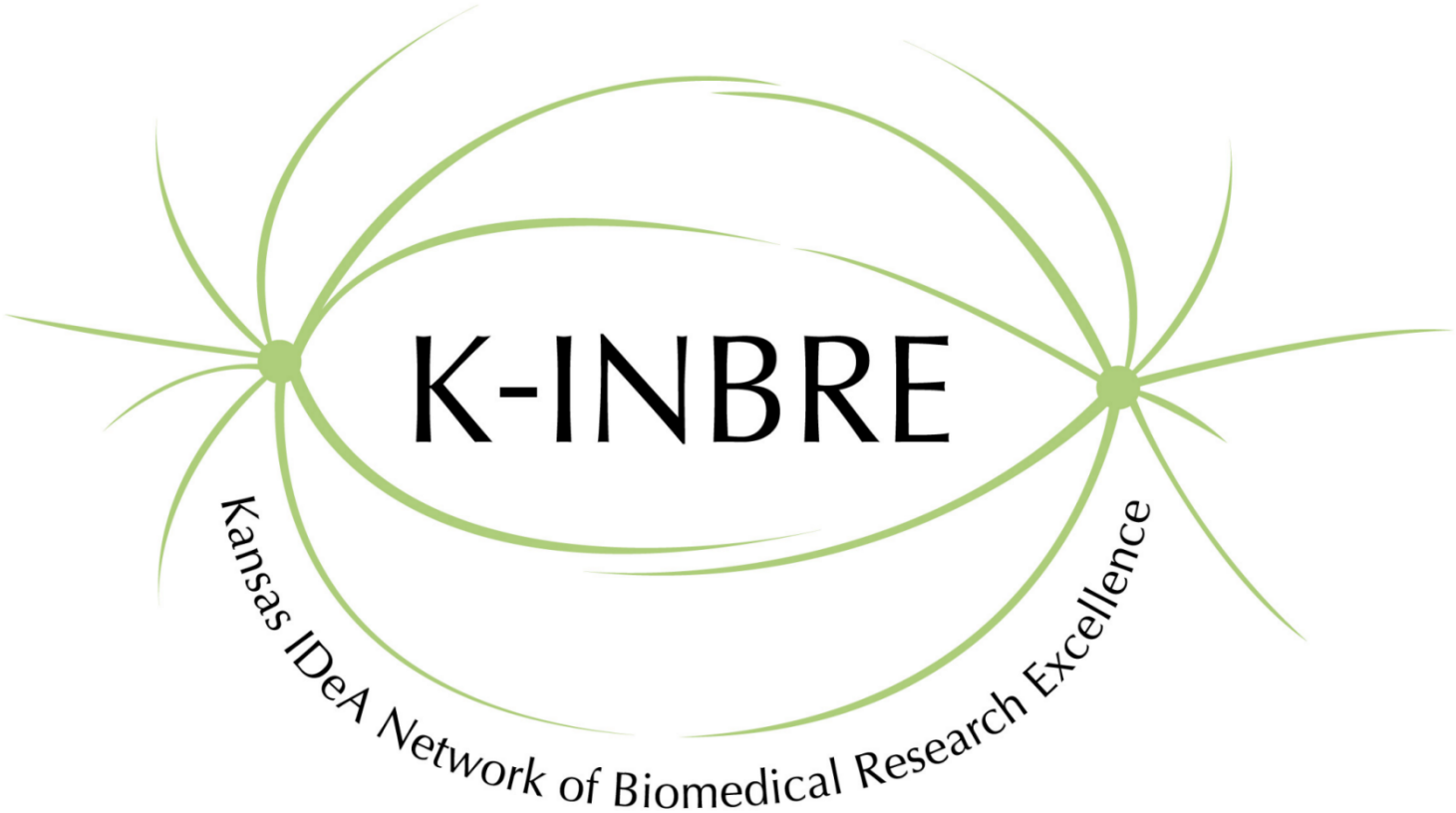
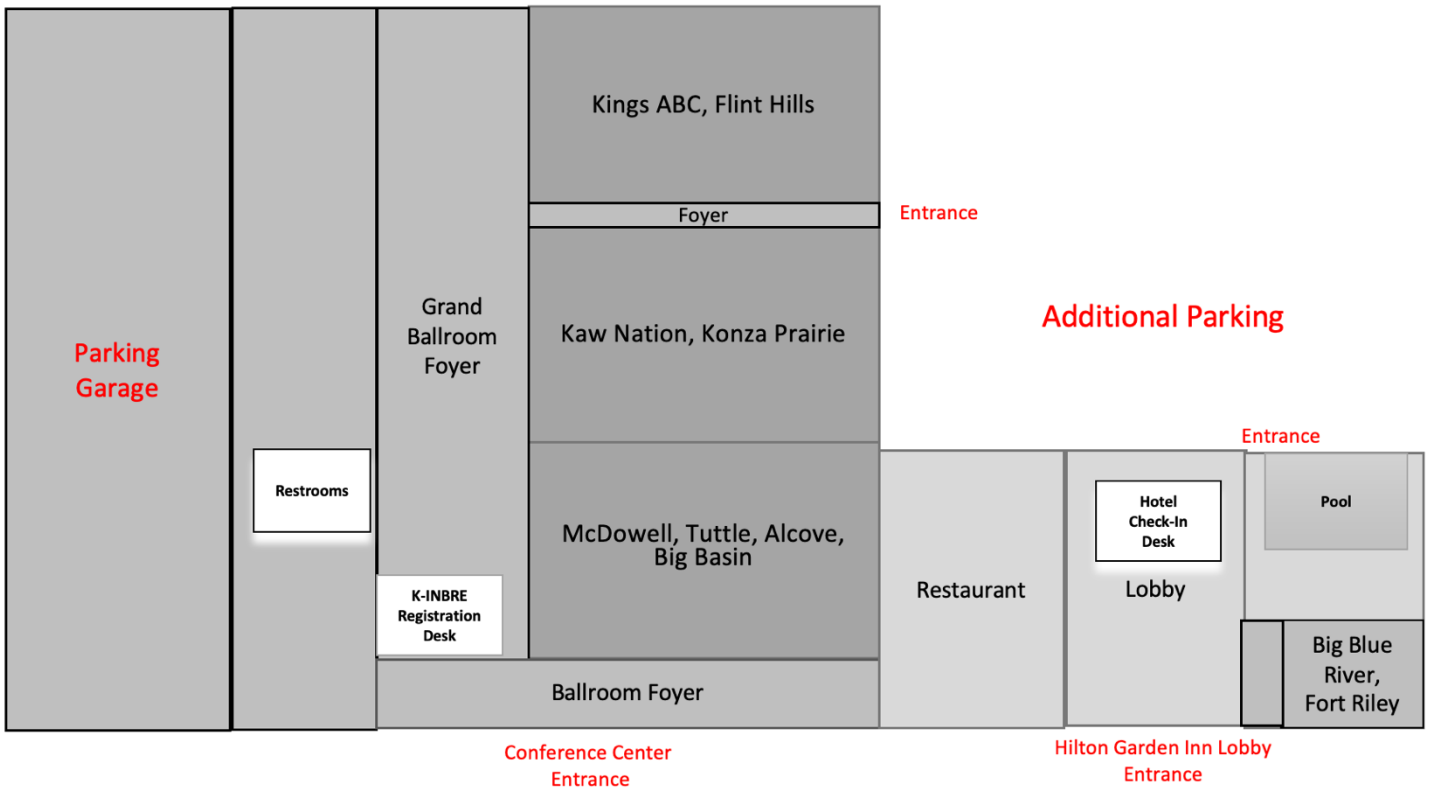
The 22nd Annual Kansas-IDeA Network of Biomedical Research Excellence Symposium



January 12-14, 2024
Hilton Garden Inn
Manhattan, 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.

Manhattan Hilton Garden Inn
Floor Plan



LOCATION OF EVENTS:

- **Registration:** Grand Ballroom Foyer
- **Friday Night Dinner:** Kaw Nation, Konza Prairie
- **Breakfast:** Kaw Nation, Konza Prairie
- **General Session:** Kings ABC, Flint Hills
- **Breaks:** Grand Ballroom Foyer
- **Lunch:** Kaw Nation, Konza Prairie
- **Poster Session/Reception:** McDowell, Tuttle, Alcove, Big Basin
- **Saturday Night Dinner:** Kaw Nation, Konza Prairie
- **Boxed Lunches:** Grand Ballroom Foyer

K-INBRE 2024 Symposium
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(4:30-5:30 PM) Poster Sessions 41-80

(5:30-6:30 PM) Poster Sessions 81-120

SUNDAY (10:10-11:10 AM) Poster Sessions 121-160

See Poster Presentation Schedule for details

IMPORTANT:

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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 period between receipt of funding and the publication or presentation.

K-INBRE 2024 Symposium
Program Schedule

Hilton Garden Inn
Manhattan, KS

Friday, January 12, 2024

3:00 PM	**Early Registration** **Open Poster practice (until 6pm)**	**Grand Ballroom Foyer** **McDowell, Tuttle, Alcove, Big Basin**
4:30 PM	**Early Registration Closes**	
6:00 PM	**Friday Night Dinner**	**Kaw Nation, Konza Prairie**
8:00 PM	**Dinner Ends**	

Saturday, January 13, 2024

7:30 AM	**Breakfast Buffet**	**Kaw Nation, Konza Prairie**
	Registration	**Grand Ballroom Foyer**
8:30 AM	**General Session**	**Kings ABC, Flint Hills**
	Doug Wright, Ph.D., K-INBRE Principal Investigator, University of Kansas Medical Center Opening Remarks	
8:50 AM	*David Rosowsky, Ph.D., Vice President for Research, Kansas State University* Welcome from Kansas State University	
9:00 AM	*V. Gustavo Blanco, M.D., Ph.D., Professor and Chairperson Molecular and Integrative Physiology, University of Kansas Medical Center* Keynote Speaker	
9:30 AM	*Erin Young, Ph.D., Assistant Professor, University of Kansas Medical Center* Moderator: The role of the microbiome in chronic abdominal pain syndromes: An Innovative Team Science Approach	
	Erin Young, Ph.D., Assistant Professor, University of Kansas Medical Center Title: Harnessing the microbiome to treat visceral hypersensitivity	
	Kyle Baumbauer, Ph.D., Assistant Professor, Ph.D., University of Kansas Medical Center Title: Combining neurophysiologic and transcriptomic data to understand functional pain disorders.	
	Anuradha Ghosh, Ph.D., Associate Professor, Pittsburg State University Title: Diagnostic applications of the microbiome	
	Sree Chintapalli, Ph.D., Assistant Professor, Arkansas Children's Hospital Title Metabolomics-Driven Protein Target Prediction: An In-Silico Methodology	
10:25 AM	**Break**	**Grand Ballroom Foyer**
	University Photos	**Hotel Lobby**
10:30 AM	Kansas State University Photo	
10:35 AM	Pittsburg State University Photo	
10:40 AM	University of Kansas Medical Center Photo	
10:45 AM	Fort Hays State University Photo	
10:50 AM	Wichita State University Photo	
10:55 AM	**General Session**	**Kings ABC, Flint Hills**
	Sherry Fleming, Ph.D., Professor, Kansas State University Moderator: Trainee Presentations	
11:00 AM	*Camryn Greving, Fort Hays State University, Hays, Kansas* Title: Distribution of the 2-micron Plasmid in Various Strains of *Saccharomyces cerevisiae*	
11:15 AM	*Kayla Smith*, *Langston University, Langston, Oklahoma* Title: Impairments in Cerebral Autoregulation and Cerebrovascular Reactivity in Cancer Survivorship	
11:30 AM	*Grace Schieferecke, Kansas State University, Manhattan, Kansas* Title: Molecular Analysis of Benzimidazole Resistance in Hookworms in Kansas Dogs	
11:45 AM	**Lunch**	**Kaw Nation, Konza Prairie**
1:00 PM	**General Session**	**Kings ABC, Flint Hills**
	Stephen Fields, Ph.D., Associate Professor, Emporia State University Moderator: Trainee Presentations	
1:05 PM	*David Claridge, Emporia State University, Emporia, Kansas* Title: Assessing Plant Derived Antioxidants for a Protective Effect Against Pesticides in the Honeybee Gut	

1:20 PM	*Alexandra Robinson, Pittsburg State University, Pittsburg, Kansas* Title: Syntheses of Co-MOF, Ni-MOF, and Fe-MOF for applications in both electrocatalysis and energy storage using a single-step microwave method.	
1:35 PM	*Bradley Olson, Ph.D. Associate Professor, Kansas State University* Moderator: What the Data Science Core can do for you	
	Dinah Davison, Division of Biology, Kansas State University Title: The reorganization of protein interaction networks during the transition to multicellularity	
	Dong Pei, Department of Biostatistics & Data Science, University of Kansas Medical Center, KS Title: optima: an open-source R package for the Tapestri platform for integrative single cell multiomics data analysis	
2:35 PM	**General Session Concludes/Break**	**Grand Ballroom Foyer**
	University Photos	**Hotel Lobby**
2:45 PM	Washburn University Photo	
2:50 PM	Haskell Indian Nations University Photo	
2:55 PM	Emporia State University Photo	
3:00 PM	Langston University Photo	
3:05 PM	University of Kansas Lawrence Photo	
3:20 PM	**Poster Judge Meeting**	**Big Blue River, Fort Riley**
3:30 PM	**Reception/Poster Session I**	**McDowell, Tuttle, Alcove, Big Basin**
4:30 PM	**Reception/Poster Session II**	**McDowell, Tuttle, Alcove, Big Basin**
5:30 PM	**Reception/Poster Session III**	**McDowell, Tuttle, Alcove, Big Basin**
6:30 PM	**Poster Session Ends**	
	Dinner	**Kaw Nation, Konza Prairie**
7:00 PM	**Award Presentations** *John Stanford, Ph.D., K-INBRE Associate Director, University of Kansas Medical Center*	**Kaw Nation, Konza Prairie**
7:30 PM	*Doug Wright, Ph.D., K-INBRE Principal Investigator, University of Kansas Medical Center* Closing Remarks	

Sunday, January 14, 2024

7:30 AM	**Breakfast Buffet**	**Kaw Nation, Konza Prairie**
8:30 AM	**General Session** *John Stanford, Ph.D., Associate Director, University of Kansas Medical Center* Opening Remarks Moderator: Regional Scientist and Trainee Presentations	**Kings ABC, Flint Hills**
8:40 AM	*Keetan Munsell, Washburn University, Topeka, Kansas* Title: Examining the Reproductive Ecology of *Terrapene ornata* in Western Nebraska; a Multi-year Study	
8:55 AM	*Ian Ensley, University of Kansas Medical Center, Kansas City, Kansas* Title: Hyaluronan synthase (Has)2, in dual Has1 and Has3 deficient mice, protects against age-associated weight gain by reducing adipocyte hypertrophy	
9:10 AM	*Alia Michaelis, Wichita State University, Wichita, Kansas* Title: Characterization of Cardiomyopathic Point Mutations in the Ig3 Domain of Myopalladin	
9:25 AM	*Scott Lovell, Ph.D., Director, Protein Structure and X-Ray Crystallography Laboratory, University of Kansas* Title: High Throughput Structural Biology Methods and Applications	
9:55 AM	General Session ends	
10:10 AM	**Poster Session IV**	**McDowell, Tuttle, Alcove, Big Basin**
11:10 AM	**Poster Session IV ends**	
11:15 AM	**General Session** *John Stanford, Ph.D., Associate Director, University of Kansas Medical Center* Oral Presentation Awards	**Kings ABC, Flint Hills**
11:45 AM	*Doug Wright, Ph.D., K-INBRE Principal Investigator, University of Kansas Medical Center* Closing Remarks	
11:45 AM	**Boxed lunches available for pickup**	**Grand Ballroom Foyer**
12:00 PM	**Hotel Checkout**	

Saturday, January 13, 2024

Distribution of the 2-micron Plasmid in Various Strains of Saccharomyces cerevisiae

Greving, Camryn, Gillock, Eric T.
Department of Biological Sciences, University of Fort Hays State University

Abstract
Along with several known viruses and prions, some strains of baker's yeast, *Saccharomyces cerevisiae,* are known to carry the 2-micron plasmid. When present, this extrachromosomal element exists as a circular, double-stranded, DNA plasmid within the nucleus of the host cell. In strains that harbor it, there is an average copy number of between 40 to 60 per haploid cell, with 60 being more common. This copy number is stabilized by the action of the host amplification system. At normal copy numbers, the plasmid doesn't seem to confer any selective advantage to the host. However, at high copy numbers, it becomes detrimental and causes cell cycle misregulation and cell death. It is thought that the plasmid utilizes a "chromosome hitchhiking" method to ensure that adequate numbers of copies are distributed into the daughter cells after cell division. The "chromosome hitchhiking" segregation method is of research interest as it is also used by papilloma and gammaherpes viruses to maintain themselves in latently infected cells. In this work, several strains of yeast were assayed by colony PCR for the presence of the 2-micron plasmid *REP2* gene, which functions in partitioning of the plasmid into daughter cells during mitosis. Our research so far shows out of 21 strains of *Saccharomyces cerevisiae* examined, 17 displayed the 2-micron plasmid. Future work will entail screening more yeast strains for the 2-micron plasmid, and examining sequence variations among the *REP2* genes in the plasmids found.

Impairments in Cerebral Autoregulation and Cerebrovascular Reactivity in Cancer Survivorship

Author(s): **Kayla Smith**[1], Britton Scheuermann[2], Shannon Parr [2], Stephen Hammond [2], Vanessa-Rose Turpin[2] , Olivia Kunkel [2], Carl Ade [2,3]
1 Department of Biology, Langston University, Langston, OK
2 Department of Kinesiology, Kansas State University, Manhattan, KS
3 Department of Physician's Assistance Studies, Kansas State University, Manhattan, KS
‡ Contributed equally to this work.

Roughly 46% of cancer survivors report cognitive dysfunction across many types of cancer, which has been associated with anti-cancer therapy and often results in reduced quality of life. Pre-clinical studies have suggested that the underlying factors of cognitive decline likely involve cerebrovascular dysfunction. We aimed to characterize local cerebrovascular regulatory functions (cerebrovascular reactivity and cerebral autoregulation) and central large artery stiffness (aortic arch stiffness) in cancer survivors, within 1-5 years of completing treatment compared to age- and sex-matched healthy controls. Aortic arch pulse wave velocity (aaPWV) was determined using Doppler ultrasound scans of the aortic valve and the descending aortic arch. Cerebrovascular reactivity was assessed as the change in middle cerebral artery velocity relative to the change in end-tidal carbon dioxide during a modified rebreathing protocol. Cerebral autoregulation was determined using Mx, a moving correlation coefficient between finger plethysmography-derived arterial blood pressure and cerebral blood velocity of the middle cerebral artery. Higher Mx values indicate poorer cerebral autoregulation. 11 women were recruited (5 healthy controls and 6 cancer survivors who had received treatment). Mx values were higher in cancer survivors. Both cerebrovascular regulatory functions were impaired in cancer survivors compared to healthy controls and decreases in cerebral autoregulation were associated with increases in aortic stiffness. The present findings highlight the importance of monitoring cerebral and global vascular function in cancer survivors who are at high risk for cognitive decline.

Molecular Analysis of Benzimidazole Resistance in Hookworms in Kansas Dogs

Grace Schieferecke[1], Theresa Quintana[2], Jeba Jesudoss Chelladurai[2]
[1] Division of Biology, College of Arts and Science, Kansas State University
[2] Department of Diagnostic Medicine Pathobiology, College of Veterinary Medicine, Kansas State University

Ancylostoma caninum (canine hookworm) primarily causes infections in dogs, but can also be zoonotic. Hookworm infections are the most commonly diagnosed parasites in dogs in the U.S., with up to 4% prevalence. Common treatment for hookworm infections includes a class of antiparasitics called benzimidazoles that hookworms have developed resistance to. A single nucleotide polymorphism (SNP) in codon 167 (F->Y) of the beta-tubulin gene is suggested to be responsible for benzimidazole resistance and is therefore a target for resistance diagnosis. There is little research on this SNP in the U.S., particularly in Kansas. We **hypothesize** that this mutation is prevalent in hookworms in Kansas dogs. We isolated hookworm eggs from the feces of naturally infected dogs and extracted DNA using a commercial kit. Using qAC167 and qACRtr1 primers, we performed quantitative polymerase chain reaction (qPCR) on ~80 samples to determine relative allele frequency rates at codon 167. We found significant variation in allele frequencies within and between samples, with variations from 1% to nearly 100%. These results are significant, novel, and have shown the existence of significant resistance within *A. caninum* in the region. These have implications for the judicious use of benzimidazoles for treating hookworm infections in dogs without contributing to more resistance development. By using molecular techniques, we demonstrate that we can detect resistance early and in individual dogs. These results can be integral for choosing an effective treatment for hookworm infections. Molecular diagnostics are integral for the treatment of infections with probable levels of resistance.

Assessing Plant Derived Antioxidants for a Protective Effect Against Pesticides in the Honeybee Gut

David Claridge, Oliver Hiszczynskyj, Meghan Cashell, Meagan Fernandez, Jacob Spidell and Dr. Joanna Gress
School of Science and Mathematics, Emporia State University, Emporia KS 66801

Apis mellifera is an invaluable pollinator for commercial crops. Long- and short-term survival of honeybees has been negatively impacted by neonicotinoid pesticides, including imidacloprid, which causes oxidative stress in the bee gut. The antioxidant pathway in the bee gut consists of 10 genes that break down ROS's and repair the damage caused by them. Little is known about what compounds can stimulate this pathway and how this may improve overall honeybee health. There are many antioxidants found in nature and in the plants that bees pollinate. One group are catechins that include epigallocatechin-3-O-gallate from green tea, that act as ROS scavengers. Another group are the anthocyanins and proanthocyanidins found in blueberries. These are flavonoid polyphenols that create red, blue, and purple hues in plants. These molecules have been shown to increase the antioxidant capacity and increase gene expression for antioxidant genes. Another antioxidant is rosmarinic acid present in *Salvia officinais* which has been implicated in radical scavenging. Mint or *Mentha piperita* has been found to contain high levels of antioxidants including phenolic compounds, ascorbic acid and carotenoids that can delay or inhibit the oxidation of different molecules and act as free radical scavengers and inhibit lipid peroxidation. To assess if these plant antioxidants offer a protective effect to honeybees, feeding trials were conducted on foragers. Each antioxidant was fed to 20 forager bees exposed to imidacloprid and their abdomens were collected for RNA extraction 48hrs later. We are conducting qPCR analysis to look at expression of the antioxidant/detoxification pathway.

Syntheses of Co-MOF, Ni-MOF, and Fe-MOF for applications in both electrocatalysis and energy storage using a single-step microwave method.
Alexandra Robinson[2], Wang Lin[1] and Ram K. Gupta[1,2*]
[1]National Institute of Material Advancement, Pittsburg, KS 66762, USA
[2]Department of Chemistry, Pittsburg State University, Pittsburg, KS 66762, USA

Abstract:
With the energy crisis at hand, many scientists are developing new ways to both obtain and store clean energy. These new techniques have the potential to revolutionize technology across the board in many different settings, such as in medical technologies. One of the most popular approaches is the utilization of hydrogen gas. The primary setback is the poor reaction kinetics of water splitting reactions. Precious metal-based catalysts are attractive to aid this; however, they are expensive, which hinders the economic aspect. So, researchers have homed in on transition-metal based catalysts. In this work, cobalt, iron, and nickel metal organic frameworks (MOFs) were synthesized on nickel foam (NF) using the single-step microwave method to achieve a highly porous crystalline structure that consequently increased the number of active sites for the water splitting reaction. Once synthesized, the electrodes underwent both electrocatalytic and supercapacitor testing at a Versastat 4-500 electrochemical workstation. The Fe-MOF proved to have the best results in OER, with a low overpotential, low Tafel slope, and good stability. The Ni-MOF proved to have the best results in the supercapacitor application, with a high specific capacitance, high energy density, and a good rate performance.

Sunday, January 14, 2024

Examining the Reproductive Ecology of the Ornate Box Turtle (*Terrapene ornata)* in Western Nebraska; A Multiyear Study
Keetan Munsell, Katie Brighton, Mason Chaney, Erica Guldner, Zoe Edlund, Aubrey Gauntt, Samantha Kim, Timothy Speer, Abigal Trautman, Patience Wagner, Brianna Wilson, Benjamin Reed
Department of Biology, *Washburn University, Topeka, Kansas, USA*

Understanding the reproductive ecology of any species is vital for determining intraspecific variation in individual fitness, modeling population growth or persistence potential, and developing effective conservation strategies. The reproductive ecology of Ornate Box Turtles (*Terrapene ornata*) including a full examination of the pattern of their egg bearing period and reproductive output is relatively understudied. The goal of this study was to specifically address the mating behavior, egg bearing cycles, body condition fluctuations, and nesting behavior of free-ranging Ornate Box Turtles via radio telemetry and ultrasonography. To do this we closely monitored a population of 32 female turtles in Nebraska over two consecutive years with each turtle being monitored for embryonic development on a four-day cycle during the presumed egg-bearing period. Individual female movements were tracked daily using radio telemetry, then an ultrasound (IBEX EVO II) was used to assess the egg bearing status, internal condition, and clutch size of that female. Our results enabled us to better describe the egg bearing period of Ornate Box Turtles and their nesting, mating, and overall movement behaviors when reproductively active. This data can be useful in understanding individual variation in reproductive output, fitness, and ultimately aid in targeted conservation plans without performing an invasive procedure.

Hyaluronan synthase (Has)2, in dual Has1 and Has3 deficient mice, protects against age-associated weight gain by reducing adipocyte hypertrophy
Ian Ensley[1], Vanessa Schmidt[1], Wendena Parkes[1], Michele T. Pritchard[1,2,3]
[1]Department of Pharmacology, Toxicology, and Therapeutics, [2]Diabetes Institute, [3]Liver Center, The University of Kansas Medical Center, Kansas City, KS 66160

Hyaluronan (HA) is a large glycosaminoglycan important for tissue structure, repair, and cell signaling. HA is important for preadipocyte maturation into adipocytes and possibly other adipose physiology. Pharmacological efforts to suppress HA reduce diet induced weight gain. However, hyaluronan-adipose physiology during aging is largely unknown. Because HA creates a soft extracellular matrix, we hypothesized that it permits age-associated adipocyte hypertrophy. To test this, we used wild type (WT) mice and Has1&3 double knock out (dko) mice. Within each genotype, we used young (7 weeks) and old (17 months) mice who were fed normal mouse chow (5% fat by weight). At euthanasia, we weighed mice, and then harvested and weighed gonadal (white) adipose tissue. We assessed adipocyte number and size using ImageJ. We semi quantitatively measured tissue hyaluronan content after fluorescent HA binding protein (HABP) staining using ImageJ. We performed ELISA-like assays to confirm HABP staining results. We found significantly reduced body and adipose mass in old dko mice compared to old WT counterparts. Moreover, we found that adipocyte hypertrophy in dko old mice was reduced compared to WT old mice adipocytes. Paradoxically, we found that adipose HA content was partially retained with age in dko animals compared to WT mice which lose adipose HA. We've concluded that Has1 and Has3 deficiency protects against age associated weight gain perhaps through HA over production by the intact Has2 synthase. Further analysis is needed to understand the possible physio-mechanical role of HA in adipose expansion with age.

Characterization of Cardiomyopathic Point Mutations in the Ig3 Domain of Myopalladin
Michaelis, Alia; Tran, Julie; Arachchige, Asha R; Beck, Moriah R.
Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS

Abstract

Myopalladin (MYPN) is a recently described actin-binding protein (ABP) located at both the Z and I lines of striated muscle. MYPN is believed to act as an anchor to other structural proteins such as actin, nebulin, and titin, which work together to facilitate contractile motion at the sarcomeres of muscle cells. However, its specific role in regulating the actin-cytoskeleton is largely unknown. Previous studies in the Beck lab have shown that MYPN was capable of binding and cross-linking filamentous actin directly with its Ig3 domain; thus, allowing us to narrow our domain of study to solely Ig3 to further investigate actin binding affinity. The purpose of the study is to examine point mutations in the Ig3 domain of MYPN that have been previously associated with various types of cardiomyopathies (hypertrophic, dilated, and restrictive). In this study, we explore the following properties of MYPN: the F-actin binding affinity and bundling capacity via actin co-sedimentation assays, stability via circular dichroism, and actin depolymerization rates via fluorescence assays. Throughout the study, a total of six cardiomyopathic mutations were investigated and compared to wild-type MYPN: C1002W, R1042C, P961L, F954L, R955W, and R955Q. Thus far, the general observation is that the mutagenic constructs of MYPN bind and bundle actin less successfully than wild-type MYPN. Further studies will aim to elucidate the role of MYPN in the context of the actin-cytoskeleton its potential link to cardiomyopathy.

