (CaCx) remains a critical clinical challenge, driven primarily by persistent expression of the HPV E6 and E7 oncogenes. Our studies demonstrate that these oncogenes fundamentally rewire DNA repair pathway choice, creating a therapeutically targetable dependence on the microhomology-mediated end joining (MMEJ) pathway mediated by DNA polymerase theta (POL θ). We show that cervical tissues exhibit among the highest POL θ mRNA levels across 34 cancer types, and that prolonged HPV16 E6/E7 expression in primary human keratinocytes produces a progressive increase in POL θ protein abundance and a 2-fold elevation in MMEJ activity, accompanied by loss of p53 and Rb. Functional assays reveal that HPV-positive cervical cancer cells and HPV16 E6/E7-expressing keratinocytes are selectively sensitive to POL θ inhibition. Combination matrices demonstrate strong synergy between the POL θ inhibitor ART812 and cisplatin, with high synergy scores observed in HPV-positive cells. Oncogene expressing cells treated with ART812 showed increased γ H2AX-marked DNA damage, and significant suppression of MMEJ reporter activity. In vivo xenograft studies using HeLa and CaSki tumors confirm that ART812 enables subtherapeutic cisplatin (4 mg/kg) to achieve tumor control equivalent to high-dose cisplatin (8 mg/kg) while minimizing weight loss and systemic toxicity. Collectively, these data define a cervical cancer-specific DNA repair vulnerability driven by HPV oncogenes and support POL θ inhibition as a potent sensitizer that enhances the efficacy and tolerability of cisplatin-based therapy.

D-5. Genetic characterization and genome analysis of bloom-forming cyanobacteria in western Kansas

Louisa Acquah¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

Cyanobacteria are photosynthetic prokaryotes ubiquitous in aquatic ecosystems and prone to mass clonal reproduction during warm summer months, often stimulated by agricultural run-off. These blooms, visible as bright-green layers on water surfaces or shorelines, can contain toxic metabolites that threaten freshwater quality and human health. Because cyanotoxin profiles vary by species, identifying the strains forming these blooms is essential. In water-scarce regions such as western Kansas, however, the cyanobacterial species responsible for local blooms are often unknown. For this study, cyanobacterial samples were isolated from multiple blooms in western Kansas and genetically characterized. Bloom water samples were cultivated into axenic cultures, genomic DNA was extracted, and strains were identified through DNA barcoding and microscopic assessment of colony morphology. Our analyses showed that the dominant isolates were related to members of the genus *Limnothrix*, but with sequence similarity values of at most 97 percent, suggesting the presence of novel species. To determine precise taxonomic placement and assess genes associated with cyanotoxin production, whole-genome sequencing was conducted for one isolate. Its complete genome was found to be not only genetically distinct but also highly rearranged relative to all previously sequenced Pseudanabaenaceae, even though genome size and gene content remain comparable to related species. This research provides the first genomic insight into the identity of bloom-forming cyanobacteria in western Kansas.

D-6. Transcription and Regulation of the *mpt* PTS in *Enterococcus faecalis*

Tolulope I. Ade and Lynn E. Hancock

Department of Molecular Biosciences, University of Kansas, Lawrence, KS

Enterococcus faecalis is a metabolically versatile organism that has been reported to encode at least 46 different phosphotransferase systems (PTS). The PTS is a phospho-relay system that is important for the uptake and phosphorylation of carbon substrates for energy production. Six of the 46 PTSs in *E. faecalis* are regulated by the alternative sigma factor, σ 54 (RpoN) that recognizes the -24/-12 promoter sequence. The regulation of RpoN-dependent PTSs also require bacterial enhancer binding proteins (bEBPs) that belong to the LevR family of transcriptional regulators and include CelR, DgaR, GfrR, MptR, and XpoR. Using biolog growth phenotype assay and sugar-specific growth phenotype assays, we have defined RpoN-dependent substrates that require CelR, DgaR, GfrR, and MptR for their uptake. We have also used luciferase assay to show that these sugars specifically induce the different promoters that are regulated by the respective bEBPs. Specifically, the *mpt* PTS, regulated by MptR, is important for the uptake of glucose, mannose, glucosamine, and N-acetylglucosamine. Bioinformatic analysis predicts that the *mpt* operon contains four open reading frames – *mptB* (EIIB), *mptA* (EIIA), *mptC* (EIIC), and *mptD* (EIID). More detailed analysis of this operon identified a second EIIB domain fused to the EIIA protein of MptA and shares ~ 50% amino acid sequence similarity with MptB. We hypothesize that the presence of two EIIB domains within the Mpt operon enables diversification of the sugar substrates recognized and are currently undertaking a genetic deletion approach to identify contributions from each EIIB domain.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-7. Exploring the Link Between Soil Microbes, Land Use, and Antibiotic Resistance through a One Health Lens.

Yaw Agyapong Antwi¹, Alfred Kusi-Appiah¹, Chloe Harmon¹, Morgan Fischer¹, Jaime Arellanes¹, Claudia Da Silva Carvalho PhD¹

¹Department of Biological Sciences, Fort Hays State University

Soil is a dynamic ecosystem that supports diverse microbial communities essential to environmental health and sustainability. These communities can serve as reservoirs for antibiotic resistance genes (ARGs), posing a growing public health concern. From a One Health perspective which recognizes the interconnectedness of human, animal, and environmental health, it is important to understand how land use influences microbial diversity and the potential spread of ARGs.

This study investigated microbial diversity and abundance in soils from agricultural, recreational, and hospital-adjacent areas across rural, urban, and metropolitan sites in Kansas. Soil samples were collected, and DNA was extracted and analyzed using 16S rRNA Next Generation Sequencing. Alpha diversity was assessed using Chao1 and Shannon indices to determine species richness and evenness.

Our results showed that while microbial richness in rural soils remained relatively stable, urban and hospital-adjacent soils exhibited significant changes in community structure and diversity. These findings suggest that land use intensity and local environmental factors may have a stronger influence on microbial dynamics than geographic location alone.

This research supports the inclusion of soil microbial surveillance in One Health-based strategies aimed at monitoring and mitigating antibiotic resistance. It also highlights the importance of engaging underrepresented communities in environmental health research to address disparities in exposure and outcomes.

D-8. The role of Notch signaling in vascular integrity of Autosomal Dominant Polycystic Kidney Disease

^{1,2}Begum, Rahima; ^{1,2}McGonigle, Mercedes; ^{1,2} Wang, Wei; ^{1,2}Sommer, Nicole; ^{1,2}Placide, Sagine; ^{1,2}Wallace, Darren; ^{1,2}Sharma, Madhulika

¹Department of Cell Biology and Anatomy, University of Kansas Medical Center; ²The Jared Grantham Kidney Institute, Department of Internal Medicine, University of Kansas Medical Center, Kansas City, Kansas, United States

Introduction: Autosomal Dominant Polycystic Kidney Disease (ADPKD) is marked by progressive growth of fluid-filled cysts and associated extra-renal manifestations, including hypertension and intracranial aneurysms. Notch signaling is crucial to maintaining vascular homeostasis, but its role in ADPKD remains unclear. Notch3 is abnormally elevated in cyst-lining epithelia of ADPKD patients and mouse models. Given its established role in regulating vascular structure and function, we hypothesize that notch signaling is also essential to maintain vascular integrity in ADPKD by regulating VSMC phenotype and contractility.

Methods: PKD mouse models with fast and slow disease progression were assessed for Notch inhibition by pharmacological (using gamma secretase inhibitor, GSI) and genetic means. α -SMA immunofluorescence was used to assess vascular smooth muscle cell (VSMC) expression in the heart and kidney. Micro-CT was used to visualize vascular structures. Dose dependent response of GSI was determined on primary VSMCs to assess Notch-dependent phenotypic switching.

Results: Pharmacological Notch inhibition caused lethality in fast-progressing PKD mice and accelerated cyst expansion in a slow-progressing model. Genetically, collecting duct specific deletion of Notch3 on a PKD model did not alter cyst progression whereas global deletion of Notch3 resulted in perinatal lethality associated with VSMC loss in heart and worsening cystic disease. Micro-CT revealed weakened vasculature in PKD mice. In vitro, GSI induced a dose-dependent switch in VSMCs from a contractile to synthetic phenotype.

Conclusion: Our findings indicate that vascular architecture is compromised in ADPKD, and that Notch may play a critical role in maintaining the vascular integrity in ADPKD.

D-9. CCUSTR: A Phylogenetic Program for Automated Clade Splicing

David Bohorquez¹, Brandon Williams², Elijah McCullough³, Michael Gruenstaedl¹

¹Department of Biological Sciences, Fort Hays State University

²Department of Computer Science, Fort Hays State University

³Department of Informatics, Fort Hays State University

There are many robust phylogenetic visualization software packages available, used both to create and visualize phylogenetic trees with support for various tree formats and displays. However, none of them have a function for automatically collapsing clades to user-defined taxonomic levels. For example, the programs Dendroscope (Huson and Scornavacca 2012) and Figtree (Rambaut 2018) only have the capacity to collapse clades manually, with no way of doing so based on recognized clades. Similarly, the Python package ETE3 (Huerta-Cepas et al. 2016) has the theoretical functionality for a reduced representation, but a long script would be needed for the feature to work, and it does not have a way of autocorrecting misspelled taxon names. The functionalities provided by the Interactive Tree of Life (ITOL; Letunic and Bork 2007) are also insufficient, as internal nodes must be specified for the automatic collapse features to work. For large phylogenetic trees, collapsing clades provides better visual feedback for a user to view than the original set of clades, but this task may prove to be time-consuming for the purposes of quick visualization with current phylogenetic software. To solve this, a software program that can handle such tasks with only an input tree and a few command-line arguments is needed. Here, we present a bioinformatics software tool called CCUSTR (Collapse Clade to User Specified Taxonomic Rank) that collapses clades, corrects invalid taxa, and handle both polyphyletic and paraphyletic relationships for tree visualization using Python.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-10. Targeting HuR Mediated Regulation of CD147 on Extracellular Vesicles to Modulate Immune Response in Triple Negative Breast Cancer (TNBC)

Alfred Buabeng, Sunghae Kim, Qi Zhang, Xiaoqing Wu, and Liang Xu.
University of Kansas/ Department of Molecular Biosciences

Triple-negative breast cancer (TNBC) is a highly aggressive subtype of breast cancer lacking estrogen, progesterone, and HER2 receptors, resulting in limited targeted treatment options and poor survival rates. EVs play a crucial role in TNBC progression and immune modulation. The RNA-binding protein HuR is overexpressed in TNBC and stabilizes oncogenic mRNAs, contributing to tumor growth and treatment resistance. CD147 (EMMPRIN) is a transmembrane protein found on EVs that drives cancer hallmark processes including cellular invasion, migration, immune evasion and treatment resistance. HuR binds to the 3'-UTR of CD147 mRNA, enhancing its stability and protein expression. CD147 is highly expressed in various cancers including TNBCs, and the expression levels correlate with tumor progression and invasion by inducing the production of matrix metalloproteinases (MMPs), degrading extracellular matrix and promoting EV release. Our preliminary data shows that HuR knockout reduces exosome secretion in MDA-MB-231 cells and subsequently reduced CD147 proteins expressed on EVs. We identified small molecule inhibitors (KH compounds) that disrupt HuR-mRNA interactions. Treatment of wild type TNBC cells with the KH compound reduced CD147 proteins on the cell line. However, the combination of immune checkpoint inhibitors and HuR inhibitors have been shown to synergistically enhance T cell activation and sensitization of TNBC tumors to immunotherapy. Based on these findings, we hypothesize that HuR regulates CD147 expression on EVs and targeting HuR mediated regulation of CD17 on EVs may improve immunotherapeutic responses in TNBC.

D-11. Investigation of neuronal nanofiber interaction of glioblastoma

Cantu, Kayla, Li Yao
Department of Biological Sciences, Wichita State University

Glioblastoma is a malignant form of brain cancer with a rapid tumor progression and poor prognosis. Glioma cells can diffuse and invade brain tissue, allowing them to interact with the extracellular matrix. These cellular interactions can result in abnormal and elevated levels of collagen, compared to low collagen levels in normal brain tissue. Previous studies revealed that collagen can support tumor cell proliferation and migration, while another cellular component hyaluronic acid (HA) is necessary for tumor invasion. Glioma cells develop from astrocytes, therefore by using nanofibers to replicate nerve cells, we can closely study the interactions between cellular components of collagen and HA with glioma cells. Fabrication of various types of nanofibers were developed: PCL + Collagen, PCL, PCL + Hyaluronic acid, Collagen, and Hyaluronic acid + Collagen + PCL. We have seeded glioblastoma cells on top of the collagen/PCL and HA/PCL fibers to study the ability of cell proliferation and migration. We have completed performing viability assays and migration recordings. This ongoing project will be laboratory research. It is expected in the spring semester to conduct gene sequence analysis and gene knockdown to gather further results.

D-12. Metabolomic analysis reveals hyaluronic acid as a novel component of ADPKD pathobiology that links altered metabolism to extracellular mechanisms of cyst formation

Aakriti Chaturvedi^{1, 5}, Chadhve Ranganathan^{1, 5}, Matthew A. Kavanaugh^{1, 5}, Saleem Ahmad^{1, 5}, Michele Pritchard^{2, 5}, Madhulika Sharma^{3, 5}, Darren P. Wallace^{3, 5}, Stephen C. Parnell^{4, 5}, Chad Slawson^{4, 5}, Pamela V. Tran^{1, 5}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Pharmacology and Toxicology, University of Kansas Medical Center, Kansas City, KS

³Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

⁴Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁵The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

Autosomal Dominant Polycystic Kidney Disease (ADPKD) is among the most common inherited, fatal diseases. It causes the progressive growth of fluid-filled cysts in the kidney, leading to renal failure typically in the 6th decade of life. Major cellular drivers include increased cell proliferation and fluid secretion, and more recently, altered cell metabolism. O-GlcNAcylation, a metabolically regulated post-translational modification, is elevated in ADPKD kidneys. Using rapidly and slowly progressive ADPKD mouse models, we show that deleting O-GlcNAc transferase (*Ogt*) reduces renal cystogenesis. While rapidly progressive *Pkd1* conditional knockout (cko) mice died before postnatal day 21, *Pkd1;Ogt* double knockout (dco) mice survived over a year. Additionally, pharmacological OGT inhibition in patient-derived renal epithelial cells reduced cysts *in vitro*. In *Pkd1;Ogt* dco kidneys, levels of phosphorylated AMPK and mitochondrial respiratory chain complexes, which sense and produce cellular energy, were maintained, while in *Pkd1* cko kidneys, these were reduced. Further, in *Pkd1;Ogt* dco kidneys, metabolomic analysis revealed correction of glycolysis and of the hexosamine and hyaluronic acid (HA) biosynthesis pathways. In contrast, in *Pkd1* cko kidneys, dysregulation of these pathways culminated in increased tricarboxylic acid cycle entry, increased O-GlcNAc, and increased HA in the extracellular matrix, respectively. In patient renal tissue, HA was also increased, and low molecular weight HA increased proliferation of cultured patient-derived renal epithelial cells. These data reveal HA as a novel component of ADPKD renal cystogenesis. Additionally, these findings identify *Ogt* as a central metabolic regulator and potential therapeutic target, linking metabolism to intracellular and extracellular mechanisms of cyst formation.