K-INBRE 2024 Symposium

Poster Presentations

1. Molecular characterization of START-Adjacent Domain (STAD) interaction with GIR1 to control cell division
Lauren E. Apprill[1], Bilal Ahmad[2], Samira R. Laytimi[1] and Kathrin Schrick[1,2]
[1]Department of Biochemistry and Molecular Biophysics and [2]Division of Biology, Kansas State University

2. Impact of *PTPN22* Autoimmunity-Associated Allele on Dendritic Cell Type-I Interferon Production
Jenna R Barnes*, Anam Shaikh, Alec Bevis, Tammy Cockerham, Nancy Schwarting, Robin C Orozco**
Department of Molecular Biosciences, University of Kansas, Lawrence, KS
Presenting Author*
Corresponding Author**

3. Effect of Heat Shock Stress on the Subcellular Localization of the tumor suppressor protein APC
Kamar Chahine[1], Eldric Carreon[2], Kristi Neufeld[2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

4. Exploring Resistance-Virulence Tradeoff in *Pseudomonas fluorescens*
Tiffany Chan, Kervens Accilien, Robert Unckless PhD
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

5. CRISPR Analysis of HIRA in Plants
Keying Chen, Claire Shippy, and Tara Phelps-Durr

6. Cardiovascular Health Monitoring Using Multiple Conformal Photoplethysmography Devices
Coffman, Lauren, Yongkuk, Lee, Department of Biomedical Engineering, Wichita State University

7. Development of Maleic/Malonic Acid Modified Gold Nanoparticles Capable of Detecting Lead in Drinking Water by Colorimetric Analysis
Ethan Conners and Dr. Said Adem
Washburn University 2023
Supported by the Kansas INBRE, P20 GM103418

8. RBPjk plays a protective role in Human immunodeficiency virus-1 (HIV-1) related chronic kidney disease.
Ashley Diaz Rocha, Nicole Sommer, Madhulika Sharma

9. Hyaluronan synthase (Has)2, in dual Has1 and Has3 deficient mice, protects against age-associated weight gain by reducing adipocyte hypertrophy
Ian Ensley[1], Vanessa Schmidt[1], Wendena Parkes[1], Michele T. Pritchard[1,2,3]
[1]Department of Pharmacology, Toxicology, and Therapeutics, [2]Diabetes Institute, [3]Liver Center, The University of Kansas Medical Center, Kansas City, KS 66160

10. Exercise as a Means to Attenuate Early Life Stress-Induced Cognitive Deficits and Hippocampus Disparities
Carly H. Gagnon, Tara E. McQuillan, Julie A. Christianson
Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS 66160

11. Rapid PCR with precise droplet temperature control using digital microfluidic chip
Hale, Joseph, Snowden, Nathan, Becerra, Jesus, Fan, Scott
Department of Mechanical and Nuclear Engineering, Kansas State University

12. *HIC2* loss may underlie cardiac anomalies in human cases with distal 22q11.2 microdeletions
Jennifer I. Interiano[1], Brittany M. Hufft-Martinez[1,2], Jeremy P. Goering[1], Majed Dasouki[3], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, [2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. [3]Department of Genetics and Genomics, Advent Health Genomics and Personalized Health, Orlando, FL.

13. Role of Palladin in Actin Dynamics Revealed by Quantitative Total Internal Reflection Fluorescence Microscopy
Tariq Izard, Wael Yessin, Sanju Ghimire, Moriah R. Beck
Department of Chemistry and Biochemistry, Wichita State University

14. A new vaccine platform based on the selective targeting of dendritic cells by the binding component of the anthrax toxin, protective antigen.
Yousaf Khan[1], Srinivas Gonti[1], Xianglei Yan[2], Nancy Meyer[3], Vamseedhar Rayaprolu[3], Robert N. Brey[4], Karin Loré[2] and James G. Bann[1]
[1]Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS
[2]Division of Immunology and Allergy, Karolinska Institute, Stockholm, Sweden
[3]Pacific Northwest Center for Cryo-EM, Portland, OR.
[4]Kinesis Vaccines LLC, Chicago, IL.

15. Using Comparative Genetics to Annotate the Insulin-Like Signaling Pathway of *Tribolium madens*
Korte, Gen; Teresa Shippy; Susan Brown
Division of Biology, Kanas State University

16. Immunohistochemical Analysis of HNSCC Cell Spheroids and Xenotransplant Tumor Masses in the Hamster Cheek Pouch
Martinez, Michael[1], Hendry, William PhD[1] Carte, Meris[1]
[1]Department of Biological Sciences, Wichita State University
Supported by the Kansas INBRE, P20 GM103418

17. Conceptual human application of RNA interference of autocrine motility factor receptor in *Acyrthosiphon pisum.*
Mull, Olivia, Balthazor, James. Department of Chemistry, Fort Hays State University.

18. Exploration of Ultraconserved Elements in Noteridae: Comparative Phylogenomic Reconstruction Methods
Authors: Murphy, Baca, et al
Haskell Indian Nations University, University of Kansas.

19. The Evolutionary History of Moray Eels
Edgar A. Nickols, Haskell Indian Nations University, University of Kansas

20. The Role of Glycogen in Clostridioides difficile Spore resilience and longevity
Joshua Ogunbase[1, 2], Revathi Govind[2]
Langston University; Department of Art & Sciences[1], Kansas State University; Division of Biology[2]

21. ManyFishes 1: A standardized test of inhibitory control in fishes using Big Team Science
Shane Rance[1] and Laurent Prétôt[2]
[1]Department of Biology, Pittsburg State University
[2]Department of Psychology and Counseling, Pittsburg State University

22. Exploring Protein-Protein Docking of the Sox2 and HDAC1 Proteins
Rorstrom, Carl J.,[1] and Allan Ayella,[1] [1]Department of Chemistry, Washburn University

23. CRISPR Analysis of the MYB Domain Transcription Factor Asymmetric Leaves 1
Gabriella Rueschhoff, Dr. Tara Phelps-Durr
Fort Hays State University Department of Biological Sciences, Fort Hays State University Honors College

24. Optimizing *C. elegans* for high throughput chemical screening
Ariana Siddique[1], John Hoopes[1], James Pressdee[1], Arnav Jain[1], Dr. Lisa Timmons[1]
[1]Department of Molecular Biosciences, The University of Kansas, Lawrence, Kansas

25. Urban heat islands are present in small Midwestern cities, but unrelated to residents' sociodemographics
Simmons, Christopher, Daniel J. Benson, and Christine C. Rega-Brodsky
Department of Biology, Pittsburg State University

26. Synthesis of a Hyaluronic Acid-Deferoxamine Conjugate for Local Treatment of Bone Regeneration
Navya Singh, Laird Forrest
Department of Pharmaceutical Chemistry, University of Kansas, Lawrence, Kansas

27. Microbial Survival and Partitioning in Layered Ices Relevant to Mars
Bao Nhu N. To and Mark A. Schneegurt
Department of Biological Sciences, Wichita State University, Wichita, KS, 67260, USA

28. cHPV E6 reduces innate immune signaling.
Emily Tolbert, Dalton Dacus, Rose Pollina, Nicholas A. Wallace
Division of Biology, Kansas State University

29. The significance of leaf venation patterns in the genus *Uromyrtus* in New Caledonia: A poorly-known genus currently under taxonomic revision
Clarissa Wedman and Neil Snow
Department of Biology, Pittsburg State University

30. Activation of β_2-adrenergic receptor enhances neonatal lung immunity to Respiratory Syncytial Virus infection
Sandeep Adhikari[1], Pankaj Baral[1*]
Corresponding Author: baral@ksu.edu
[1]Division of Biology, Kansas State University, Manhattan, KS, USA, 66506.

31. A PROTAC-Based Degrader to Colorectal Cancer Relevant *N*-Terminal Methyltransferase 1 (NTMT1)
Chao An,[1] Wei Wu,[1] Ping Li[1]
[1]Department of Chemistry, Kansas State University, Manhattan, Kansas, 66506, U.S.A

32. Impact of *PTPN22* and its Autoimmunity-Associated Minor Allele During Coronavirus Infection
Alec M. Bevis[1,2], Anam Shaikh[1,2], Catherine Kerr[1,2], Jenna Barnes[1], Kate Rosa[1], Tammy Cockerham[1], Nancy Schwarting[1], Anthony R. Fehr[1], Robin C. Orozco[1].
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA;
[2]The Office of Graduate Studies, University of Kansas, Lawrence, KS, USA

33. Determining Nuclear APC's role in Mediating UV-Induced DNA Damage
Carreon, Eldric and Kristi L. Neufeld
Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

34. Presence of PERV-C among Feral Pigs in Eastern Kansas
Cesur, Robin. Gillock, Eric. Fort Hays State University, Hays, KS

35. Oxidative Stress Regulator NRF2 controls Inflammatory T-helper (Th) Subset differentiation by Modulating Glycolysis
Debolina Dasgupta[1], Aprajita Tripathi[1], Ashlyn Bugbee[2] and Kalyani Pyaram[1]
[1]Department of Cancer Biology, University of Kansas Medical Center
[2]Division of Biology, Kansas State University

36. Water extract from *Euglena gracilis* attenuates lung cancer growth and increases PD-1 expression in tumor infiltrating lymphocytes
Authors: Sarah DeVader, Susumu Ishiguro, Jeffery Comer, Masaaki Tamura
Department of Anatomy and Physiology, Kansas State University College of Veterinary Medicine, Manhattan, KS 66506

37. Higher yield isolation method of alveolar macrophages for functional studies
Surya Prasad Devkota[1], Prabhu Raj Joshi[1], Sandeep Adhikari[1], Chinemerem Onah[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State university, Manhattan, Kansas, USA, 66506

38. Extracellular vesicle miRNA signatures as novel biomarkers in mouse model of allergic asthma
Santhosh Kumar Duraisamy[1], Chandrashekhar Prasad[1], Rachel Griffard[2], Dong Pei[2], Navneet Dhillon[1], Mario Castro[1], Isaac Kirubakaran Sundar[1]
[1]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, [2]Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS, USA

39. Unused
40. Unused

41. Characterizing the *AT3G05510* gene product in *Arabidopsis thaliana* using lipid profiling
Adamson, Summer,[1,2] Ruth Welti,[1,2] and Zolian Zoong Lwe[2,3]
[1]Division of Biology, Kansas State University, [2]Kansas Lipidomics Research Center, Kansas State University, [3]Department of Biochemistry and Molecular Biophysics, Kansas State University

42. The Effect of NKG2D on The Fate of CD8+ T-cells
Aikin, Tatum,[1] Zoe Bedrosian,[1] Mary Markiewicz[1,2]
[1]Department of Microbiology, Molecular Genetics, and Immunology, University of Kansas Medical Center; [2]Flow Cytometry Core Laboratory, University of Kansas Medical Center

43. Understanding the role of neurotransmitter receptors in anti-*Aspergillus fumigatus* immunity
Michael Bartkoski[1], Chinemerem Onah[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

44. The differentiation and characterization of dental pulp stem cells on nanofiber matrices
Kayla Cantu, Neema Fathi, Li Yao
Department of Biological Sciences, Wichita State University

45. Kansas Small Mammal Survey Abstract
Oscar Casillas-Vallejo[1], Andrew Hope[2], and Kaitlyn Headlee[2]
[1]Department of Biology, Langston University, Langston, Oklahoma [2]Division of Biology, Kansas State University, Manhattan, Kansas

46. Fitness Effects and Transmission of a B chromosome in *Drosophila putrida*
Evelyn Cuellar*, Paul S. Ginsberg, Robert Unckless*
University of Kansas, Department of Molecular Biosciences

47. EXPLORING THE GUT MICROBIOTA OF GRAY BATS IN KANSAS FOLLOWING CULTURABLE AND METAGENOMIC APPROACHES
Ayushee Dasgupta, Bobbi Monroe, Andrew George, and Anuradha Ghosh
Biology Department, Pittsburg State University, Pittsburg, KS

48. Fine-tuning of Cell-ECM Assembly by Transglutaminase
Dylan Feist, Nicole Green, Ziwei Zhao, Erika R. Geisbrecht
Department of Biochemistry and Molecular Biophysics, Kansas State University

49. ANNEXIN A2 EXPRESSION IN PROSTATE CANCER CELLS.
Charles R. Gates[1,2], Amit Kumar Tripathi[1], Jamboor K. Vishwanatha[1], Pankaj Chaudhary[1]
[1]Department of Microbiology, Immunology & Genetics, University of North Texas Health Science Center, Fortworth, TX
[2]Department of Biology, Langston University, Langston, OK.

50. Distribution of the 2-micron Plasmid in Various Strains of Saccharomyces cerevisiae
Greving, Camryn, Gillock, Eric T.
Department of Biological Sciences, University of Fort Hays State University

51. A gradient-based assay for analyzing microbial community interactions.
Makayla Hallacy, Alexa McGann, Ashlynn Booth and Stephen Fields
School of Science and Mathematics, Emporia State University, Emporia KS

52. Fitness Testing of Adults Ages 60 and Older
Jessica Jones, Dr. Laura Covert Miller, Dr. Mike Carper
Pittsburg State University - Health Human Performance and Recreation

53. Role of b- adrenergic Receptors in Innate Immune Response to *Burkholderia thailandensis* Infection
Abigail Judd[1], Prabhu Joshi[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

54. Nitrification and Denitrification Rates in Intermittent Streams during a Wet-up Event at Youngmire Ranch (Elk County, Kansas)
Genevieve Knotts[1], Sarah Flynn[2], Amy Burgin[2]
Haskell Indian Nations University[1], University of Kansas[2]

55. Investigating how miRNA modifications influence strand selection in the nematode *Caenorhabditis elegans.*
Sumire Kurosu, Jeff Medley, and Anna Zinovyeva
Division of Biology, Kansas State University, Manhattan, Kansas

56. Small Molecule KRAS Inhibition in Colorectal Cancer
Alexa N. Magstadt[1], Andrew E. Evans[1], and Dan A. Dixon[1,2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, [2]University of Kansas Cancer Center, Kansas City, KS

57. Cloning and Expression of the AAA+ ATPase ClpA from *Escherichia coli*
Eleanor Martin, Zachary Spaulding, and Michal Zolkiewski
Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, Kansas

58. Sex differences in active avoidance strategies
Authors: Halle Ness, Shannon Ruble, Cassie Kramer, Maria Diehl
Affiliation: Kansas State University, Department of Psychological Sciences

59. Investigation of Visual Data Analysis Skills and the Impact on Clinical Decision Making
Halle Panter,[1] Paige Boydston[1]
[1]Department of Psychology and Counseling, Pittsburg State University

60. Analysis of OSCP Deregulation in Alzheimer's Disease
Albert Park, Tienju Wang, Jing Tian, Heng Du
University of Kansas School of Pharmacology and Toxicology, Lawrence KS, 66046

61. Computational Prediction of Chloroplast Outer Envelope β-barrel Proteins
Emily Proctor[1], Daniel Montezano[1], Joanna S. G. Slusky[1,2]
[1]Computational Biology Program, University of Kansas, Lawrence, KS 66045
[2]Department of Molecular Biosciences, The University of Kansas, Lawrence, KS 66045

62. Comparing the Sugar Profile of Infant Formulas in The United States from 1988-2022
Audrey R. Rips-Goodwin[1,2], Daiil Jun[1], Tera L Fazzino[1]
[1]Department Psychology, University of Kansas, [2]Department of Chemistry, University of Kansas

63. An Analysis of Presence of Antibiotic-Resistant Bacteria in Wastewater Systems: A Strategy to Assess Population Health in Kansas Counties
Audrey Rymer[1], Jonathan Ferguson[1], Garret Rymer[1], Claudia Da Silva Carvalho[1], Brooklyn Schaffer[1], Jeff Sekavec[2], and Courtney McCullough[2]
[1]Department of Biological Sciences, Fort Hays State University, [2]Colby Community College

64. Deciphering DMXAA Binding: A Computational Exploration of Interactions with Human and Mouse STING Proteins
Emily A. Schulte and Masakatsu Watanabe
Department of Chemistry, Fort Hays State University, Hays, Kansas

65. Movement Ecology of Ornate Box Turtles (*Terrapene ornata*) across Different Life Stages
Timothy Speer, Katie Brighton, Mason Chaney, Erica Guldner, Zoe Edlund, Aubrey Gauntt, Samantha Kim, Keetan Munsell, Abigail Trautman, Patience Wagner, Brianna Wilson, Benjamin Reed
Dept of Biology, Washburn University, Topeka, KS, USA

66. Irisin-mediated Exercise Neuroprotection
Carter Stanley, Zachary White, Keshari Sudasinghe and Stephanie Hall
Department of Biology and Department of Anatomy and Physiology, Kansas State University, Manhattan, Kansas, USA

67. Identifying and Characterizing a Genetic Suppressor of *let-7* in *C. elegans*
Will Sydzyik[1], Jeff Medley[1], and Anna Zinovyeva[1]
[1]Division of Biology, Kansas State University, Manhattan, KS

68. Characterization of cardiomyopathic point mutations of the Ig3 domain in myopalladin
Tran, Julie; Michaelis, Alia; Arachchige, Asha R.; Beck, Moriah R.
Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS

69. Oxygen consumption sex differences in intermittent-fasted animals
Sabrina Veith, Stephanie Hall, Keshari Sudasinghe
Kansas State University Department of Anatomy and Physiology

70. Development of a novel drug delivery platform from the Lagunamide family of natural products
Kameron R. Wildeman, Shashika Perera, Anthony Fatino, and Ryan J. Rafferty
Kansas State University, Department of Chemistry

71. Reconstructing the evolutionary history of a Neotropical aquatic beetle species complex using phylogenomic inference methods
Liam Wrixon[1], Stephen Baca[2]
[1]Natural Sciences Department, Haskell Indian Nations University, [2]Department of Ecology and Evolutionary Biology, University of Kansas

72. Glycosylation Unveiled: Exploring the Structure and Function of FSH Hormone Glycoforms
Yara Abdine, Alan R. Brown, Viktor Y. Butnev, William K. White, Jeffrey V. May, and George R. Bousfield
Department of Biology, Wichita State University, Wichita, KS.

73. Equipment and Services of the Kansas University Nanofabrication Facility
Ryan Grigsby[1] and Susan M. Lunte[1,2,3,4]
[1]The Center for Molecular Analysis of Disease Pathways, [2]The Ralph N. Adams Institute for Bioanalytical Chemistry, [3]Department of Pharmaceutical Chemistry, [4]Department of Chemistry, University of Kansas

74. Developing bioinformatic tools for the data mining of archived organellar genomes – A productive setting for online student-led research
Michael Gruenstaeudl[1], Phongsavahn E. Mongkhovilay[2], Gregory Smith[2], and Keaton Rowley[2]
[1]Department of Biological Sciences, Fort Hays State University; [2]Department of Computer Science, Fort Hays State University

75. Next Generation Sequencing at KU Genome Sequencing Core
Hackett, Jennifer L.[1,2,3], Kristen M. Cloud-Richardson[1,2,3], Erik A. Lundquist[1,2,3], Susan M. Lunte[1,4,5]
[1]Center for Molecular Analysis of Disease Pathways, [2]Genome Sequencing Core, [3]Department of Molecular Biosciences, [4]Department of Chemistry, [5]Department of Pharmaceutical Chemistry, University of Kansas, Lawrence KS, USA

76. Global Transcriptional Network Changes of Temperature on Sex Dimorphism
Jane A. Ibude[1], Edziu Franczak[2], Michael E. Ponte[2], John C. Prom[2], and E. Matthew Morris[2].
[1]Department of Dietetics and Nutrition, University of Kansas Medical Center
[2]Cell Biology and Physiology, University of Kansas Medical Center.

77. The role of nuclear APC in regulating MUC2 expression and colonic inflammation
Anika James, Kristi L. Neufeld
University of Kansas, Lawrence, KS, USA

78. The Effects of Alcohol Use in the Risk for Cancer
Trisha Rastogi, Varun Rastogi
Blue Valley High School

79. Unused
80. Unused

81. RNA Interference of TorsinA protein on *Acyrthosiphon pisum*
Allphin, Braden, Balthazor, James. Department of Chemistry, Fort Hays State University

82. NMR structural studies of a growth-blocking peptide, *Manduca sexta* SRP-6
Blake Arria[1], Andy Su[1], Tomohiro Kimura[1,2], Xiao Iong Cao[3], Yang Wang[3], Haobo Jiang[3] and Om Prakash[1]
[1]Department of Biochemistry and Mol. Biophysics, Kansas State University, Manhattan, KS 66506
[2]Department of Chemistry, Kansas State University, Manhattan, KS 66506
[3]Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK 74078

83. Vector Construction to Generate Charcoal Rot Resistant Transgenic Soybeans
Bolick, Abby, Daniel Zurek
Pittsburg State University Department of Biology

84. Role of β-adrenergic signaling in neonatal myeloid cell response to TLR Ligands
Camille Carrier[1], Sandeep Adhikari[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

85. RNA Interference of Heat Shock 70 kDa Protein 1L in *Acyrthosiphon pisum*
Griffin Davies, James Balthazor

86. Flavonoid-Rich Alimentary Intervention: Investigating Food Components in Cancer Prevention and Therapy (FLAVOR-CAP)
Duru Dogan, Kansas State University, Department of Political Science, Department of Statistics Hande Kucuk McGinty, Kansas State University, Department of Computer Science

87. Role of PARP14 in HSV-1 Viral Replication
Anna Ferkul, Hongping Hao, Srivatsan Parthasarathy, Anthony Fehr, David Davido
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

88. Isolation and Identification of Microbes from Commercial Kombucha
Abigail Fette, Susan Bjerke
Washburn University, Department of Biology

89. CDKs-1 and -2 Enhance HSV-1 IE Gene Expression and Replication
Drew Honeycutt[1], Maxim Rodzkin[1], and David Davido[1]
[1] Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas, USA

90. Stalk cell movement in Drosophila: a model to understand how migrating cells shape tissues and organs
Author(s): Daysha Isaac[1], Sally Horne-Badovinac[2], and Jocelyn A. McDonald[3]
Affiliations: [1]Department of Biology, Langston University, Langston, OK; [2]Department of Molecular Genetics and Cell Biology, The University of Chicago, Chicago, IL; [3]Division of Biology, Kansas State University, Manhattan, KS.

91. Antifungal Bacteria in Soil
Brandon Kennemer and Dr. Eric Gillock
Fort Hays State Biology Department

92. Mechanisms underlying the development of plastic cellular differentiation in the volvocine green algae
Lidia S. Lopez Vazquez[1], Dinah R. Davison[1], Bradley J.S.C. Olson[1]
[1]Division of Biology, Kansas State University, Manhattan, KS

93. Cadmium exposure induces fibroblast-to-myofibroblast transition and pulmonary fibrosis
Kushala Madduru,[1] Kylie Cushing,[1] Jackson Hagen, [2] Chandrashekhar Prasad,[3] Santhosh Kumar Duraisamy, [3] and Isaac Kirubakaran Sundar[3]
[1]University of Missouri – Kansas City, Kansas City, KS, USA
[2]Pomona College in Claremont, Claremont, CA, USA
[3]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, University of Kansas Medical Center, Kansas City, KS, USA

94. Screening Environmental Soil Samples for Antibiotic Production
Paige Mattick, Eric Gillock, Fort Hays State University Department of Biological Sciences

95. Downregulation of the nutrient-sensitive post-translational modification, O-GlcNAcylation, attenuates Autosomal Dominant Polycystic Kidney Disease
Nikhitha Muthineni[1, 4], Matthew A. Kavanaugh[1, 4], Dona G. Isai[1,4], Vincent Lam[1, 4], Rayyan Abid[1, 4], Maria T. Villar[2], Antonio Artigues[2], Stephen C. Parnell[2, 4], Chad Slawson[2, 4], Darren P. Wallace[3, 4], Pamela V. Tran[1, 4]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS
[4]The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

96. Micro Fabry-Perot Cavity for Characterizations of Nanoscale Particles in Liquid Phase
Girish Paudyal and Hoang Nguyen
Department of Chemistry, Washburn University, Topeka, KS 66621, USA

97. Understanding Mechanisms of Tumor Resistance in Murine Cell Lines
Payne, Carlie and Peter A.Chung. Department of Biology, Pittsburg State University

98. Phosphorylation State of the Intermediate Protein Partner RsbV1 Impacts Growth and Progeny Production of *Chlamydia trachomatis*
Diego Prieto, Alexandra P. Cutter, and P. Scott Hefty
Department of Molecular Biosciences, University of Kansas

99. Role of asparagine synthetase and other transcription factor targets in epidermal morphogenesis
Jillian K. Rockley, Bibek Subedi, Bradley J.S.C. Olson, and Kathrin Schrick
Division of Biology, Kansas State University

100. Using DNA repair inhibitors to increase the efficacy of chemotherapy in cervical cancer
Sandoval, Allison,[1] Wendel, Sebastian,[1] Wallace, Nicholas,[1] Division of Biology, Kansas State University

101. Understanding the mechanisms of *Clostridioides difficile* resistance to Cycloserine
Madelyn Seiler, Victoria Droge and Revathi Govind, Division of Biology, Kansas State University

102. Assessment of the Impact and Outcomes of the K-INBRE Program on Undergraduate Research Experiences
Michael Shi[1], Sarah E. Velasquez, PhD[2]
[1]Department of Computer Science, Cornell University, [2]Department of Anesthesiology, University of Kansas Medical Center

103. Determination of Psychoactive Compounds in CBD Oils via RP-HPLC-UV/Vis Analysis
Steigner, Sofia, Dr. Qiyang Zhang, Department of Biological Sciences, Emporia State University

104. Regional volume changes during adolescence in the valproic acid model parallels human findings
Hunter Strating[1], Cole King[1], Macy Payne[2], Ivina Mali[2], Stefan H Bossmann[2], Bethany Plakke[1]
[1]Department of Psychological Sciences, Kansas State University
[2]Department of Chemistry, Kansas State University

105. Changing Macrophage Differentiation by Treatment of B2-GPI Derived Peptides
Mia Thompson[1], Jen Rowe[1], Sherry Fleming[1,2]
[1]Division of Biology, [2]Johnson Cancer Research Center, Kansas State University, Manhattan, Kansas

106. Design of Peptide Amphiphiles for Selective Aggregation in Gram-Positive Bacterial Membranes
Walker, Greyson, Jeffrey Comer
Department of Anatomy and Physiology, Kansas State University

107. The Effects of Circuit Resistance Training on Psychosocial and Physiological Outcomes in Underactive Latinos
Jack Watson[1] and Erin M. Blocker[1], [1]Department of Health, Physical Education & Recreation, Emporia State University

108. Isolation and Characterization of Fungi Tolerant to High Concentrations of Ammonium Sulfate
Wolf, Jaylynn, Schneegurt, Mark. Department of Biological Sciences, Wichita State University

109. Hydrogen Bonds Impact on Function of PhoU Homologs and Dimers
Nikolas Yackovich[1], Sakib Mahmud[1], Ryan Rodriguez[1], Katelyn Schmalz[1], Stewart Gardner[1]
[1]School of Sciences and Mathematics, Emporia State University, KS.

110. The bidirectional impact of arginine-vasopressin receptor 1a (*Avpr1a*/AVPR1A) and the gut microbiome on visceral hypersensitivity (VH).
Leena Kader[1], Adam Willits[1], Julie A. Christianson[2], Kyle Baumbauer[2], Jun-Ho La[3], Bin Feng[3], and Gerald F. Gebhart[3,4,5], Erin E. Young[1,2]
[1]Department of Anesthesiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Integrative Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Anesthesiology, University of Pittsburgh School of Medicine, Pittsburgh, PA
[4]Department of Medicine (GI), University of Pittsburgh School of Medicine, Pittsburgh, PA
[5]Department of Psychiatry, University of Pittsburgh School of Medicine, Pittsburgh, PA

111. Friend or Foe? Determining how social interactions improve or impair learning behaviors in a platform-mediated active avoidance task in rats.
Authors: Cassandra Kramer, Shannon Ruble, Ivy Auletti, Maria M. Diehl
Affiliation: Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA

112. PhoU homologs in *Staphylococcus aureus* form Homodimers
Sakib Mahmud[1], Nikolas Yackovich[1], Ryan Rodriguez[1], Katelyn Schmalz[1], Stewart Gardner[1]
[1]School of Sciences and Mathematics, Emporia State University, KS.

113. Maternal heterozygosity in mice for the ciliary *Thm1* gene protects against cleft palate
Brittany M. Hufft-Martinez[1,2], Jeremy P. Goering[1], Sarah C. Wilson[1], An Tran[1], Dana N. Thalman[1], Michaella Rekowski,[3] Michael Washburn[3,4], Pamela V. Tran[1,5], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center,
[2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, [3]Department of Cancer Biology, University of Kansas Medical Center, [4]Kansas University Cancer Center,[5]Jared Grantham Kidney Institute, University of Kansas Medical Center

114. Flow Cytometry Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory.
Peter R. McDonald [1], 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 and 2 Department of Molecular Biosciences, The University of Kansas, Lawrence, KS, USA

115. Targeted mutations of miRNA duplexes reveal asymmetries important for proper strand selection *in vivo*
Jeff Medley[1], Sumire Kurosu[1], Ganesh Panzade[2], Sarah Coffey[1], Will Sydzyik[1], Joel Sydzyik[1], Mira Bhandari[3] and Anna Zinovyeva[1]
[1]Division of Biology, Kansas State University
[2]Frederick National Laboratory for Cancer Research, National Institutes of Health
[3]Department of Molecular and Integrative Physiology, University of Michigan

116. Stroke and Neural Dynamics: Exploring the impact of focal ischemic infarcts in the latent space
Authors: Nishimoto, Matthew,[1] Federico Barban[2,3], Heather Hudson[4], Michela Chiappalone[2,3], Randolph J. Nudo[4,5], David J. Guggenmos[4]
[1]Department of Neurosurgery, University of Kansas Medical Center; [2]Department of Informatics, Bioengineering, Robotics System Engineering (DIBRIS), University of Genoa, Genoa, IT; [3]Rehab Technologies Lab, Istituto Italiano di Tecnologia, Genoa, IT; [4]Department of Physical Medicine and Rehabilitation, [5]Landon Center on Aging, University of Kansas Medical Center

117. Prescence of Porcine Endogenous Retrovirus Class C in Domestic pigs in selected areas in Kansas
Isaac Odoi, Eric T. Gillock, Fort Hays State University, Biology department

118. Unused

119. Unused

120. Unused

121. Effect of XPO1 inhibition on colorectal cancer tumorigenesis
Andrew E. Evans[1], Dan A. Dixon[1,2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, [2]University of Kansas Cancer Center, Kansas City, KS

122. "Pleiotropic Prioritization: Unraveling Shared Genetic Threads in Insomnia and Chronic Pain Through an Advanced Gene Prioritization Pipeline"
Morgan A. Ewald[1,2,3], Olivia J. Veatch[3], Erin E. Young[1]; University of Kansas Medical Center
[1]Department of Anesthesiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Integrative Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Psychiatry, University of Kansas Medical Center, Kansas City, KS

123. Harnessing the power of *C. elegans* genetics to model neurodevelopmental disorder-associated *AGO1* and *AGO2* mutations.
Belén Gaete Humada[1], Ye Duan[2,3], Li Li[1], Ganesh Prabhakar Panzade[1], Sumire Kurosu[1], Amélie Piton[4], Victor Ambros[2], Anna Zinovyeva[1]
[1] Division of Biology, Kansas State University, Manhattan, KS; [2] Program of Molecular Medicine, University of Massachusetts Chan Medical School, Worcester, MA; [3] Department of Organismic and Evolutionary Biology, Museum of Comparative Zoology, Harvard University, Cambridge, MA; [4] Institute of Genetics and Molecular and Cellular Biology, Strasbourg University, France

124. Unraveling a novel role of DCLK1 in IBD and colon cancer
Kafayat Yusuf[1,2], Badal C. Roy[1,2], Shrikant Anant[2], Shahid Umar[1,2]
[1]Department of Surgery, University of Kansas Medical Center
[2]Department of Cancer Biology, University of Kansas Medical Center

125. A novel method based on field-amplified sample injection coupled with electrokinetic supercharging for the sensitivity detection of glyphosate in flow-gated capillary electrophoresis
Ying Gong, Maojun Gong
Department of Chemistry and Biochemistry, Wichita State University, Kansas

126. Iridium Containing Artificial Dye-decolorizing Peroxidases with Non-canonical Axial Ligand for Catalysis of Unnatural Chemical Reactions
Samiksha Khadka, Chao An and Ping Li
Department of Chemistry, Kansas State University, Manhattan, KS, 66502

127. CRISPR-Mediated Endogenous NTMT1 Tagging for NTMT1 PROTAC Characterization, Design, and Optimization
Wei Wu, Chao An, and Ping Li
Department of Chemistry, Kansas State University, Manhattan, Kansas

128. Gestational Choline Modulates Adolescent Cognitive Outcomes in a Maternal Immune Activation Model of Neurodevelopmental Disorders
Cole King[1,2], Bethany Plakke[2]
[1]Master of Public Health Program, Kansas State University
[2]Department of Psychological Sciences, Kansas State University

129. Nociceptor sensory neurons promote pneumonic sepsis during carbapenem-resistant *Klebsiella pneumoniae* lung infection
Prabhu R. Joshi[1], Pankaj Baral*[1]
*Corresponding author
[1]Section of Microbiology and Immunology, Division of Biology, Kansas State University, Manhattan, KS, USA, 66506.

130. Assessing the Incidence of Methicillin-Resistant (MRSA) and Methicillin-Susceptible Staphylococcus aureus (MSSA) in Pigs at the FHSU Animal Farm's Swine Unit
Kofi Addo Okyere-Addo[1], Dr. Claudia Da Silva Carvalho[1]
[1]Department of Biological Sciences, Fort Hays State University, Hays, Kansas.

131. Lung-innervating Nociceptor Sensory Neurons augment lung defense against *Aspergillus fumigatus* Pneumonia
Chinemerem Onah,[1] Michael Bartkoski,[1] and Pankaj Baral[1]
[1]Kansas State University Division of Biology, Manhattan, Kansas.

132. optima: an open-source R package for the Tapestri platform for integrative single cell multiomics data analysis
Dong Pei 1,2, Rachel Griffard 1, Nanda Kumar Yellapu 1,2, Emily Nissen 1, Devin C. Koestler 1,2
1 Department of Biostatistics & Data Science, University of Kansas Medical Center, KS, Kansas City, USA. 2 The University of Kansas Cancer Center, Kansas City, KS, USA.

133. The Synthetic Chemical Biology Core (SCB): A Resource for Research in Chemical Biology
Chamani T. Perera[1]
[1]Synthetic Chemical Biology Core Laboratory, University of Kansas, Lawrence, KS, USA

134. Musashi1 affects intestinal epithelium growth by regulating mTORC1 pathway
Bikash Pokhrel[1], Dr Kristi Neufeld[1]
[1] Department of Molecular Biosciences, University of Kansas, Lawrence, USA

135. The Hepatic-Brain Axis in Obesity Related Hypertension Development
Michael E. Ponte[1], John C. Prom[1], Jane A. Ibude[1], and E. Matthew Morris[1]
[1]Dept. Cell Biology and Physiology, University of Kansas Medical Center

136. Extracellular Vesicle MicroRNAs as Novel Biomarkers in Asthma Pathobiology
Chandrashekhar Prasad[1], Santhosh Kumar Duraisamy[1], Alexander Alsup[2], Rachel Griffard[2], Dong Pei[2], Navneet Dhillon[1], Mario Castro[1], Isaac Kirubakaran Sundar[1]
[1]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, [2]Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS, USA

137. Reduced Hepatic Mitochondrial Energy Metabolism Decreases Food Intake Inhibition by Oral Preloads in Mice.
John C. Prom[1], Michael E. Ponte[1], Jane A. Ibude[1], and E. Matthew Morris[1]
[1]Dept. Cell Biology and Physiology, University of Kansas Medical Center

138. Gene expression of oncolytic virus receptors in human head and neck squamous cell carcinomas
Silas Rosiere, Sara Akhtar, Christopher Simmons, and Phillip Harries
Department of Biology, Pittsburg State University

139. Active avoidance is acquired more rapidly when learned through observation compared to direct experience in rats.
Authors: Shannon Ruble, Cassandra Kramer, Lexe West, Ivy Auletti, Maria M. Diehl
Affiliation: Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA

140. The cellular behavior and molecular regulation of neural cells in response to electrical signals
Audrey Scherrman, Li Yao
Department of Biological Sciences, Wichita State University

141. EWS is upregulated in Ewing sarcoma and a potentially targetable dependency
Evan Schulz, Harsha Hapugaswatta, Mizuki Azuma – University of Kansas

142. Enhancing the immune response during chronic virus infection using an autoimmunity-associated allele of PTPN22
Shaikh, Anam F,* Bevis, Alec, Jenna Barnes, Schwarting, Nancy, Cockerham, Tammy, and Orozco, Robin C**
Department of Molecular Biosciences, University of Kansas, Lawrence, KS
*Presenting author
**Corresponding author

143. The Kansas State University KINBRE Data Science Core
Teresa Shippy
KSU Data Science Center, Division of Biology, Kansas State University

144. Role of Malvolio, the *Drosophila* ortholog of human NRAMP2 metal ion transporter, in salivary gland morphogenesis
Contributors:
Mary Short[1] (Presenting Author), Srihitha Akula[2], Aditi Kulkarni[2], Tony Zou[2], Rika Maruyama[2], Deborah Andrew[2], Raj Logan[1]
Institution: 1. Department of Biological Sciences, Wichita State University, KS 67260; 2. Department of Cell Biology, Johns Hopkins University, Baltimore, MD 21205.

145. Methylation Patterns Across Tissue Type and Time in *Peromyscus leucopus*: A Targeted Museum Study
Smith, Loryn[1], Nicholas Stewart[2], Alexandra DeCandia[3], Lorelei Patrick[1]
[1]Department of Biology at Fort Hays State University, [2]Department of Biology at Southern Oregon University, [3]Department of Biology at Georgetown University

146. Leukemia inhibitory factor signaling in human trophoblast stem cells
Savannah L. Speckhart[1], Khursheed Iqbal[1], Ayelen Moreno-Irusta[1], Marija Kuna[1], Regan L. Scott[1], and Michael J. Soares[1,2,3]
[1]Institute for Reproductive and Developmental Sciences, Department of Pathology and Laboratory Medicine, [2]Department of Obstetrics and Gynecology, University of Kansas Medical Center, Kansas City, KS, [3]Center for Perinatal Research, Children's Research Institute, Children's Mercy, Kansas City, MO

147. NMR insights into the structural/functional differences of *Manduca sexta* pro-moricin-6 and moricin-6
Andy Su[1], Aprajita Jha[1], Nitin Mishra[1], Tomohiro Kimura[1,2], Chunxiang Hou[3], Haobo Jiang[3] and Om Prakash[1]
[1]Department of Biochemistry and Mol. Biophysics, Kansas State University, Manhattan, KS [2]Department of Chemistry, Kansas State University, Manhattan, KS
[3]Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK

148. Characterization of polymorphic mitochondrial tRNA fragments that correlate with severity of metastasis
Katy L. Swancutt[1], Adam D. Scheid[1], Christian Foster[1], Raymond E. Preston[2], Sydney P. Quijano[1], Emily Nissen[3], Devin C. Koestler[3], Tony Vanden Bush[1], Isidore Rigoutsos[4], Danny R. Welch[1]
[1]Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, [2]Parker B. Francis Summer Research Fellowship, University of Missouri Columbia, Columbia, MO, [3]Department of Biostatistics, University of Kansas Medical Center, Kansas City, KS, [4]Computational Medicine Center, Sidney Kimmel Medical College, Thomas Jefferson University, Philadelphia, PA

149. Loss of *Specc1l* causes disorganization of Blood-CSF Barrier resulting in Congenital Hydrocephalus
Dana Thalman[1], Brittany M. Hufft-Martinez[1,2], Jeremy Goering[1], Luke Wenger[1], An Tran[1], Zaid Umar[1], Benjamin Kelm[1], Sarah C. Wilson[1], Marta Stetsiv[1], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS, [2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City KS

150. Presence of Porcine Endogenous Retrovirus C in Domestic Pig Populations
Welton, Avery[1], Eric Gillock[1]
[1]Department of Biological Sciences, Fort Hays State University

151. Mitochondrial ATPase ClpB is essential for neutrophil differentiation of myeloid precursor cells
Tomasz Wenta, Guanpeng Wang, Lexi Ziolo, Michal Zolkiewski, Anna Zolkiewska
Department of Biochemistry and Molecular Biophysics, Kansas State University

152. Investigating medium-chain fatty acid production in developing fruits of Chinese elm.
P A D B Vinusha Wickramasinghe, Ruth Welti
Division of Biology, Kansas State University

153. A Novel Role for the 'Migraine Molecule' Calcitonin Gene-Related Peptide in Neurogenic Bowel Pain and Dysfunction
Adam Willits[1], Leena Kader[1], Olivia Eller[2], Kyle Baumbauer[2], Erin Young[1]
[1]Department of Anesthesiology, University of Kansas Medical Center
[2]Department of Cell Biology and Physiology, University of Kansas Medical Center

154. Infectious Disease Assay Development Core: High Throughput Screening Laboratory at the University of Kansas
Anuradha Roy, PhD
IDAD-HTS Laboratory, University of Kansas, Lawrence, KS, USA

1. Molecular characterization of START-Adjacent Domain (STAD) interaction with GIR1 to control cell division

Lauren E. Apprill[1], Bilal Ahmad[2], Samira R. Laytimi[1] and Kathrin Schrick[1,2]
[1]Department of Biochemistry and Molecular Biophysics and [2]Division of Biology, Kansas State University

Arabidopsis thaliana MERISTEM LAYER1 (ATML1) is a HD-Zip IV transcription factor required for proper cell type differentiation of the epidermis in *Arabidopsis*. Understanding cell division regulation is critical for developing cancer therapeutics**.** HD-Zip IV transcription factors contain four functional domains: a homeodomain (HD), a leucine zipper dimerization domain (ZLZ), a Steroidogenic Acute Regulatory (StAR) protein-related lipid/sterol Transfer (START) domain, and a START-adjacent domain (STAD). Our research focuses on a proposed transcriptional repression model which contains an interaction between ATML1 STAD and the small protein GLABRA2 INTERACTING REPRESSOR1 (GIR1). A giant cell phenotype discovered in sepals of *gir1* mutants supports its function as a repressor of ATML1. The aim of this project is to further characterize the interaction between ATML1 STAD and GIR1 and determine how GIR1 represses ATML1 activity. Using yeast two-hybrid (Y2H) experiments, we identified *gir1* mutants in highly conserved cysteine residues found in zinc finger motifs that abolish ATML1 interaction. Conversely, several missense mutants affecting charged residues in ATML1 STAD negatively impact interaction with GIR1. Our current studies focus on assessing GIR1 repression of ATML1 target genes involved in epidermal development using reverse transcription-quantitative PCR (RT-qPCR)**.** Determining the function of ATML1 STAD and GIR1 interaction will aid in gaining knowledge of the molecular mechanisms underlying gene expression in plant growth and development as well as provide further insights about cell division regulation in humans.

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2. Impact of *PTPN22* Autoimmunity-Associated Allele on Dendritic Cell Type-I Interferon Production

Jenna R Barnes*, Anam Shaikh, Alec Bevis, Tammy Cockerham, Nancy Schwarting, Robin C Orozco**
Department of Molecular Biosciences, University of Kansas, Lawrence, KS
Presenting Author*
Corresponding Author**

PTPN22's alternative allele, 1858C>T, is expressed in 5-15% of the North American population and is associated with autoimmunity. Previous data shows *Ptpn22* promotes IFN-I production in myeloid cells following LPS exposure. Little is known about how *PTPN22* and its alternative allele regulate IFN-I production following non-LPS stimuli. Our hypothesis is that bone marrow dendritic cells (BMDCs) expressing the *Ptpn22* alternative allele have decreased IFN-I production following virus-relevant stimulus. To test this, we used Flt3L differentiated BMDCs from wild type (PEP-WT), *Ptpn22* knockout (PEP-null), and *Ptpn22* alternative allele expressing mice (PEP-619WW). *Ptpn22* inhibitor was also utilized in additional experiments. After overnight exposure to LPS or 3p–hp-RNA, we observed no significant difference in IFN-I production between PEP-WT, PEP-null, and PEP-619WW BMDCs. Also, incubation with *Ptpn22* inhibitor did not impact IFN-I production. This data suggests that *Ptpn22* does not mediate IFN-I production in BMDCs following RNA or LPS exposure. Results of this study inform future projects to define the molecular mechanisms by which *PTPN22* and its alternative allele impact myeloid cell signaling pathways.

3. Effect of Heat Shock Stress on the Subcellular Localization of the tumor suppressor protein APC

Kamar Chahine[1], Eldric Carreon[2], Kristi Neufeld[2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

Colorectal cancer, a prominent malignancy in the United States, frequently arises from mutations in the Adenomatous Polyposis Coli (APC) gene. This gene encodes a protein critical for suppressing tumor growth and regulating the Wnt signaling pathway. Intriguingly, APC's ability to shuttle between the nucleus and cytoplasm implies diverse roles. Heat shock, a cellular response to stressors like high temperatures, might upregulate APC expression, yet the link between APC and heat shock remains unclear. This study aimed to investigate the relationship between heat shock and APC in cancer cells, particularly focusing on the subcellular localization of APC. Using RKO colon cancer cells with wild-type APC, we subjected them to heat shock treatment. Immunofluorescence microscopy captured APC signal, which was quantified using ImageJ software. The results demonstrate a significant increase in the proportion of carcinoma cells with nuclear APC localization upon heat shock compared to cells exhibiting equal nuclear and cytoplasmic APC distribution. In conclusion, this study sheds light on the subcellular dynamics of APC in response to heat shock stress in colon carcinoma cells. The observed nuclear translocation of APC during heat shock implicates potential novel functions for this tumor suppressor. These findings contribute to a deeper comprehension of the cellular behavior of colon carcinoma cells under stress, holding promise for the advancement of targeted cancer therapies.

4. Exploring Resistance-Virulence Tradeoff in *Pseudomonas fluorescens*

Tiffany Chan, Kervens Accilien, Robert Unckless PhD
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

The rapid emergence of antimicrobial resistance in bacteria is a worldwide crisis that puts the effectiveness of antibiotics at risk. Several studies suggest, however, that where there is an adaptive advancement in one trait, in this case, antimicrobial resistance, there is a decreased performance in another, such as growth or virulence. This is referred to as resistance-virulence tradeoff. The goal of this project is to determine the relationship between those traits in experimentally evolved resistant *P. fluorescens* using *Drosophila melanogaster* as an *in vivo* infection model. We started off by optimizing the bacterial infection conditions for the wildtype bacteria. We observed that a larger sample size was needed to detect a pronounced effect. On the bacterial side, an OD600 of 5 was required to kill roughly 50% of the flies by day 4. Finally, allowing the bacteria to enter a late stationary growth phase increased its virulence potential. There was no significant difference in mortality between sexes. Next, we infected the flies with different antibiotic-resistant strains of *P. fluorescens* and tracked mortality for 7 days. This insight into how bacteria evolve, proliferate, and adapt to their environment may drive the development of new countermeasures against drug resistance.

5. CRISPR Analysis of HIRA in Plants

Keying Chen, Claire Shippy, and Tara Phelps-Durr

The purpose of this study is to mutate the Histone Repressor A (HIRA) gene in *Arabidopsis* (a mustard plant) via a CRISPR vector. HIRA is a chromatin remodeling protein that is required for proper development in both plants and animals. In animals, HIRA suppresses the cell cycle proliferation genes involved in early development by packaging them in heterochromatin. HIRA is unlikely to function exactly the same in both plants and animals since development is regulated very differently between the two. In plants, development happens throughout the entire lifecycle and differentiation of cells is more flexible. While HIRA may be involved in gene suppressing gene expression in plants, it's unlikely that HIRA permanently suppresses early development genes in plants. Understanding how HIRA functions in plants will help us understand how cellular differentiation is flexible in plants. HIRA is known to regulate the transcription of genes during leaf development by interacting with a myb domain transcription factor which represses the KNOX genes. Once the KNOX genes are repressed, cellular differentiation occurs. Thus, HIRA is involved in regulating genes that promote cellular differentiation in plants; however, the exact mechanism is currently unknown. The purpose of creating CRISPR mutations is to better understand the function of HIRA in plants. So far, we have made the CRISPR tools and transformed the plants. An early examination of our CRISPR mutants has revealed phenotypes consistent with HIRA's involvement in leaf development.

6. Cardiovascular Health Monitoring Using Multiple Conformal Photoplethysmography Devices

Coffman, Lauren, Yongkuk, Lee, Department of Biomedical Engineering, Wichita State University

In space, it is important to continuously monitor astronauts' cardiovascular health because of microgravity since the human body is evolved to function optimally in the presence of Earth's gravity. However, existing medical devices are bulky, so they are often not suitable for use in spacecrafts, which have very limited rooms. Photoplethysmography (PPG) devices, which use lights to penetrate beneath the skin to measure blood flow which can determine heart rate and oxygen levels, have great potential as small, lightweight, cost-effective cardiovascular health monitoring devices in space. In the present work, we designed conformal PPG devices, which are wireless, light, and skin-wearable devices. Multiple conformal PPG devices were placed on the body to first identify precise locations where signal-to-noise ratio (SNR) are best. These locations included the forehead, wrist, and ankle. Simultaneous synchronized data collection was performed at all three locations for a sixty second period. Using MATLAB software, peak detection was used to pinpoint each systolic peak in a wave and create a plot, which measures the time distance between two peaks. Plots from each location were then stacked together and used to find the delay of blood flow to each location on the body. Those findings can be utilized for pulse rate variability analysis and pulse wave velocity measurement. Future testing includes cardiovascular health monitoring using multiple conformal PPG devices in ambulatory environments as well as low-pressure environments.

7. Development of Maleic/Malonic Acid Modified Gold Nanoparticles Capable of Detecting Lead in Drinking Water by Colorimetric Analysis

Ethan Conners and Dr. Said Adem
Washburn University 2023
Supported by the Kansas INBRE, P20 GM103418

The purpose of this research was to develop gold nanoparticles (GNPs) capable of detecting lead in drinking water through colorimetric sensing. The surface of the gold nanoparticles was modified using trisodium citrate and malonic acid/maleic acid (MAMA) in a 1:1 ratio by volume to create a MAMA-GNP sensor capable of detecting a nanomolar range of lead ions. We studied the effect of pH and the lead ion to GNP ratio to find the optimum conditions in which MAMA-GNP was most sensitive to Pb^{2+} detection. Selectivity tests were carried out to study interference by other metal ions commonly found in contaminated drinking water. The carboxyl group of malonic and maleic acids bound to the surface of the GNP allowed the MAMA-GNP to show strong affinity towards Pb^{2+} thereby increasing its selectivity over other ions (Ca^{2+}, Cd^{2+}, Cu^{2+}, Co^{2+}, Fe^{2+},Fe^{3+}, Mg^{2+}, Ni^{2+}, Zn^{2+},) and anions (Cl^{-}). The MAMA-GNP only aggregated in the presence of Pb^{2+} changing the color of the solution from red to purple. UV-VIS spectroscopy was used to follow the change in the absorption spectrum of these colorimetric analyses. The color intensity as a function of Pb^{2+} concentration provided a linear response range from 10 µM to 200 µM with a detection limit of 6.44 µM (R^2= 0.981). A similar linear range was observed with the naked eye. Stability testing showed the MAMA-GNP to be stable for 7 months. The results obtained in this research showed MAMA-GNP can detect Pb^{2+} through colorimetric sensing that is reliable, quick, and inexpensive.

8. RBPjk plays a protective role in Human immunodeficiency virus-1 (HIV-1) related chronic kidney disease.

Ashley Diaz Rocha, Nicole Sommer, Madhulika Sharma

Background: Antiretroviral therapy (ART) has increased the life expectancy in patients living with HIV-1. However, latently infected cells remain in the body and slowly release viral proteins leading to inflammation and comorbidities including chronic kidney disease (CKD). Efforts have focused on the HIV-1 long terminal repeat (LTR) promoter manipulations. RBPj (Recombination signal Binding Protein for immunoglobulin kappa J region) is a strong repressor of the LTR promoter in T cells. However, its functional role is not known. Thus, we sort to examine the role of LTR-RBPj interactions in kidneys. Methods: The Tg26 mouse model of HIV-CKD harbors the active HIV-LTR promoter, hence increased expression of HIV genes. Tg26 mice were bred with floxed RBPj mice and Podocin Cre mice to drive RBPjk knockout (KO) in podocytes. The resulting mice: WT (wild type), RBPjKO, Tg26, Tg26: RBPjKO-Pod were compared for renal histology, renal function, inflammation and HIV gene expression (as a proxy for LTR activation). Results: Deletion of RBPjk alone in podocytes of Tg26 mice, led to a drastic aggravation of disease severity and reduced life span. Compared to Tg26 positive littermate controls, Tg26: RBPjkKO-Pod mice presented with increased focal segmental glomerulosclerosis, tubular dilations and reduced serum albumin levels. Glomerular NFkB (p65) expression increased, and this was associated with a significant increase in inflammation and HIV-gene (*Nef*) expression. Conclusions: RBPj is a strong functional repressor of the LTR promoter in renal cells. Thus, RBPj overexpression in HIV-1 latent cells may have therapeutic potential.

9. Hyaluronan synthase (Has)2, in dual Has1 and Has3 deficient mice, protects against age-associated weight gain by reducing adipocyte hypertrophy

Ian Ensley[1], Vanessa Schmidt[1], Wendena Parkes[1], Michele T. Pritchard[1,2,3]
[1]Department of Pharmacology, Toxicology, and Therapeutics, [2]Diabetes Institute, [3]Liver Center, The University of Kansas Medical Center, Kansas City, KS 66160

Hyaluronan (HA) is a large glycosaminoglycan important for tissue structure, repair, and cell signaling. HA is important for preadipocyte maturation into adipocytes and possibly other adipose physiology. Pharmacological efforts to suppress HA reduce diet induced weight gain. However, hyaluronan-adipose physiology during aging is largely unknown. Because HA creates a soft extracellular matrix, we hypothesized that it permits age-associated adipocyte hypertrophy. To test this, we used wild type (WT) mice and Has1&3 double knock out (dko) mice. Within each genotype, we used young (7 weeks) and old (17 months) mice who were fed normal mouse chow (5% fat by weight). At euthanasia, we weighed mice, and then harvested and weighed gonadal (white) adipose tissue. We assessed adipocyte number and size using ImageJ. We semi quantitatively measured tissue hyaluronan content after fluorescent HA binding protein (HABP) staining using ImageJ. We performed ELISA-like assays to confirm HABP staining results. We found significantly reduced body and adipose mass in old dko mice compared to old WT counterparts. Moreover, we found that adipocyte hypertrophy in dko old mice was reduced compared to WT old mice adipocytes. Paradoxically, we found that adipose HA content was partially retained with age in dko animals compared to WT mice which lose adipose HA. We've concluded that Has1 and Has3 deficiency protects against age associated weight gain perhaps through HA over production by the intact Has2 synthase. Further analysis is needed to understand the possible physio-mechanical role of HA in adipose expansion with age.

10. Exercise as a Means to Attenuate Early Life Stress-Induced Cognitive Deficits and Hippocampus Disparities

Carly H. Gagnon, Tara E. McQuillan, Julie A. Christianson
Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS 66160

Early life stress (ELS) is highly prevalent in the United States, with 64% of US adults having experienced at least one adverse childhood experience and 17% having experienced four or more. It has been shown that ELS negatively impacts the hippocampus, resulting in reduced neuronal proliferation, decreased hippocampal volume, and altered plasticity. Given the hippocampus's vital role in memory formation, memory retrieval, and spatial memory, identifying methods to counteract these effects is important. While exercise has been shown to help slow cognitive decline and improve hippocampal integrity, its use in attenuating specifically ELS-induced cognitive and hippocampal deficits has not been investigated. In this study, mice underwent neonatal maternal separation (NMS) during the first three postnatal weeks and gained access to a running wheel at 4 weeks of age. Two cognitive assessments, the y-maze and the radial arm maze, were used to evaluate memory and learning at 6 and 12 months of age. Percent alternation in the y-maze, which measures working memory, was surprisingly higher in NMS males at 6 months of age, compared to naïve mice. Additionally, although not statistically significant, sedentary female mice had more overall errors in the radial arm maze compared to exercised mice, indicating better working and reference memory. In conclusion, this study investigated the use of exercise as a method to improve the cognitive and hippocampus disparities observed in NMS mice, but it did not identify conclusive trends, possibly due to the study's small sample sizes. Accordingly, further studies will aim to increase sample sizes.