D-13. Identification of a Genetic Suppressor of Antimorphic *alg-1* Mutations

Heather Crawshaw, Jeff Medley, and Anna Zinovyeva
Division of Biology, Kansas State University

Regulation of gene expression is a fundamental process that controls the magnitude, timing, and location of gene activity, enabling diverse cellular functions and proper development. Disruptions in this regulation are linked to cancers and developmental disorders. Among the major regulators of gene expression are microRNAs (miRNAs), a class of non-coding RNAs that mediate post-transcriptional gene silencing by repressing target gene activity. During miRNA biogenesis, mature miRNAs are loaded into Argonaute proteins, forming complexes that recognize and silence specific transcripts through complementary base pairing. The let-7 miRNA is evolutionarily conserved across metazoans and is essential for development in *Caenorhabditis elegans*. In *C. elegans*, the Argonaute protein ALG-1 is one of two primary effectors of the miRNA pathway and associates with let-7 to regulate its targets. Loss of let-7 or *alg-1* function leads to misexpression of target genes and failure to progress through normal developmental stages. Here, we identified a spontaneous suppressor mutation that restores proper development and stage-specific gene expression in antimorphic *alg-1(ma202)* and *alg-1(ma192)* mutants. Genetic mapping places this suppressor on the left side of Chromosome I within an interval containing six candidate variants identified by whole-genome sequencing. We are currently using CRISPR/Cas9 genome editing to determine which of these variants corresponds to the *alg-1* suppressor. Further characterization of this suppressor will provide insight into mechanisms that fine-tune miRNA-mediated gene regulation during animal development.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-14. Targeting oxidative stress regulator Nrf2 to improve T-cell responses in inflammatory bowel disease and in colorectal cancers

Debolina Dasgupta¹, Aprajita Tripathi¹, Nadine Santana Magal¹, Rachel Griffard-Smith², Emily Burt¹, Jennifer S. Davis¹, and Kalyani Pyaram¹

¹Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, USA.

²Department of Biostatistics & Data Science, University of Kansas Medical Center, Kansas City, KS, USA.

Ulcerative colitis (UC) is a chronic, relapsing form of inflammatory bowel disease (IBD) characterized by inflammation of the colon, which can further progress to colorectal cancers (CRCs). Antioxidation protein Nrf2 (nuclear factor erythroid 2-related factor 2), regulated by Keap1 (Kelch-like ECH-associated protein 1), has been studied to be anti-inflammatory, however, if Nrf2 could be targeted in T-cells as a therapeutic against IBD and CRCs is largely unknown. Therefore, in this study, we aimed to examine if/how Nrf2 manipulation in T-cells impacted the disease outcome of IBD and the viability of CRC cell lines. We used mice with T-cell specific knockout (KO) of Nrf2 (N-KO, no Nrf2), and Keap1 (K-KO, high Nrf2) and performed CD4⁺ T-cell adoptive transfers into immunodeficient Rag1^{-/-} mice to address if Nrf2 manipulation could affect T-cell-driven IBD progression in these mice. Pharmacological inhibition of Nrf2 in CD8⁺ T-cells was also performed *in vitro*, to test its effect on the killing potential of these cells. We found that while high Nrf2 in CD4⁺ T-cells significantly reduced disease severity in Rag1^{-/-} mice, pharmacological inhibition of Nrf2 in CD8⁺ T-cells enhanced their killing potential against mouse colorectal adenocarcinoma (MC38) cells. These results highlight that Nrf2 activation in CD4⁺ T-cells could be targeted as a novel therapeutic by dampening inflammatory responses of these cells. On the other hand, in CD8⁺ T-cells, Nrf2 inhibition could enhance their tumor cell killing potential, thus highlighting the dual role of Nrf2 in inflammation and in cancers.

D-15. Efficacy of Antibiotic Prophylaxis for Infective Endocarditis Recommended for Dental Patients

Gabriela C. Chianca^{1,2,3}, Helvécio C. C. Póvoa¹, Bruna A. Thurler^{1,2}, Raiane C. Chamon², Fábio F. da Mota⁴, Heidi Pauer³, Rosana B. R. Ferreira³, Natalia L. P. P. Iorio¹.

¹Department of Basic Sciences, Universidade Federal Fluminense (UFF), Nova Friburgo, Brazil, ²Department of Pathology, UFF, Niterói, Brazil,

³Department of Molecular Biosciences, University of Kansas and ⁴Department of Systems and Computational Biology, Instituto Oswaldo Cruz, Rio de Janeiro, Brazil.

To prevent the development of infective endocarditis (IE) caused by oral *Streptococcus* in patients subject to invasive dental procedures, clinical guidelines recommend the use of antimicrobial prophylaxis, but its efficacy is debated. This study aimed to define the susceptibility profile of oral *Streptococcus* isolated from IE and evaluate the ability of some species to produce biofilms. An *in silico* study was conducted to understand the susceptibility profile of *Streptococcus* isolated from patients with IE. Then, biofilm formation was evaluated for *Streptococcus sanguinis*, *Streptococcus gordonii*, *Streptococcus oralis* and *Streptococcus mitis* isolated from patients with IE, under static and continuous flow conditions. Our *in silico* analysis revealed that *S. oralis* is the most prevalent species in IE. Potential resistance to at least one antimicrobial was detected on 38.4% of the genomes, most belonging to oral *Streptococci* (79.5%). None of the genomes showed potential resistance to the antimicrobial used as primary prophylaxis for IE (amoxicillin). However, resistance genes for azithromycin and/or doxycycline (currently recommended as alternatives for allergic patients) were observed in all genomes of oral samples that were resistant to at least one antimicrobial. *S. gordonii* and *S. sanguinis* were able to form stronger biofilms than *S. mitis* and *S. oralis* under static conditions. Under continuous flow (which better mimics *in vivo* conditions), *S. gordonii* was able to form significantly more biofilm than *S. sanguinis*. Investigating oral Streptococci antimicrobial susceptibility and ability to form biofilms is crucial to understand the impact of antibiotic prophylaxis on the prevention of IE.

Keywords: Microbiology, Endocarditis, Dentistry, Disease Prevention, Biofilm

D-16. Human SPECC1L mutation knock-in mouse model reveals the role of cytoskeletal regulation in palatogenesis

Iman Dilower¹, Brittany M Hufft-Martinez^{1,2}, An Tran¹, Dana Thalman¹, Michael Kuehn¹, Everett Hall¹, Jeremy Goering¹, Andras Czirok³, Irfan Saadi^{1,2}

¹Department of Cell Biology and Physiology, ²Institute of Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. ³Department of Biological Physics, Eotvos University, Budapest, Hungary.

Normal embryonic development requires dynamic tissue remodeling through movement and fusion events. Disruption of these events can lead to congenital structural anomalies including cleft palate (CP), exencephaly and ventral body wall defects (VBW). CP affects ~1/1,200 live-births worldwide. A critical step in palate development is the elevation and fusion of bilateral palatal shelves (PS), which requires coordinated cell proliferation, orientation, actomyosin contractility and tissue mechanics. Human mutations in *SPECC1L* result in several tissue movement and fusion congenital anomalies. *SPECC1L* is a cytoskeletal scaffolding protein that interacts with filamentous actin (F-actin), microtubules, and non-muscle myosin II. We previously generated a *Specc1l* null allele and an in-frame deletion of the coiled-coil domain 2 (Δ CCD2), which facilitates binding with microtubules and harbors most human pathogenic variants. Δ CCD2 mutant embryos exhibit exencephaly (~50%), CP (~50%) and VBW (~60%). Throughout cultured primary cells, *SPECC1L* largely associates with F-actin. Complete loss of *SPECC1L* results in increased F-actin staining, indicating participation in F-actin turnover. In contrast, *SPECC1L*- Δ CCD2 protein fails to traffic within the cell due to loss of microtubule association but retains F-actin turnover, causing severe intracellular cytoskeletal disorganization. To investigate human disease relevance, we developed a knock-in mouse model carrying the patient-derived T397P mutation within CCD2. The *SPECC1L*-T397P mutant embryos displayed ~80% CP and 100% VBW. Unlike Δ CCD2, *SPECC1L*-T397P protein exhibited normal intracellular trafficking but impaired F-actin turnover in cells, revealing allele-specific effects. AlphaFold modelling predicts local changes in T397P-CCD2 that might disrupt protein-protein interactions. These findings reveal novel mechanisms of cytoskeletal regulation during palate morphogenesis.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-17. Functional Characterization of Argonaute Syndromes Variants in *Caenorhabditis elegans*

Belén Gaete Humada¹, Rebecca Mitchell¹, Amélie Piton², Davor Lessel³, Hans-Jürgen Kreienkamp⁴, Victor Ambros⁵, Anna Zinovyeva¹

¹ Division of Biology, Kansas State University, Manhattan, KS

² Department of Translational Medicine and Neurogenetics, Institute of Genetics and Molecular and Cellular Biology, Strasbourg University, Strasbourg, France

³ Institute of Human Genetics, University of Regensburg, Regensburg, Germany

⁴ Institute of Human Genetics, University Medical Center Hamburg-Eppendorf, Hamburg, Germany

⁵ Program of Molecular Medicine, UMass Chan Medical School, Worcester, MA

Gene regulation is essential for animal development. Argonaute (AGO) proteins, guided by microRNAs (miRNAs), play key roles in post-transcriptional regulation by silencing target genes. Recently, coding variants in human AGO1 and AGO2 genes have been identified as causative for rare developmental disorders termed Argonaute Syndromes (AS). The AS variants, primarily missense alleles, are associated with clinical manifestations that range from mild to severe. As the number of distinct AS variants increases, there is a need to rapidly characterize their effects on molecular AGO functions. Given that human and *Caenorhabditis elegans* miRNA-associated AGOs are highly conserved, modeling AS variants in *C. elegans* allows for their rapid *in vivo* functional characterization. We previously modeled four human AGO1 AS mutations in the *C. elegans* homolog *alg-1*, revealing allele-specific developmental and miRNA-related molecular phenotypes. In this study, we used CRISPR-Cas9 genome editing to engineer 13 additional *alg-1* AS variants, further increasing our coverage of AS variations. Genetic analysis of these *alg-1* AS strains revealed varying degrees of developmental defects. While some variants cause only mild effects, a subset of *alg-1* AS alleles disrupt development more strongly than loss of *alg-1*, exhibiting antimorphic phenotypes. Introducing wildtype *alg-1* into *alg-1* AS mutant strains partially restores normal development, consistent with dosage-dependent effects of ALG-1 function. Our current work aims to characterize the molecular effects of *alg-1* AS variations in miRNA biogenesis and activity. Genetic and molecular analysis will enable functional classification of AS variants, contributing to our understanding of genotype-phenotype causalities and disease mechanism of AS.

D-18. Deep Learning Framework for Temporal Data Imputation in Longitudinal Electronic Health Records: Sequence-to-Sequence with Multi-Head Cross-Attention

Barsha Halder

Department of Biostatistics, University of Kansas Medical Center, Kansas

In longitudinal Electronic Health Records (EHRs), missing data is a fundamental challenge. Health-related features such as biomarkers are commonly missing at large scales. In addition, EHR datasets presents unique difficulties in handling missing values, including (a) inconsistent number of clinical visits across patients, (b) missing entries within observed records, and (c) irregular sampling intervals at which the biomarkers were observed. To address these challenges, and accurately impute missing information, this study introduces a deep learning framework that enhances the robustness of longitudinal EHR data analyses. A neural network-based sequence-to-sequence architecture with long short-term memory (LSTM) units, augmented by multi-head cross-attention was developed to impute missing biomarker values in longitudinal EHRs. The model was designed to work with irregular sampling intervals, variable number of clinical visits, enabling robust imputation in both univariate and multi-task imputation settings. The model performance was evaluated on two real-world datasets and one simulated dataset, consistently outperformed Last Observation Carried Forward (LOCF), Multivariate Imputation by Chained Equations (MICE), and K-Nearest Neighbors (KNN) across MAE, MSE, RMSE and R^2 metrics, thereby demonstrated robust performance in imputing missing values in longitudinal EHRs. Imputing missing biomarkers in longitudinal EHRs necessitates modeling temporal dynamics across patients visits. Large datasets with values missing at different time points pose significant challenges in downstream analyses. This study demonstrates that a deep learning framework without distributional assumptions can effectively outperform conventional imputation methods in imputing missing temporal data in EHRs.

D-19. Scalable extraction, alignment, and annotation validation for thousands of plastid genomes through a novel bioinformatic software

Thanina Hamitouche¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

Large-scale plastid phylogenomics has become a central approach in plant phylogenetics, but extracting homologous genes across thousands of plastid genomes remains a complex task. Here we present a software tool designed to automatically extract homologous regions across large sets of plastid genomes and detect annotation discrepancies before performing automated multiple sequence alignment (MSA) across the extracted regions. Our software, *plastburstalign*, was written in Python and provides a computational procedure that autonomously extracts and aligns genes, introns, and intergenic spacers across hundreds or thousands of plastid genomes. The tool addresses five key difficulties inherent to plastid genome alignment: the mosaic organization of plastid genomes, which requires precise identification and grouping of homologous gene regions; the presence of annotation errors that necessitate automatic detection and exclusion of incorrect annotations; the need to apply different alignment strategies for coding versus noncoding regions; the practical need to process hundreds to thousands of genomes within reasonable computational time; and the complexity of manually excluding user-specified regions, which needs automated region filtering before alignment. These capabilities enable scalable, accurate, and efficient evaluation of plastid genome annotations in large comparative datasets within a reasonable time compared to existing state-of-the-art methods.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-20. Interferon hypersensitivity in Down syndrome primes microglial dysfunction from development

Hayden C. Hawks¹, Lexe M. West¹, Katherine I. McCarthy¹, Sunita N. Varghese¹, Abhik Saha¹, Greta Foye¹, Luke Johnson¹, Keith P. Smith², Heather M. Wilkins², and Katherine A. Waugh¹

Departments of Cell Biology and Physiology¹ and Neurology², University of Kansas Medical Center, Kansas City, KS 66160
Individuals with Down syndrome (DS) caused primarily by trisomy 21 (T21) are susceptible to a wide variety of neurological conditions across their lifespan, including autism spectrum disorder, Alzheimer's disease (AD) and intellectual disability. However, the symptomatic progression of these conditions shows significant heterogeneity that is mechanistically poorly understood. There is emerging evidence that chronic neuroinflammation influences progression of these conditions, neuroinflammation which is detectable in DS fetuses as early as the second trimester. A hallmark of immune perturbation in DS is hyperactive interferon (IFN) signaling driven largely by the triplication of 4 of 6 interferon receptor (IFNR) subunits located on chromosome 21. Interferonopathies have been implicated in cognitive impairment and accelerated neurodegeneration, and correction of *IFNR* dosage has been shown to ameliorate aberrant cognitive and developmental phenotypes in mouse models of DS. Hyperactive IFN signaling also drives microglial dysfunction in human iPSC models of DS and AD. Given that microglia originate from the inflammation vulnerable yolk sac during embryogenesis, we hypothesize heightened IFN signaling aberrantly "trains" DS progenitors establishing durable epigenetic programs that shape microglial function. To investigate, we differentiated T21 and euploid human induced pluripotent stem cells (hiPSCs) into yolk sac embryoid bodies, stimulated them with interferon, and generated microglia. We characterized karyotype-specific activation marker profiles via flow cytometry and dissected morphological phenotypes using Fiji. These studies will test whether IFN hypersensitivity in DS programs microglial dysfunction early in development. Defining these vulnerabilities may uncover opportunities to delay dementia in DS and reveal mechanisms relevant to AD.