11. Rapid PCR with precise droplet temperature control using digital microfluidic chip

Hale, Joseph, Snowden, Nathan, Becerra, Jesus, Fan, Scott
Department of Mechanical and Nuclear Engineering, Kansas State University

Polymerase Chain Reaction (PCR) has been an increasingly valuable and evolving tool in diagnostic research and the gold standard in various diagnostic applications. A typical PCR protocol requires cycling between different activation temperatures – upwards of 45 cycles lasting an hour in total. However, by optimizing the polymerase and increasing the concentrations of the polymerase, primers, and template, this time can be reduced considerably. In the present work, we developed a digital microfluidic (DMF) chip which uses electrowetting to control the motion and temperature of microdroplets on a field of electrodes. We investigated rapid PCR using an optimized mix and protocol based on a Klentaq polymerase, with COVID mRNA as an example template. Combining this model of rapid PCR with DMF, we provided a PCR result in less than 15 minutes. This type of rapid droplet PCR further provides better options for point-of-care testing and more accessible PCR diagnostics, with affordable and easy to use technology that allows PCR to be conducted in a short amount of time.

12. *HIC2* loss may underlie cardiac anomalies in human cases with distal 22q11.2 microdeletions

Jennifer I. Interiano[1], Brittany M. Hufft-Martinez[1,2], Jeremy P. Goering[1], Majed Dasouki[3], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, [2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City, KS. [3]Department of Genetics and Genomics, Advent Health Genomics and Personalized Health, Orlando, FL.

Small deletions on the long arm of chromosome 22, region 22q11.2, are the most common microdeletions in humans, occurring in 1/4000 births. Among these, proximal 22q11.2 deletions result in common DiGeorge or CHARGE syndromes while distal 22q11.2 deletions result in a variety of cardiac and craniofacial anomalies. We identified a patient with a distal 22q11.2 microdeletion who demonstrated a rare combination of phenotypes, including cleft palate and cardiac ventricular septal defect (VSD). We hypothesized that the minimal deleted genetic interval in our patient would contain one or more genes responsible for the observed anomalies. We found 69 other patients with distal 22q11.2 deletions and focused on 29 patients with a direct deletion overlap with our patient. Minimum deleted regions for both phenotypes led to Hypermethylated in Cancer 2 (HIC2) being the "candidate" gene. Consistently, knockout of *Hic2* in mice resulted in cardiovascular phenotypes, including VSD. While *Hic2* knockout mice did not show cleft palate, knockout for closely related *Hic1* did. So, we hypothesized that perhaps *Hic2* may also play a role in craniofacial development. One way to associate a gene's role in the development of a particular tissue is to show that the gene's expression is enriched in the tissue during critical stages of development. Using SYSFACE (Systems Tool for Craniofacial Expression-Based Gene Discovery), we were able to identify enrichment of *Hic2* expression in the embryonic mandible, defects in which can affect palatogenesis. Taken together, *HIC2* loss may underlie cardiac and craniofacial defects observed in cases with distal 22q11.2 microdeletions.

13. Role of Palladin in Actin Dynamics Revealed by Quantitative Total Internal Reflection Fluorescence Microscopy

Tariq Izard, Wael Yessin, Sanju Ghimire, Moriah R. Beck
Department of Chemistry and Biochemistry, Wichita State University

Actin is an intracellular protein that is highly abundant in eukaryotic cells. It is responsible for the formation of contractile filaments with myosin in muscle cells and is essential for controlling and maintaining cell shape. Actin binding proteins assist in the formation of various actin structures by forming crosslinks and bundles of actin filaments. The actin binding protein of particular interest in this study is palladin, as it aids in localizing actin structures for assembly and maintenance. A key finding of palladin is that it is overexpressed in cancer-associated fibroblasts of multiple types of tumors, such as pancreatic and breast cancer. Previous studies have observed the effects of palladin on actin's polymerization and structure using bulk fluorescence assays and a co-polymerization bundling assay respectively. These studies have shown that the isolated Ig3 domain of palladin promotes the polymerization of actin and both the Ig3 domain and 90 kDa isoform of palladin formed actin bundles. To monitor actin structures formed during polymerization induced by palladin directly, total internal reflection fluorescence microscopy (TIRFm) was used to analyze both the rate of polymerization and organization of actin filaments in real time. The study compared actin polymerization without the influence of any actin binding proteins versus with either the Ig3 domain or 90 kDa palladin. The results from this project clearly show differences in how the Ig3 domain and 90 kDa isoform of palladin influence the polymerization and structure of actin.

14. A new vaccine platform based on the selective targeting of dendritic cells by the binding component of the anthrax toxin, protective antigen.

Yousaf Khan[1], Srinivas Gonti[1], Xianglei Yan[2], Nancy Meyer[3], Vamseedhar Rayaprolu[3], Robert N. Brey[4], Karin Loré[2] and James G. Bann[1]
[1]Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS
[2]Division of Immunology and Allergy, Karolinska Institute, Stockholm, Sweden
[3]Pacific Northwest Center for Cryo-EM, Portland, OR.
[4]Kinesis Vaccines LLC, Chicago, IL.

The anthrax toxin is an AB toxin. The B component, protective antigen (PA) is known to directly target and disrupt host immune cells as part of its pathology. In particular, PA exhibits high affinity binding to capillary morphogenesis protein 2 (CMG2), a receptor expressed on dendritic cells, macrophages, and other antigen presenting cells. Dendritic cells are the most potent antigen presenting cells and can induce activation of T cells, crucial for a sustained immune response. Given the high affinity binding between PA and CMG2 and targeting of dendritic cells, we hypothesize that PA can be used as a vector for targeted delivery of conjugated antigens to dendritic cells. To test this hypothesis, we have generated a conjugate between PA and Spy0469, a putative 42 kDa surface protein of *Streptococus pyogenes*. Since memory T-cell responses to Spy0469 are common in the human population, we surmise that activation of T-cells by the PA-Spy0469 conjugate would be stronger than Spy0469 or PA alone. We show here that the ability to bind CMG2 and formation of the heptameric structure is not perturbed with the conjugate attached to domain 4 of PA. Preliminary flow cytometry analysis is indicative of T-cell activation by the PA-Spy0469 conjugate. Although activation of CD4+ T-cells is not enhanced by the PA-Spy0469 conjugate, we find a greater activation of CD8+ T-cells, suggesting that PA is able to be cross presented.

15. Using Comparative Genetics to Annotate the Insulin-Like Signaling Pathway of *Tribolium madens*

Korte, Gen; Teresa Shippy; Susan Brown
Division of Biology, Kanas State University

The insulin/insulin-like peptide signaling pathway (Ilp pathway) is a highly conserved pathway in multicellular organisms functioning in development through cell growth and proliferation. Insulin signaling also plays a critical role in metabolism and disruption of the Ilp pathway with diabetes in many organisms. The Ilp pathway is triggered by insulin binding to insulin receptors, which activates intracellular signaling components. Insects have an Ilp pathway very similar to that of mammals and have been used as model systems to understand the regulation of this critical pathway. We used genes of the Ilp pathway from the model insects *Drosophila melanogaster* and *Tribolium castaneum* to identify homologs in the genome of the black flour beetle, *Tribolium madens*. We then manually annotated these genes in Apollo using evidence from RNA-seq data and orthologous genes. This work was part of a comparative genomics project between *T. madens* and its close relative *T. castaneum*, which seeks to understand the changes that have occurred in these two species since their evolutionary separation. Twelve genes were found and annotated in the *T. madens* pathway, with all gene quantities matching those of *T. castaneum;* though variations in gene numbers of the *Tribolium* species and *D. melanogaster* varied on five accounts. Therefore, this comparative analysis in *T. madens* can be used to convey the Ilp pathway's conserved nature in insects and how regulation in this pathway may be applied to humans after being studied in insect species.

16. Immunohistochemical Analysis of HNSCC Cell Spheroids and Xenotransplant Tumor Masses in the Hamster Cheek Pouch

Martinez, Michael[1], Hendry, William PhD[1] Carte, Meris[1]
[1]Department of Biological Sciences, Wichita State University
Supported by the Kansas INBRE, P20 GM103418

Cancer, one of the most pressing health concerns of our time, stands as a formidable adversary that knows no boundaries and affects individuals regardless of age, gender, or nationality. Among the various types of cancer, head and neck squamous cell carcinoma (HNSCC) has emerged as a significant concern, and is characterized by malignancies affecting the oral cavity, throat, larynx, salivary glands, and nasal passages. Human HNSCC spheroid masses from two different cell lines were xenotransplanted by taking advantage of the immune privileged hamster cheek pouch. The donor spheroids and xenotransplant tumor masses were then fixed onto slides and analyzed using immunohistochemistry to visualize their proteomics. Interesting staining patterns were observed for antibodies that targeted the (Insert here the protein names) proteins.

17. Conceptual human application of RNA interference of autocrine motility factor receptor in *Acyrthosiphon pisum.*
Mull, Olivia, Balthazor, James. Department of Chemistry, Fort Hays State University.

Autocrine motility factor receptor (AMFR) is one of the seven transmembrane proteins that acts as a metabolic pathway receptor. AMFR primarily functions to bind autocrine motility factor (AMF), a cytokine for glycolysis and gluconeogenesis. AMFR also induces protein degradation via the activation of ubiquitin ligases. The AMF-AMFR interaction results in actin fiber rearrangements. Overexpression of this interaction is a known contributor to musculoskeletal tumor cell growth and metastasis. Aphids (*Acyrthosiphon pisum)* are small insects that are known to cause damage and spread diseases to plants. The application of RNA interference in aphids can be utilized to decrease or inhibit the AMF-AMFR interaction and alter the lifespan of aphids. RNA was obtained from aphids to induce reverse-transcription to produce cDNA. The cDNA obtained was used alongside an AMFR primer-template to isolate the dsRNA of the AMFR gene. An aphid feeding study was then conducted using dsRNA. The lifespan of aphids was overall decreased compared to the control group, indicating that decreasing or inhibiting AMFR expression may prove to be a potential treatment option for musculoskeletal cancers in humans.

18. Exploration of Ultraconserved Elements in Noteridae: Comparative Phylogenomic Reconstruction Methods
Authors: Murphy, Baca, et al
Haskell Indian Nations University, University of Kansas.

Ultraconserved Elements (UCEs), consistent through millions of years, are pivotal for evolutionary reconstructions in non-model organisms. Extending Baca et al.'s research on Notomicrus (Coleoptera: Noteridae), this study contrasts UCEs harvested via targeted enrichment and genome skimming. Our analysis at the University of Kansas examines method efficacy and bias in data capture strategies. Comparing phylogenetic reconstructions from both techniques, we observed congruent tree topologies, underscoring that capture methodologies do not distort phylogenetic estimates. This finding confirms UCEs' reliability as genetic markers for lineage tracing and the effectiveness of integrating diverse data capture methods. Our results enrich phylogenetic tools, supporting conservation biology.

19. The Evolutionary History of Moray Eels
Edgar A. Nickols, Haskell Indian Nations University, University of Kansas

Among the 35,000 fish species, the true eels are a diverse group, representing nearly 3% of all fishes. While eels can be found in habitats ranging from rivers to the deep sea, the most charismatic group is the Moray eels. In order to explore their evolution and adaptations, we need a better understanding of how different Morays are related to each other. Therefore, I have combined new and existing DNA sequence data for one quarter of all Moray species to provide a new evolutionary framework for moray eels. My results corroborated many previous hypotheses for Moray eel relationships, but also recovered the Redface Moray (Monopenchelys acuta) as the earliest diverging Moray. Given this surprising finding, I will need to describe a new subfamily of eels to place this enigmatic species. Beyond my DNA data, the Redface Moray can be separated from all other Moray eels by the presence of a single branchial pore, a unique cartilaginous pectoral skeletal element, and a dorsal-fin origin well behind the anus. This more comprehensive analysis of Moray eels will allow us to explore the evolution of their raptorial jaws in light of this recognition of the Redface Moray as the earliest Moray lineage.

20. The Role of Glycogen in Clostridioides difficile Spore resilience and longevity
Joshua Ogunbase[1, 2], Revathi Govind[2]
Langston University; Department of Art & Sciences[1], Kansas State University; Division of Biology[2]

Clostridioides difficile, a spore-forming bacterium, is notorious for healthcare-associated infections, notably in hospital settings. It's a primary cause of antibiotic-associated diarrhea and pseudomembranous colitis. These infections arise from disturbances in the gut microbiota, often due to antibiotic use, enabling C. difficile proliferation and toxin production. The bacterium's enduring spores persist in the environment, contributing to its contagiousness. Effectively managing its spread in healthcare facilities requires robust infection prevention and control measures.
This study delves into the significance of glycogen in *C. difficile* spores concerning their resilience and longevity. Spores were obtained from both the wild-type (WT) bacterial strain and a mutant strain (*glyC* mutant) lacking glycogen production or utilization capabilities. Subsequently, these spores were exposed to various physical and chemical disinfectants. Our findings reveal that spores from the *glyC* mutant exhibited high susceptibility to most disinfectants, highlighting the importance of glycogen in shielding *C. difficile* spores from heat, hydrogen peroxide, and alkali treatments. Surprisingly, both WT and *glyC* spores demonstrated significant resistance to acid treatment. We also noted that *glyC* mutant spores losing their viability approximately two months into storage, while 90% of the WT spores remained viable at this time point.

21. ManyFishes 1: A standardized test of inhibitory control in fishes using Big Team Science
Shane Rance[1] and Laurent Prétôt[2]
[1]Department of Biology, Pittsburg State University
[2]Department of Psychology and Counseling, Pittsburg State University

Although fish behavior research has a reasonably long history, the past decade has seen a dramatic increase in the number of studies on fish cognition. Yet, there exist important limitations to our assessment of fish cognition that can lead to replicability issues, including the use of small sample sizes, nonrepresentative samples, and unstandardized protocols. Recently, several Big Team Science initiatives have begun to address this problem in various taxa (e.g., ManyBabies, ManyPrimates, ManyBirds, ManyDogs). In the same spirit as its predecessors, ManyFishes uses an approach based on large-scale collaboration across researchers and institutions in an attempt to increase both the number and diversity of fish samples used in cognitive and behavioral research. Here, we tested Lamarck's angelfish (*Genicanthus lamarck*, N = 7) in a pilot version of ManyFishes 1, the first-ever study of the ManyFishes project that uses a standardized version of the cylinder task—a detour paradigm widely used in comparative psychology—to assess inhibitory control capacities in fishes. In the task, subjects must swim around a clear cylinder to obtain a food reward located inside the cylinder; importantly, to succeed, they must "detour" the obstacle by inhibiting their motor impulses to reach for the food directly, thus avoiding to bump or touch the cylinder walls along the way. We discuss the results of our pilot study, both advantages and challenges of the experimental procedure, and the implication of our findings for the ManyFishes project.

22. Exploring Protein-Protein Docking of the Sox2 and HDAC1 Proteins
Rorstrom, Carl J.,[1] and Allan Ayella,[1] [1]Department of Chemistry, Washburn University

The Sox2 protein has been shown to associate with many different proteins to produce large-scale genomic changes. In this research, we choose to study the binding between Sox2 and the epigenetic protein histone deacetylase 1 (HDAC1). From previous literature, we know Sox2 123-180 destabilized loop region (DLR) binds with HDAC1 protein. However, this binding is inhibited by the Sox2 HMG region. Thus, we hypothesized, the binding sites for the Sox2 HMG and DLR regions may be with the same HDAC1 region due to close proximity. To analyze this, we first used the InterEvDock3 program to predict the docking site of the Sox2 HMG region with a known model structure of the HDAC1 protein. This showed a predicted docking site with the Sox2 HMG region to the HDAC1 325-343 region. Thus, with these predicted regions of docking, three different oligopeptides from the Sox2 DLR region were synthesized and tested for association with one oligopeptide of the HDAC1 325-343 region on native tris-tricine PAGE gel electrophoresis and electronic circular dichroism. Tris-tricine gel electrophoresis results showed light bands of high molecular weight aggregation when Sox2 DLR oligos 1 and 2 were run with the HDAC1 oligo. Circular dichroism results showed a positive shift in absorbance with all the Sox2 DLR oligos and the HDAC1 oligo. Therefore, the results show that Sox2 DLR regions bind with the chosen 325-343 HDAC1 region. This verifies our hypothesis that both the Sox2 DLR region, and the Sox2 HMG region are binding with the same HDAC1 325-343 region.

23. CRISPR Analysis of the MYB Domain Transcription Factor Asymmetric Leaves 1
Gabriella Rueschhoff, Dr. Tara Phelps-Durr
Fort Hays State University Department of Biological Sciences, Fort Hays State University Honors College

The goal of this study is to create new mutations in the *ASYMMETRIC LEAVES 1* (*AS1*) gene of Arabidopsis using CRISPR technology. *AS1* is a myb domain transcription factor that represses the KNOX genes, a group of genes involved in maintaining an undifferentiated cell state. *AS1* binds to the chromatin remodeling protein Histone Repressor A (HIRA). In animals, HIRA is involved in the permanent suppression of proliferation genes required for early development. The interaction between *AS1* and HIRA provides clues to how *AS1* maintains suppression at the KNOX genes; however, there are key differences between plant and animal development. Most notably, plant development occurs throughout the lifecycle, and unlike animals, plant cells more readily un-differentiate and re-differentiate. We intend to create new *AS1* CRISPR mutants in order to better understand the structure of the *AS1* protein and its function during cellular differentiation during leaf development. This work will allow us to better understand how genes are regulated during cellular differentiation.

24. Optimizing *C. elegans* for high throughput chemical screening
Ariana Siddique[1], John Hoopes[1], James Pressdee[1], Arnav Jain[1], Dr. Lisa Timmons[1]
[1]Department of Molecular Biosciences, The University of Kansas, Lawrence, Kansas

This study explores RNAi strategies to enhance membrane permeability for improved high throughput drug screening in *Caenorhabditis elegans*. As a small, genetically tractable multicellular animal, *C. elegans* is an excellent system for compound library screening; however, the cuticle poses a formidable barrier for many chemicals. Traditional chemical library screens rely on ingestion to deliver drugs to internal cells in the animal, limiting cellular exposure to the drug. We are undertaking a new approach to drug delivery by using RNAi to reduce cuticle integrity gene expression.

The *C. elegans* system facilitates large-scale RNAi experiments, affecting treated animals and their progeny. *C. elegans* ingest bacteria as food source, which can easily be manipulated to express gene targeted double stranded RNA. This bacterial-mediated feeding protocol for dsRNA delivery is used to reduce the level of cuticular proteins and lipids. Permeability will be assessed by the time to lethality for small molecules (e.g., bleach, boric acid) in treated versus untreated animals. We will also extend this approach using small molecule dyes and larger fluorescent nanoparticles to determine the extent of permeability. To obtain reproducible breaches in cuticle integrity in live animals, we will manipulate the environment using osmotic agents and physical forces. The goal is to devise a protocol that reproducibly produces a large population of worms that are permeabilized but remain viable and fertile. This experiment's results will improve the efficiency of toxicity assessments and establish a pathway for the entry of larger molecules to penetrate the cuticle barrier.

25. Urban heat islands are present in small Midwestern cities, but unrelated to residents' sociodemographics
Simmons, Christopher, Daniel J. Benson, and Christine C. Rega-Brodsky
Department of Biology, Pittsburg State University

Urban centers tend to be warmer than their surrounding rural areas due to increased infrastructure and heat-absorbing asphalt, and lack of vegetative cover. Thus, cities become "islands" of heat, resulting in an Urban Heat Island (UHI) effect. Certain groups of urban residents tend to be disproportionately burdened with urban heat, such as low-income residents and people of color. Urban heat is the leading cause of weather-related deaths in the United States, exacerbating medical issues of these residents. While the UHI has been studied in cities around the world, most of the research has been focused on large metropolitan cities located far away from agricultural or rural landscapes. Our objective was to document the UHI in small southwestern Missouri cities. We surveyed 25 locations during the summer of 2023 within three small cities: Monett, Joplin, and Springfield. At each sampling location, we measured canopy coverage, temperature, relative humidity, and heat stress. We evaluated the impact of tree canopy and sociodemographic variables on urban heat with a linear regression. Preliminary results indicate that areas with greater tree canopy coverage were cooler; however, median household income, percent Hispanic/Latino population, and percent Black/African American population were not related to temperature differences. Thus, urban vegetation is an important feature for regulating UHIs, which is particularly important in an era of climate crisis. As climate predictions indicate that heat will become an increasing issue, more research is needed to test the UHI across both micro- and metropolitan areas.

26. Synthesis of a Hyaluronic Acid-Deferoxamine Conjugate for Local Treatment of Bone Regeneration

Navya Singh, Laird Forrest
Department of Pharmaceutical Chemistry, University of Kansas, Lawrence, Kansas

Medically based efforts and alternative treatment strategies to prevent or remediate the corrosive effects of radiotherapy on pathologic fracture healing have failed to produce clear and convincing evidence of success. Establishing an effective pharmacologic option to prevent or treat the development of non-unions in this setting could have immense therapeutic potential. Experimental studies have shown that deferoxamine (DFO), an iron-chelating agent bolsters vascularity and subsequently enhances normal fracture healing when injected locally into a fracture callus in long-bone animal models. However, due to its short half-life and rapid clearance, maintaining DFO at the callus site during peak fracture angiogenesis has remained challenging. In this study, we set out to strategically enhance the therapeutic efficacy of the DFO via covalently attaching the drug molecule hyaluronic acid (HA). HA plays a critical role in cell differentiation, tissue morphogenesis, proliferation, and wound healing. Herein, we first prepared a HA-DFO conjugated deferoxamine (HA-DFO) using a two-step synthesis method. We then examined the biodegradability and in vitro release characteristics of the HA-DFO. Our results suggested that HA-DFO bio-conjugate offered the sustained release of the active DFO.

27. Microbial Survival and Partitioning in Layered Ices Relevant to Mars

Bao Nhu N. To and Mark A. Schneegurt
Department of Biological Sciences, Wichita State University, Wichita, KS, 67260, USA

Layered ice systems are novel analogs of natural systems relevant to Mars. The presence of liquid water on Mars's surface suggests the possibility that life may exist within the brine trapped between layers of pure water ice and soils formed by deposition of frost and aeolian dust. As temperatures warm, frozen brine layers melt before water ice layers, which creates liquid lenses trapped in icy deposits. We are investigating the survival of bacteria and their partitioning in layers of frazil, brine, and water ice. Halotolerant bacterial isolates (*Halomonas* sp. str. BLE7 and *Oceanobacillus* sp. str. SAF16) were grown in R2A medium supplemented with 15% NaCl. Layered ice systems were created with pure water and this 15% NaCl brine, which were first frozen at –20 °C. After melting of the brine layer at –12 °C, the brine fractionated into a denser brine and a frazil ice layer that was less salty, while the top and bottom layers of water ice remained frozen. Exposing cells to a freeze-thaw cycle reduced their viability somewhat. Despite the frazil layer's higher volume, more cells partitioned into the brine than into the frazil. Similar experiments were performed with media supplemented with 20% $NaClO_3$, an important salt on Mars. *Oceanobacillus* sp. str. SAF16 in 20% $NaClO_3$ appeared to partition more cells into the much larger frazil than the brine. Microbial responses in layered ice systems informs planetary protection protocols and suggests qualities of native life should it exist on Mars. Supported by NASA and K-INBRE.

28. cHPV E6 reduces innate immune signaling.

Emily Tolbert, Dalton Dacus, Rose Pollina, Nicholas A. Wallace
Division of Biology, Kansas State University

Each year 3 million Americans are diagnosed with non-melanoma skin cancer (NMSC) and spend approximately $4.8 billion on treatments. Cutaneous human papillomaviruses (cHPV) are hypothesized to promote NMSC by destabilizing the host genome. Supporting this, the E6 protein from these viruses (cHPV E6) dysregulates DNA repair signaling pathways. Inhibition of DNA repair is believed to promote viral replication by promoting cell cycle progression in UV exposed skin. They may also dysregulate other pathways to promote cHPV replication. The cGAS-STING (cyclic GMP-AMP synthase-stimulator of interferon genes) pathway prevents viral infection (and maintains genomic integrity) by activating innate immunity in response to cytoplasmic double stranded DNA (dsDNA). I hypothesize that cHPV E6 also impairs the cGAS-STING innate immune response. To test this, transfected dsDNA was used to simulate cGAS-STING signaling and pathway activation was monitored by immunoblot. This demonstrated that cHPV E6 impairs cGAS-STING signaling downstream of STING activation. Our current efforts use RNA-sequencing to obtain an unbiased measure of how broadly cHPV E6 blocks the innate immune response to cytoplasmic DNA. These data support the hypothesized role of cHPV in NMSC.

29. The significance of leaf venation patterns in the genus *Uromyrtus* in New Caledonia: A poorly-known genus currently under taxonomic revision

Clarissa Wedman and Neil Snow
Department of Biology, Pittsburg State University

The Myrtle family (Myrtaceae) includes approximately 5500 species in over 140 genera. Some species are eaten (e.g., guava, Brazilian plum, Java plum), used as spices (cloves, allspice), and valued for their medicinal and therapeutic uses (e.g., Eucalyptus and tea tree oils). *Uromyrtus* is a genus of shrubs and short trees in the Myrtle family (Myrtaceae), comprises approximately 20–25 species, ranging from Malesia to Australia and New Caledonia (NC). Its highest diversity occurs in NC, with approximately ten known species and four new species to be described. However, taxonomic boundaries between the species remain poorly understood, and additional species may still be unrecognized. Patterns of leaf venation often have taxonomic value in members of Myrtaceae and may help clarify species' boundaries among living taxa, including the identification of fossilized taxa. This study examined leaves from 28 samples representing approximately 9 species of NC members of *Uromyrtus*. Preliminary results indicate variation in venation among species; however, analyses are still ongoing.

30. Activation of β_2-adrenergic receptor enhances neonatal lung immunity to Respiratory Syncytial Virus infection

Sandeep Adhikari[1], Pankaj Baral[1*]
Corresponding Author: baral@ksu.edu
[1]Division of Biology, Kansas State University, Manhattan, KS, USA, 66506.

Respiratory Syncytial Virus (RSV) is the most common cause of acute bronchiolitis and pneumonia in neonates with no effective antiviral drug or vaccine for treatment. The respiratory tract is heavily innervated by sympathetic neurons that mediate bronchodilation and immunomodulation through β-adrenergic receptors. Exploring neuroimmune interaction involved in RSV infection could provide therapeutic strategies against RSV infection. β-adrenergic receptors are highly upregulated in lung macrophages and monocytes. β-agonists, albuterol and xamoterol activate β_1AR and β_2AR respectively. Albuterol is an FDA-approved drug for asthma and COPD. We hypothesize that β_2-adrenergic receptors activation in neonates mediate antiviral immunity and host defense to RSV. Rapid virus clearance in the infected lungs, coupled with lesser immunopathology, is critical for the host protection against RSV. We stimulated bone marrow-derived macrophages (BMDMs) with R848 (TLR7/8 agonist) in the presence and absence of β-adrenergic agonists. Furthermore, we intranasally inoculated neonates with RSV-A2 and followed up with albuterol treatment to determine its therapeutic efficacy. In BMDM culture, albuterol suppressed the production of pro-inflammatory cytokine TNF-α, but upregulated the anti-inflammatory cytokine IL-10 production, suggesting albuterol might suppress the lung immunopathology during RSV infection. Further, we observed suppression of viral replication and reduced lung damage in albuterol-treated neonates. We also noticed enhanced B-cell and RSV-specific $CD8^+$ T-cell responses together with significant weight gain. Overall, our data suggests the protective role of β_2-adrenergic receptor in regulation of lung inflammation and immune response to RSV infection in neonates.

Keywords: Albuterol, β_2-adrenergic, RSV-A2, Immune cell, Sympathetic neuron

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31. A PROTAC-Based Degrader to Colorectal Cancer Relevant *N*-Terminal Methyltransferase 1 (NTMT1)

Chao An,[1] Wei Wu,[1] Ping Li[1]
[1]Department of Chemistry, Kansas State University, Manhattan, Kansas, 66506, U.S.A

Protein N-terminal methylation catalyzed by N-terminal methyltransferase 1 (NTMT1) is an emerging methylation present in eukaryotes, playing important regulatory roles in various biological and cellular processes. Although dysregulation of NTMT1 has been linked to many diseases such as colorectal cancer, their molecular and cellular mechanisms remain elusive due to inaccessibility to an effective cellular probe. Here we report the design, synthesis, and characterization of the first-in-class NTMT1 degraders based on proteolysis-targeting chimera (PROTAC) strategy. PROTAC is a new technology that uses bifunctional small molecules to degrade proteins of interest. Compared with traditional occupancy-driven enzyme inhibitors, PROTAC molecules display many advantages, making them ideal candidates for drug development.

32. Impact of *PTPN22* and its Autoimmunity-Associated Minor Allele During Coronavirus Infection

Alec M. Bevis[1,2], Anam Shaikh[1,2], Catherine Kerr[1,2], Jenna Barnes[1], Kate Rosa[1], Tammy Cockerham[1], Nancy Schwarting[1], Anthony R. Fehr[1], Robin C. Orozco[1].
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, USA;
[2]The Office of Graduate Studies, University of Kansas, Lawrence, KS, USA

Allelic variation can impact the outcome of viral disease. Mice expressing the autoimmune-associated allelic variant of *Ptpn22* can clear Lymphocytic choriomeningitis virus clone 13 (LCMV-cl13) infection, but little is known regarding its impact during other virus infections. This research investigates how the loss of *Ptpn22* (PEP-null) and its minor allelic variant (PEP-619WW) impacts antiviral immunity during coronavirus infection**. We hypothesize that PEP-null and PEP-619WW mice will have enhanced antiviral immunity during coronavirus infection.** This hypothesis was tested using a common murine model of coronavirus, Mouse Hepatitis Virus (MHV) A59, in our PEP-WT, PEP-null, and PEP-619WW mouse models. Following infection, PEP-null and PEP-619WW mice have reduced weight loss and increased survival over PEP-WT mice. Next, we determined if lymphocytes were necessary for disease recovery using lymphocyte-deficient $Rag1^{-/-}$ PEP-WT and $Rag1^{-/-}$ PEP-619WW mice. We show that PEP-619WW innate cells mediate some protection against MHV A59, but T and B cells are necessary for survival. Additionally, we investigated MHV A59 viral tropism and IFN-I production using PEP-WT, PEP-null, and PEP-619WW bone marrow-derived macrophage (BMM) and dendritic cell (BMDC) cultures. These experiments show that *Ptpn22* does not mediate viral permissiveness or IFN-ß production. Lastly, we performed flow cytometry at 3 days post-infection to assess the impact of *Ptpn22* on the innate immune response. The results described above demonstrate that PEP-619WW is beneficial during coronavirus infection and sets the precedent to interrogate its role in other RNA virus infections.

33. Determining Nuclear APC's role in Mediating UV-Induced DNA Damage

Carreon, Eldric and Kristi L. Neufeld
Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas

Colorectal cancer (CRC) is the second most common cancer in the US, with an estimated 152,020 new diagnoses and 52,550 projected deaths in 2023. Mutation of *Adenomatous polyposis coli (APC)* is a crucial early step in ~80% of CRC cases. Our lab has shown that APC, a known cytoplasmic regulator of Wnt signaling, is capable of nucleocytoplasmic shuttling and have identified nuclear roles for APC in Wnt signaling. Other proposed nuclear APC functions include in DNA repair, with APC levels increasing in cells exposed to DNA damaging agents. Additionally, skin fibroblasts isolated from patients with germline APC mutations exhibited heightened sensitivity to UV irradiation, implicating APC in UV-induced DNA damage response. We hypothesize that APC is a crucial component in the UV-induced DNA damage response.

We compared human colon carcinoma cells with wild-type APC (*APC+*) and CRISPR-generated APC- deficient cells (*APC-*) exposed to various UV doses. *APC-* cells displayed increased cell death while *APC+* showed recovery with lower doses. To assess DNA damage, we stained for phosphorylated H2AX (p-H2AX) which serves as a marker for double stranded DNA breaks and plays a role in sensing DNA damage. The staining results showed that *APC-* cells had a higher percentage of cells with widespread presence of p-H2AX in sham irradiated and 10 J/M^2 exposed samples as compared to *APC+*. This observation was further supported by Western blots which showed elevated p-H2AX levels in sham irradiated *APC-* cells compared to *APC+* cells. These findings suggest that the loss of APC leads to increased DNA damage when exposed to UV, indicating a potential role for APC in the early stages of the UV-induced DNA damage response.

34. Presence of PERV-C among Feral Pigs in Eastern Kansas
Cesur, Robin. Gillock, Eric. Fort Hays State University, Hays, KS

Allotransplantation (human to human transplant) is not a service most people in the United States can utilize readily due to lack of human organs. Xenotransplantation offers the benefit of having more cells, tissues, or organs available. Pigs are an appropriate animal that may be used for this due to similar organ size and physiology to humans. Pigs (wild and domestic) can be a problem when it comes to Porcine Endogenous Retrovirus (PERV). This is a retrovirus that can become integrated in all cells of an organism through the germ line. Infectious viral particles have been released in some immortalized pig cell lines causing immunodeficiencies and lymphomas. There are three subtypes based on cell tropism, sequence variation, and receptor interference; A, B, and C. A and B are present in all pigs and infects pigs and humans. C is only present in some pigs and only infects pigs. A and C can recombine in two known varieties, long and short. Since A can infect humans, so can these hybridizations. By looking at recombinant envelope regions, it can be hypothesized how prevalent this hybridization is in feral and domestic samples. This study is using PCR to detect the presence of PERV-C in samples from Eastern Kansas. This will also guide further studies in learning structure and function in retroviruses and their related family members (koala retrovirus, murine leukemia virus, etc.) It was found that 44/53 (83%) were positive for PERV-C and 13/31 (42%) were positive for PERV A/C hybrid long.

35. Oxidative Stress Regulator NRF2 controls Inflammatory T-helper (Th) Subset differentiation by Modulating Glycolysis
Debolina Dasgupta[1], Aprajita Tripathi[1], Ashlyn Bugbee[2] and Kalyani Pyaram[1]
[1]Department of Cancer Biology, University of Kansas Medical Center
[2]Division of Biology, Kansas State University

CD4 T cells are the orchestrators of adaptive immunity and a disbalance in their effector responses is implicated in multiple inflammatory diseases, like Ulcerative Colitis (UC). In this project, we aim to identify if/how Nrf2 (nuclear factor erythroid 2–related factor2), an oxidative stress regulator controlled by Keap1 (Kelch-like ECH-associated protein1), impacts the differentiation of inflammatory (Th1) or regulatory (Treg) T-cell subsets and in turn, the disease outcome of UC. To answer this, we used mice with T-cell specific knock out (KO) of Nrf2 (N-KO) or Keap1 (K-KO). We performed *in vitro* T-cell differentiation assays to compare the effects of high and low Nrf2 using KO mice and validated the results *in vivo* using mice models of Colitis. Cytokine IFN-γ secretion and T-bet expression were assessed for measuring Th1 while Foxp3 was assessed for Treg differentiation. Glycolysis is indispensable for Th1 differentiation. To dissect the metabolic mechanisms, the levels of glycolytic intermediates lactate and pyruvate were measured. Our data revealed lower Th1 differentiation by K-KO T-cells alongside lower glycolysis compared to the Wild type (WT) and N-KO CD4 T-cells. Conversely, we observed increased Foxp3 expression with high Nrf2 indicating that Nrf2 promotes Treg cell differentiation. To elucidate if T-cell intrinsic Nrf2 plays a protective role in UC, we employed adoptive transfer model of Colitis. Expectedly, $Rag1^{-/-}$ mice adoptively transferred with high Nrf2-bearing K-KO CD4 T-cells showed a milder disease than mice transferred with WT T-cells suggesting a protective role of NRF2 in UC, making it an attractive therapeutic target.

36. Water extract from *Euglena gracilis* attenuates lung cancer growth and increases PD-1 expression in tumor infiltrating lymphocytes
Authors: Sarah DeVader, Susumu Ishiguro, Jeffery Comer, Masaaki Tamura
Department of Anatomy and Physiology, Kansas State University College of Veterinary Medicine, Manhattan, KS 66506

Lung cancer is the leading cause of cancer related death in the US. In human lung cancers, a high tumor infiltration of lymphocytes (TILs) and a high expression of immune checkpoint proteins programmed death-ligand 1 (PD-L1) and programmed death 1 (PD-1) in early stages is linked to susceptibility to immune checkpoint inhibitor (ICI) therapy and shown to increase survival rate after ICI therapy. Our previous studies revealed daily oral administration of *Euglena gracilis* water extract (EWE) significantly attenuated lung cancer growth in mice. *In vitro,* EWE stimulates T cell-induced cytolysis of cancer cells. Here, we investigated the relationship between EWE-induced attenuation of lung cancer growth and EWE-induced T cell stimulation with a special interest in PD-1 and PD-L1 expressions in a murine lung cancer model. This study found that treatment with EWE *in vitro* increased both mRNA and protein expressions of PD-1 and PD-L1 in murine lung carcinoma cells. EWE was revealed to increase the amount of PD-1 and PD-L1 in murine tumor tissues, which was correlated with a decrease in tumor weights. This study also discovered that EWE increases the PD-1 expressing TILs in tumor nodules. These results suggest the EWE-induced attenuation of lung cancer growth is associated with an increase of PD-1 expressing TILs in the lung tumor microenvironment. It is further suggested that EWE may stimulate the efficacy of ICI therapy against lung cancer. Determining the mechanisms by which EWE stimulates PD-1 expression in TILs and the specific subpopulation affected by EWE await future studies.

37. Higher yield isolation method of alveolar macrophages for functional studies
Surya Prasad Devkota[1], Prabhu Raj Joshi[1], Sandeep Adhikari[1], Chinemerem Onah[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State university, Manhattan, Kansas, USA, 66506

Alveolar macrophages (AMs) are long-lived tissue-resident immune cells, representing a critical component of the lung innate immunity to infection and injury. AM culture represents an excellent *ex vivo* culture system for the studies of innate immune activation such as phagocytosis and cytokine production. For *ex vivo* studies, the quantity and quality of AMs after isolation from bronchoalveolar lavage is critical. Most of the methods have reported the yield less than 100,000 AMs per mouse. We found the novel method that increased the yield significantly higher (2.5 times) than the traditional method. While traditional method used the ice-cold phosphate buffered saline (PBS) buffer (4°C) for AM isolation, we used the warm PBS buffer (37°C) with 2mM EDTA for higher number recovery of AMs. We also examined the viability and functional characteristics of AMs in new method vs. traditional method. Flow cytometry analysis was performed for the measurements of AM numbers (AMs were characterized as $CD45^{+}CD11b^{-}Siglec\text{-}F^{+}CD11c^{+}F4/80^{+}$ population). Further, we compared the viability of AMs using Annexin V/PI kit. For functional studies, we parallelly evaluated the production of cytokines and chemokines in LPS-stimulated AM cultures by ELISA (for protein levels) and real-time qPCR (for mRNA levels). The apoptosis assay revealed that there was no difference in viability of AMs isolated using both methods as the viability was around 80%. Hence, the novel method we are proposing for the higher yield of AMs is highly suitable for ex vivo functional analysis of these cells.
Keywords: Alveolar macrophages, cytokines, ex vivo studies.

38. Extracellular vesicle miRNA signatures as novel biomarkers in mouse model of allergic asthma

Santhosh Kumar Duraisamy[1], Chandrashekhar Prasad[1], Rachel Griffard[2], Dong Pei[2], Navneet Dhillon[1], Mario Castro[1], Isaac Kirubakaran Sundar[1]
[1]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, [2]Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS, USA

Extracellular vesicles (EVs) are membrane-bound nanovesicles that contain proteins, nucleic acids, and other biomolecules, and which play an essential role in intercellular communications. In chronic inflammatory diseases such as asthma, variations in EV size and concentration may be associated with pathophysiological phenotypes. We hypothesized that acute house dust mite (HDM) exposure augments EV release in systemic circulation, and that EV-enriched miRNAs can serve as novel circulating biomarkers in preclinical models of asthma. Adult C57BL/6 (WT; female and male mice; ~2-3 months old) were intranasally exposed to HDM (30 µg) or PBS for 10 consecutive days; serum was obtained 48 hours after final exposure. EVs were isolated from serum by ultracentrifugation, followed by total RNA extraction and small RNA sequencing. HDM exposure significantly increased the EV counts and total protein compared to the PBS control. Analysis of EVs using small RNA-seq revealed 9 differentially expressed (DE) miRNAs (6 miRNAs upregulated: miR-205-5p, miR-206-3p, miR-2137, miR-466f, miR-466f-5p and miR-8109, and 3 miRNAs downregulated: miR-138-5p, miR-215-5p and miR-8117). mirPathV.3 analysis and identified fatty acid metabolism, thyroid hormone signaling, adherens junction, and lysine degradation as KEGG pathways specific to upregulated miRNAs. Similarly, fatty acid metabolism, amino acid metabolism, and axon guidance pathways were the KEGG pathways specific to downregulated miRNAs. Integrative pathway analysis of DE miRNAs revealed key metabolic pathways linked to asthmatic phenotypes. Ongoing studies will validate the miRNAs and associated target genes that directly contribute to asthma pathobiology. ***Funding*****:** K-INBRE P20 GM103418, R01 HL142543, *and KUMC School of Medicine, Internal Medicine Start-up Funds.*

39. Unused

40. Unused

41. Characterizing the *AT3G05510* gene product in *Arabidopsis thaliana* using lipid profiling

Adamson, Summer,[1,2] Ruth Welti,[1,2] and Zolian Zoong Lwe[2,3]
[1]Division of Biology, Kansas State University, [2]Kansas Lipidomics Research Center, Kansas State University, [3]Department of Biochemistry and Molecular Biophysics, Kansas State University

The *Arabidopsis thaliana* gene *AT3G05510* is hypothesized to encode an enzyme with acyltransferase activity involved in the synthesis of cardiolipin, which is found in mitochondria. The enzyme is potentially a homolog of the human protein tafazzin, which acts as an acyltransferase, altering cardiolipin fatty acid composition by “remodeling”. Like tafazzin, the AT3G05510 protein is predicted to be an acyltransferase, but its association with mitochondria is unknown. By looking at the lipid phenotypes of plants with T-DNA insertions in or near the *AT3G05510* gene and comparing them to the lipid phenotypes of wild-type plants, we will determine whether the AT3G05510-encoded enzyme affects the fatty acyl composition of cardiolipin like tafazzin does. We will also compare the *AT3G05510* mRNA levels in wild-type and mutant samples to confirm that the T-DNA insertions in the mutants act as predicted to reduce the expression of *AT3G05510.* Taken together, these studies will clarify whether the *AT3G05510* gene product is a plant homolog of tafazzin. If the cardiolipin composition in the mutants is unaffected compared to wild type, indicating that the protein is not catalyzing the same reaction as tafazzin, we will compare other analyzed lipids in wild-type vs mutant plants to provide insight as to what reaction is catalyzed by the AT3G05510 protein.

42. The Effect of NKG2D on The Fate of CD8+ T-cells

Aikin, Tatum,[1] Zoe Bedrosian,[1] Mary Markiewicz[1,2]
[1]Department of Microbiology, Molecular Genetics, and Immunology, University of Kansas Medical Center; [2]Flow Cytometry Core Laboratory, University of Kansas Medical Center

Diabetes is a condition characterized by a decrease in the production or processing of the blood sugar homeostasis hormone insulin. This results in increased levels of glucose in the bloodstreams of the millions that are affected, leading to a multitude of health problems. In type 1 diabetes, the buildup of glucose is caused by an autoimmune attack on the beta islet cells of the pancreas, which decreases or cuts off the production of insulin. The autoreactive cells causing this reaction include cytotoxic CD8 effector T cells, one of the multiple fates of a CD8+ T cell post-differentiation. The receptor NKG2D, which signals cytotoxic effector action, has been investigated in the differentiation of CD8+ effectors. Based on previous studies in the Markiewicz lab, we hypothesize that NKG2D signaling affects the differentiation of naïve CD8+ T cells. We are testing this hypothesis via the isolation and coculture of antigen presenting cells with naïve CD8+ T cells, and analysis of transcription factors, extracellular receptors, and cytokines expressed by the T cells. These studies will help to better understand the implication of NKG2D signaling on the generation of the CD8+ T cells that kill islet cells during type 1 diabetes development.

43. Understanding the role of neurotransmitter receptors in anti-*Aspergillus fumigatus* immunity

Michael Bartkoski[1], Chinemerem Onah[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

Aspergillus fumigatus, a major respiratory pathogen, causes deadly invasive aspergillosis among immunocompromised individuals. The increasing prevalence of immunosuppression worldwide has elevated *A. fumigatus* to a common cause of life-threatening pneumonia. Our unpublished data suggests a crucial role of nociceptor sensory neurons in orchestrating immune cell recruitment and fungal clearance in the lungs during *A. fumigatus* infection. Additionally, we determined the immunomodulatory potential of Calcitonin Gene-Related Peptide (CGRP) on neutrophils and macrophages *in vitro*. This study hypothesizes that various neuropeptide and neurotransmitter (NT) receptors, including CGRP receptor, are instrumental in immune cell activation and host defense against *A. fumigatus*.

To delve deeper into the unidentified receptors governing host defense, we have identified NT receptors of interest through the ImmGen database. Specifically, we will investigate ADRB1&2 (norepinephrine receptor), 5-HTR2C (serotonin receptor), nAChR (acetylcholine receptor), and GABBR1 (gamma-aminobutyric acid receptor) for their potential roles in intracellular killing and immune activation against *A. fumigatus*. Our approach includes intracellular killing assays to assess conidial viability and confocal imaging for phagocytosis using bone marrow-derived macrophages (BMDMs) in the presence and absence of receptor agonists and antagonists. Preliminary results suggest the beta-adrenergic receptors plays an important role in macrophage activation and fungal killing. Furthermore, receptor-deficient BMDMs will be employed to elucidate the role of receptor signaling pathways in anti-*A. fumigatus* immune responses. This research aims to enhance our understanding of NT receptors involved in the immune response to *A. fumigatus*, with the potential to pave the way for more targeted therapeutics and expedited recovery for immunocompromised individuals.

44. The differentiation and characterization of dental pulp stem cells on nanofiber matrices

Kayla Cantu, Neema Fathi, Li Yao
Department of Biological Sciences, Wichita State University

Dental pulp stem cells (DPSCs) have become an attractive cell source of stem cells because they have a similar differentiation capability as other mesenchymal stem cells (MSCs) and they are relatively easy to obtain. Studies have shown that DPSCs can be differentiated into chondrogenic cells that expresses chondrocyte phenotype markers such as sox 9, collagen type II, and aggrecan. DPSCs derived chondrogenic cells may replace chondrocytes cells for cartilage regeneration. In previous study, we differentiated the DPSCs into chondrogenic cells and studied the migration of DPSC-derived chondrogenic cells in the collagen hydrogels. We demonstrated the motility of the cells in the hydrogels. However, the differentiation efficiency of DPSCs into chondrogenic cells was low. Electrospinning techniques have shown potential in developing fibrous scaffolds for tissue engineering application. Nanofibers provide 3D matrix for cellular growth and therefore may potentially promote the DPSC cell differentiation to chondrocyte phenotype. In this study we fabricated the nanofibers using polycaprolactone (PCL) and gelatin copolymer. The fibers were prepared by co-axial electrospinning. We grew and differentiated the DPSCs on top of the nanofibers. The differentiated cells were labeled with rhodamine phalloidin and the result confirmed the cell growth on the nanofibers. We also further examined the differentiated cells morphology and attachment on nanofiber using scanning electron microscope. Our preliminary results showed that the polymer and protein hybrid nanofibers can support DPSC growth and the differentiated cell morphology on the fibers. The nanofibers carrying stem cells can be potentially used for cartilage repair.

45. Kansas Small Mammal Survey Abstract

Oscar Casillas-Vallejo[1], Andrew Hope[2], and Kaitlyn Headlee[2]
[1]Department of Biology, Langston University, Langston, Oklahoma [2]Division of Biology, Kansas State University, Manhattan, Kansas

One Health embraces an understanding that human well-being depends on healthy environments and intact biodiversity. Since the global pandemic, connections between humans, mammal species, and zoonotic diseases have become apparent to society broadly. However, it is possible that whole species are not the best scale of analysis and narrowing scientific focus to intra-specific relationships between mammal hosts and their diseases may provide more comprehensive understanding of risks. The Great Plains is recognized as a potential hotspot for future disease outbreaks. I studied the evolutionary history of eight small mammals to identify the geographic extent of within-species lineages. Kansas supports mammals from multiple distinct communities across North America that all meet in the middle. I contributed genetic data to refine our knowledge of how mammal diversity is distributed across the Great Plains. This will be important for future research on the co-evolution between mammals and their diseases.

46. Fitness Effects and Transmission of a B chromosome in *Drosophila putrida*

Evelyn Cuellar*, Paul S. Ginsberg, Robert Unckless*
University of Kansas, Department of Molecular Biosciences

B chromosomes are non-essential for the basic functioning or survival of an organism. Two defining characteristics of B chromosomes are negative fitness consequences at high copy number and biased transmission into the gametes. *Drosophila putrida*, is a widespread mushroom-feeding fly species found across the eastern US. Its prevalence in diverse ecological habitats provides a unique opportunity to investigate the genetic mechanisms associated with its adaptation to different environments. In *D. putrida,* B chromosomes are found from a 33%-75% frequency depending on the population, and in 0 to 4 copies per individual. Here, we aim to determine whether the B chromosome of *D. putrida* affects the fitness of wild-caught females, and whether the B chromosome follows the rules of Mendelian inheritance. We found no influence of the B chromosome on either offspring production or hatch rate. B chromosomes are important to study to provide insight into various aspects of genetic, evolution, and genome dynamics. Initial indications propose that the inheritance of B chromosomes in *D. putrida* follows the standard Mendelian segregation. Currently, we are broadening this dataset through controlled genetic crosses. *Drosophila* is a preferred species to study B chromosomes due to its short generational time, high reproductive rate, small genome, and cost-effectiveness. Additionally, ethical considerations and the complexity of human genetics make some aspects of genetic research more challenging in human populations.

47. EXPLORING THE GUT MICROBIOTA OF GRAY BATS IN KANSAS FOLLOWING CULTURABLE AND METAGENOMIC APPROACHES

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

Humans have historically had an ambivalent relationship with bats. Bats perform important services by reducing populations of insect pests. They also act as reservoirs of diseases, as highlighted by the recent Coronavirus pandemic. This study aims to characterize the bacterial diversity associated with the Gray Bat (*Myotis grisescens*) in Southeast Kansas. A total of 32 bacterial isolates with different colony morphology were recovered from guano samples on tryptic soy agar media after enrichment. The majority (21/32, 65%) of isolates were Gram positive. All isolates were tested for growth on selective and differential media. Sugar fermentation profiles showed that 78% (25/32) fermented all four sugars, 9% (3/32) fermented three sugars, another 9% (3/32) fermented two sugars, and one isolate (3%) fermented only one sugar. Urea was hydrolyzed by seven (21%) isolates while one isolate (3%) was positive for indole production. Pooled isolates were sequenced using an Illumina miniSequencer. A total of 2,909,555 reads were completed. The most common genus being *Serratia* (26.36%) followed by *Achromobacter* (20.17%), *Lysinibacillus* (19.93%), and *Bacillus* (17.01%). Currently, sequencing experiments are underway to determine the microbiota of male and female bats GI tract. Identification of known and novel bacteria/fungi in bats is important for prevention of disease spread and long-term preservation of bat populations.

48. Fine-tuning of Cell-ECM Assembly by Transglutaminase

Dylan Feist, Nicole Green, Ziwei Zhao, Erika R. Geisbrecht
Department of Biochemistry and Molecular Biophysics, Kansas State University

The *Drosophila melanogaster* myotendinous junction (MTJ) is a unique model to understand how secretion and assembly of the extracellular matrix (ECM) contributes to cell adhesion during development and growth. MTJ formation requires myotube targeting to the appropriate tendon cell followed by the secretion and binding of ECM proteins to transmembrane integrin heterodimers on opposing muscle and tendon cells. This stable network not only links the ECM to the internal actin cytoskeleton, but also transmits tension between muscles and tendons to withstand contractile forces. Thus, knowledge of the molecular composition of the MTJ throughout development is essential to understand how forces vary at the muscle-tendon interface. We performed a targeted RNA interference (RNAi) screen to uncover secreted proteins that are required for cell-matrix adhesion in the contractile muscles of third instar larvae (L3). One candidate that emerged is Transglutaminase (Tg), a protein with known scaffold and crosslinking activity. Therefore, our hypothesis that the crosslinking function of Tg is important for maintaining extracellular adhesion and ECM integrity is exciting and may change current dogma suggesting that integrins are the primary mediator for MTJ stability. RNAi knockdown of Tg in the embryonic tendon cells resulted in smaller muscle attachment sites and occasionally led to fully detached muscles by the L3 stage. Preliminary studies indicate that Tg activity is required as an antibody generated against the epsilon-(gamma-glutamyl)lysine-isopeptide bond can be visualized at muscle attachment sites. Current and future experiments will focus on examining Tg mutants and further characterizing if the crosslinking role of Tg is essential through expression of a catalytically inactive Tg.

49. ANNEXIN A2 EXPRESSION IN PROSTATE CANCER CELLS.

Charles R. Gates[1,2], Amit Kumar Tripathi[1], Jamboor K. Vishwanatha[1], Pankaj Chaudhary[1]
[1]Department of Microbiology, Immunology & Genetics, University of North Texas Health Science Center, Fortworth, TX
[2]Department of Biology, Langston University, Langston, OK.

Metastasis is a major cause of morbidity in prostate cancer patients; the primary mortality is metastasis of bone tissue. Despite substantial efforts to understand prostate cancer metastasis, the mechanisms involved in preparing the metastatic niche for colonizing the prostate cancer cells are still unknown. Therefore, there is an urgency to identify essential regulators of bone metastasis in prostate cancer for therapeutic targets. Annexin A2 is a calcium-dependent phospholipid-binding protein overexpressed in prostate cancer's poorly differentiated high-grade adenocarcinomas. Phosphorylation of AnxA2 at tyrosine-23 creates an important event for the localization of AnxA2 to the cell surface. It provides a binding site for tissue plasminogen activators at the cell surface and converts plasminogen into plasmin, which plays an essential role in the invasion and metastasis of cancer. However, the cell surface expression of AnxA2 in prostate cancer is unknown. Therefore, in the present study, we demonstrated the cell surface expression of AnxA2 in prostate cancer cells to delineate the mechanism of bone metastasis. Prostate cancer cell lines, PC3, and DU145 were grown. Immunoblotting was used to detect the expression of pAnxA2-Y23 and AnxA2 proteins in cells. Our results demonstrated that the expression of pAnxA2-Y23 is very high in prostate cancer cells (PC3 and DU145 cells) compared to normal prostate epithelial cells. However, the expression of total AnxA2 in both prostate normal and cancer cell lines is comparable. Results suggest that the cell surface expression of AnxA2 is high in prostate cancer cells due to increased phosphorylation of AnxA2 at tyrosine 23.

50. Distribution of the 2-micron Plasmid in Various Strains of Saccharomyces cerevisiae

Greving, Camryn, Gillock, Eric T.
Department of Biological Sciences, University of Fort Hays State University

Along with several known viruses and prions, some strains of baker's yeast, *Saccharomyces cerevisiae,* are known to carry the 2-micron plasmid. When present, this extrachromosomal element exists as a circular, double-stranded, DNA plasmid within the nucleus of the host cell. In strains that harbor it, there is an average copy number of between 40 to 60 per haploid cell, with 60 being more common. This copy number is stabilized by the action of the host amplification system. At normal copy numbers, the plasmid doesn't seem to confer any selective advantage to the host. However, at high copy numbers, it becomes detrimental and causes cell cycle misregulation and cell death. It is thought that the plasmid utilizes a "chromosome hitchhiking" method to ensure that adequate numbers of copies are distributed into the daughter cells after cell division. The "chromosome hitchhiking" segregation method is of research interest as it is also used by papilloma and gammaherpes viruses to maintain themselves in latently infected cells. In this work, several strains of yeast were assayed by colony PCR for the presence of the 2-micron plasmid *REP2* gene, which functions in partitioning of the plasmid into daughter cells during mitosis. Our research so far shows out of 21 strains of *Saccharomyces cerevisiae* examined, 17 displayed the 2-micron plasmid. Future work will entail screening more yeast strains for the 2-micron plasmid, and examining sequence variations among the *REP2* genes in the plasmids found.