D-21. Identification and Optimization of Peptide Inhibitors of the Classical Complement Pathway

Author: Aprajita Jha¹, Shannon S. Allen², Hailee N. Nerber², Jon T. Skare², Brandon Garcia¹,

¹Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, KS

² Department of Microbial Pathogenesis and Immunology, College of Medicine, Texas A&M University, Bryan/College Station, TX

Aberrant activation of the complement system is a major driver of autoimmune and inflammatory diseases, where uncontrolled protease activity amplifies immune responses and causes tissue injury. The classical pathway, triggered by the proteases C1r and C1s, represents a critical control point that remains underexplored by current therapeutics. Interestingly, the Lyme disease pathogen *Borrelia burgdorferi* has evolved specialized proteins such as BBK32 and Elps that selectively block C1r and C1s respectively. These natural immune evasion molecules provide a powerful evolutionary template for therapeutic design. Building on this principle, our project applies biomimicry to develop short peptides that mimic the inhibitory motifs of BBK32 and Elps. Peptides offer distinct advantages over larger biologics, including structural tunability, access to defined binding sites, and reduced immunogenic potential while maintaining high specificity. Using phage display, we identified multiple C1r- and C1s-binding candidates, with two advancing as promising leads. The structural features of each peptide are being assessed through ongoing NMR and crystallography trials aimed at resolving peptide-C1r complexes at atomic resolution. Functional characterization by surface plasmon resonance has established binding kinetics, while competition assays with BBK32 and Elps confirm target engagement. Enzyme-based assays are also being performed to evaluate classical pathway inhibition, with current efforts directed toward enhancing inhibitory potency. Collectively, this integrative approach demonstrates how microbial immune evasion strategies can be translated into minimal synthetic peptides, establishing a novel platform for the development of pathway-specific complement inhibitors with therapeutic potential.

D-22. Profiling the NTMT1 Protein Network Using Spectrometry-based Proximity Labeling

Sahadev Khadka, Wei Wu, Ping Li

Kansas State University, Department of Chemistry, Manhattan, KS, USA

N-terminal methyltransferase 1 (NTMT1) regulates diverse cellular processes by catalyzing α -N-terminal methylation, a modification whose dysregulation has been linked to multiple cancers. However, the broader protein environment that shapes NTMT1 activity remains poorly defined. Conventional biochemical approaches, such as co-immunoprecipitation, often miss weak, transient, or compartment-restricted interactions, creating a need for tools capable of capturing NTMT1's molecular neighborhood with greater sensitivity. BioID2 and TurboID are engineered biotin ligases that covalently attach biotin to lysine residues of nearby proteins in living cells. BioID2 provides high specificity and low background labeling but requires extended incubation times. TurboID enables rapid labeling and efficiently captures dynamic, short-lived interactions, though its larger size and higher background can be limiting relative to BioID2. Their complementary properties make proximity biotinylation a powerful strategy for mapping protein interaction landscapes. In this project, NTMT1 will be fused to both BioID2 and TurboID to biotinylate proximal proteins under native conditions. Biotin-tagged proteins will be enriched by streptavidin affinity purification and identified through high-resolution mass spectrometry. Using two biotinylation systems will enable comparison of labeling depth and specificity, allowing the identification of both stable partners and transient interactors of NTMT1. Because NTMT1's substrates and regulators may interact only briefly during methylation cycles or occupy specific nuclear microenvironments, this dual-enzyme approach is particularly advantageous. Overall, this work aims to generate a comprehensive map of NTMT1-associated proteins and establish a framework for future functional studies.

D-23. Coordinated collective cell invasion requires balanced levels of the stress response transcription factor ATF4

Rehan Khan¹, Emily Burghardt¹, Jocelyn McDonald¹

¹Division of Biology, Kansas State University, USA

Collective cell migration is critical for development and is utilized by cancer cells to invade as cohesive groups. A key to improving cancer outcomes is tackling metastasis, the deadly spread of cancer cells. Studying metastasis in human models is difficult. Thus, our research uses the fruit fly as a simpler *in vivo* genetic model. In fruit flies, the "border cell" cluster, a group of 6-10 cells, migrates through the ovary as the egg develops, mirroring how cancer cells navigate tissues and organs. We focus on how endoplasmic reticulum stress response pathways control collective invasion. We hypothesize that balanced levels of the key stress-response gene ATF4 promote collective cell migration. Using genetic tools, we increased or decreased ATF4 expression in border cells. The results were striking; too much or too little ATF4 significantly affected the journey of border cells. Live time-lapse imaging of migrating clusters revealed that ATF4-altered cells consistently shifted to the back of the cluster. Using ImageJ software, we quantified the overall cluster speed and position of ATF4-altered cells relative to those of wild-type neighbors. ATF4-altered cells showed a marked reduction in lead position occupancy without affecting their speed. Thus, altering ATF4 disrupts the ability to take the lead, suggesting that ATF4-deficient cells are unable to drive the movement of the entire cluster. Thus, balancing internal stress signals is vital for coordinated collective cell migration. Understanding how cells migrate collectively will help us identify new strategies to prevent the spread of cancer and to better understand developmental defects.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

D-24. Voltage-Gated Sodium Channels in Cancer Cells: Implications for Anesthetic Mechanisms and Clinical Sensitivity

Yousaf Khan¹, Will Krogman¹

¹Department of Anesthesiology, KU School of Medicine-Wichita

Voltage-gated sodium channels (VGSCs) are essential for cellular excitability and represent established molecular targets of anesthetic agents. Emerging evidence demonstrates that VGSCs—particularly the Nav1.5 and Nav1.7 isoforms—are markedly upregulated and functionally active in multiple carcinomas, including breast and colon cancers, where they promote invasion, metastasis, and poor clinical outcomes. These cancer-associated channels often exhibit embryonic splice variants that enhance persistent sodium influx, intracellular acidification, and extracellular matrix degradation, distinguishing them from their counterparts in normal tissues. Anesthetics, including local, inhalational, and intravenous agents, modulate VGSC activity through direct pore blockade, alterations of voltage-sensing domains, and interactions with lipid rafts that regulate membrane organization and ion conductance. This narrative review synthesizes evidence suggesting that the heightened abundance and altered regulation of VGSCs in cancer cells may modify their responsiveness to anesthetics. Consequently, anesthetic exposure could have distinct cellular effects in malignant versus non-malignant tissues, potentially influencing tumor biology and perioperative outcomes. Understanding these interactions may refine anesthetic selection and inspire future investigations into channel-targeted anesthetic strategies that optimize oncologic and anesthetic care.

D-25. Novel truncation variants expand the role of *SPECC1L* in neurodevelopmental disorders

Michael Kuehn¹, Jeremy Goering¹, Luke Wenger¹, Yomna Badawi¹, Marta Stetsiv¹, Preethi Kunchala¹, An Tran¹, Brittany Martinez¹, Dana Thalman¹, Iman Dilower¹, Shubhangi Singh¹, Emily Farrow⁴, Olivia Veatch^{1,2}, Hiroshi Nishimune^{1,5}, Irfan Saadi^{1,3}

¹Department of Cell Biology and Physiology, ² Department of Psychiatry and Behavioral Sciences, ³ Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. ⁴Genomic Medicine Center, Children's Mercy Hospital, Kansas City, MO. ⁵Department of Physical Medicine and Rehabilitation, University of Missouri, Columbia, MO.

Neurodevelopmental disorders (NDDs) affect about 1 in 12 children yet remain some of the most challenging conditions to diagnose and treat. Many NDDs are associated with cytoskeleton gene variants. One such gene encodes a cytoskeletal scaffolding protein *SPECC1L*. Missense variants in *SPECC1L* have been associated with structural birth anomalies. Some of these patients also present with NDDs, but little is known about *SPECC1L*'s role in brain development and function. In collaboration with Children's Mercy Hospital, we identified five patients with autosomal-dominant *SPECC1L* protein-truncating variants (PTVs). Notably, phenotype scoring of all published case reports of *SPECC1L* variants showed a significant increase in NDD phenotypes in patients with PTVs compared to those with missense variants in the Calponin Homology Domain (CHD) or Coiled Coil Domain 2 (CCD2). All newly identified PTVs encode protein isoforms missing the C-terminal CHD. We developed a *Specc1l-ΔC510* mouse model mirroring patient PTVs with a resultant isoform lacking the CHD. Heterozygotes for this allele (*Specc1l^{ΔC510/+}*) showed behavioral abnormalities associated with NDDs, including reduced sociability, learning and motor deficits, and reduced anxiety behaviors/fear response. We identified strong expression of *SPECC1L* in cerebellar Purkinje cells (PC). Analyses of cerebella from *Specc1l^{ΔC510/+}* mice showed reduced PC density compared to WT littermates, a phenotype also associated with NDD patients. Global and Phospho-proteomic analyses of these cerebella revealed a reduction in signaling pathways associated with maintenance and cellular export, a possible cause of the observed PC reduction. These data suggest a model for the mechanistic exploration of phenotypes associated with patients with NDDs.

D-26. The ABC transporter EF2223-EF2221 of *Enterococcus faecalis* imports high mannose glycans, and is dependent on a three-component signal transduction system

Abdulrahman M. Naeem¹, Tolupe I. Ade¹, Zakria H. Abdullahi¹, Rupa Addanki², Mark P. Farrell², Ana Flores-Mireles³, and Lynn E. Hancock¹

¹Department of Molecular Biosciences, University of Kansas, Lawrence, KS

²Department of Medicinal Chemistry, University of Kansas, Lawrence, KS

³Department of Biological Sciences, Notre Dame University, South Bend, IN

In the absence of preferred carbon sources, the opportunistic pathogen, *Enterococcus faecalis*, utilizes a diverse array of carbon substrates for metabolism including host glycans. Through transcriptomic studies, we identified a 6 gene operon comprised of an ABC transporter and signal transduction system that was abundantly expressed in the presence of high mannose N-linked glycans. Using luciferase reporter assays, we show that operon expression is dependent on the signal transduction system, in particular the response regulator YesN, and requires endoglycosidase activity to liberate the glycans from glycoproteins. We hypothesized that YesN would contribute to physiological adaptations at sites of infection and tested the parental and *yesN* mutant in a catheter associated urinary tract infection model in mice. The *yesN* mutant was attenuated in dissemination to distal sites from the initial inoculation in the bladder, suggesting that this glycan sensing and import system are important to *E. faecalis* as a pathogen. We are presently testing the ability of the ABC transporter to recognize distinct host glycans for nutrient uptake. We have purified the solute binding protein, EF2221, and will be testing several distinct forms of high mannose glycans for binding affinities using microscale thermophoresis. We are also interested in the signal transduction pathway connecting the histidine kinase, YesM, for its ability to phosphorylate YesN to initiate signal transduction. We have purified the cytoplasmic domain of YesM and the YesN protein and will be conducting phosphotransfer assays along with gel mobility shift assays to establish their function in signal transduction.

E-1. Up-Regulating the cGAS-STING Pathway via HuR Inhibition in Prostate Cancer

Ngoc Huan Nguyen¹, Sunghae Kim¹, Xiaoqing Wu¹, and Liang Xu¹

¹Department of Molecular Biosciences, University of Kansas

Prostate cancer is the most common cancer type in men and the second leading cause of cancer deaths worldwide. Cancer immunotherapies have achieved significant success compared to traditional methods including chemotherapy and radiotherapy; however, they face challenges such as low response rate. Therefore, discovering new approaches is crucial to enhance the treatment efficacy and patients' survival. The cGAS-STING pathway is a cytosolic dsDNA sensor that is part of the innate immune system and responds to cancer cells. Human antigen R (HuR), also known as HuA or ELAVL1, is an RNA-binding protein that is involved in various post-transcriptional regulatory processes, including mRNA splicing, maturation, nuclear export, stability, and translation. Consequently, HuR dysfunction contributes to the development of various diseases including cancers; and ubiquitous cytoplasmic HuR levels are found in various cancer types. Our lab has discovered HuR small molecule inhibitors (KHs) that inhibit the HuR-mRNA interaction. We hypothesize that HuR promotes cancer immune evasion by suppressing the cGAS-STING pathway, HuR inhibition can overcome the immune-resistance and improve the response of cancer immunotherapies. This study will offer a promising strategy to improve cancer immunotherapy and further research is required to understand the mechanisms of how HuR regulates the cGAS-STING pathway, hence leads to the activation of immune system.

K-INBRE 2026 Symposium Poster Presentation Abstracts

E-2. Characterizing the HuR-ID1 Regulatory Network in Pancreatic Cancer

Candice Osaqie¹, Xiaoqing Wu¹, Liang Xu.¹ ¹Department of Molecular Biosciences, University of Kansas
Name of Institution to be credited - University of Kansas - Lawrence

Pancreatic ductal adenocarcinoma (PDAC) remains one of the most lethal malignancies, driven by aggressive growth and resistance to therapy. HuR (ELAVL1), an RNA-binding protein overexpressed in PDAC, stabilizes oncogenic transcripts and supports tumor progression. Our preliminary data indicate that HuR inhibition downregulates inhibitor of DNA binding 1 (ID1), a transcriptional regulator associated with tumor aggressiveness. We hypothesize that the HuR-ID1 axis plays a critical role in PDAC maintenance and may represent a novel therapeutic vulnerability. Current efforts focus on characterizing this axis through HuR modulation strategies and transcriptomic profiling to define its contribution to PDAC biology. These findings could inform future approaches to disrupt HuR-ID1 signaling for improved treatment outcomes.

E-3. Characterization of the Role of *BODYGUARD2* in the Formation of Cuticle in *Arabidopsis thaliana*

Zanri Pieterse^{1,2}, Yu Nj^{1,3}, Libin Yao^{1,3}, Zolian S. Zoong Lwe^{1,4}, and Ruth Welti^{1,3}

¹Kansas Lipidomics Research Center, ²Department of Anatomy and Physiology, ³Division of Biology, ⁴Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, KS 66506

In higher plants, as in humans and other mammals, there is a cross-linked lipid matrix on the outside of the epidermal cells protecting the organism from pathogens and other environmental threats. In plants, this matrix is called the cuticle. These cross-linked lipid barriers prevent evaporation of water, though some degree of permeability still exists. In *Arabidopsis thaliana*, a gene called *BODYGUARD2* (*BDG2*) encodes an α/β hydrolase fold protein and is a member of a family of five proteins. Of this family, only one gene, called simply *BODYGUARD* (*BDG*), has been characterized. *BDG* has been found to affect cutin biosynthesis, and stimulates, at the transcriptional level, genes encoding enzymes involved in the induced synthesis of the hormone abscisic acid (ABA) in response to osmotic or drought stress perceived at the organismal surface. Gene sequence alignment showed that *BDG2* is ~80% identical to *BDG*. Very little research has been done on *BDG2*, but it is hypothesized that it is essential for proper cuticle formation, influencing both the cutin and wax biosynthesis pathways. Current work focuses on assessing cuticle permeability in *BDG2* mutant plants to determine whether loss of *BDG2* alters cuticle function. In addition, we are investigating whether *BDG2* plays a role in osmotic stress responses and whether *BDG2* mutants display altered germination patterns compared to wild-type plants under control and stress conditions.