51. A gradient-based assay for analyzing microbial community interactions.

Makayla Hallacy, Alexa McGann, Ashlynn Booth and Stephen Fields
School of Science and Mathematics, Emporia State University, Emporia KS

Most natural environments have inherent obstacles to bacterial growth that result from antibiotics, toxins, immune responses, plant-based secondary products, competition, or nutrient inaccessibility. Cellulose, for example, is a glucose homopolymer that is inaccessible to most microbes. Hydrolysis of cellulose requires the activity of three different cellulase subfamilies, so only a small fraction of bacteria can break down cellulose. The goal of this project is to develop an assay testing the hypothesis that bacterial species are more adaptive in the context of communities than as individual populations. To accomplish this goal, we are developing a gradient-based growth system for examining tolerance and adaptive strategies to a broad spectrum of barriers. For an initial test of the system, we isolated eight species of carboxymethylcellullose (CMC)-competent bacteria from a soil community, sequenced each species with Illumina NextSeq and Oxford Nanopore MinION platforms, and annotated assembled genomes. The assay, which utilizes a stepwise concentration gradient of the "challenge substrate" (CMC), begins with individual populations or communities started at the end without CMC (+glucose). To grow into agar quadrants with progressively higher CMC concentrations (and lower glucose), bacteria must overcome the inhibitory concentration through accumulation of adaptive mutations, HGT or metabolite exchange. Microbes isolated from the highest concentrations of challenge substrate are characterized according to migration distance and speed, genomic changes, and synergistic pairings. This assay may be used to gain broad insights into community-level adaptive processes that help maintain viable communities in various habitats, including the human gut.

52. Fitness Testing of Adults Ages 60 and Older

Jessica Jones, Dr. Laura Covert Miller, Dr. Mike Carper
Pittsburg State University - Health Human Performance and Recreation

A more thorough understanding of physical fitness (PF) levels in older adults may help improve physical activity (PA) recommendations and delay disease onset. **Purpose:** The purpose of this study was to collect PF data in older adults in Southeast Kansas through functional fitness and cardiopulmonary exercise (CPET) testing. **Methods:** Older adults (n = 15 [M = 3, F = 12]; age = 73.6 ± 5.6 yrs) were recruited to participate. Informed consent, demographic, and health history data were obtained for all participants. Physician consent was obtained when necessary. The CHAMPS survey for PA was completed as well as measures of hand grip strength, 30-second chair stand, 8-foot up and go, back scratch, and the Berg balance tests. Body composition was obtained via DEXA scan and CPET via treadmill VO_{2MAX} test (e.g., modified Bruce). **Results:** Participant's (BMI: 25.6 ± 4.5; body fat = 39.9 ± 8.4%) preliminary data revealed sit to stand (13.4 ± 3.1 reps), sit and reach (11.7 ±7.0 cm), back scratch (3.1 ± 6.5 cm), 8-foot up and go (5.6 ±1.0 sec), hand grip strength (22 ± 8.1 kg), Berg balance single leg stance (3.8 ± 0.4), Berg balance tandem stance (3.8 ± 0.8), and VO_{2Max} (n = 12; 19.9 ± 6.2 $ml \cdot kg^{-1} \cdot min^{-1}$). Survey data were not included in preliminary analysis. **Discussion:** Preliminary data indicates subjects' functional fitness results fall within average norms. Data collection is ongoing. **Conclusion:** Additional data are needed to be collected to better understand functional fitness in older adult population.

53. Role of b- adrenergic Receptors in Innate Immune Response to *Burkholderia thailandensis* Infection

Abigail Judd[1], Prabhu Joshi[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

Burkholderia thailandensis is an opportunistic intracellular pathogen that causes lung infections. This pathogen can be used as a model organism for the more virulent pathogen *Burkholderia pseudomallei* that causes chronic lung infection known as melioidosis. Lungs are highly innervated with sympathetic neurons which release the neurotransmitter noradrenaline during homeostasis and infection/inflammation. The innate immune cells, including monocytes and macrophages, express the b-adrenergic receptor for noradrenaline (NA). The role of b-adrenergic receptors during *B. thailandensis* infection is unknown. We hypothesized that b-adrenergic receptor signaling in innate immune cells plays a role in host defense during *B. thailandensis* infections. We performed *In-vitro* coculture of bone marrow-derived macrophages (BMDMs) and *B. thailandensis* with and without NA, b-1 adrenergic receptor agonist (xamoterol), and b-2 adrenergic receptor agonist (albuterol) to determine their affects in intracellular survival of bacteria. Both NA and albuterol enhanced the intracellular killing abilities of BMDMs. Also, NA increased the cytokines TNF-a and IL-6 secretion from BMDMs stimulated with *B. thailandensis in vitro.* This data suggests that b-2 adrenergic receptor signaling plays a critical role in innate immunity against *B. thailandensis* infection.
Key words: BMDMs, *B. thailandensis,* Noradrenaline, Cytokines, intracellular killing

54. Nitrification and Denitrification Rates in Intermittent Streams during a Wet-up Event at Youngmire Ranch (Elk County, Kansas)

Genevieve Knotts[1], Sarah Flynn[2], Amy Burgin[2]
Haskell Indian Nations University[1], University of Kansas[2]

While intermittent streams are widely prevalent across the world, little research has been put into their inner workings. The purpose of this study is to see how nitrification and denitrification rates are affected by a wet-up event where the intermittent streams become flowing after a period of dry or pooling conditions. This study sampled water and soil during both the month of June, when there was little water in the system, and in July, after a large amount of rain caused the sites to have majority flowing or pooling conditions. Once the samples were collected, they were processed at the Burgin Laboratory with separate samples being used to determine nitrification and denitrification rates through use of a spectrometer and soil weight to determine nitrification rates, and a gas chromatograph to determine denitrification rates. These rates are important to study due to the devastating effects of nitrite in river systems on the local populations. Fish kills can easily occur when large amounts of nitrite or ammonia are concentrated in one area. Since intermittent streams can go dry for long periods of time, leaf litter can be trapped in their soil until a wet-up event occurs. The dangerous levels of nitrite can be swept downstream all at once into a lake or other water-holding area, killing large amounts of fish and invertebrates and even having the potential to hurt human infants or the elderly. From an initial look at the data using the average rates, both nitrification and denitrification increased significantly a majority of the time in July compared to the June results. This leads me to believe that wet-up events cause an increase in nitrification and denitrification rates in intermittent streams.

55. Investigating how miRNA modifications influence strand selection in the nematode *Caenorhabditis elegans.*

Sumire Kurosu, Jeff Medley, and Anna Zinovyeva
Division of Biology, Kansas State University, Manhattan, Kansas

Gene regulation allows for cells to express different sets of genes despite DNA content remaining the same in all cells, a process that is crucial for animal development. miRNAs are small non-coding RNA molecules that negatively regulate gene expression, which is critical for proper developmental timing. For example, in worms, the let-7 miRNA regulates genes important for the transition from larval development into adulthood. As worms approach adulthood, let-7 accumulates, leading to downregulation of let-7 gene targets. Thus, the levels of miRNAs play a key role in regulating miRNA activity. Interestingly, dysregulation of miRNA levels is often observed in human diseases, possibly due to abnormal gene regulation. While it is clear that many miRNAs are developmentally regulated, it remains unclear how they are regulated throughout development. One possible mechanism is that miRNAs are modified post-transcriptionally by factors such as adenylases or uridylases, which may modify miRNA function. In this study, we are exploring how adenylases or uridylases regulate miRNA activity and its possible influence in the stability, function, and strand selection of miRNAs. Our preliminary data suggests that both adenylases and uridylases regulate miRNA-dependent gene regulation, suggesting a broad role of miRNA modifications in regulating miRNA activity. To further understand how adenylases or uridylases regulate miRNA levels and stability throughout development I will perform qPCR and analysis of small RNA sequencing data. These findings will establish how adenylases and uridylases influence miRNA activity, which will be an important first step into understanding how modification of miRNAs influences their activity.

56. Small Molecule KRAS Inhibition in Colorectal Cancer

Alexa N. Magstadt[1], Andrew E. Evans[1], and Dan A. Dixon[1,2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, [2]University of Kansas Cancer Center, Kansas City, KS

In the United States, colorectal cancer (CRC) is the third-most diagnosed and second-most lethal cancer for both men and women. Thus, there is a need to develop novel therapeutics limiting CRC tumorigenesis. In CRC, 30-40% of tumors contain a mutation in the small GTPase protein Kirsten Rat Sarcoma (KRAS). When *KRAS* is mutated and constitutively active, numerous cell signaling pathways are activated that increase cell division and proliferation. Due to KRAS's high mutation prevalence in CRC and role in progression, it is an intriguing chemotherapeutic target. For many years, KRAS was considered "undruggable" due to its protein structure and lack of targetable binding pockets. However, recent advancements in binding affinity optimization have led to the development of new small-molecule therapeutics that allosterically suppress KRAS GDP/GTP cycling. MRTX1133 is one such drug that binds to the switch II pocket of G12D mutated KRAS. Phase 1/2 clinical trials of MRTX1133 are currently ongoing on the basis of encouraging mouse xenograft evidence. At this point, the treatment effects of MRTX1133 in CRC are largely unknown. We are currently working to understand the effects of this inhibitor in both mutated and wild type KRAS cell lines. Through cell viability assays, we have demonstrated that MRTX1133 is particularly effective at inhibiting KRAS G12D mutant CRC cell lines in the nanomolar range. Further studies examining MRTX1133's ability to impact CRC cell growth will be discussed. Future studies will be aimed to characterize cell signaling pathway disruption and post-transcriptional gene regulation in CRC cell lines upon MRTX1133 treatment.

57. Cloning and Expression of the AAA+ ATPase ClpA from *Escherichia coli*

Eleanor Martin, Zachary Spaulding, and Michal Zolkiewski
Department of Biochemistry and Molecular Biophysics, Kansas State University, Manhattan, Kansas

Living organisms must maintain the quality of their proteins to survive various environmental stresses that affect protein stability and biological activity. Maintaining a balanced set of cellular proteins (a.k.a. proteostasis) requires specialized protein factors, including those that mediate degradation of damaged proteins. ClpA is a member of the AAA+ protein family found in gram-negative bacteria. In combination with the peptidase ClpP, ClpA forms a large complex that threads protein substrates through its central channel into the proteolytic site of ClpP, which leads to their degradation. The inhibition of ClpA serves as a promising strategy for the development of novel antimicrobials. For further studies on ClpA it is necessary to reliably overexpress and purify this protein from *Escherichia coli.* To achieve that goal, we performed cloning of the ClpA DNA coding sequence into the bacterial expression vector. Using PCR, we produced a DNA construct containing the *E. coli* ClpA gene with a polyhistidine tag at the C-terminus and the restriction enzyme cloning sites. The PCR product was digested with XhoI and NdeI and cloned into pET-20B plasmid vector. Insertion of the ClpA sequence into the vector was confirmed by DNA sequencing and restriction enzyme analysis. The pET-20B-ClpA plasmid was transformed into the BL21(DE3) strain of *E. coli* and the ClpA expression was tested after induction with IPTG, followed by gel electrophoresis (SDS-PAGE).

58. Sex differences in active avoidance strategies

Authors: Halle Ness, Shannon Ruble, Cassie Kramer, Maria Diehl
Affiliation: Kansas State University, Department of Psychological Sciences

Prior research indicates that women are twice as likely to develop anxiety-related disorders compared to men. Avoidance behaviors, prevalent in these disorders, can significantly disrupt daily life. Despite established sex differences, fear response studies primarily use male animal models, creating a crucial gap in understanding female responses. Using the Platform-Mediated Avoidance (PMA) task adapted from traditional fear conditioning studies, we observed active avoidance, where a rat learns to avoid a tone-signaled shock at the cost of a sucrose reward. Our findings demonstrate sex differences in avoidance behavior during the solitary PMA task, with females displaying higher avoidance tendencies. We modified the task to include a social condition where one rat completes the task, and the other rat watches from behind a transparent barrier. Previous aversive learning studies have found that females tend to engage in darting behavior as an active fear response strategy, exhibiting rapid movements in response to a negative stimulus, while male rats primarily engage in a fear response strategy called freezing, characterized by very little movement. In this study, we will evaluate darting behavior in rats across solitary and social PMA. We hypothesize that female rats will display more darting behavior than males, mirroring results in fear conditioning studies. Additionally, we expect that rats paired with a partner will exhibit increased darting behavior compared to solitary rats, as seeing such behavior may lead the observer rat to adopt it more quickly. This study contributes to understanding sex-specific fear responses, potentially influencing future research on anxiety-related disorders.

59. Investigation of Visual Data Analysis Skills and the Impact on Clinical Decision Making

Halle Panter,[1] Paige Boydston[1]
[1]Department of Psychology and Counseling, Pittsburg State University

Visual inspection of data in behavioral research and practice requires an understanding of varied processes, such as fluency with trend and variability. Determining the appropriate time to modify independent variables based on behavioral responses is imperative during repeated measurement procedures. The primary purpose of the current project is to conduct a preliminary investigation of behavioral practitioner abilities to review data in multiple formats (e.g., raw data, line graphs) and their resultant ability to make appropriate data-based decisions. Data-based decisions may vary, including recommendations to continue or alter an intervention, and their ability to identify at what point in time an intervention should have been modified. The secondary purpose of the current project is to evaluate the potential difference in data-based decision-making skill levels based on training modality (e.g., electronic versus paper training). Methods and procedures for the project include creating, administering, and analyzing an anonymous survey with hypothetical data sets presented in varied formats, with participants required to make a data-based decisions. Participation will have no specific restrictions, but recruitment efforts will target Board Certified Behavior Analysts. The survey will be distributed through multiple platforms including email, Facebook, and recruitment posters. The survey will include sections such as demographics, an initial 20-30 question "quiz" with varied data and varied data presentations, a short informational section on components of analyzing data, and an additional 20-30 question "quiz." Data will be analyzed in several ways, including scores per participant group, scores based on length of experience, and scores based on training modality.

60. Analysis of OSCP Deregulation in Alzheimer's Disease

Albert Park, Tienju Wang, Jing Tian, Heng Du
University of Kansas School of Pharmacology and Toxicology, Lawrence KS, 66046

Alzheimer's disease (AD) is a chronic and irreversible neurodegenerative disease that affects more than 44 million people worldwide. There are currently no effective therapies for this devastating neurological disorder and the detailed molecular mechanisms of AD etiopathogenesis remain unelucidated. Mitochondrial dysfunction is emerging as a vital contributor to the development of AD. The molecular pathways that lead to disease-associated mitochondrial abnormalities including impaired ATP production via oxidative phosphorylation (OXPHOS) are under intensive investigation. Previous studies have implicated loss of oligomycin sensitivity conferring protein (OSCP), a key protein of the F1Fo ATP synthase, in AD pathology; however, the precise mechanism for OSCP degradation in AD conditions remains unknown.

Our study aims to establish a link between oligomeric amyloid beta protein and the deregulation of ubiquitinated-OSCP in AD. We have discovered through immunostaining that human oligomeric Aß42 increases ubiquitin and decreases in OSCP expression in primary cultured hippocampal neurons. Mitochondrial membrane potential and total ATP level were also compromised in cortical neurons treated with oligomeric Aß42. However, these phenotypes were mitigated with nanomolar treatment with tanespimycin (17-AAG), an HSP90 inhibitor. These observations further implicate a link between Aß42 and ubiquitin dependent OSCP loss. Further studies will be performed to add clarity to OSCP degradation in an AD context and will be a key to understanding the precise mechanism behind OSCP loss in AD and integrating it as a potential therapeutic target.

61. Computational Prediction of Chloroplast Outer Envelope β-barrel Proteins

Emily Proctor[1], Daniel Montezano[1], Joanna S. G. Slusky[1,2]
[1]Computational Biology Program, University of Kansas, Lawrence, KS 66045
[2]Department of Molecular Biosciences, The University of Kansas, Lawrence, KS 66045

Chloroplasts are plant cell organelles responsible for photosynthesis, which requires a very different set of reactants than glucose-based metabolic systems. These reactions consequentially need different import machineries for different reactants, and the movement of these reactants across the membrane is understood to be accomplished by outer envelope β-barrel proteins. To date, we remain largely unaware of the variety of proteins that participate in outer envelope import and export. Our laboratory has recently developed a computational algorithm, named IsItABarrel, to identify bacterial outer membrane β-barrels. Chloroplast outer envelope β-barrels are likely related to bacterial β-barrels as chloroplasts most likely originated from a primitive prokaryotic cell. We are working to adapt our prokaryotic outer membrane β-barrel identifier for chloroplast outer membrane β-barrels. This will allow us to understand some sequence-based differences between bacterial and chloroplast outer membrane proteins, while also develop a database of chloroplast β-barrels, furthering our understanding of chloroplast biology. So far, we have reimplemented a database of predicted chloroplast β-barrel sequences for all organisms in the domain Eukarya. We present an overview of this database containing 4,801 unique sequences of chloroplast outer envelope proteins. With these sequences, we can test and adapt our program for accurately predicting chloroplast outer envelope β-barrels.

62. Comparing the Sugar Profile of Infant Formulas in The United States from 1988-2022

Audrey R. Rips-Goodwin[1,2], Daiil Jun[1], Tera L Fazzino[1]
[1]Department Psychology, University of Kansas, [2]Department of Chemistry, University of Kansas

Objective: Infant formulas provide an alternative source of nutrition for infants and are advertised to closely mimic the nutrient profile of human breastmilk. Lactose is the principal sugar in human milk and should be the sole sugar present in formula. The infant formula market has expanded since the 1980s as brand ownership and formula compositions have changed. This study examined how the sugar profile of infant formulas differed between 1988 and 2022. Methods: Nutrient data containing a representative sample of infant formulas were obtained from the US department of Agriculture (USDA) to represent 1988 and the Nutrition Data System for Research (NDSR) Software for 2022. Formulas that were matched across timepoints were excluded from analysis. Infant formulas were classified as lactose-containing or lactose free. Differences in overall sugar content, sugar composition, and total carbohydrates were examined using independent samples t-tests. A total of n=11 formulas represented the 1988 infant formula market and n=64 formulas represented the 2022 market. Results: In 2022, the percentage of sugars from galactose (t= -6.05, p= <.0001) and sucrose (t= -2.89, p= .005) were significantly higher in lactose-containing formulas relative to formulas in 1988. Regarding lactose-free formulas, the percentage of sugars from glucose was significantly higher (t= -2.83, p = 0.017) than products in 1988. Conclusions: The sugar profile of infant formulas has changed over time. Infants may be at risk of ingesting sucrose, glucose, and galactose when consuming US-produced infant formulas.

63. An Analysis of Presence of Antibiotic-Resistant Bacteria in Wastewater Systems: A Strategy to Assess Population Health in Kansas Counties

Audrey Rymer[1], Jonathan Ferguson[1], Garret Rymer[1], Claudia Da Silva Carvalho[1], Brooklyn Schaffer[1], Jeff Sekavec[2], and Courtney McCullough[2]
[1]Department of Biological Sciences, Fort Hays State University, [2]Colby Community College

The development and spread of antibiotic resistance and the emergence of novel human pathogens are progressively limiting the treatment and prevention of bacterial infections. This poses a threat to critical components of modern medicine. The emergence of antibiotic-resistant microorganisms that evade all water treatment technologies poses a growing threat to community health. Research has shown that water in sewer systems can serve as an early warning system for disease outbreaks (Hutinel et al., 2019). Surveillance and tracking of microorganisms in wastewater play a crucial role in this early warning system (EWS). Furthermore, analyzing sewage samples has the potential to complement clinical surveillance systems for antibiotic-resistant bacteria efficiently. Thus, it is important to establish the relationship between resistance rates in sewage waters in different parts of the United States. In this study, influent and effluent wastewater samples, along with municipal water samples, were collected from Hays and Colby, KS, for a period of ten months. Each sample underwent a viable plate count technique, bacterial isolation, and an antibiogram profile analysis. A total of 22 resistant microbe isolates were identified. Ten Gram-negative isolates appeared in treated water. An ANOVA analysis of the rate of antibiotic resistance between Hays, Colby, and the nation was performed. Results showed no significant difference in the rate of antibiotic resistance compared to nationwide (F_2, 15 = .411, p>0.05).

64. Deciphering DMXAA Binding: A Computational Exploration of Interactions with Human and Mouse STING Proteins

Emily A. Schulte and Masakatsu Watanabe
Department of Chemistry, Fort Hays State University, Hays, Kansas

The stimulator-of-interferon-genes (STING) protein plays a pivotal role in innate immunity, demonstrating its potential as a target for an aggressive antitumor response. Despite initial therapeutic promise observed in mouse models with the drug DMXAA (5,6-dimethylxanthenone-4-acetic acid) against solid tumors, it faced setbacks in human clinical trials. DMXAA exhibited selectivity by binding exclusively to murine STING (mSTING) rather than its human counterpart (hSTING). While DMXAA is no longer viable for hSTING, investigating why it failed to bind to the wild-type hSTING is crucial for developing novel agonist drugs. We employed computational modeling to unravel the intricacies of the interaction between DMXAA and STING proteins, focusing on both mouse and human STING. This analysis aimed to decipher the mechanism underpinning DMXAA's preference for mSTING over hSTING. Comprehending the binding process is pivotal for designing compounds that are efficacious against hSTING. These insights serve as a foundation for the development of DMXAA analogs engineered to bind and stimulate hSTING. Through a rational design approach, mimicking the effects of amino acid substitutions observed in the study could pave the way for the creation of potent human-active STING agonists with applications in antitumor, antiviral, and vaccine adjuvant scenarios.

65. Movement Ecology of Ornate Box Turtles (*Terrapene ornata*) across Different Life Stages

Timothy Speer, Katie Brighton, Mason Chaney, Erica Guldner, Zoe Edlund, Aubrey Gauntt, Samantha Kim, Keetan Munsell, Abigail Trautman, Patience Wagner, Brianna Wilson, Benjamin Reed
Dept of Biology, Washburn University, Topeka, KS, USA

Understanding the movement ecology of individuals/populations is critical for predicting future needs and success in any species, especially as viable habitats become scarce, and climates continue to change. The movement ecology of many species has been extensively studied (particularly in mammals); however, other taxonomic groups including many ectotherms have not been well documented. One such ectotherm is the Ornate Box Turtle (*Terrapene ornata*), which has rarely had its movement ecology examined across multiple life stages, especially at the western edge of their range. Here, we examined the micro habitat association and movement ecology of juveniles (ranging from 35g to 250g) to capture the full extent of movement patterns as they relate to the various life stages of an Ornate Box Turtle. By comparing the movement ecologies of these different groups our findings are helpful in understanding the habitat needs, space-use, and day-to-day behaviors of Ornate Box Turtles.

66. Irisin-mediated Exercise Neuroprotection

Carter Stanley, Zachary White, Keshari Sudasinghe and Stephanie Hall
Department of Biology and Department of Anatomy and Physiology, Kansas State University, Manhattan, Kansas, USA

Introduction: Irisin is a myokine, released in response to exercise. Once released, irisin has been found to function through αVβ5 integrin receptors and requires Hsp90α for binding. Upon binding, irisin mediates exercise induced neuroprotection. In humans, cold environment exercise serum irisin levels are higher than room temperature exercise. However, the interaction between cold environment exercise and irisin has never been studied in rats.
Methods: Female Fisher rats were stratified randomly into 2 groups: 5°C exercise and 20°C exercise. Both groups completed the same treadmill training protocol, 40 cm/sec, 10° incline, 20-30 minutes per day for 5 consecutive days. The brain, skeletal muscle, and blood were extracted and weighted 24 hours following the last exercise session.
Results: All animals completed the exercise protocol. There were no differences in body or tissue weights between the groups. Skeletal muscle and brain tissues will be processed for western blot protein quantification (Jess, Simple Western) of irisin, BDNF and Hsp90α. In addition, irisin will be quantified in the serum samples with Irisin ELISA protocol (Phoenix Pharmaceuticals).
Discussion: Given the short exercise protocol we expected there to not be a difference in tissue mass. However, our future biochemical analysis will identify the effect of cold on the skeletal muscle, irisin, and brain axis. These results can later be applied to the exercise-induced neuroprotective benefits of irisin in correlation with neurodegenerative brain diseases.

67. Identifying and Characterizing a Genetic Suppressor of *let-7* in *C. elegans*

Will Sydzyik[1], Jeff Medley[1], and Anna Zinovyeva[1]
[1]Division of Biology, Kansas State University, Manhattan, KS

During animal development, gene expression is coordinated to give rise to diverse cellular functions. Gene expression must be tightly regulated to ensure that genes are expressed at the right time and place. Towards this end, microRNAs (miRNAs) are key regulators of gene expression. miRNAs are small non-coding RNAs that repress their target genes, which plays a key role in animal development. In the nematode *Caenorhabditis elegans,* the *let-7* miRNA is critical for the developmental transition from a larva into an adult. The loss of function *let-7(n2853)* mutation leads to a heterochronic phenotype where animals reiterate key developmental events and fail to properly develop into adults. Here, we have identified a genetic suppressor of *let-7* that restores proper developmental timing to *let-7(n2853)* mutants. We hypothesize that the suppressor may directly regulate *let-7* or affect downstream *let-7* targets. To determine the molecular identity of the *let-7* suppressor, we performed whole genome sequencing and identified 43 homozygous variations present in the suppressor strain and have narrowed down the genetic location of the *let-7* suppressor to intervals on chromosomes II or III. We are using genetic mapping to further define the genomic location of suppressor and will validate the suppressor using CRISPR/Cas-9 genome editing. *let-7* is highly conserved in metazoans and dysregulation of *let-7* has been observed in human cancers. Therefore, identifying genes that regulate *let-7* may provide insights into how *let-7* is dysregulated in human disease.

68. Characterization of cardiomyopathic point mutations of the Ig3 domain in myopalladin
Tran, Julie; Michaelis, Alia; Arachchige, Asha R.; Beck, Moriah R.
Department of Chemistry and Biochemistry, Wichita State University, Wichita, KS

Myopalladin (MYPN) is a recently described actin-binding protein (ABP) located at both the Z and I lines of striated muscle. MYPN is believed to act as an anchor to other structural proteins such as actin, nebulin, and titin, which work together to facilitate contractile motion at the sarcomeres of muscle cells. However, its specific role in regulating the actin-cytoskeleton is largely unknown. Previous studies in the Beck lab have shown that MYPN was capable of binding and cross-linking filamentous actin directly with its Ig3 domain; thus, allowing us to narrow our domain of study to solely Ig3 to further investigate actin binding affinity. The purpose of the study is to examine point mutations in the Ig3 domain of MYPN that have been previously associated with various types of cardiomyopathies (hypertrophic, dilated, and restrictive). In this study, we explore the following properties of MYPN: the binding affinity with F-actin (via actin co-sedimentation assays) and molecular stability (via circular dichroism). Throughout the study, a total of six cardiomyopathic mutations were investigated and compared to wild-type MYPN: C1002W, R1042C, P961L, F954L, R955W, and R955Q. Thus far, the general observation is that the mutagenic constructs of MYPN bind and bundle actin less successfully than wild-type MYPN. Further studies will aim to elucidate the role of MYPN in the context of the actin-cytoskeleton and its potential link to cardiomyopathy.
Word Count: 224

69. Oxygen consumption sex differences in intermittent-fasted animals
Sabrina Veith, Stephanie Hall, Keshari Sudasinghe
Kansas State University Department of Anatomy and Physiology

Introduction- Intermittent fasting (IF) is a promising strategy to protect against cognitive impairment, such as in the case of Alzheimer's Disease (AD). Our recent studies have found that young male rats introduced to 10 weeks of alternate-day fasting had significantly reduced body weights, compared to the ad-libitum (AL) control group. However, no significant differences were observed in female body weights even though both males and females had reduced food intake. This sexual dimorphism might be due to changes in resting whole-body metabolism. The study aimed to explore whether IF impacts overall oxygen consumption and carbon dioxide production and whether these effects vary between sexes. Methods- Forty 10-week-old female and male Fisher-344 rats were randomly assigned to either a four-week IF group or AL group. Two weeks into the intervention resting oxygen consumption was measured by placing the animal in an air-tight chamber with O2 and CO2 analyzers in order to calculate oxygen consumption, carbon dioxide production, and respiratory exchange ratio (RER). Results- After two weeks of IF, females had reduced O2 consumption and CO2 production compared to the AL group (30.6 vs. 41.4 mL/min/kg, $p<.01$ and 25.1 vs. 36.1 mL/min/kg, $p<.001$, respectively), however, no significant changes were seen in the males. Conclusion- The results have confirmed that IF elicits significant sexual dimorphism in both O2 consumption and CO2 production where females exhibited declines in both while males did not change. This shift to a slower metabolism is likely the cause for maintained body mass during IF.