E-4. Efforts Towards Enhancing Potency of PROTACs Specific to NTMT1

Arti Pujari, Chao Ann, Ping Li
Department of Chemistry, Kansas State University

Protein N-terminal methyltransferase 1 (NTMT1) plays essential roles in genome stability, cell-cycle regulation, and tumor progression. Its dysregulation has been implicated in many cancers, especially the colorectal cancer. Our laboratory has recently developed the first cell-permeable PROTAC degrader 1 targeting NTMT1 specifically in colorectal carcinoma cell lines HCT116 and HT29, achieving DC₅₀ values as low as 7.53 μ M and >90% NTMT1 degradation (Li et al., 2022). Advances in PROTAC design highlight that modifying linker characteristics such as rigidity, geometry, and polarity through incorporation of cyclic linkers, as well as adopting a new E3 ligase ligand can enhance degradation potency significantly. Building on these insights, we are redesigning degrader 1 with either an optimized cyclic linker structure or ligand recruiting DCAF16 E3 ligase to improve its metabolic stability, spatial orientation, and compartment selectivity. This effort aims to generate next-generation NTMT1 degraders with enhanced cellular performance for degradation efficiency and therapeutic potential. These findings will provide a roadmap for future rational PROTAC development and establish targeted NTMT1 degradation as a compelling modality for mechanistic study and therapeutic exploration in oncology.

E-5. Distinct behavioral phenotypes exhibit unique brain-wide neural activation patterns during observational avoidance learning.

Authors: Shannon Ruble, Helen Durrett, Cassidy Stecher, Cassandra Kramer, Lexie West, and Maria M. Diehl
Affiliation: Kansas State University, Department of Psychological Sciences

Observational learning allows individuals to gain information about potential outcomes without directly experiencing those outcomes and is particularly advantageous when learning to actively avoid danger without risking harm to themselves. To assess observational learning of active avoidance, Observer rats witnessed a Beginner or an Advanced Demonstrator rat undergo platform-mediated avoidance (PMA), in which rats learn to avoid a tone-signal footshock by stepping onto a safe platform. We found that Observers acquired PMA regardless of their Demonstrator's experience in the task. We were then interested in the behavioral phenotypes of Observers and how these phenotypes were related to experimental conditions. We identified three distinct behavioral phenotypes based on the time they spent avoiding, freezing, or food-seeking. Exposing Observers to footshock prior to Observational PMA increased the ratio of Avoiders to Freezers or Lever-Pressers. We then used c-Fos immunohistochemistry to quantify neural activation correlated with Observational PMA. Avoiders and Lever-Pressers showed differences in neural activation in the prelimbic (PL) and infralimbic (IL) cortices as well as distinct correlations in activation between these and other brain areas measured including the anterior cingulate cortex, nucleus accumbens, and basolateral amygdala. Ongoing work is investigating the role of PL and IL in Observational PMA and how chemogenetically inhibiting these areas affects PMA acquisition in different behavioral phenotypes.

E-6. Unoccupied

E-7. Directed Evolution of Iridium-Containing TcDyP for Stereo-controlled Cyclopropanation for Drug Precursors

Tinky Sharma, Samiksha Khadka, Ping Li
Department of Chemistry, Kansas State University, Manhattan, Kansas, U.S.A.

Artificial metalloenzymes (ArMs) are engineered catalytic systems formed by incorporating a non-native metal cofactor or metal complex into a biological protein scaffold, resulting in an integrated catalytic system enabling stereo control of a broad spectrum of substrates and thereby overcoming the functional limitations of natural metalloproteins to produce various drug precursors. **In this study, an Ir-porphyrin-based artificial metalloenzyme was generated through the incorporation of a synthetically derived iridium cofactor into the native heme-binding pocket of TcDyP, replacing the endogenous Fe-porphyrin. Ir(Me)MPIX was prepared from hemin chloride through a streamlined multistep sequence and confirmed by UV-Vis, NMR, and mass spectrometry.** Assembly of Ir(Me)TcDyP was achieved by expressing the apo-TcDyP enzyme with *E. coli* Nissle 1917 cells in the presence of Ir(Me)MPIX. The resulting ArM exhibits catalytic activity toward the cyclopropanation between styrene and ethyl diazoacetate, exhibiting both diastereoselectivity and enantioselectivity of the products. This work highlights the ability of employing protein scaffolds to tune the reactivity and stereocontrol of non-natural metal centers and demonstrates the potential of Ir-porphyrin-based ArMs to serve as versatile catalysts for abiological transformations to produce drug precursors.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

E-8. Cognitive and behavioral impairment in *FMR1* knockout rats across the lifespan

Bhavana Sivayokan, Tsam Myu Shawng Maji, Bethany Plakke
Department of Psychological Sciences, Kansas State University

Fragile X syndrome (FXS) is an X-linked dominant disorder caused by a triplet repeat expansion in the *FMR1* gene, which codes for the protein FMRP. The loss of FMRP in FXS results in immature dendritic spines and higher spine density, which causes disrupted synaptic plasticity leading to multiple cognitive and behavioral impairments. This study used homozygous and heterozygous *FMR1* knockout (KO), and wild type (WT) Long-Evans rats (at least 12 per group) to examine cognitive and behavioral impairment across the lifespan. All animals underwent grooming, nesting removal, rotarod, and grip strength tests. A subgroup of animals was trained on a touchscreen-based categorization task assessing cognitive flexibility. Results showed that older animals spent less time grooming than younger animals ($p=.037$), had fewer bouts of grooming ($p<.001$), and a later onset of grooming ($p<.001$). KO rats spent significantly more time digging during the nesting removal test than WT rats ($p<.001$). Latency to fall from the rotarod and the relative grip strength were greater among aged animals, irrespective of genotype, $p<.001$. Results of the categorization task showed that while the overall accuracy improved with days of training, both KO and WT rats struggled to reach the criterion of 70% correct for each category. They seemed to rely on a side bias which was more prominent among the KO than WT rats. These findings suggest repetitive behaviors manifest differently in both young and old KO rats, motor deficits emerge later in life, and aged rats, irrespective of genotype, struggle with cognitive flexibility.

E-9. Disruption of the Blood–CSF Barrier by *Specc1l* Deficiency Causes Embryonic Ventriculomegaly and Hydrocephalus

Dana Thalman¹, Brittany M. Hufft-Martinez^{1,2}, An Tran¹, Abigail Truong¹, Jeremy Goering¹, Luke Wenger¹, Zaid Umar¹, Benjamin Kelm¹, Sarah C. Wilson¹, Marta Stetsiv¹, Timothy C. Cox³, Erin E. Young^{1,4}, Irfan Saadi^{1,2}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS, ²Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS, ³Departments of Oral & Craniofacial Sciences, School of Dentistry, and Pediatrics, School of Medicine, University of Missouri-Kansas City, MO, ⁴Department of Anesthesiology, Pain, and Perioperative Medicine, KU Medical Center, Kansas City, KS

Ventriculomegaly and congenital hydrocephalus are genetically heterogenous conditions that affect ~1/500 and ~1/1000 live births, respectively. Ventriculomegaly arises when cerebrospinal fluid (CSF) accumulates in brain ventricles, enlarging them. It can progress to hydrocephalus with elevated pressure and skull deformation. Both conditions cause brain compression and impaired function. CSF is produced in the choroid plexus (ChP), with production regulated by the Blood-CSF barrier (BCB). SPECC1L, a cytoskeletal scaffolding protein that interacts with actin, microtubules, and cell-cell junction proteins, is expressed in the ventricular ependyma and ChP. Patients with missense *SPECC1L* mutations often show ventriculomegaly. *Specc1l* null mice on homogenous FVB/NJ and C57BL/6J backgrounds showed edema at embryonic day (E) 13.5, enlarged lateral ventricles and disorganized ChP at E16.5, and perinatal lethality. *In vivo* dye injections indicated leakage from ChP of *Specc1l* null mutants into the ventricles and brain at E16.5, confirming BCB dysfunction. ChP immunostaining revealed abnormal membrane-associated β -catenin (adherens junctions) and Occludin (tight junctions) expression at E16.5, consistent with BCB dysfunction. Interestingly, C57BL/6J:FVB/NJ (50:50) F1 hybrid homozygous mutants lacked gestational edema and ventriculomegaly, survived postnatally, but most developed hydrocephalus around postnatal day 21, suggesting late-onset BCB defects. F2 mice exhibited three phenotypes: perinatal lethal, hydrocephalic, and non-hydrocephalic, consistent with segregation of modifier SNPs. SNP genotyping (Transnetyx) and minimal region mapping identified two candidate genomic regions harboring the modifiers. These findings revealed a novel role for SPECC1L in BCB formation and suggested that common genetic variants can modulate this function, informing the etiology of ventriculomegaly and congenital hydrocephalus.

E-10. Assessment of GenBank-archived human mitochondrial genomes through modern quality filtering and reassembly

Buddha Thapa Magar¹ and Michael Gruenstaeudl¹

¹Department of Biological Sciences, Fort Hays State University

Many biomedical investigations rely on retrieving and analyzing complete human mitochondrial genomes archived on GenBank. However, a substantial proportion of mitochondrial genome records on GenBank display incorrect assembly, incomplete annotation, or both. A careful evaluation of these genome records is needed to ensure that only accurate and reliable genomes are used in biomedical research. For this study, we compiled a set of more than 1,000 human mitochondrial genomes archived on GenBank and assessed their data quality so that scientists can make informed decisions and data reuse and select only high-quality genomes. Specifically, we developed a computational pipeline to evaluate the assembly quality of complete human mitochondrial genomes on GenBank by comparing each archived genome sequence to a modern de novo reassembly generated with contemporary assembly software. The pipeline includes a quality control process for short read sequence data, a contamination check, a mapping process against mitochondrial reference sequences, and genome assembly using modern assembly software. Our preliminary results illustrate that a large proportion of GenBank-archived human mitogenomes cannot be replicated under contemporary assembly standards.

E-11. Nrf2 as a therapeutic target to improve T cell function in muscle invasive bladder cancer (MIBC)

Aprajita Tripathi, Nadine Santana-Magal, Jared Rack, Debolina Dasgupta, Benjamin L. Woolbright and Kalyani Pyaram
Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, USA

Introduction: Bladder cancer is seventh most common malignancy in the United States, causing an estimated 16,840 deaths in 2024. Despite therapeutic advances, MIBC shows poor survival, with only ~20% of MIBC patients showing durable responses to immunotherapy. Nrf2, a Keap1-regulated transcription factor, is highly activated in tumor-infiltrating T cells in BC patients. We and others have reported that Nrf2 loss enhances IFN- γ and Granzyme B expression supporting a cytotoxic T cell phenotype. We therefore *hypothesized* that Nrf2 inhibition would improve T cell-mediated anti-tumor immunity in MIBC. **Methods:** We used mice with T cell-specific deletion of Nrf2 (Nrf2-KO) or constitutive activation of Nrf2 by deleting Keap1 (Keap1-KO) to evaluate T cell-intrinsic role of Nrf2 in MIBC. *In vivo*, we assessed tumor growth of BBN963 cells in a syngeneic bladder cancer model. *In vitro*, we performed tumor-killing assays by coculturing CD8⁺ T cells treated with the Nrf2 inhibitor ML385 and with BBN963 cells. **Results:** BBN963 tumors implanted in Nrf2-KO mice (with Nrf2-depleted T cells) exhibited remarkably reduced tumor growth compared to wildtype mice while Keap1-KO mice (elevated Nrf2 in T cells) displayed significantly larger tumors compared to WT. Pharmacological inhibition of Nrf2 using ML385 improved the tumor-killing ability of CD8⁺ T cells against BBN963 bladder cancer cells. **Conclusions:** These findings reveal a previously unrecognized T cell-intrinsic role for Nrf2 in suppressing antitumor immunity and promoting bladder cancer progression. Our work identifies Nrf2 as a potential immune checkpoint and highlights its inhibition as a promising therapeutic strategy to improve outcomes for MIBC patients.

K-INBRE 2026 Symposium Poster Presentation Abstracts

E-12. Interactions of PhoU in *Staphylococcus aureus*

Nikolas Yackovich, Stewart Gardner

School of Science and Mathematics, Emporia State University

Staphylococcus aureus is a Gram-positive bacterium; it is an opportunistic pathogen found on the skin and in the nose. Invasive staph infections can be fatal and lead to sepsis, pneumonia, endocarditis, and osteomyelitis. This is especially concerning in healthcare-associated environments where many of the people who are contracting *S. aureus* are more likely to develop a serious infection. PhoU (PhoU1 and PhoU2) are proteins in *S. aureus* that have multiple roles; like regulating virulence factors, persister formations, and phosphate metabolism. In *Escherichia coli* PhoU forms a phosphate signaling complex with PhoR, PstB, and metals. This is not the case in *S. aureus* where PhoU does not interact with other proteins within the phosphate signaling complex. Both PhoU proteins form homodimers with themselves, but they do not strongly interact with one another. We are currently working on three different projects to understand PhoU better. The first project is using site-directed mutagenesis to mutate specific residues that are believed to form hydrogen bonds within the homodimer of PhoU1. This may confirm our model of the PhoU1 homodimer. The second project is a β -galactosidase assay with the PhoU proteins and certain Histidine Kinases within *S. aureus* that are known to regulate virulence and antibiotic resistance. The final project is creating a yeast two-hybrid prey library and screening against our "bait" proteins (PhoU) to find any other protein interactions with *S. aureus* PhoU proteins.

E-13. Next Generation Sequencing at KU Genome Sequencing Core

Hackett, Jennifer^{1,2,3}, Kristen M. Cloud-Richardson^{1,2,3}, Erik A. Lundquist^{1,2,3}, Susan M. Lunte^{1,4,5}

¹Center for Molecular Analysis of Disease Pathways, ²Genome Sequencing Core, ³Department of Molecular Biosciences, ⁴Department of Chemistry, ⁵Department of Pharmaceutical Chemistry, University of Kansas, Lawrence KS, USA

The Genome Sequencing Core (GSC) is one of three research service core labs in the NIH COBRE Center for Molecular Analysis of Disease Pathways (CMADP) at the University of Kansas (KU). The major mission of the GSC is to provide researchers with next-generation sequencing (NGS) technologies. NGS, carried out in a massively parallel fashion, has been revolutionizing bio-medical research and used in a growing list of applications. Projects supported by the GSC include de novo genome assembly, genome re-sequencing for identification of mutations and polymorphisms, transcriptome analysis (RNA-seq), and epigenomic and gene regulation studies such as ChIP-seq, Methyl-seq, and small RNA analysis. The GSC enhances the genomics infrastructure at KU by providing a range of Illumina sequencing platforms including the NextSeq2000 and NextSeq550 (mid-sized genome re-sequencing or transcriptome projects) and the MiSeq (metagenomic or targeted amplicon sequencing projects) to researchers at KU-Lawrence and across the region. To capture the full power of NGS, we provide a range of project support, including project consultation, sample quality check, sequencing library construction, Illumina sequencing, and FASTQ generation and demultiplexing. For latest pricing, current sequencing queue, or other information, visit the Genome Sequencing Core's website: <https://gsc.ku.edu/>.

E-14. The Synthetic Chemical Biology Core (SCB): A Resource for Research in Chemical Biology

Chamani Perera

Synthetic Chemical Biology Core Laboratory, University of Kansas, Lawrence, KS, USA

The Synthetic Chemical Biology Core strives to provide comprehensive synthetic chemistry capabilities to investigators under one roof. The synthetic expertise of the core includes, but is not limited to, novel and commercially unavailable small molecules, fluorescent molecules and custom peptides. The core assists in identifying hits for medicinal chemistry optimization in infectious disease targets and provides synthesis capabilities for structure activity studies of said hits. The core staff will work with investigators to design and synthesis novel molecular probes to facilitate their research. SCB core provides purification, analysis and quality control of compounds via LC/MS. The SCB core also offers MALDI-TOF analysis of biomolecules.