70. Development of a novel drug delivery platform from the Lagunamide family of natural products
Kameron R. Wildeman, Shashika Perera, Anthony Fatino, and Ryan J. Rafferty
Kansas State University, Department of Chemistry

Natural products (NPs) have served as an unparalleled source of inspiration for pharmaceutical research and development for more than 40 years. Because of this, our lab has warranted a total synthesis effort toward lagunamide C (LagC). Along with development of a synthetic route towards this macrocyclic NP, which alone possesses nanomolar IC_{50} biological activities against ovarian and lung cancer, we also envision the potential for LagC to be augmented into a novel drug delivery platform (DDP). Utilizing the fact that the polypeptide motif is identical in all lagunamide family members, and the biological activities only deviate with polyketide differentiation, we believe that the polypeptide is imperative to the cellular penetration ability of the molecule. Derivatization of this polypeptide will potentially lead to the development of a novel DDP. A linear form of the polypeptide will allow for tandem drug conjugation on both the N- and C-termini. However, if a macrocyclic structure is imperative for maintaining cellular penetration, a biologically inert tether equipped with drug docking sites will be developed and appended to the linear polypeptide to mimic the macrocyclic structure of the NP.

71. Reconstructing the evolutionary history of a Neotropical aquatic beetle species complex using phylogenomic inference methods
Liam Wrixon[1], Stephen Baca[2]
[1]Natural Sciences Department, Haskell Indian Nations University, [2]Department of Ecology and Evolutionary Biology, University of Kansas

Suphisellus sensu lato is a diverse genus of the aquatic beetle family Noteridae. Individuals attributed to the species Suphisellus nigrinus (Aube) are among the most widespread and commonly collected in the Neotropics. However, preliminary taxonomic observations suggest the species comprises multiple superficially cryptic lineages without clear delimiting morphology. To resolve the relationships within the group, we apply a phylogenomics approach with the target capture of ultraconserved elements (UCEs). Using a tailored, Noterid-specific, UCE probe-set, we capture UCE sequence data from 46 individuals from within the *nigrinus* complex with broad geographic sampling and infer the phylogeny of the group. Resulting data matrices include thousands of captured UCE loci, despite stringent filtering for missing data. We recover strongly supported phylogenetic estimates across data treatments and confirm the existence of multiple distinct lineages within the *nigrinus* complex, with relationships depicting geographic structuring. This is the highest resolution phylogenetic study within *Suphisellus* to date. Presented are data capture results and phylogenetic trees. Evolutionary implications and future directions are discussed.

72. Glycosylation Unveiled: Exploring the Structure and Function of FSH Hormone Glycoforms
Yara Abdine, Alan R. Brown, Viktor Y. Butnev, William K. White, Jeffrey V. May, and George R. Bousfield
Department of Biology, Wichita State University, Wichita, KS.

Follicle-stimulating hormone (FSH), luteinizing hormone (LH), and human chorionic gonadotropin (hCG) play a pivotal role in human reproduction by initiating the growth, differentiation, and maturation of ovarian follicles. FSH, synthesized in the anterior pituitary gland in response to GnRH from the hypothalamus at low pulse frequencies, stimulates the release of fully developed follicles, leading to the development and release of a mature oocyte capable of fertilization by sperm. In the testes, FSH supports spermatogenesis. FSH is a glycoprotein composed of alpha (shared with thyroid-stimulating hormone, hCG, and LH) and beta (exclusive to FSH) subunits.
Our research focuses on unraveling the intricate roles of FSH N-glycans, elucidated through genetic modifications involving the removal of individual glycosylation sites. Glycosylation, the attachment of sugar molecules (carbohydrates) to the protein backbone, is crucial for the structural stability and functionality of glycoproteins. Both alpha and beta subunits of FSH possess two N-linked glycosylation sites; however, the occupancy of glycans on the beta-subunit sites may vary.
The three-dimensional structures of glycoproteins are dictated by the addition of N-linked and O-linked glycans, along with the degree of glycosylation, giving rise to diverse glycoforms with distinct structural stability and functionality. Our research aims to develop a clinical method for determining the relative quantities of FSH21, FSH18, and FSH24 glycoforms using a quick serum ELISA, contributing to a deeper understanding of the glycosylation patterns in FSH and their implications in reproductive processes.
Keywords: Follicle-stimulating hormone, Glycosylation, Glycoforms, Reproductive biology, ELISA.

73. Equipment and Services of the Kansas University Nanofabrication Facility
Ryan Grigsby[1] and Susan M. Lunte[1,2,3,4]
[1]The Center for Molecular Analysis of Disease Pathways, [2]The Ralph N. Adams Institute for Bioanalytical Chemistry, [3]Department of Pharmaceutical Chemistry, [4]Department of Chemistry, University of Kansas

The Kansas University 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 accommodate broad research applications with micro- and nanofabrication needs. The core lab consists of about 1,300 ft^2 of ISO class 5, 1,700 ft^2 of ISO class 6 and 1,250 ft^2 of ISO class 7 cleanroom space, housing tools and materials for techniques including photolithography, nano-imprint lithography, plasma (dry) etching (ICP-RIE), wet etching, metal and dielectric material thin film deposition, scanning electron microscopy (VP-SEM), contact angle goniometry, ellipsometry, profilometry, wafer dicing, 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, dedicated process fume hoods and filtered lighting for photolithography.

This facility is under the direction of Dr. Susan Lunte. 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. Hourly and per-use rates apply for facility access, equipment usage, and staff labor. Consultation is free.

74. Developing bioinformatic tools for the data mining of archived organellar genomes – A productive setting for online student-led research
Michael Gruenstaeudl[1], Phongsavahn E. Mongkhovilay[2], Gregory Smith[2], and Keaton Rowley[2]
[1]Department of Biological Sciences, Fort Hays State University; [2]Department of Computer Science, Fort Hays State University

Mitochondria and plastids are multi-membrane cell organelles that sustain key metabolic processes in eukaryotic cells and possess their own bacteria-like genomes. Tens of thousands of mitochondrial and plastid genomes have so far been sequenced, primarily as by-products of whole genome, RNA, or metagenomic sequencing experiments. Their accumulation on nucleotide sequence databases represents an invaluable resource for exploring genomic patterns. Almost 130,000 records of complete mitochondrial genomes across the eukaryotic diversity have been archived on GenBank; approximately half of them constitute human mitochondrial genomes which represent hundreds of different haplotypes, including such associated with clinically relevant mitochondriopathies. Similarly, almost 44,000 complete plastid genomes of different photosynthetic eukaryotes have been archived on GenBank, including from taxa relevant to human health. By bioinformatically mining this vast collection of genomic data, fundamental aspects of organellar genome structure, sequence, and evolution can be explored. However, only a few scientific investigations have so far explored this wealth of archived genome data, primarily due to a lack of suitable bioinformatics analysis tools, as most of them do not account for the structural and genetic idiosyncrasies of organellar genomes. Here, I describe the development and application of two bioinformatics tools for the data mining of archived organellar genomes and highlight that the software development and testing was conducted together with three undergraduate students of an online degree program at Fort Hays State University. I report that undergraduate research experiences in bioinformatics are productive settings for student-led research and training in this critical field between biology and computer sciences.

75. Next Generation Sequencing at KU Genome Sequencing Core
Hackett, Jennifer L.[1,2,3], Kristen M. Cloud-Richardson[1,2,3], Erik A. Lundquist[1,2,3], Susan M. Lunte[1,4,5]
[1]Center for Molecular Analysis of Disease Pathways, [2]Genome Sequencing Core, [3]Department of Molecular Biosciences, [4]Department of Chemistry, [5]Department 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 already 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/.

76. Global Transcriptional Network Changes of Temperature on Sex Dimorphism

Jane A. Ibude[1], Edziu Franczak[2], Michael E. Ponte[2], John C. Prom[2], and E. Matthew Morris[2].
[1]Department of Dietetics and Nutrition, University of Kansas Medical Center
[2]Cell Biology and Physiology, University of Kansas Medical Center.

Physical activity has been observed to improve metabolic disease outcomes. However, it is unclear whether these improvements are due to increased energy expenditure of activity or physical action alone. Further, it is unknown whether systemic energy expenditure differences impact tissue transcriptional regulation. This research aims to provide an answer to the question: Is there a sex difference in transcriptional regulation in the liver and adipose during different energy expenditure levels? Method: RNAseq was performed on liver and subcutaneous adipose tissue from low-fat diet-fed male and female C57Bl6/J mice housed at 20 or 30 degrees Celsius. IPA analysis was used to generate a canonical pathway. Cytoscope software was used to create a transcriptional network for the most dynamic pathways. These were performed within sex comparing 30 to 20 degrees Celsius. **Results:** Tissue-specific alterations were observed in the liver and adipose tissue of both males and females. In the case of females, the liver displayed dynamic changes, whereas in males, the adipose tissue exhibited temperature-induced dynamic changes. **Conclusion:** These data show that differences in energy expenditure result in differential transcriptional pathway regulation in the liver and adipose tissues of male and female mice.

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77. The role of nuclear APC in regulating MUC2 expression and colonic inflammation

Anika James, Kristi L. Neufeld
University of Kansas, Lawrence, KS, USA

Adenomatous polyposis coli (APC) functions to maintain intestinal homeostasis. Although widely appreciated for cytoplasmic tumor suppressor functions, APC roles in other subcellular compartments, or in inflammation are less defined. To study nuclear APC functions, we previously developed a mouse model with compromised nuclear Apc import. These $Apc^{mNLS/mNLS}$ mice were more susceptible to experimentally induced colitis than their wild-type littermates and displayed lower levels of the RNA encoding mucin-2 (MUC2), the main protein of the intestinal mucus barrier. We hypothesize that nuclear APC promotes gut barrier integrity by regulating *MUC2* expression. In cultured human colon cells, we showed a positive regulation of *MUC2* RNA level by APC and have used chromatin immunoprecipitation (ChIP) to demonstrate an association of APC with *MUC2* DNA. $Apc^{mNLS/mNLS}$ mice displayed significantly thinner colonic mucus layers than wildtype mice and also harbored different bacterial species. Overall, this study provides preliminary evidence that nuclear APC regulates colonic *MUC2* expression and the mucus barrier, potentially impacting colonic inflammation and its downstream effects, such as colorectal tumorigenesis.

78. The Effects of Alcohol Use in the Risk for Cancer

Trisha Rastogi, Varun Rastogi
Blue Valley High School

Heightened alcohol consumption has proved to possess carcinogenic effects on the body, increasing the relative risk of various cancers, especially those of the oral cavity, pharynx, larynx, esophagus, breast, and liver. The cytotoxicity of alcohol is a major factor accounting for its risk; even short-term exposure of human epithelial cells to alcohol can account for cellular degradation. Enzymes in the liver facilitate the metabolism of ethanol into acetaldehyde, a genotoxic compound that causes DNA mutations when circulated throughout the body. Research evidence corroborates the production of ROS under conditions of heavy alcohol exposure, aiding in the proliferation of cancer stem cells. This project further delves into discrepancies in drinking patterns between genders and underscores the importance of risk awareness campaigns regarding the dangers of alcohol.

79. Unused

80. Unused

81. RNA Interference of TorsinA protein on *Acyrthosiphon pisum*

Allphin, Braden, Balthazor, James. Department of Chemistry, Fort Hays State University

Pea Aphids, *Acyrthosiphon pisum*, are “sap-sucking” insect pests to the legume (Fabaceae) plant family. In low population densities, they are typically harmless; however, large populations can lead to decreased growth and production. Currently, pea aphids are managed by introducing natural predators and insecticides. However, these methods are imperfect because insecticides often kill natural predators and negatively impact the environment. RNA interference presents an alternative method to the regulation of aphid populations. TorsinA is a protein that is closely related to protein folding, processing, and catabolizing misfolded proteins. It is primarily located in the endoplasmic reticulum and nuclear envelope within the cell. The introduction of excess TOR1A RNA could result in a buildup of the torsinA gene and negatively impact these protein folding processes. The buildup of torsinA could lead to cell death, shorter life expectancy, and reproductive inabilities in pea aphids. RNA from *A. pisum* was isolated and then reverse-transcribed to obtain cDNA. Using the *A. pisum* cDNA and a TOR1A primer-template, the TOR1A gene was isolated in the form of dsRNA. This dsRNA was then used in feeding studies. Using the TOR1A in feeding studies decreased the lifespan of the pea aphids compared to the control in preliminary studies and shows promise as a potential pest control method.

82. NMR structural studies of a growth-blocking peptide, *Manduca sexta* SRP-6

Blake Arria[1], Andy Su[1], Tomohiro Kimura[1,2], Xiao Iong Cao[3], Yang Wang[3], Haobo Jiang[3] and Om Prakash[1]
[1]Department of Biochemistry and Mol. Biophysics, Kansas State University, Manhattan, KS 66506
[2]Department of Chemistry, Kansas State University, Manhattan, KS 66506
[3]Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK 74078

A family of stress-responsive peptides (SRPs) have been identified in many insects including the tobacco hornworm, *Manduca sexta*. They function as cytokines to regulate immune responses. SRPs are secreted into hemolymph as inactive precursors and proteolytically activated at times of stress, such as pathogen invasion, wounding, crowdedness, and heat or cold shock. After injection into the hemocoel, synthetic *M. sexta* SRP6 efficiently suppressed the larval feeding behavior and affected growth. The growth-blocking effect was not observed after injection of SRP1 or SRP2, which induces antimicrobial peptide synthesis. According to our previous structural studies, the two SRP homologs exhibit a well-defined structure consisting of two beta strands and a beta turn in the core region. We now know that the biological functions of different SRPs are diverse and that the relative stability and secondary structural features of the core region are likely necessary for their biological activity. SRP-6 is a 26-residue peptide (NMIVVPPNCPPGQQMGSDGVCRVVFN) stabilized with a disulfide bond between residues C9 and C21. By using homo and hetero-nuclear multi-dimensional NMR spectroscopy, we are now trying to elucidate the solution structure of SRP6 and identify the activating protease(s) of proSRP1, 2, and 6.

83. Vector Construction to Generate Charcoal Rot Resistant Transgenic Soybeans

Bolick, Abby, Daniel Zurek
Pittsburg State University Department of Biology

Charcoal rot fungus is the leading cause of soybean crop death in Kansas. Despite causing millions of dollars in loss to Kansas farmers each year, there are currently no cost-effective methods to prevent this disease. The purpose of this work is to create a transgenic resistance against charcoal rot. BOZO is a B-1,4 glucanase whose function is to cleave load bearing bonds in plant cell walls during growth. Prior experiments revealed that the protein encoded by this gene inhibits fungal growth, presumably due to the cleavage of charcoal rot fungal cell walls as well. Currently, experiments are being done to clone the BOZO gene under the control of a strong inducible promoter into a plant transformation vector. One putative BOZO clone was constructed but confirmation of the presence of the gene in the vector construct has been ambiguous. This protein is also toxic to gram-negative bacteria used in the cloning process, so we are employing multiple cloning strategies to obtain a mutation-free, functional construct.

84. Role of β-adrenergic signaling in neonatal myeloid cell response to TLR Ligands

Camille Carrier[1], Sandeep Adhikari[1], Pankaj Baral[1]
[1]Division of Biology, Kansas State University

Respiratory Syncytial Virus (RSV) is a major public health issue in infants and toddlers. There are currently no FDA-approved preventive options for RSV infection. So, research into novel therapeutic potential to treat RSV infection is critical. The mouse neonatal model is critical for fully understanding the pathogenesis of RSV in infants. Identification of new therapeutic targets by manipulation of the β-adrenergic receptor in myeloid cell population might be of importance in development of the antiviral immune response in neonates during RSV infection. We hypothesize that β_2-adrenergic receptor signaling in neonatal macrophage plays a significant role in altering antiviral immunity during RSV infection. To determine the effect of β-adrenergic signaling we will isolate bone marrow from 14 days old C57BL/6J (Wild type) and β-adrenergic receptor knockout neonates and differentiate them into bone marrow-derived macrophages (BMDMs). In order to mimic RSV infection we will use viral ligand (R848) to stimulate BMDM and cotreat with β-adrenergic receptors agonists. Preliminary results suggest that during *In vitro* stimulation of wild type BMDMs with R848 in the presence of albuterol (β_2-receptor agonist) showed suppression of proinflammatory cytokine TNF-α, but not in the presence of xamoterol (β_1- receptor agonist) suggesting possible immunomodulatory role of β_2-adrenergic receptor signaling in the antiviral immune response during RSV infection.
Keywords: Albuterol, β_2-adrenergic receptor, RSV, Macrophage

85. RNA Interference of Heat Shock 70 kDa Protein 1L in *Acyrthosiphon pisum*

Griffin Davies, James Balthazor

Acyrthosiphon pisum, more commonly known as pea aphids, are a pest to many species of *Febaceae* (legumes) mainly due to the species being prone to carrying *Febaceae* diseases. Protection against *A. pisum* currently includes insecticides and natural predators, both of which bring potential negative effects to other organisms in the surrounding area. In this study, the use of RNA interference (RNAi) provides an alternative and species-specific elimination of *A. pisum.* The targeted protein in this study, Heat Shock 70 kDa Protein 1L (HSPA1L), is involved with the stabilization of existing proteins as well as mediating the folding of newly translated proteins in the cytosol and organelles. Targeting the HSPA1L gene could potentially result in an increase in improperly folded proteins in the cytosol and other organelles, which would eventually result in increased apoptosis (cell death) and death of the organism. In this study, RNA was isolated from *A. pisum* and reverse transcribed into cDNA. This cDNA was combined with HSPA1L primers to synthesize HSPA1L dsRNA that would be fed to multiple groups of *A. pisum.* In preliminary studies, this method has shown reasonable evidence of increased death rate of *A. pisum.*

86. Flavonoid-Rich Alimentary Intervention: Investigating Food Components in Cancer Prevention and Therapy (FLAVOR-CAP)

Duru Dogan, Kansas State University, Department of Political Science, Department of Statistics Hande Kucuk McGinty, Kansas State University, Department of Computer Science

Flavonoids are polyphenolic compounds found in plants and naturally occur in fruits, vegetables, teas, wines, and chocolate. Flavonoids also have known health benefits due to their anti- oxidative, anti-inflammatory, anti-mutagenic, and anti-carcinogenic properties and their ability to inhibit/modulate enzymatic systems (Panche et al., 2016). During this research we explored the relationships among different flavanoids, different foods, and different cancers using knowledge graphs and statistical methods. Our preliminary results show that the relationships among these concepts are more complex than the insights simple statistical methods can provide. In this poster, we present our approach to data collection, data cleaning, and representation in addition to the preliminary results of our statistical approaches. As we continue our research, we're enriching our knowledge graph by incorporating data on known cancer drugs and drug targets to the knowledge graph and adopting more complex analysis approaches to understand the dynamic interplay of flavanoid-food-cancer interactions.

87. Role of PARP14 in HSV-1 Viral Replication

Anna Ferkul, Hongping Hao, Srivatsan Parthasarathy, Anthony Fehr, David Davido
Department of Molecular Biosciences, University of Kansas, Lawrence, KS

Herpes simplex virus 1 (HSV-1) is a common linear double-stranded DNA virus that currently has no cure or vaccine, which is why we continue to study factors that impact viral replication. The virus manifests as oral and facial sores within humans. There are two phases of infection, lytic and latent with lytic infection occurring in epithelial cells and latent infection within sensory ganglia neurons. In lytic infection there is expression of immediate early, early, and late genes. Latent infection results in the virus being transcriptionally repressed, through genome chromatinization. For the virus to become lytic from a latent stage reactivation is required, and the initiation of lytic infection occurs from conditions of stress. My specific research focuses on poly-ADP ribose polymerases (PARPs) and their interactions with HSV-1 within the host. PARPs have many functions like repair of DNA thorough the DNA damage response, glycolysis regulation, and the restriction of viral replication. My research focuses on the specific PARP, PARP14 that has many different domains still being studied and discovered. We examined how HSV-1 replicate in the presence and absence of PARP14 both intracellularly and extracellularly. Preliminary data from our studies has shown the viral replication is increased significantly within PARP14 knockout cell lines as compared to a control cell line that expresses the PARP14. In the future, we will investigate further impacts that PARP14 has on viral gene expression, how certain inhibitors of PARP14 will affect viral replication, and the expression of type 1 interferons and interferon-stimulated genes.

88. Isolation and Identification of Microbes from Commercial Kombucha

Abigail Fette, Susan Bjerke
Washburn University, Department of Biology

Kombucha is a fermented tea that is consumed as a beverage and offers health benefits from probiotic microbes. The probiotics are fermenting microbes and usually, flavoring is added to increase the palatability of the tea. The fermenting microbes are the target of the isolation and identification experiment. The purpose of the research was to identify individual microbes that are present in kombucha because that information was not listed on the ingredients label of the bottle. Five microbes were cultured from three different brands of Kombucha, two of which were the same flavor and one of which did not have multiple flavors available. To identify the microbes, their genomic DNA was extracted using a kit. Then, the 16S rDNA from the bacteria and 28S rDNA from the yeast was analyzed using PCR. Gel electrophoresis showed DNA bands from two yeast and one bacterium indicating successful amplification. DNA from the two yeast microbes was successfully extracted and purified. The yeast DNA was sequenced and put through a BLAST search which resulted in the identification of a yeast in the Pichia genus. Future experiments aim to amplify and sequence 16s and 28s rDNA from the microbes that were not sequenced in this research. The results of this research will help other scientists gain insight into the identity of microbes commonly found in commercial kombucha.

89. CDKs-1 and -2 Enhance HSV-1 IE Gene Expression and Replication

Drew Honeycutt[1], Maxim Rodzkin[1], and David Davido[1]
[1] Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas, USA

Cyclin-dependent kinases (CDKs) are a group of cellular kinases that modulate, in part, the host cell cycle. Herpes simplex virus 1 (HSV-1) is an enveloped, large DNA virus that requires host factors for viral replication. Previous studies have shown that the broad spectrum CDK inhibitor, Roscovitine, inhibits HSV-1 lytic replication in cell culture. Furthermore, specific CDKs have been reported to interact with HSV-1 proteins, supporting a role for CDKs in the HSV-1 life cycle. Because Roscovitine inhibits several CDKs, it is unclear which specific CDKs are involved in HSV-1 productive infection. We hypothesized that distinct CDKs are required for efficient HSV-1 replication and gene expression. Our approach was to test the effects of specific inhibitors for CDK-1 (CDK1i) and -2 (CDK-2i) on virus progeny production and immediate-early (IE) gene expression in cell culture. Viral replication was examined 24 hours post-infection (hpi) in the presence and absence of CDK1i or CDK2i. Wild type HSV-1 titers were reduced by 3- to 2-fold upon CDK1i and CDK2i treatment in at least 2 cell lines. In addition, CDK-1i or -2i appreciably reduced levels of the IE proteins, ICP0 and ICP4, by 4 hpi. Future studies will examine the impact of CDK1i or CDK2i on HSV-1 IE transcript levels using reverse transcriptase-quantitative PCR (RT-qPCR). Our results suggest that CDK-1 and CDK-2 regulate HSV-1 during an early stage of lytic infection, most likely via IE transcription.

90. Stalk cell movement in Drosophila: a model to understand how migrating cells shape tissues and organs

Author(s): Daysha Isaac[1], Sally Horne-Badovinac[2], and Jocelyn A. McDonald[3]
Affiliations: [1]Department of Biology, Langston University, Langston, OK; [2]Department of Molecular Genetics and Cell Biology, The University of Chicago, Chicago, IL; [3]Division of Biology, Kansas State University, Manhattan, KS.

Many cells move dynamically during development to form complex tissues and organs. Disruption of cell migration can lead to virous birth defects, including spina bifida, microcephaly (small brain), and congenital heart defects. To better understand how cells move in development, we use a powerful genetic model organism, *Drosophila*. Many genes required for cell migration are conserved between files and humans, making this a useful system. During fly oogenesis, a string of cells called the stalk forms between egg chambers, future eggs, to form the ovariole. Multiple Ovarioles then buddle together to form the ovary. Loss of the stalk prevents egg formation, but nothing is known about the mechanisms that control stalk movement. In this study, we hypothesized that the stalk activity starts moving early in oogenesis and stops moving at mid-oogenesis. To address this question, we developed methods to image and analyze stalk movement. We report that the conserved STE20-like serine-threonine Kinase Misshapen (MSN) is required, as a knockdown of *msn* prevents stalk movement. Thus, stalk movement is an active process and occurs from early-to-mid-oogenesis. Future work will focus on how the stalk movement is a new model of tissue migration during development with implications for understanding human birth defects.

91. Antifungal Bacteria in Soil
Brandon Kennemer and Dr. Eric Gillock
Fort Hays State Biology Department

New antifungal drugs are desperately needed because new strains of pathogenic fungi are continually arising, and many are resistant to known antifungals. This issue is exacerbated by the fact that relatively few antifungals are available to clinicians and even fewer are in development. We are screening environmental soil samples to find bacteria that have antifungal properties. The bacteria are cultured from the soil by placing 1 gram of soil into 9 milliliters of distilled water. Serial dilution is used to create 1/100 and 1/1000 solutions. The dilutions are swabbed onto tryptic soy agar (TSA) plates and incubated at 30°C to grow any bacteria present in soil samples. The grown bacteria are then screened against a lawn of yeast (*Saccharomyces cerevisiae*) and examined for the production of a clear zone. The bacteria producing a clear zone are isolated in pure culture by successive streaking on TSA plates. The isolated bacteria are then submitted for partial 16S rDNA sequencing to determine a tentative identification. We have isolated a strain of *Bacillus amyloliquefaciens* that exhibits antifungal activity. We are currently in the process of further characterizing this organism. Future work will entail isolating and characterizing any antifungal compounds it produces.

92. Mechanisms underlying the development of plastic cellular differentiation in the volvocine green algae
Lidia S. Lopez Vazquez[1], Dinah R. Davison[1], Bradley J.S.C. Olson[1]
[1]Division of Biology, Kansas State University, Manhattan, KS

How new cell types arise is a central question in the study of cellular evolution. While genetic modifications can lead to the evolution of novel cell types in multicellular species, it's unclear whether differentiation be ancestrally plastic and then stabilized by genetic assimilation. To address this possibility, we use the volvocine green algae as a model system. Previous research has demonstrated that *Eudorina* species, initially characterized as undifferentiated, develop plastic somatic cells following cold shock. We focus on identifying the mechanisms underlying this response. We will use transcriptomics to investigate the genetic mechanisms underlying plastic somatic cell development in *Eudorina* sp. NIES 3984, a genome-sequenced species. We will extract RNA after cold shock and then engage in RNA sequencing. This approach will allow us to examine gene expression changes following cold shock and during development. By collecting and sequencing cells every four hours for two days, we will characterize the gene expression alterations tied to plastic somatic cell development. Combining phenotypic, developmental data, and single-cell transcriptomics, we aim to understand how gene interactions with environmental conditions lead to a new trait's emergence.