E-15. University of Kansas Nanofabrication Facility: Equipment and Capabilities

Ryan Grigsby^{1,2} and Susan M. Lunte^{2,3,4,5}

¹The KU Office of Research, The University of Kansas, Lawrence, KS, USA; ²The Center for Molecular Analysis of Disease Pathways, The University of Kansas, Lawrence, KS, USA; ³The Ralph N. Adams Institute for Bioanalytical Chemistry, The University of Kansas, Lawrence, KS, USA; ⁴Department of Pharmaceutical Chemistry, The University of Kansas, Lawrence, KS, USA; ⁵Department of Chemistry, University of Kansas, The University of Kansas, Lawrence, KS, USA

The University of Kansas Nanofabrication Facility (KUNF) is a Core Lab supported by the KU Office of Research and the Center for Molecular Analysis of Disease Pathways COBRE. The KUNF primarily caters to researchers who are manufacturing micro- and nanofluidic devices for biomedical research, but has the equipment and resources to also accommodate broad research applications with micro- and nanofabrication needs. The facility consists of about 1,300 ft² of ISO class 5, 1,700 ft² of ISO class 6 and 1,250 ft² of ISO class 7 cleanroom space, housing tools and materials for techniques including photolithography, nano-imprint lithography, plasma (dry) etching (ICP-RIE), wet etching, thin film deposition, scanning electron microscopy (VP-SEM), atomic force microscopy, contact angle goniometry, ellipsometry, profilometry, wafer dicing, wire bonding, laser ablation and engraving, 3D printing, hot embossing, and COMSOL software for device modeling. In addition, the facility has numerous microscopes for general inspection, ovens and furnaces, ultrapure water, and dedicated process fume hoods.

This facility is under the leadership of Dr. Susan Lunte, and the direction of Ryan Grigsby. Services and usage of the facility are available to researchers from all Kansas universities. Training is provided to new investigators and graduate students in the use of micro- and nanofabrication procedures and equipment. In addition, researchers from both non-Kansas academic and private industry institutions may contract with the facility for consultation and services, including access to the facility. Hourly and per-use rates apply for facility access, equipment usage, and staff labor. Consultation is free.

K-INBRE 2026 Symposium
Poster Presentation Abstracts

E-16. The Computational Chemical Biology and Molecular Modeling Core

David K. Johnson¹ (dkjohnson@ku.edu)

¹Computational Chemical Biology and Molecular Modeling Core, University of Kansas, Lawrence, KS, USA;

Part of the Chemical Biology of Infectious Disease COBRE at the University of Kansas, the Computational Chemical Biology and Molecular Modeling Core (CCBMM) provides the computational resources and expertise to enhance the productivity of researchers studying infectious diseases, in addition to other projects. The CCBMM has the tools and expertise to perform virtual screening, small molecule docking, cheminformatics analysis of high-throughput screening hits, binding site prediction, protein/peptide/antibody modeling and docking (including AlphaFold modeling), protein design, and molecular dynamics simulations.

Recent highlights include the identification inhibitors of ACMS decarboxylase and DNAJA1 via virtual screening, using modeling to identify the functional activity of *Legionella pneumophila* effector protein SidI, using modelling to assess the structural impact of clinically relevant point mutations of TRIM32, modeling the interaction between the Type III secretion system basal body and sorting platform proteins SctK and SctD from *Pseudomonas aeruginosa*, and the optimization of an inhibitor of PTPRD.

With the software and expertise to perform virtual screening, protein-small molecule docking, protein/peptide modeling/docking, and cheminformatic analysis, the CCBMM is a valuable resource to enhance the productivity of researchers studying infectious diseases, in addition to other projects.

The CBID COBRE is funded by the NIH NIGMS grant 1P20GM113117.

E-17. Spatial and temporal dynamics of darting behavior during platform-mediated active avoidance in rats.

Helen Durrett, Karissa Payne, Halle Ness, Shannon Ruble, and Maria M. Diehl.

Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA.

Post-traumatic stress disorder and other anxiety disorders are commonly characterized by excessive fear and avoidance, in which patients avoid cues that remind them of their trauma at the cost of pursuing daily activities. In order to gain a better understanding of these maladaptive behaviors in humans, preclinical studies have developed rodent models of fear and avoidance behavior. In rodent studies, fear responses are typically measured by "freezing", defined as the cessation of all movement except for breathing. However, recent research has identified another fear-related behavior called "darting", which is characterized by a rapid movement across a chamber in response to a conditioned stimulus. Studies have reported darting in conditioned fear (Gruene, et al., 2015) and active avoidance tasks (Ruble et al., 2025); but the spatial and temporal dynamics of darting are unknown. In our lab, we use the platform-mediated active avoidance task (PMA) in which a rat learns to avoid a tone-signaled footshock by stepping onto a safe platform while forgoing access to a food reward across 10 days of training. Our lab modified this task to include a social context in which rats learn the task in the presence of another rat, called social partner PMA. The purpose of this project was to determine the spatial trajectories of darting across social and solitary PMA contexts and whether darting is correlated with other behaviors such as freezing or food seeking.

E-18. Cadmium-Induced Circadian Dysregulation Drives Epithelial to Mesenchymal Transition and Apoptosis in Alveolar Type 2 Cells

Stefanie Cravens¹, Chandrashekar Prasad², Santhosh Kumar Suraisamy², Issac Sundar²

¹Kansas City University, College of Osteopathic Medicine

²Department of Internal Medicine, University of Kansas Medical Center

Cadmium (Cd), a toxic heavy metal found in environmental pollutants and cigarette smoke, contributes to lung injury and chronic disease. Circadian rhythm disruption plays a key role in pulmonary pathophysiology. Alveolar Type 2 (AT2) cells are critical for epithelial repair and integrity, yet the impact of Cd on their circadian regulation and epithelial-mesenchymal transition (EMT) remains unclear. Immortalized mouse alveolar epithelial (MLE-15) cells were cultured and treated with cadmium chloride (CdCl₂; 5 or 10 μM) for 24 hours. Proteins were extracted for Western blot analysis of circadian regulators (BMAL1, REV-ERBα), epithelial markers (E-cadherin, pan-cytokeratin), mesenchymal markers (α-SMA, vimentin), and apoptotic markers (cleaved and total PARP). Densitometry was performed using ImageJ. Cd exposure increased BMAL1 expression and reduced REV-ERBα in a dose-dependent manner. Epithelial markers decreased, while mesenchymal and apoptotic markers (α-SMA, vimentin, cleaved PARP) increased, indicating activation of EMT and apoptosis. Cd exposure disrupts circadian clock protein balance and promotes EMT and apoptosis in alveolar epithelial cells. These findings suggest circadian dysregulation as a key mechanism of Cd-induced epithelial injury and a potential therapeutic target in Cd-related lung disease.

E-19. Identification of interneurons in stress resistance and longevity

Mingyi Liu¹, Shelby Innes¹, Lizzie Vetter¹, Sophia Mccune¹, Moussa Gacko¹, and Shijiao Huang¹

¹ Biochemistry and Molecular Biophysics, Kansas State University

Organisms lose functions with age and must overcome environmental stressors to survive. Studies have shown that stress responses and aging are correlated. We aimed to reveal aging mechanisms in the nervous system by focusing on interneurons, which are central in integrating signals from sensory neurons perceiving environmental cues. PVQ neurons are interneurons in *C. elegans* and identified as one of the key neural network hub neurons through connectome analyses. Our results showed that PVQ ablated *C. elegans* worm strain showed increased resistance to heat stress, endoplasmic reticulum (ER) stress and mitochondria stress, suggesting PVQ neurons negatively regulate stress responses. We further found that lipid levels of PVQ ablated strain are lower compared to the wild-type strain and did not further decrease after heat stress as in wild-type worms. These results suggest that lipid metabolism may be responsible for the increased stress resistance seen in PVQ ablated strain. In addition, multiple longevity models, including mitochondrial unfolded protein response (UPR), hypoxic response, dietary restriction, and ER UPR, were used to test the necessity of PVQ neurons in extending lifespan. Our results showed that these longevity interventions still extend lifespan of PVQ ablated worms, which suggests that PVQ neurons are not necessary in these longevity pathways. We will next observe the neuronal activities of PVQ neurons under different stress conditions, aiming to demonstrate the role of PVQ neurons in stress response pathways and underlying mechanisms. This study will advance our understanding of how neurons regulate stress response and aging processes.

K-INBRE 2026 Symposium Poster Presentation Abstracts

E-20. Primary ciliary homeostasis and the metabolic sensor, O-GlcNAc, are interconnected

Chadhve Ranganathan^{1,6}, Matthew A. Kavanaugh^{1,6}, Saleem Ahmad^{1,6}, Brittany M. Hufft-Martinez¹, Brenda Magenheimer^{2,6}, Madhulika Sharma^{3,6}, Stephen C. Parnell^{4,6}, Chad Slawson^{4,6}, Darren P. Wallace^{3,6}, Mihaela E. Sardiou⁵, Robin L. Maser^{2,6}, Pamela V. Tran^{1,6}

¹Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS

²Department of Clinical Laboratory Sciences, University of Kansas Medical Center, Kansas City, KS

³Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS

⁴Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS

⁵Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS

⁶The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

Primary cilia are antenna-like sensory organelles essential for tissue development and homeostasis. Disruption of cilia function results in ciliopathies, which are syndromic and often cause renal cysts. Autosomal Dominant Polycystic Kidney Disease (ADPKD) is a ciliopathy, yet the mechanism by which ciliary dysfunction promotes ADPKD is unknown. Increased renal primary cilia lengths and impaired ciliary sensory function are associated with ADPKD renal cystogenesis. Moreover, deletion of certain ciliary genes in ADPKD mouse models attenuates disease severity and ciliary lengthening. We have shown that the metabolically regulated post-translational modification, O-GlcNAcylation, is upregulated in ADPKD kidneys. Importantly, deleting O-GlcNAc transferase (*Ogt*) in ADPKD mice restrains O-GlcNAcylation and reduces disease severity and ciliary lengthening. Here we report a direct role for O-GlcNAcylation on renal cilia lengths. Acetylated α -tubulin, which comprises the ciliary axoneme, is hyper-O-GlcNAcylated in *Pkd1* conditional knockout mouse kidneys. Additionally, in cultured patient-derived ADPKD epithelial cells, primary cilia lengths were modified by O-GlcNAc pharmacological modulators. Proteomic and phosphoproteomic analyses reveal these cilia length changes coincided with changes in the abundance and phosphorylation of actin-related proteins, suggesting O-GlcNAc regulates cilia length also via the actin cytoskeleton, a regulator of ciliogenesis. Since primary cilia are mechanosensors, we subjected cultured mouse renal epithelial cells to physiological levels of fluid shear stress (FSS). FSS reduced O-GlcNAcylation and increased phosphorylated AMPK, a key cellular energy sensor, indicating a role for cilia mechanosensing in regulating metabolism. Thus, renal primary ciliary homeostasis and O-GlcNAc are inter-regulated. We propose this inter-regulation is designed to fine-tune cell sensing and metabolism.

E-21. Exploring Non-Invasive Biomarkers of ADPKD Progression

Singh, Siraj¹, Placide, Sagine¹, Sommer, Nicole¹, Chakraborty, Anubhav¹, Vanamamaly, Krishi¹, Wallace, Darren¹, Yu, Alan¹, and Sharma, Madhulika¹.

¹University of Kansas Medical Center, Department of Internal Medicine, Kansas City KS 66160.

Introduction: Autosomal Dominant Polycystic Kidney Disease (ADPKD) is characterized by the relentless expansion of renal cysts, leading to kidney failure. Currently, no safe and effective therapies exist, and reliable non-invasive biomarkers are urgently needed. Ferritin, an iron-storage protein, was unexpectedly detected in cyst-lining epithelial cells from ADPKD patients and mouse models. Given that ferritin is secretory and serves as a biomarker in lupus nephritis, we hypothesized that abnormal ferritin release by cyst cells contributes to elevated levels in cyst fluid and urine, making it a potential biomarker of ADPKD progression, and that cyst fluid proteins may translate into urinary biomarkers of cyst growth.

Methods: Normal human kidney (NHK) epithelial cells, ADPKD cyst cells, cyst fluid from ADPKD patients, and extracellular vesicles (EVs) were obtained from the PKD RRC Core. EV number and size were quantified by NanoSight. Ferritin expression in EVs was assessed by Western blots and normalized to CD9. Mass spectrometry profiled the cyst fluid proteome.

Results: Conditioned media from ADPKD cells showed significantly higher ferritin secretion compared to NHK cells, and cyst fluid was enriched in ferritin. Urinary EVs from ADPKD patients exhibited elevated ferritin levels, which correlated with disease progression. Additionally, mass spectrometry identified DCR2 as a novel mediator of cyst progression and a potential sex-specific biomarker.

Conclusion: Ferritin may serve as promising non-invasive biomarker of disease progression in ADPKD, while DCR2 represents a novel sex-specific candidate biomarker. Together, these studies provide new avenues for biomarker discovery and clinical monitoring in ADPKD.

E-22. Using auxin-inducible degron to investigate the loss of glycosylation genes in adult *Drosophila melanogaster*

Authors: Viet Hoang Le, Hans Dalton

Department of Molecular Biosciences, The University of Kansas, Lawrence, Kansas.

Glycosylation is a common post-translational modification in which sugar residues are attached to proteins or lipids. It is responsible for several biological processes, such as protein folding, cell signaling, and cell-cell interactions. Defects in glycosylation genes lead to Congenital Disorders of Glycosylation (CDGs) which are rare diseases that can cause delay in neurological development, poor growth, facial dysmorphism, and seizures, among others. In this project, we use *Drosophila melanogaster* as an animal model to investigate the impact of impairing one of three different CDG-related genes – *DPAGT1*, *DPM1*, and *PIGA* – during adult life. *DPAGT1* and *DPM1* are involved in N-glycosylation, while *PIGA* is involved in the biosynthesis of glycosylphosphatidylinositol (GPI) anchors. To inhibit gene expression in adult flies, we utilize the auxin-inducible (degron) gene expression system (AGES) where gene knockdown only occurs in the presence of the hormone auxin. Therefore, we can avoid developmental complications due to the loss of these essential genes by only feeding auxin to adult animals. We collected progeny from 1 to 4 days old and transferred them to auxin containing food at two different concentrations – 0mM and 5mM of auxin, separated by sex. The loss of glycosylation genes in adult *D. melanogaster* shortened their life span, indicating that these genes continue to maintain its critical role for survival, not only during development. This finding suggests that most deficiencies during the glycosylation pathway decrease survival. Future directions include searching for seizure phenotypes and investigating if drugs that fix developing glycosylation-deficient flies can also restore viability post-developmentally.

E-23. University of Kansas High Throughput Screening/ Infectious Disease Assay Development Laboratory

Anuradha Roy, University of Kansas, Lawrence, KS

IDAD-HTS Laboratory, University of Kansas, Lawrence, KS, USA

High Throughput Screening/Infectious Disease Assay Development Laboratory (KU-HTS/IDAD) is a fee-for-service, state-of-the-art facility dedicated to providing academia, nonprofit institutions, biotech, and pharmaceutical industries with exceptional assay development and high throughput screening services at economical rates. The staff has experience in executing cell-based, biochemical, siRNA as well as high content screening campaigns against a plethora of target classes. HTS-IDAD Lab has a collection of 400,000 small molecules that are available for screening campaigns. KU-HTS/IDAD lab is innovative and flexible in providing superior service to the drug discovery research community, including assay development, screening, compound profiling and data mining. The labs have capabilities of executing miniaturized assays using all available platform technologies in 384/1536-well microplates. KU-HTS/IDAD lab further leverages the strengths of the medicinal chemistry/ computational modeling cores under CoBRE Chemical Biology of Infectious diseases (CBID) program to support your tool/lead discovery research.

K-INBRE 2026 Symposium Poster Presentation Abstracts

E-24. Flow Cytometry Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory

Peter R. McDonald¹, Robin C. Orozco^{1,2}, and P. Scott Hefty^{1,2}.

¹ Flow Cytometry Core, Chemical Biology of Infectious Disease, The University of Kansas, Lawrence, KS, USA; ² Department of Molecular Biosciences, The University of Kansas, Lawrence, KS, USA

The University of Kansas Flow Cytometry Core (FCC) provides access to flow cytometry and cell sorting instrumentation and expertise to researchers. Services and training are provided for flow cytometry: cell sorting and multi-parametric analysis of individual cells in solution, calculated from their fluorescent or light scattering characteristics. The FCC provides assistance in sample processing, data analysis, instrument training, software support, method and grant assistance, manuscript support, and consulting. The FCC is a 980 ft² BSL-2 facility equipped with BD FACSymphony S6 and FACSAria Fusion cell sorters, a Cytex Aurora spectral flow cytometer, an Agilent NovoCyte Advanteon conventional flow cytometer, and other supplemental assay instrumentation (Bio-Rad QX600 ddPCR, C.T.L ImmunoSpot). The flow cytometry analyzers provide users with tube- and plate-based, conventional and spectral flow cytometry. The BD FACS instruments allow measurement and sorting of up to 6 resolved populations of cells simultaneously, based on up to 50 parameters of detection using 18 simultaneous fluorochromes. The facility is equipped to handle BSL-2 samples and perform aseptic and single cell sorting into tubes or 96-well plates. The facility provides instrument training for users who desire to become self-operators of the facility instruments. The FCC will equip CBID researchers with tools directly applicable to infectious disease research, such as identifying and characterizing infectious agents such as bacteria and parasites, quantification and sorting of cells infected with microbial pathogens, and assessing chemical probe efficacy against infectious agents. The University of Kansas Flow Cytometry Core seeks to assist the academic community in achieving their research goals.

E-25. G_{αq} Subunits Engage Targets in the Nucleus

Joseph F. Loomis¹, Naincy R. Chandan², Michael Burroughs², Saji Abraham², Gregory G. Tall², Rongxi Zhang² and Alan V. Smrcka²

¹University of Michigan Program in Chemical Biology, ²Department of Pharmacology, University of Michigan Medical School, Ann Arbor, Michigan 48109

G_{αq} is a critical mediator of cells' responses to G_q-coupled receptor agonists. G_{αq}-dependent signaling regulates many physiological processes, and dysregulated G_{αq}-dependent signaling has been linked to uveal melanoma and maladaptive cardiomyocyte hypertrophy. One mechanism by which activated G_{αq} subunits promote these processes involves activation of phospholipase C beta isoforms (PLCβ); however, G_{αq} subunits also signal independently of PLCβ, notably through p63RhoGEF and Trio. Recently, our lab conducted a proximity labeling proteomic screen in HEK293 cells in which we compared wild-type G_{αq} to constitutively active G_{αq} Q209L. Each G_{αq} variant was fused to TurboID, a promiscuous biotin ligase. From this, we identified numerous proteins that were selectively enriched in cells expressing G_{αq}-Q209L-TurboID compared to cells expressing G_{αq}-WT-TurboID. These enriched proteins included known G_{αq} interactors—PLCβ, Trio, and GRK2—thus validating the ability of this approach to detect G_{αq} interactors. Intriguingly, several nuclear proteins, such as SMARCD3 (SWI/SNF complex component) and BCAS2 (spliceosome component), were enriched in our Q209L samples. Subsequently, we found that SmBIT-tagged versions of these proteins preferentially interact with constitutively active G_{αq}-LgBIT in a nanoluciferase complementation (NanoBiT) assay. Furthermore, we confirmed that purified G_{αq} directly interacts with purified SMARCD3 in an *in vitro* GST pulldown assay. Additional luciferase complementation and PLA experiments revealed that a small fraction of G_{αq} is present in the nucleus and engages SMARCD3. This nuclear G_{αq} increases following GPCR activation or the introduction of an activating mutation in G_{αq}. Taken together, these data suggest that G_{αq} engages nuclear proteins and may directly influence nuclear processes.

E-26. 3' Nucleotide Asymmetry Directs miRNA Strand Selection

Jeffrey C. Medley¹, Sumire Kurosu Moriya¹, Huiwu Ouyang², Heather Crawshaw¹, Sarah Y. Zhang¹, Ganesh Panzade^{1,3}, Will J. Sydzzyk¹, Joel T. Sydzzyk^{1,4}, Mira Bhandari^{1,5}, Christopher M. Hammell² and Anna Zinovyeva¹

¹ Division of Biology, Kansas State University, Manhattan, KS.

² Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

³ Laboratory of Human Retrovirology and Immunoinformatics, Frederick National Laboratory for Cancer Research, Frederick, MD.

⁴ University of Kansas School of Medicine, Kansas City, KS.

⁵ Department of Molecular Genetics and Cell Biology, University of Chicago, Chicago, IL.

During miRNA biogenesis, double-stranded precursors are processed into duplexes comprising functionally distinct strands. The guide strand directs the miRNA-induced silencing complex (miRISC) to complementary mRNA targets, while the passenger strand is degraded. As each strand has different molecular targets, strand selection effectively determines the target repertoire of the miRISC. Previous studies suggest that 5' nucleotide identity and thermodynamic asymmetries determine miRNA strand choice *in vitro*. However, these guidelines cannot fully explain the observed strand preference of all miRNAs *in vivo*. Here, we demonstrate a conserved role for 3' nucleotide asymmetry in facilitating miRNA strand selection in *Caenorhabditis elegans* and human HEK293T cells. Our data show that a favorable 3' nucleotide on miRNA passenger strands can promote selection of the opposing guide strand. We propose that terminal nucleotide asymmetries on both strands of miRNA duplexes promote accurate strand selection *in vivo*.

E-27. Uncovering common molecular pathways of kidney-brain dysfunction in chronic kidney disease using spatial transcriptomics

Wei Wang¹, Henrietta Ehirim¹, Nicole Sommer¹, Sumedha Gunewardena², Aditi Gupta¹ and Madhulika Sharma^{1,2}

¹Nephrology and Hypertension, Department of Internal Medicine, University of Kansas Medical Center; ²Department of Cell Biology and Physiology, University of Kansas Medical Center

The interaction between the kidneys and the nervous system plays a critical role in maintaining overall homeostasis in the body. Patients with chronic kidney disease often experience cerebrovascular complications and cognitive impairment. Conversely, brain injury can negatively affect kidney function. However, the molecular mechanisms underlying communication between the nervous system and the kidneys remain poorly understood. To access whether there are common targetable mediators of both brain and kidney injury, here we applied spatial transcriptomics using the Visium platform (10x Genomics) to analyze gene expression in kidneys and brains of a diabetic kidney disease mouse model (*db/db*), which develops both renal and neurological complications. Unsupervised clustering revealed distinct cell clusters in both tissues. Differential gene expression analysis identified more than 200 DEGs exhibiting similar directional changes in the brain and kidney. Gene Ontology analysis showed that pathways related to cytoplasmic translation, regulation of epithelial cell proliferation, response to steroid hormone and memory were commonly altered in both tissues. Among the shared DEGs, *Rnaset2b* and *Sgk1* were among the most upregulated genes across multiple cellular clusters in the diabetic kidney and brain. We validated the increased expression of RNaseT2 and SGK1 in the brains and kidneys of *db/db* mice, suggesting that these genes might be the common molecular pathways driving disease progression in both tissues. As such, they may serve as potential therapeutic targets capable of mitigating both neurological complications and renal dysfunction, ultimately contributing to more effective clinical interventions.

Symposium Participants

Name	University/Company	Position/Title	Email Address
Abassah-Oppong, Samuel	Fort Hays State University	Assistant Professor	s_abassahoppong@fhsu.edu
Abdine, Yara	Wichita State University	Undergraduate student	yaraabdine@gmail.com
Abraham, Kj	Langston University	Associate Professor & K-INBRE Campus Coordinator	kj.abraham@langston.edu
Abraham, Susan	Langston University	Assistant Professor	susan.abraham@langston.edu
Ackley, Brian	University of Kansas - Lawrence	K-INBRE Campus Coordinator	bdackley@ku.edu
Acquah, Louisa	Fort Hays State University	Graduate student	l_acquah@mail.fhsu.edu
Ade, Tolulope	University of Kansas - Lawrence	Graduate student	tolulope.iorwuese@ku.edu
Adefuye, Ifelayo	Fort Hays State University	Assistant Professor	iiadefuye@fhsu.edu
Adem, Seid	Washburn University	Professor	seid.adem@washburn.edu
Ahuja, Mehak	University of Kansas Medical Center	Graduate student	mahuja@kumc.edu
Aikin, Tatum	University of Kansas - Lawrence	Undergraduate student	t261a017@ku.edu
Akhtar, Sara	Pittsburg State University	Undergraduate student	akhtar.sara2004@gmail.com
Alfailakawi, Ameerah	Kansas State University	Undergraduate student	ameerahalfailakawi@gmail.com
Alrid, Natalie	Emporia State University	Undergraduate student	nalrid@g.emporia.edu
An, Junqiao	Emporia State University	Undergraduate student	junqiao@gmail.com
Antunes, Caetano	University of Kansas - Lawrence	Assistant Professor	caetano@ku.edu
Antwi, Yaw	Fort Hays State University	Graduate student	y_antwi@mail.fhsu.edu
Arb, Jackson	Emporia State University	Undergraduate student	jarb2@g.emporia.edu
Arias, Meghan	University of Kansas - Lawrence	Undergraduate student	meghanaarias@ku.edu
Azmi, Zeeshan	Wichita State University	Undergraduate student	zeeshan.azmi2964@gmail.com
Azuma, Mizuki	University of Kansas - Lawrence	Associate Professor	azumam@ku.edu
Baldwin, Kinsey	Pittsburg State University	Undergraduate student	kinsey.baldwin@gus.pittstate.edu
Balthazor, James	Fort Hays State University	K-INBRE Campus Coordinator, judge, moderator	jralthazor@fhsu.edu
Bann, James	Wichita State University	Associate Professor	jim.bann@wichita.edu
Bansal, Aanya	University of Kansas Medical Center	Undergraduate student	aanyabansal13@gmail.com
Barrager, Shelby	Pittsburg State University	Undergraduate student	Shelbybarrager592@gmail.com
Beck, Moriah	Wichita State University	Talaty Endowed Professor	moriah.beck@wichita.edu
Begum, Rahima	University of Kansas Medical Center	Graduate student	rbegum@kumc.edu
Behbod, Fariba	University of Kansas Medical Center	Professor	fbehbod@kumc.edu
Berndt, Isabella	Kansas State University	Undergraduate student	imberndt@ksu.edu
Berryhill, Justin	Langston University	Undergraduate student	justin.berryhill@okstate.edu
Berzansky, Marion	University of Kansas - Lawrence	Undergraduate student	marion.berzansky@gmail.com
Bjerke, Susan	Washburn University	Associate Professor of Biology	susan.bjerke@washburn.edu
Blake, Caden	Kansas State University	Undergraduate student	ccblake@ksu.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Blocker, Erin	Emporia State University	Assistant Professor	eblocker@emporia.edu
Bohach, Carolyn	University of Idaho	INBRE EAC member	cbohach@uidaho.edu
Bohorquez, David	Fort Hays State University	Graduate student	debohorquez@mail.fhsu.edu
Bon, Susan	Pittsburg State University	University Administrator & Committee member	sbon@pittstate.edu
Bousfield, George	Wichita State University	Professor	george.bousfield@wichita.edu
Boydston, Paige	Pittsburg State University	Assistant Professor	paigeboydston@pittstate.edu
Braasch-Turi, Margaret	Fort Hays State University	Assistant Professor	mmbraaschturi@fhsu.edu
Briggs, Anna	Fort Hays State University	Undergraduate student	annabriggs551@gmail.com
Brown, Braylon	Pittsburg State University	Undergraduate student	braylon.brown@gus.pittstate.edu
Browning, Colson	Fort Hays State University	Undergraduate student	cjbrowning2@mail.fhsu.edu
Brunet, Marie	Wichita State University	Graduate student	p348h457@wichita.edu
Buabeng, Alfred	University of Kansas - Lawrence	Graduate student	a545b289@ku.edu
Bui, Abby	Wichita State University	Undergraduate student	atbui3@shockers.wichita.edu
Burnett, Tim	Emporia State University	INBRE committee member	tburnett@emporia.edu
Busick, Zane	University of Kansas - Lawrence	Undergraduate student	zanebusick@ku.edu
Caniza Velazquez, Eliceo	Wichita State University	Undergraduate student	eliceocaniza2001@gmail.com
Cantu, Kayla	Wichita State University	Graduate student	Kacantu@shockers.wichita.edu
Carey, Vanessa	Wichita State University	Undergraduate student	vlc Carey@shockers.wichita.edu
Carter, Kearstin	Pittsburg State University	Undergraduate student	kearstin.carter@gus.pittstate.edu
Chacon-Araya, Sofia	University of Kansas - Lawrence	Undergraduate student	schacon@ku.edu
Chalise, Prabhakar	University of Kansas Medical Center	Associate Professor	pchalise@kumc.edu
Chan, Vincent	University of Kansas - Lawrence	Undergraduate student	v970c527@ku.edu
Chapes, Stephen	Kansas State University	Invited Guest	skcbiol@ksu.edu
Chapin, Bridgett	Haskell Indian Nations University	K-INBRE Campus Coordinator and Department Chair	bchapin@haskell.edu
Chapman, Heiata	University of Kansas Medical Center	K-INBRE Assistant Director and Chief Administrative Officer	hchapman@kumc.edu
Chartier, Julia	Kansas State University	Undergraduate student	jchartier@ksu.edu
Chaturvedi, Aakriti	University of Kansas Medical Center	Graduate student	aakritichaturvedi17@gmail.com
Cheng, Nikki	University of Kansas Medical Center	Professor, IGPBS Associate Director	ncheng@kumc.edu
Chianca, Gabriela	University of Kansas - Lawrence	Graduate student	gchianca@ku.edu
Chicas-Mosier, Ana	University of Kansas - Lawrence	Invited Guest	amcm@ku.edu
Childers, Christopher	Pittsburg State University	University Administrator	rchilders@pittstate.edu
Christenson, Lane	University of Kansas Medical Center	Professor	lchristenson@kumc.edu
Chung, Peter	Pittsburg State University	Professor	pchung@pittstate.edu
Clark, Elijah	Langston University	Undergraduate student	Elijacl@langston.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Collier, Brynn	Kansas State University	Undergraduate student	brynncollier@ksu.edu
Colson, Ella	Fort Hays State University	Undergraduate student	e_colson@mail.fhsu.edu
Consani, Angela	BCSI	Invited guest	angela@bcsi.bio
Cottrill, Gauge	Langston University	Undergraduate student	gauge.cottrill@langston.edu
Covert Miller, Laura	Pittsburg State University	Professor	Lcovert@pittstate.edu
Coykendall, Alison	Fort Hays State University	Undergraduate student	a_coykendall@mail.fhsu.edu
Craig, Madison	University of Kansas Medical Center	Undergraduate student	madisoncraig200323@gmail.com
Cranor, Kendall	University of Kansas - Lawrence	Undergraduate student	kendallcranor@ku.edu
Cravens, Stefanie	Kansas City University	Medical Student	stefaniecravens23@gmail.com
Crawshaw, Heather	Kansas State University	Graduate student	hncrawsh@ksu.edu
Da Silva Carvalho, Claudia	Fort Hays State University	Assistant Professor	cmdasilvacarvalho@fhsu.edu
Danner, Jacob	Emporia State University	Undergraduate student	jdanner@g.emporia.edu
Dasgupta, Ayushee	University of Kansas - Lawrence	Graduate student	ayu.dasgupta@ku.edu
Dasgupta, Debolina	University of Kansas Medical Center	Graduate student	ddasgupta@kumc.edu
David, David	University of Kansas - Lawrence	Professor of Molecular Biosciences	ddavido@ku.edu
Davis, Aiyanna	Langston University	Undergraduate student	aiyanna.davis@langston.edu
Davis, Jennifer	University of Kansas Medical Center	Assistant Professor/Mentor of INBRE Scholar	jdavis57@kumc.edu
Davis, Lindsay	Langston University	Assistant Professor of Chemistry	dalin@langston.edu
Dean, Tara	Piestar	Vendor	Tara@piestar.com
Delmas, Olivia	University of Kansas Medical Center	Graduate student	odelmas@kumc.edu
Diab, Christina	Pittsburg State University	Undergraduate student	cdiab@gus.pittstate.edu
Diehl, Maria	Kansas State University	Assistant Professor	mmdiehl@ksu.edu
Dilower, Iman	University of Kansas Medical Center	Graduate student	idilower2@kumc.edu
Doubrava, Gavin	Pittsburg State University	Undergraduate student	gdoubrava@gus.pittstate.edu
Draper, Kaitlyn	Pittsburg State University	Undergraduate student	kdraper@gus.pittstate.edu
Durrett, Helen	Kansas State University	High school student	durrett_helen@hotmail.com
Dutta, Amit	Kansas State University	Graduate student	amit49@ksu.edu
Eichhorn, David	Wichita State University	Associate Dean and Professor	david.eichhorn@wichita.edu
Erby, Kelly	Washburn University	University Administrator	kelly.erby@washburn.edu
Estes, Sarah Beth	Wichita State University	Dean, Fairmount College of Liberal Arts and Sciences	sarahbeth.estes@wichita.edu
Fairchild, Corbin	University of Kansas - Lawrence	Undergraduate student	cfairchild347@gmail.com
Fardipour, Komron	University of Kansas - Lawrence	Undergraduate student	fardipourkomron@ku.edu
Farrell, Mark P.	University of Kansas - Lawrence	Associate Professor	markfarrell@ku.edu
Fehr, Anthony	University of Kansas - Lawrence	Associate Professor	arfehr@ku.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Ferkul, Anna	University of Kansas Medical Center	Graduate student	aferkul@kumc.edu
Ferreira, Rosana	University of Kansas - Lawrence	Assistant Professor	rosana@ku.edu
Fields, Stephen	Emporia State University	Associate Professor and K-INBRE Campus Coordinator	sfields1@emporia.edu
Finnerty, Halle	Pittsburg State University	Undergraduate student	haleffinnerty@gmail.com
Fleming, Sherry	Kansas State University	Professor Emeritus	sdflamin@ksu.edu
Folscroft, John	University of Kansas - Lawrence	Undergraduate student	j741f664@ku.edu
Forbush, Kelsie	University of Kansas - Lawrence	Professor/Center Director	kforbush@ku.edu
Frans, Hazel	Fort Hays State University	Undergraduate student	hazelfrans2006@gmail.com
Frantz, Clare	University of Kansas Medical Center	K-INBRE Staff	cfrantz2@kumc.edu
Freedman, Abegel	Wichita State University	Postdoc	Abegel.freedman@wichita.edu
Freiburger, Asher	Pittsburg State University	Undergraduate student	afreiburger@gus.pittstate.edu
Freiburger, Noah	Pittsburg State University	Undergraduate student	noman5050@icloud.com
Gacko, Moussa	Kansas State University	Undergraduate student	gmpa@ksu.edu
Gaete Humada, Belen	Kansas State University	Graduate student	bgate@ksu.edu
Gardner, Jamie	Emporia State University	Academic Advisor	jpgardne7@emporia.edu
Gardner, Stewart	Emporia State University	Associate Professor	sgardne4@emporia.edu
Gartelos, Ava	University of Kansas Medical Center	Undergraduate student	agartelos@icloud.com
Gast, Elaine	University of Kansas Medical Center	Undergraduate student	gastelaine@gmail.com
Geisbrecht, Erika	Kansas State University	Professor	geisbrechte@ksu.edu
Ghosh, Anuradha	Pittsburg State University	Professor & K-INBRE Campus Coordinator	aghosh@pittstate.edu
Gillock, Eric	Fort Hays State University	Professor	egillock@fhsu.edu
Gilmore, Caleb	University of Kansas - Lawrence	Undergraduate student	c621g776@ku.edu
Glover, Logan	Kansas State University	Undergraduate student	lglover@ksu.edu
Gong, Maojun	Wichita State University	Associate Professor	maojun.gong@wichita.edu
Graber, Alexis	Kansas State University	Graduate student	alexis_graber@ku.edu
Gray, Carter	University of Kansas - Lawrence	Undergraduate student	cartergray@ku.edu
Greeves, Emmalyn	Kansas State University	Undergraduate student	emmalyn@ksu.edu
Gress, Joanna	Emporia State University	Assistant Professor	jgress@emporia.edu
Grigsby, Ryan	University of Kansas - Lawrence	Core Lab Director	ryan.grigsby@ku.edu
Grotheer, Savannah	Pittsburg State University	Undergraduate student	sgrotheer@gus.pittstate.edu
Gruenstaeudl, Michael	Fort Hays State University	Assistant Professor	m_gruenstaeudl@fhsu.edu
Guillen, Andrea	University of Kansas - Lawrence	Undergraduate student	nicolle.guillen@ku.edu
Gupta, Avani	Washburn University	Undergraduate student	guptaavani07@gmail.com
Gupta, Ram	Pittsburg State University	Associate Vice President for Research Strategy and Advancement	rgupta@pittstate.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Gutierrez, Avery	Emporia State University	Undergraduate student	agutie11@g.emporia.edu
Hackett, Jennifer	University of Kansas - Lawrence	Core Director	jhackett@ku.edu
Hailemariam, Yesem	University of Kansas - Lawrence	Undergraduate student	y747h854@ku.edu
Halder, Barsha	University of Kansas Medical Center	Graduate student	bhalder@kumc.edu
Hamitouche, Thanina	Fort Hays State University	Graduate student	t_hamitouche@mail.fhsu.edu
Hancock, Lynn	University of Kansas - Lawrence	Associate Professor of Molecular Biosciences	lynnh@ku.edu
Harmon, Chloe	Fort Hays State University	Undergraduate student	ceharmon@mail.fhsu.edu
Harries, Phillip	Pittsburg State University	Professor of Biology	pharries@pittstate.edu
Hartley, Meredith	University of Kansas - Lawrence	Assistant Professor	hartley@ku.edu
Hawks, Hayden	University of Kansas Medical Center	Graduate student	hhawks@kumc.edu
Hefty, Scott	University of Kansas - Lawrence	Professor/Chair/CoBRE Director	pshefty@ku.edu
Hendry, Bill	Wichita State University	Wichita K-INBRE Coordinator	william.hednry@wichita.edu
Henry, Benjamin	Pittsburg State University	Undergraduate student	bphenry@gus.pittstate.edu
Higgins, Lauren	University of Kansas Medical Center	Undergraduate student	l127h101@ku.edu
Hinrichs, Kylie	Washburn University	Undergraduate student	kylie.hinrichs@washburn.edu
Hinton, Duane	Washburn University	Faculty	duane.hinton@washburn.edu
Hiszczynskij, Hannah	Emporia State University	Graduate student	hhiszczy@g.emporia.edu
Hodges, Reed	University of Kansas - Lawrence	Undergraduate student	reed.hodges@ku.edu
Hoff, Joselyn	Emporia State University	Undergraduate student	Everdeen416@gmail.com
Huang, Shijiao	Kansas State University	Assistant Professor	shijiaoh@ksu.edu
Hufft- Martinez, Brittany	University of Kansas Medical Center	Postdoc	bmartinez3@kumc.edu
Hughes, Lauren	Wichita State University	Undergraduate student	F875A287@wichita.edu
Hunter, Chad	University of Kansas Medical Center	Professor	chunter7@kumc.edu
Hupert, Patryk	University of Kansas - Lawrence	Undergraduate student	p643h463@ku.edu
Huynh, Cassidy	Kansas State University	Undergraduate student	chuynh06@ksu.edu
Innes, Shelby	Kansas State University	Graduate student	sinnes3@ksu.edu
Jackson, Ruth	Langston University	University Administrator	president@langston.edu
Jain, Auditya	Pittsburg State University	Undergraduate student	auditya.jain@gus.pittstate.edu
Janzen, Carly	University of Kansas - Lawrence	Undergraduate student	carly.janzen@ku.edu
Jha, Aprajita	Kansas State University	Graduate student	ajha@ksu.edu
Ji, Yan	Kansas State University	Research Associate	yanj@ksu.edu
Johnson, David	University of Kansas - Lawrence	Core Lab Director	dkjohnson@ku.edu
Johnson, Maddox	Pittsburg State University	Undergraduate student	maddox.johnson@gus.pittstate.edu
Joseph, Caitlyn	Wichita State University	Undergraduate student	crjoseph@shockers.wichita.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Kapapula, Jedidah	University of Kansas - Lawrence	Undergraduate student	j384k145@ku.edu
Kasirosafar, Nazanin	Wichita State University	Undergraduate student	nxcasirosafar@shockers.wichita.edu
Khadka, Sahadev	Kansas State University	Graduate student	skhadka2353@ksu.edu
Khan, Rehan	Kansas State University	Graduate student	rehank@ksu.edu
Khan, Yousaf	University of Kansas Medical Center	Graduate student	ykhan@kumc.edu
King, Kara	Washburn University	Undergraduate student	kara.king@washburn.edu
Klein, Robert	University of Kansas Medical Center	Vice Chancellor	rklein@kumc.edu
Koehn, Amelia	Kansas State University	Undergraduate student	ameliakoehn@ksu.edu
Kohno, Satomi	Fort Hays State University	Assistant Professor	s_kohno@fhsu.edu
Kouadio, Kenny	Pittsburg State University	Undergraduate student	kkouadio@gus.pittstate.edu
Krentzel, Jim	University of Kansas - Lawrence	Undergraduate student	jkrentzel@ku.edu
Kriley, Luke	Emporia State University	Assistant Professor	lkriley@emporia.edu
Kuehn, Michael	University of Kansas Medical Center	Graduate student	mkuehn@kumc.edu
Kusena, Blessing	Kansas State University	Graduate student	bzkusena@ksu.edu
Lad, Darsh	University of Kansas - Lawrence	Undergraduate student	laddarshmed@gmail.com
Lane, Suzanne	Kansas State University	Graduate School table staff	suzlane@ksu.edu
Lawrence, Ben	Kansas State University	Undergraduate student	benmlawrence@ksu.edu
Le, Viet Hoang	University of Kansas - Lawrence	Staff	lehoangviet161102@ku.edu
Leach, Breanna	Wichita State University	Undergraduate student	bnleach@shockers.wichita.edu
Lee, Yongkuk	Wichita State University	Chair and Associate Professor in BME at WSU	yongkuk.lee@wichita.edu
Legleiter, Leah	University of Kansas - Lawrence	Undergraduate student	llegleiter@ku.edu
Leung, Sam	Washburn University	Professor & K-INBRE Campus Coordinator	sam.leung@washburn.edu
Lewis, Sharon	Langston University	Associate Professor	lewissa@langston.edu
Li, Ping	Kansas State University	Associate Professor	pli@ksu.edu
Liska, Zoie	Wichita State University	Undergraduate student	Zoeliska@gmail.com
Liu, Mingyi	Kansas State University	Postdoc	liu2024@ksu.edu
Logan, Raj	Wichita State University	Assistant Professor	raj.logan@wichita.edu
Long, Owen	Pittsburg State University	Undergraduate student	olong@gus.pittstate.edu
Loomis, Joseph	Formerly KU-Lawrence	Postdoc	loomisjoseph97@gmail.com
Lunte, Susan	University of Kansas - Lawrence	Professor	slunte@ku.edu
Macdonald, Stuart	University of Kansas - Lawrence	Professor	sjmac@ku.edu
Magstadt, Alexa	University of Kansas Medical Center	Undergraduate student	alexamagstadt@ku.edu
Markiewicz, Mary	University of Kansas Medical Center	Associate Professor	mmarkiewicz@kumc.edu
Martin, Eleanor	Kansas State University	Undergraduate student	eleanor3martin@ksu.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Mason, Rylan	Pittsburg State University	Undergraduate student	rylan.mason@gus.pittstate.edu
Matthias, Emily	Emporia State University	Undergraduate student	ematthi1@g.emporia.edu
Maxfield, Kala	Emporia State University	ESU Executive Director for Engagement	kmaxfie1@emporia.edu
Mays, Liz	University of Kansas - Lawrence	Undergraduate student	e733m513@ku.edu
McCammon, Miranda	Washburn University	Undergraduate student	miranda.mccammon@washburn.edu
McCarthy, Kate	University of Kansas Medical Center	Undergraduate student	katemccarthy1000@gmail.com
McCormick, Brynn	Emporia State University	Undergraduate student	brynnmccormick2022@gmail.com
McCormick, Lucas	Emporia State University	Associate Professor of Chemistry	lmccormi@emporia.edu
McCreight, Rebecca	Washburn University	Undergraduate student	rebecca.mccreight@washburn.edu
McDonald, Brianna	Langston University	Undergraduate student	bri.mcdonald2022@gmail.com
McDonald, Peter	University of Kansas - Lawrence	Staff - Core Director	petemcd@ku.edu
McGann, Alexa	Emporia State University	Undergraduate student	amcgann@g.emporia.edu
McGuire, Jessica	Fort Hays State University	Graduate Enrollment Professional	jmmcguire2@fhsu.edu
McMillan, Riley	Wichita State University	Undergraduate student	rrmcmillan@shockers.wichita.edu
Medley, Jeff	Kansas State University	Postdoc	jcmedley@ksu.edu
Meriano, Sebastian	University of Kansas - Lawrence	Undergraduate student	sebastian.a.meriano@gmail.com
Michel, Kristin	Kansas State University	Professor	kmichel@ksu.edu
Middendorf, Riley	Washburn University	Assistant Professor	Riley.middendorf@washburn.edu
Mitchell, Rebecca	Kansas State University	Undergraduate student	Rlmitche@ksu.edu
Molesworth, Jessica	EPSCoR/IDeA Foundation	Executive Director, EPSCoR/IDeA Foundation	jmolesworth@eifdc.org
Montezano, Daniel	University of Kansas - Lawrence	Postdoc	montezano@ku.edu
Montney, Justin	Fort Hays State University	Assistant Prof., Dir. FHSU HEART Research Lab	JLMontney@fhsu.edu
Moore, Lauren	Langston University	Undergraduate student	lauren.moore10@langston.edu
Morgan, Cortnie	Langston University	Undergraduate student	cortnie.morgan@langston.edu
Morgan, Dyan	University of Kansas - Lawrence	Associate Teaching Professor	dyan.morgan@ku.edu
Mountain, Isaac	Pittsburg State University	Undergraduate student	imountain374@gmail.com
Naeem, Abdulrahman	University of Kansas - Lawrence	Graduate student	abdulrahman21@ku.edu
Neef, Jody	Pittsburg State University	Professor	cneef@pittstate.edu
Newman, Jack	Fort Hays State University	Undergraduate student	jgnewman@mail.fhsu.edu
Newton, Madison	Emporia State University	Undergraduate student	mnewton6@g.emporia.edu
Nguyen, Hoang Long	Washburn University	Assistant Professor	hoang.nguyen@washburn.edu
Nguyen, Ngoc	University of Kansas - Lawrence	Graduate student	huannguyen@ku.edu
Nguyen, Vanessa	University of Kansas - Lawrence	Undergraduate student	vanessa.nguyen@ku.edu
Nimmo, Hannah	Fort Hays State University	Undergraduate student	hannah.nimmo@gmail.com

Symposium Participants

Name	University/Company	Position/Title	Email Address
Nolen, Tessa	Wichita State University	Graduate student	tjnolen2@shockers.wichita.edu
O'Dell, Riley	University of Kansas Medical Center	School of Medicine Admissions	rodell5@kumc.edu
O'Donnell, Lillian	University of Kansas - Lawrence	Undergraduate student	lilyodo06@gmail.com
Orozco, Robin	University of Kansas - Lawrence	Assistant Professor	orozco.robin@ku.edu
Osagie, Candice	University of Kansas - Lawrence	Graduate student	candice.johnson@ku.edu
Padamati, Divyanka Sri	Wichita State University	Graduate student	q443f787@wichita.edu
Pangeni, Bishnu	Fort Hays State University	Graduate student	b_pangeni@mail.fhsu.edu
Panter, Halle	Pittsburg State University	Graduate student	hpanter@gus.pittstate.edu
Park, Jeyun	Fort Hays State University	Undergraduate student	j_park13@mail.fhsu.edu
Parker, Alauna	Langston University	Undergraduate student	alauna.parker@langston.edu
Parvinzadeh Gashti, Mazeyar	Pittsburg State University	Assistant Professor	mpg@pittstate.edu
Patel, Sakshi	University of Kansas - Lawrence	Undergraduate student	sakshipatel4599@ku.edu
Patrick, Lorelei	Fort Hays State University	Associate Professor	lepatrick@fhsu.edu
Patterson, Riley	Emporia State University	Undergraduate student	rpatter6@g.emporia.edu
Peak, Mandy	Pittsburg State University	Professor of Biology	mpeak@pittstate.edu
Peltzer, Jill	University of Kansas Medical Center	Associate Dean for Graduate Programs & Associate Professor	jpeltzer2@kumc.edu
Perera, Chamani	University of Kansas - Lawrence	Core Facility Director	chamani@ku.edu
Peterson, Alonzo	Langston University	Vice President for Academic Affairs	alonzo.peterson@langston.edu
Peterson, Grace	Washburn University	Undergraduate student	grace.peterson1@washburn.edu
Peterson, Maggie	Fort Hays State University	Undergraduate student	maggiepeterson497@gmail.com
Pfaff, Cody	Fort Hays State University	Undergraduate student	cmpfaff@mail.fhsu.edu
Phelps, Jamie	Pittsburg State University	Assistant Instructional Professor	jmphelps@pittstate.edu
Phelps-Durr, Tara	Fort Hays State University	Professor/Chair of Biology	tlphelpsdurr@fhsu.edu
Piccini, Paula	Pittsburg State University	Undergraduate student	ppiccini@gus.pittstate.edu
Pieterse, Zanri	Kansas State University	Graduate student	zanpiet@ksu.edu
Pirani, Karim	University of Kansas Medical Center	Research Associate	kpirani@kumc.edu
Plakke, Bethany	Kansas State University	Associate Professor	bplakke@ksu.edu
Posterick, Hannah	Pittsburg State University	Undergraduate student	hannahposterick@gmail.com
Powell, Alexis	Emporia State University	Associate Professor, Biological Sciences	aapowell@emporia.edu
Powell, Brookelynn	Washburn University	Undergraduate student	brookelynn.powell@washburn.edu
Powers, Beth	Kansas State University	KSU Director, Scholar Development and Undergraduate Research	bethpowers@ksu.edu
Prakash, Om	Kansas State University	Professor	omp@ksu.edu
Pritchard, Michele	University of Kansas Medical Center	IGPBS director	mpritchard@kumc.edu
Pugh, Coleen	Wichita State University	Dean of Graduate School	coleen.pugh@wichita.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Pujari, Arti	Kansas State University	Graduate student	Artip@ksu.edu
Ranganathan, Chadhve	University of Kansas Medical Center	Research Technician	c329r363@kumc.edu
Reed, Aliyana	Langston University	Undergraduate student	aliyana.reed@langston.edu
Reed, Benjamin	Washburn University	Associate Professor of Biology	benjamin.reed@washburn.edu
Reh, Shelley	Piestar	Vendor	shelley@piestar.com
Rice, Gavin	Kansas State University	Assistant Professor	gavinrice@ksu.edu
Rice, Paige	University of Kansas Medical Center	Vendor for Education Programs for the Dept. of Biostatistics & Data Science, KUMC	price3@kumc.edu
Riddle, Colby	Pittsburg State University	Undergraduate student	criddle@gus.pittstate.edu
Rider, Kaylee	Pittsburg State University	Undergraduate student	kaylee.rider@gus.pittstate.edu
Rider, Virginia	Pittsburg State University	Retired Faculty	vrider@pittstate.edu
Ridgway, Maggie	University of Kansas - Lawrence	Undergraduate student	m322r197@ku.edu
Robinson, Alexandra	Pittsburg State University	Undergraduate student	anrobinson@gus.pittstate.edu
Roccaro, Sophia	University of Kansas - Lawrence	Undergraduate student	smre05@icloud.com
Rockenbach, Larissa	University of Kansas - Lawrence	Undergraduate student	Larissa-rockenbach@ku.edu
Rockley, Jillian	Kansas State University	Undergraduate student	jnrockley@gmail.com
Rodriguez, Brodryk	Wichita State University	University Recruitment	brodryk.rodriguez@wichita.edu
Rosario, Hannah Grace	Wichita State University	Undergraduate student	hxrosario@shockers.wichita.edu
Ross, Derek	Pittsburg State University	Undergraduate student	deross@gus.pittstate.edu
Roy, Anuradha	University of Kansas - Lawrence	Staff	anuroy@ku.edu
Ruble, Shannon	Kansas State University	Graduate student	sharuble11@gmail.com
Ruliffson, Ella	Emporia State University	Undergraduate student	ellapruliffson@gmail.com
Saadi, Irfan	University of Kansas Medical Center	Professor	isaadi@kumc.edu
Sadikot, Takrima	Washburn University	Professor	takrima.sadikot@washburn.edu
Saif, MD Saiful Islam	University of Kansas Medical Center	Graduate student	msaif@kumc.edu
Samek, Peyton	Washburn University	Undergraduate student	peytonsamek@washburn.edu
Sanderson, Brian	University of Kansas - Lawrence	DSC research staff	brian.sanderson@ku.edu
Santana - Magal, Nadine	University of Kansas Medical Center	Postdoc	nsantanamagal@kumc.edu
Sarma, Debmalyo Rudra	Pittsburg State University	Undergraduate student	drudrasarma@gus.pittstate.edu
Schlingensiepen, Ephraim	Washburn University	Undergraduate student	Ephraim.schlingensiepen@washburn.edu
Schmidt, Shaun	Washburn University	Professor and Chair	shaun.schmidt@washburn.edu
Schroeder, Kaylie	University of Kansas - Lawrence	Undergraduate student	kayliem2025@gmail.com
Seitz, Lucas	Wichita State University	Undergraduate student	lsseitz@shockers.wichita.edu
Shah, Udit	University of Kansas - Lawrence	Undergraduate student	uditashah03@gmail.com
Shanafelt, Elizabeth	Washburn University	Undergraduate student	Elizabeth.shanafelt@washburn.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Sharma, Tinky	Kansas State University	Graduate student	tinky@ksu.edu
Shiew, Grace	Fort Hays State University	Undergraduate student	gmshiew@gmail.com
Sim, Kristina	University of Kansas - Lawrence	Undergraduate student	kristinaysim@gmail.com
Simmons, Emma	Wichita State University	Undergraduate student	essimmons1@shockers.wichita.edu
Simmons, Juliane	Langston University	Undergraduate student	juliane.simmons@langston.edu
Simons, Kim	Emporia State University	Professor	ksimons@emporia.edu
Singh, Siraj	University of Kansas Medical Center	Speaker	sirajsingh2018@gmail.com
Sivayokan, Bhavana	Kansas State University	Graduate student	bhavana@ksu.edu
Smith, Joseph	iPosterSessions	iPoster Technician	joe@amuze-interactive.com
Smith, Madison	Kansas State University	Undergraduate student	madison368@ksu.edu
Spinelli, Taylor	Wichita State University	Undergraduate student	trspinelli@shockers.wichita.edu
Stanford, John	University of Kansas Medical Center	Program Coordinator	jstanford@kumc.edu
Steffan, Bryce	Fort Hays State University	Undergraduate student	b_steffan@mail.fhsu.edu
Steigner, Devi	Emporia State University	Undergraduate student	devi@steigner.com
Steigner, Sofia	Emporia State University	Undergraduate student	ssteigne@g.emporia.edu
Stewart, Nancy	University of Kansas Medical Center	Faculty	nstewart5@kumc.edu
Stewart, Savannah	Emporia State University	Undergraduate student	sstewa12@g.emporia.edu
Stewart-ricks, Kiaorie	Langston University	Undergraduate student	Kiaorie.stewart-ricks@langston.edu
Sundar, Isaac Kirubakaran	University of Kansas Medical Center	Associate Professor	isundar@kumc.edu
Swider, Alex	Emporia State University	Undergraduate student	Patrickswider2004@gmail.com
Sydzyk, Joel	University of Kansas Medical Center	Speaker	jsydzyk@kumc.edu
Tate, Caitlynn	Pittsburg State University	Undergraduate student	ctate@gus.pittstate.edu
Thalman, Dana	University of Kansas Medical Center	Graduate student	dthalman@kumc.edu
Thapa Magar, Buddha	Fort Hays State University	Graduate student	b_thapamagar@mail.fhsu.edu
Thomas, Brent	Emporia State University	Provost and Vice President for Academic Affairs, Prof. of Biol.Sci.	rthomas2@emporia.edu
Thomas, Ryan	Kansas State University	Undergraduate student	rthomas02@ksu.edu
Timmons, Lisa	University of Kansas - Lawrence	Faculty	timmons@ku.edu
Todd, Richard	Kansas State University	Associate Professor/Dr	rbtodd@ksu.edu
Tran, Pamela	University of Kansas Medical Center	Associate Professor	ptran@kumc.edu
Tripathi, Aprajita	University of Kansas Medical Center	Graduate student	atripathi3@kumc.edu
Trower, Vivian	Wichita State University	Undergraduate student	H452G568@wichita.edu
Tse, Hubert	University of Kansas Medical Center	University Administrator	htse@kumc.edu
Unckless, Robert	University of Kansas - Lawrence	Associate Professor	unckless@ku.edu
Veatch, Olivia	University of Kansas Medical Center	Assistant Professor	oveatch@kumc.edu

Symposium Participants

Name	University/Company	Position/Title	Email Address
Visser, Kendra	Kansas State University	Undergraduate student	kkv@ksu.edu
Vo, Gia	University of Kansas - Lawrence	Undergraduate student	g820v289@ku.edu
Wagner, Paul	Washburn University	Associate Professor	paul.wagner@washburn.edu
Wagner, Tracy	Washburn University	Associate Professor	tracy.wagner@washburn.edu
Wallace, Nick	Kansas State University	Associate Dean for Research	nwallac@ksu.edu
Wang, Wei	University of Kansas Medical Center	Postdoc	wwang3@kumc.edu
Ward, Christopher	Pittsburg State University	Assistant Professor	christopherward@pittstate.edu
Warner, Hannah	Pittsburg State University	Undergraduate student	hwarner@gus.pittstate.edu
Watanabe, Masakatsu	Fort Hays State University	Associate Professor	m_watanabe@fhsu.edu
Waugh, Katherine	University of Kansas Medical Center	Faculty	kwaugh@kumc.edu
Wedman, Clarissa	Pittsburg State University	Graduate student	cwedman@gus.pittstate.edu
Weishaar-Wilson, August	Washburn University	Undergraduate student	aawilsonks@gmail.com
Welti, Ruth	Kansas State University	Professor	welti@ksu.edu
Wendel, Sebastian	Kansas State University	Research Assistant Professor	sw87@ksu.edu
Whitehouse, Katrina	University of Kansas - Lawrence	Undergraduate student	k688w954@ku.edu
Wicks, Simon	Pittsburg State University	Undergraduate student	Swicks@gus.pittstate.edu
Wiedemann, Leanne	Stowers (and KUMC affiliated)	INBRE committee member	lmw@stowers.org
Wilkins, Heather	University of Kansas Medical Center	Associate Professor	hwilkins@kumc.edu
Wolf, Jasmine	Kansas State University	Undergraduate student	jasminewolf05@gmail.com
Wolfe, Michael	University of Kansas - Lawrence	Professor	mswolfe@ku.edu
Wozniak, Ann	University of Kansas Medical Center	Associate Professor	awozniak@kumc.edu
Wright, Doug	University of Kansas Medical Center	Principal Director	dwright@kumc.edu
Wright, Jeff	Piestar	Vendor	wright@piestar.com
Xu, Liang	University of Kansas - Lawrence	Professor	xul@ku.edu
Yackovich, Nikolas	Emporia State University	Graduate student	nyackovi@g.emporia.edu
Yang, Shang-You	University of Kansas Medical Center	Research Professor	shang-you.yang@wichita.edu
Yao, Li	Wichita State University	Professor	li.yao@wichita.edu
Young, Erin	University of Kansas Medical Center	Associate Professor	eyoung6@kumc.edu
Zarate, America	Kansas State University	Undergraduate student	americaz@ksu.edu
Zhang, Qiyang	Emporia State University	Professor	qzhang2@emporia.edu
Zhu, Ninghao	Kansas State University	Assistant Professor	nzhu@ksu.edu
Zidarita, Amelie	Wichita State University	Undergraduate student	axzidarita@shockers.wichita.edu
Zinovyeva, Anna	Kansas State University	K-INBRE Campus Coordinator	zinovyeva@ksu.edu
Zoong Lwe, Zolian	Kansas State University	Graduate student	zolian@ksu.edu

Thank You:



National Institute of General Medical Sciences

NIGMS

Basic Discoveries for Better Health



National Institutes of Health

Turning Discovery Into Health