93. Cadmium exposure induces fibroblast-to-myofibroblast transition and pulmonary fibrosis
Kushala Madduru,[1] Kylie Cushing,[1] Jackson Hagen, [2] Chandrashekhar Prasad,[3] Santhosh Kumar Duraisamy, [3] and Isaac Kirubakaran Sundar[3]
[1]University of Missouri – Kansas City, Kansas City, KS, USA
[2]Pomona College in Claremont, Claremont, CA, USA
[3]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, University of Kansas Medical Center, Kansas City, KS, USA

Cadmium (Cd) is a toxic heavy metal associated with adverse health effects and is widely distributed in the environment, and natural air due to emission from volcanoes, forest fires, coal-fired plants, coke factories, smelting industries, etc. Humans are exposed to Cd ~30 µg/day from dietary intake and cigarette smokers are predisposed to higher Cd exposure (~2-4 µg/pack of cigarettes). Cd exposure in human lung fibroblasts (HLF) induces fibroblast-to-myofibroblast transition (FMT) and low-dose Cd exposure causes peri-bronchial fibrosis. We hypothesize that cadmium exposure affects circadian clock function associated with augments profibrotic phenotypes in human lung fibroblasts and in mouse models. WI-38 cells were treated with $CdCl_2$ (5 µM) for 3 hours followed by treatment with REV-ERBα agonist (GSK4112: 20 µM) for 72 hours. Protein abundance of the circadian clock and profibrotic markers were measured using Western blotting and immunocytochemistry. C57BL/6 (~4-6 months) mice were administered with PBS or low-dose (0.016 mg/kg body weight) or high-dose (0.5 mg/kg body weight) $CdCl_2$ via oropharyngeal aspiration. All the parameters such as protein abundance of circadian clock and profibrotic markers were analyzed at day 14 post-injury. GSK4112 treatment reduced the $CdCl_2$-induced COL1A1 protein expression in HLF. $CdCl_2$-exposed mice show increased lung inflammation, mucus production, and collagen deposition. Additionally, we found that $CdCl_2$ exposure dose-dependently altered the circadian clock proteins and augmented profibrotic markers in the lungs. GSK4112 treatment reduced the Cd-induced profibrotic response in WI-38 cells, and Cd exposure in mice altered the circadian clock and pro-fibrotic markers. ***Funding: K-INBRE P20 GM103418 & R01 HL142543.***

94. Screening Environmental Soil Samples for Antibiotic Production
Paige Mattick, Eric Gillock, Fort Hays State University Department of Biological Sciences

Antibiotic resistance is a detrimental worldwide challenge, producing bacterial infections that are progressively more difficult to treat and cure. To attempt to help alleviate this issue, we screened soil samples for the presence of antibiotic-producing microorganisms. Soil samples were collected and diluted to 1:100 and 1:1000 ratios of soil and distilled water. These soil mixtures were then streaked onto tryptic soy agar (TSA) plates and incubated at 30℃ until colonies developed. These colonies were then selected and plated on a lawn of *Serratia marcescens,* which was utilized as the target organism. *Serratia marcescens* was selected due to its known resistance to many widely prescribed antibiotics such as penicillin and ampicillin. Colonies that produced clear zones on the *Serratia marcescens* lawns, indicating antibiotic production, were then isolated into pure cultures by sequential rounds of streaking. Isolated organisms were submitted for partial 16S rDNA sequencing and preliminary identification. Using this approach, we isolated three bacterial strains that have antibiotic activity. The results of sequencing verified that our organisms were *Bacillus mojavensis* and two individual strains of *Bacillus amyloliquefaciens* with 0.09%, 0.47%, and 0.28% genetic differences from known partial 16S rDNA sequences in the database, respectively. In the future, further characterization of each of these organisms and isolation of each compound of interest will be executed to further investigate each organism's antibacterial properties.

95. Downregulation of the nutrient-sensitive post-translational modification, O-GlcNAcylation, attenuates Autosomal Dominant Polycystic Kidney Disease

Nikhitha Muthineni[1, 4], Matthew A. Kavanaugh[1, 4], Dona G. Isai[1,4], Vincent Lam[1, 4], Rayyan Abid[1, 4], Maria T. Villar[2], Antonio Artigues[2], Stephen C. Parnell[2, 4], Chad Slawson[2, 4], Darren P. Wallace[3, 4], Pamela V. Tran[1, 4]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Internal Medicine, University of Kansas Medical Center, Kansas City, KS
[4]The Jared Grantham Kidney Institute, University of Kansas Medical Center, Kansas City, KS

Autosomal dominant polycystic kidney disease (ADPKD) is a leading cause of renal failure and causes the progressive growth of fluid-filled cysts in the kidney. A major component of ADPKD pathogenesis is altered cell metabolism, although drivers of these alterations are not understood. Addition of O-linked β-N-acetylglucosamine (O-GlcNAc) onto protein substrates by O-GlcNAc transferase (OGT) is a nutrient-sensitive post-translational modification that integrates multiple metabolic signals. We have reported that protein O-GlcNAcylation is increased in kidneys of ADPKD patients and mouse models, particularly in cyst-lining epithelia. Here we show that *Ogt* deletion in *Pkd1* conditional knockout (cko) mice protects kidney function; reduces renal cystogenesis, kidney weight:body weight ratios, cilia lengths, inflammation and fibrosis; and increases phosphorylation/activation of the energy sensor, AMPK. Additionally, while *Pkd1* cko mice die between postnatal day (P)14-P20, *Pkd1;Ogt* double ko mice thrive beyond 9 months of age. Immunoprecipitation of P14 mouse kidney lysates revealed AMPKα1 is hyper-O-GlcNAcylated in *Pkd1* cko kidneys, and mass spectrometry identified Serine184 of AMPKα1 as an O-GlcNAcylation site. This lies within the activation loop of AMPKα1 adjacent to Threonine183, a phosphorylation site critical for enzymatic activity. Because phosphorylation and O-GlcNAcylation are often antagonistic, we propose that O-GlcNAcylation at Ser184 may impede phosphorylation at Thr183 and activation of AMPK. Finally, OGT pharmacological inhibition reduced *in vitro* cyst formation by cultured ADPKD patient-derived cells, indicating clinical significance. We conclude that hyper-O-GlcNAcylation is a driver of ADPKD progression (in part through AMPK inactivation) and that suppression of OGT limits cystogenesis and disease-related processes, suggesting therapeutic potential.

96. Micro Fabry-Perot Cavity for Characterizations of Nanoscale Particles in Liquid Phase

Girish Paudyal and Hoang Nguyen
Department of Chemistry, Washburn University, Topeka, KS 66621, USA

A micro Fabry-Perot cavity is an optical device capable of amplifying optical signal from nanoparticles for physical and chemical characterizations. This optical device consists of two high-reflectivity mirrors positioned micrometers apart. The resonance condition of the cavity is finely tuned by fixing one mirror and moving the other one precisely using a shear piezo. The on-resonant optical signal emitted or scattered by the nanoscale particles inside the cavity will be enhanced and then detected by a spectrometer to quantify their physical properties and identify their chemical compositions. This quantitative method is non-destructive and thus can be used to study a variety of nanoscale structures, from quantum dots to molecular assemblies. We are currently working on the introduction of UV light to this cavity to excite quantum dots to collect their emission spectrum. We are expecting a 100-time enhancement for infrared emission and a few-tens-time enhancement for visible light inside the microcavity. Additionally, we are working on revising our optical setup to accommodate liquid-phase samples.

97. Understanding Mechanisms of Tumor Resistance in Murine Cell Lines

Payne, Carlie and Peter A.Chung. Department of Biology, Pittsburg State University

A fibroblast is a type of cell that contributes to the formation of connective tissue, a fibrous cellular material that supports and connects other tissues or organs in the body. This cell type secretes collagen proteins to help keep up the structural framework of tissues. Cancer-associated ones are critical in tumor growth; they create a tumor-promoting environment. The murine, or mouse model, is utilized to study the role of various genetic factors within the tumor growth and sensitivities. Our project uses mouse fibroblasts transformed with SV40 virus, a long-standing technique used to create murine oncogenic cell lines. Two resulting phenotypes were created: the F5m cell line and the F5b cell line. F5m is resistant to macrophage-mediated cytotoxicity while F5b is sensitive to macrophage-mediated cytotoxicity. Utilizing previous generated data with various proposed gene targets, our project's goal is to use protein analysis to follow up on transcript expression data, with therapeutic targets in mind.

98. Phosphorylation State of the Intermediate Protein Partner RsbV1 Impacts Growth and Progeny Production of *Chlamydia trachomatis*

Diego Prieto, Alexandra P. Cutter, and P. Scott Hefty
Department of Molecular Biosciences, University of Kansas

Chlamydia trachomatis is the most prevalent sexually transmitted bacterial infection worldwide, representing a major public health concern. This obligate intracellular bacterium has a phylum-defining biphasic developmental cycle whose regulatory signals and mechanisms are still poorly understood. One protein system that has been shown to govern the cycle's regulation is the Rsb system. This system works based on the phosphorylation state of an intermediate, $RsbV_1$, which determines the activity of a periplasmic sensor phosphatase and a terminal protein partner kinase, RsbU and RsbW respectively. Although genetic disruption of RsbU has been shown to cause a dramatic decrease in progeny production, disruption of RsbW does not, making the Rsb system's role in *C. trachomatis*' development unclear. We examined the importance of $RsbV_1$'s phosphorylation state by studying the effect of its overexpression on progeny production and growth with a tetracycline inducible system. We also examined the overexpression of a phosphodeficient mutant for $RsbV_1$, $RsbV_1$S56A, and used immunofluorescent microscopy to determine effects on morphology and size. Induction between 16 and 24 hours post infection led to a significant decrease in progeny production with overexpression of both wildtype and phosphodeficient $RsbV_1$. Furthermore, we found that the expression of $RsbV_1$S56A led to a significant reduction in inclusion size. Future studies with different induction periods will be performed to clarify the role of $RsbV_1$'s phosphorylation state in the system, which could provide a better insight on *C. trachomatis*' development and potential ways to address its public health impact.

99. Role of asparagine synthetase and other transcription factor targets in epidermal morphogenesis
Jillian K. Rockley, Bibek Subedi, Bradley J.S.C. Olson, and Kathrin Schrick
Division of Biology, Kansas State University

Asparagine synthetase is an enzyme responsible for generating asparagine and glutamine from aspartate and glutamate. Expression of this enzyme is tightly controlled in both plant and animal tissues. Mutations in the human *ASNS* gene lead to asparagine synthetase deficiency (ASD) and neurological pathologies. Additional evidence supports a regulatory function for *ASNS* in several cancers. In the plant model, *Arabidopsis thaliana*, asparagine synthetase controls nitrogen distribution throughout development. An RNA-sequencing experiment in our laboratory led to the recent discovery that *ASPARAGINE SYNTHETASE1/DARK INDUCIBILE6* (*ASN1/DIN6*, At3g47340) is upregulated in leaves displaying an abnormal “curly leaf” phenotype due to overexpression of the homeodomain leucine-zipper (HD-Zip) transcription factor GLABRA2 (GL2). Other HD-Zip transcription factors are involved in cellular events ranging from stress responses to regulation of morphogenesis. A previous DNA Affinity Purification Sequencing (DAP-seq) experiment was performed with PROTODERMAL FACTOR2 (PDF2), an HD-Zip factor needed for shoot epidermal cell differentiation. The data showed DNA binding peaks in the promoter region of *ASN1,* suggesting that *ASN1* is a transcriptional target of PDF2. To address whether *ASN1* expression is up- or down-regulated by PDF2, we performed RNA extractions from *pdf2-4, gl2-5*, and wild type leaf tissue for use in reverse transcription-quantitative PCR (RT-qPCR) analysis. Future work will include the investigation of light regulation of *ASN1* and its role in PDF2-mediated growth control related to epidermal morphogenesis. Understanding the function of asparagine synthetase and other light-regulated genes in plants may facilitate further understanding of the importance of similar genes in human cells.

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100. Using DNA repair inhibitors to increase the efficacy of chemotherapy in cervical cancer
Sandoval, Allison,[1] Wendel, Sebastian,[1] Wallace, Nicholas,[1] Division of Biology, Kansas State University

Cervical cancer (CaCx) caused by HPV takes the life of someone every 90 seconds, making it the fourth most common cancer among women globally. Because these cancers occur in working aged women, there are additional economic hardships compared to other cancers that occur more commonly in older people. Effective treatment options are limited. The standard chemotherapy for CaCx is Cisplatin, which damages DNA in all cells. Cisplatin is, in part, effective because CaCx has a reduced capacity to repair DNA damage in comparison to untransformed cells. However, there are two frequently arising issues: (i) development of resistance and (ii) dose limiting side effects. Side effects can consist of kidney issues and can cause heartbeat irregularity. Additionally, there is no consensus second line treatment for CaCx. Thus, there is a critical need to develop alternative approaches to CaCx chemotherapy. We have shown that CaCx rely on a microhomology-mediated end joining or MMEJ pathway for DNA-repair. I hypothesize that CaCx cells will be sensitive to polymerase-theta inhibitors with and without other damage. I have begun testing this hypothesis by treating cells with the small molecule inhibitor Novobiocin (NVB) that targets polymerase-theta, an essential step in MMEJ. NVB is an FDA-approved drug with a well-defined and favorable safety-profile. We will test this hypothesis *in vitro systems* with MTT assays and *in vivo* systems with CaCx xenograft models. These studies will allow us to define the extent to which NVB sensitizes CaCx cells to other chemotherapy agents like cisplatin.

101. Understanding the mechanisms of *Clostridioides difficile* resistance to Cycloserine
Madelyn Seiler, Victoria Droge and Revathi Govind, Division of Biology, Kansas State University

Clostridium difficile is a rod shaped, Gram positive, spore forming, anaerobic bacteria most commonly associated with hospital acquired diarrhea and pseudomembranous colitis. Patients staying in the hospital receiving an antibiotic are at risk for acquiring *C. difficile* infection because antibiotics deplete natural microbiome. This allows *C. difficile* spores present in hospital settings to germinate in the colon. Once *C. difficile* spores have germinated, they cause damage by secreting exotoxins produced by TcdA and TcdB proteins. TcdR is a regulator of tox genes that controls the transcription of tcdA and tcdB genes. This project is investigating a tcdR mutant in *C. difficile* strain R20291, a highly studied strain of *C. difficile*. In previous experiments, it was observed that tcdR mutant is unable to grow in the presence of TY+Di-Cycloserine suggesting sensitivity to the antibiotic. The spores are being prepped and plated on TY+Di-Cycloserine plates as well as normal TY plates to test germination rate and to positively select for the suppressor mutants that would allow tcdR mutant spores to germinate and grow even in the presence of Di-cycloserine.

102. Assessment of the Impact and Outcomes of the K-INBRE Program on Undergraduate Research Experiences
Michael Shi[1], Sarah E. Velasquez, PhD[2]
[1]Department of Computer Science, Cornell University, [2]Department of Anesthesiology, University of Kansas Medical Center

The purpose of this quality improvement (QI) study within the Kansas IDeA Network of Biomedical Research Excellence (K-INBRE) was to assess participants’ satisfaction with the program research experience, including aspects such as funding, as well as determine the program’s impact on education and career outcomes. Two surveys were developed using RedCap and distributed via email. The first survey concerning the overall satisfaction and impact of the program was sent out to participants between 2001 and 2023. The second survey was concerned with collecting current student feedback on funding. A focus group supplemented the wage survey, allowing for the collection of valuable opinions and perspectives. A comprehensive analysis was then conducted accounting for both quantitative and qualitative data. The study garnered a strong response: 60 of 138 current students (46.5%) participated in the wage survey, while 22% of the 1110 contacted past students responded to the impact survey. Most (83.3%) found compensation fair, yet many had concerns including pay relative to experience and suggestions for alternative compensation like tuition aid or equipment. Feedback from the impact survey was overwhelmingly positive: 98% rated the program "good" or "excellent," citing its strong impact on student development (97%) and its role in shaping career choices (82%). Using these insights, we will formulate well-informed recommendations aimed at bettering the program.

103. Determination of Psychoactive Compounds in CBD Oils via RP-HPLC-UV/Vis Analysis
Steigner, Sofia, Dr. Qiyang Zhang, Department of Biological Sciences, Emporia State University

Cannabinoids represent a diverse array of psychoactive substances, with more than a hundred different compounds currently recognized. Concerns surrounding the accuracy of content labeling in cannabinoid products are increasing, particularly regarding unregulated CBD oils sold online and in stores, which the FDA has officially announced are not fully evaluated or approved. Cannabinoid product labeling may not correctly reflect the real contents of the product; for example, while many CBD oil products only list THC in their labels, they may harbor undisclosed cannabinoid compounds, posing potential risks to consumers. Furthermore, certain inactive cannabinoids (THC-A), can easily convert to the psychoactive form (THC-H) under elevated temperatures.
Prior studies have demonstrated the feasibility of separating three or four compounds in cannabinoid products using HPLC (high performance liquid chromatography). Our research analyzes the concentration of both THC-H and THC-A using HPLC with a new quick, easy, cheap, effective, rugged, and safe (QuEChERS) approach. Employing RP-HPLC-UV/VIS (reverse phase high-performance liquid chromatography coupled with ultraviolet/visible light detector), we established calibration curves for THC-A and THC-H using commercially available standards. Utilizing this method, four cannabinoid product samples, were analyzed, the concentrations (in mg/mL) of THC-A and THC-H in the samples were determined. Although all samples claimed to contain neither THC-A nor THC-H, two samples contained significant amounts of THC-A and one exhibited a significant amount of THC-H.

We acknowledge and thank Emporia State University and the K-INBRE for their invaluable support in conducting this research.

104. Regional volume changes during adolescence in the valproic acid model parallels human findings
Hunter Strating[1], Cole King[1], Macy Payne[2], Ivina Mali[2], Stefan H Bossmann[2], Bethany Plakke[1]
[1]Department of Psychological Sciences, Kansas State University
[2]Department of Chemistry, Kansas State University

Regional volume changes in the hippocampus, cerebellum, and frontal areas are commonly observed in adolescents with autism spectrum disorder (ASD). The valproic acid (VPA) model was used to model ASD in rodents. Previous research has found cerebellar pathology in adult VPA animals. The current work examined volumetric dysregulation in the cerebellum, hippocampus, and frontal regions throughout adolescence. Pregnant Long-Evans dams were given intraperitoneal injections of 600 mg/kg sodium valproate (VPA) or vehicle control at gestational day 12.5. Rats were reared and aged to postnatal day (P) 28 or P40, which correspond to early and middle adolescence, respectively. At P28 or P40, animals were euthanized, and heads were fixed in PFA. MRI brain volumes were segmented with ITK snap for anterior cingulate cortex (ACC), posterior cingulate cortex (PCC), hippocampus and cerebellum by blind-to-condition researchers. Structure volumes were normalized to total brain volume. Regions were analyzed with ANOVAs (condition, age) and separated by sex for areas based on past research. The hippocampus was not enlarged in VPA animals relative to controls at P28, but significant enlargement was observed bilaterally in VPA animals at P40. No significant volumetric changes were observed in the cerebellum. Within frontal regions, VPA female animals had enlarged ACC at P40 relative to controls. These results show that the VPA model displays similar volumetric changes that are also observed in adolescent humans with ASD.

105. Changing Macrophage Differentiation by Treatment of B2-GPI Derived Peptides
Mia Thompson[1], Jen Rowe[1], Sherry Fleming[1,2]
[1]Division of Biology, [2]Johnson Cancer Research Center, Kansas State University, Manhattan, Kansas

Skin cancer is one of the most common types of cancer. Among these, melanoma is known to be the most dangerous due to its ability to rapidly metastasize. Previous studies have shown that peptides derived from the serum protein, Beta2 Glycoprotein I (B2-GPI), diminished tumor growth in male but not female mice. The peptides may be linked to macrophage polarization. M1 macrophages are known to be hyperactive and tumoricidal while M2 macrophages are quiescent. It is hypothesized that male mice treated with B2-GPI derived peptide will have increased differentiation of macrophages toward the M1 phenotype. However, peptide treated female mice are hypothesized to maintain the M2 macrophage phenotype. The goal of this project is to study this differentiation by treating mice with B2-GPI derived peptides or a control treatment. The cDNA made from tumors of these various groups of mice were used for Real Time Polymerase Chain Reaction (RT-PCR). Through RT-PCR, specific genes that have a known association to either M1 or M2 macrophage phenotypes were tested. Some genes include iNOS, IL-12 for the M1 macrophage phenotype and Arginase 1, STAT3, YM1, and PD-L1 for the M2 macrophage phenotype. Initial data suggests an increasing trend of M1 macrophage associated genes in treated male mice expression compared to its control group. It also shows treated female mice expressing higher levels of M2 macrophage associated genes compared to its control group. These studies will increase our understanding of the different mechanisms in which peptides and sex affect macrophage differentiation in tumors.

106. Design of Peptide Amphiphiles for Selective Aggregation in Gram-Positive Bacterial Membranes
Walker, Greyson, Jeffrey Comer
Department of Anatomy and Physiology, Kansas State University

Antibiotic-resistant bacteria are a growing threat to human and veterinary health, increasing the need for novel antibiotic treatments. Taking inspiration from naturally occurring antimicrobial peptides that selectively disrupt bacterial membranes, synthetic peptide derivatives hold great promise for a new generation of antimicrobials. For the potential use as a treatment, it is a requirement that these peptides specifically disrupt the membranes of bacteria and not the host's cells. Molecular dynamics simulations offer insight into the atomic scale interactions and thermodynamics that drive aggregation and insertion in membrane disruption. We generated multi-component models of gram-positive *Staphylococcus aureus* and mammalian membranes and analyzed the atomic-scale differences in their structures. With this knowledge, we designed lipopeptides, consisting of straight-chain and cyclic carbon tails, with the aim of discovering what structural features are associated with selective insertion and aggregation in *S. aureus* membranes. We found that lipopeptides with cyclic hydrophobic tails show selective aggregation in *S. aureus* membranes over mammalian membranes. Using free-energy calculation techniques, we discovered that polylysine peptides conjugated with civetone (a 17-carbon macrocyclic ketone) exhibited much more favorable insertion and aggregation in *S. aureus* membranes than in mammalian membranes. Moreover, these lipopeptides were shown to have greater *S. aureus* selectivity than similar lipopeptides with more conventional straight-chain lipid groups.

107. The Effects of Circuit Resistance Training on Psychosocial and Physiological Outcomes in Underactive Latinos
Jack Watson[1] and Erin M. Blocker[1], [1]Department of Health, Physical Education & Recreation, Emporia State University

The Latino population in the United States has higher rates of numerous chronic diseases compared to their non-Latino counterparts. Research has consistently shown that exercise is an effective strategy to reduce the risk for chronic diseases, including neurodegenerative diseases. This randomized controlled trial investigated the physical and psychological impact of an 8-week circuit resistance training program among underactive Latino adults. Participants, randomly assigned to an intervention or control group, underwent assessments for cholesterol levels, triglycerides, glucose, blood pressure, weight, and BMI, along with psychosocial measures including the Perceived Stress Scale (PSS), Barriers to Being Active Quiz (BBAQ), and Self-Efficacy Exercise Scale (SEES). Following the 8-week exercise intervention, significant improvements were found in psychosocial outcomes, evidenced by reduced perceived stress ($t(16) = 1.965$, $p = 0.033$), diminished barriers to physical activity ($t(12.38) = 2.777$, $p = 0.008$), and heightened exercise self-efficacy ($t(16) = -2.932$, $p = 0.005$). While no significant changes were observed in physiological biomarkers, factors like the program's duration, sample size and individual metabolic responses may have influenced these outcomes. Importantly, the enhanced exercise attitudes and self-efficacy lay the groundwork for sustained physical activity, which could lead to long-term improvements in physiological health. This study underscores the value of integrating such training programs to foster positive behavioral changes essential for ongoing health benefits.

Keywords: Circuit Resistance Training, Psychosocial Outcomes, Physiological Measures, Underactive Latinos, Physical Activity, Mental Health, Exercise Self-Efficacy.

108. Isolation and Characterization of Fungi Tolerant to High Concentrations of Ammonium Sulfate
Wolf, Jaylynn, Schneegurt, Mark. Department of Biological Sciences, Wichita State University

Abstract: The exploration of celestial bodies in the solar system has become a significant part of history, as technology expands and advances. Policies and procedures are in place to prevent the contamination of planets and moons by microorganisms from Earth. As the search for life continues, it is essential to study even the conditions that do not meet the typical criteria for life. Ammonia is frequently observed throughout the solar system in oceans of icy moons. Ammonia is well known as a disinfectant, suggesting that microbial tolerance might be limited. To study the tolerance of microbes to high concentrations of ammonia, enrichment cultures at 1 M ammonium sulfate were inoculated with Kansas soils to isolate tolerant microbes. Only fungi were observed and 8 were isolated, including one yeast. Growth curves of triplicate yeast cultures at 0, 1, and 2 M ammonium sulfate were measured by turbidity at 600 nm. The yeast isolate grew at 0, 1, and 2 M ammonium sulfate, reaching stationary phase at 3, 4, and 5 d, respectively. As expected, increasing ammonium concentrations delayed growth, but the yeast was highly tolerant. The goal is to test tolerance at higher ammonium concentrations and examine the tolerance of the molds isolated. These results are applicable for both planetary protection and the detection of life off Earth. It crucial to know that terrestrial microbes could potentially survive the harsh conditions of other worlds and informs our understanding of the nature of native life should it exist.

109. Hydrogen Bonds Impact on Function of PhoU Homologs and Dimers
Nikolas Yackovich[1], Sakib Mahmud[1], Ryan Rodriguez[1], Katelyn Schmalz[1], Stewart Gardner[1]
[1]School of Sciences and Mathematics, Emporia State University, KS.

Staphylococcus aureus is a Gram-positive bacterium that causes a variety of diseases, including skin infections, bacteremia, endocarditis, pneumonia, and food poisoning. S. aureus infection is a significant public health concern because of its diverse virulence factors, antibiotic resistance, and biofilm formation. The PhoU protein in S. aureus plays an important role in the regulation of virulence and pathogenesis. Genome analysis revealed that S. aureus has two PhoU homologs, PhoU1 and PhoU2, located in the pst operon and pit operon, respectively. PhoU1 and PhoU2 have some similar functions but are not redundant. The function and quaternary structure of PhoUs is different among bacterial species. In different bacterial species PhoU monomer, dimer, trimer, and even hexamer structures have been reported. In our study, we found that both PhoU1 and PhoU2 interact with themselves to form homodimers. Moreover, size exclusion chromatography analysis confirmed this claim by eluting at the predicted dimer size. The computer-predicted model of homodimer quaternary structures also showed several hydrogen bonds between monomers. We hypothesized that this PhoU dimerization is important for successful signal transduction in S. aureus. To validate this point, we plan to perform site-specific mutations and replace those amino acids involved in hydrogen bonding without changing the overall structure of PhoUs. The aberration from their regular function will confirm the role of the PhoUs dimer. These results may help explain the molecular function of PhoU homologs and the importance of dimerization.

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110. The bidirectional impact of arginine-vasopressin receptor 1a (*Avpr1a*/AVPR1A) and the gut microbiome on visceral hypersensitivity (VH).
Leena Kader[1], Adam Willits[1], Julie A. Christianson[2], Kyle Baumbauer[2], Jun-Ho La[3], Bin Feng[3], and Gerald F. Gebhart[3,4,5], Erin E. Young[1,2]
[1]Department of Anesthesiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Integrative Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Anesthesiology, University of Pittsburgh School of Medicine, Pittsburgh, PA
[4]Department of Medicine (GI), University of Pittsburgh School of Medicine, Pittsburgh, PA
[5]Department of Psychiatry, University of Pittsburgh School of Medicine, Pittsburgh, PA

Visceral hypersensitivity (VH) is an understudied peripheral factor that drives chronic abdominal pain in disorders of gut-brain interactions (DGBI) where persistent and/or recurrent abdominal pain is a primary symptom regardless of any alterations in bowel habits. The complexity of VH is in part influenced by genetic factors and individual differences in gut microbiome composition, yet specific mechanisms that generate VH are incompletely understood. Correspondingly, current treatments primarily focus on symptom management rather than targeting pathophysiological mechanisms responsible for generating VH. We have begun to examine the role of genetic susceptibility and microbiome response dynamics in VH development using intracolonic zymosan (ZYM), which is a preclinical model of post-inflammatory irritable bowel syndrome (IBS). Preliminary data reveals differential susceptibility between ZYM-induced VH in two closely related C57BL/6 sub strains; one from Taconic Biosciences (C57BL/6NTac) and the other from Jackson Laboratory (C57BL/6J). Using genomic comparisons, we have identified a VH candidate gene that encodes the arginine-vasopressin receptor 1A (*Avpr1a*/AVPR1A) protein. We have subsequently observed dynamic strain differences in the location and composition of the gut microbiome in response to ZYM corresponding to VH susceptibility. Further, we've identified colon-specific alterations in enteric neuron response properties that covary with *Avpr1a* expression and the microbiota alterations corresponding to VH development. Through manipulation of the expression of *Avpr1a* and of the microbiome in the colon, we can develop tissue-specific pharmacological interventions that decrease the reliance of opioids and better manage chronic abdominal pain by targeting the mechanisms underlying VH.

111. Friend or Foe? Determining how social interactions improve or impair learning behaviors in a platform-mediated active avoidance task in rats.

Authors: Cassandra Kramer, Shannon Ruble, Ivy Auletti, Maria M. Diehl
Affiliation: Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA

Social species rely on interactions to gain information about their environment and potential threats. Further, social interactions between conspecifics have been known to reduce fear responses to adverse situations. However, social deficits may accompany excessive avoidance in individuals experiencing PTSD or other anxiety disorders, leading to a disconnect in imperative information for an individual's wellbeing that could be gained from a partner. To study how social behavior influences aversive learning, we used an active avoidance task in which rats learn to avoid a tone-signaled foot-shock by stepping onto a safe platform at the cost of a sucrose reward. During PMA under social conditions, rats are separated by a perforated plexiglass barrier, allowing individual access to the platform and reward while visual, auditory, and olfactory cues can be obtained from the partner. We have previously reported that food-seeking behaviors decrease while freezing increases in rats trained in PMA under social vs. solitary conditions, indicating that the presence of a partner influences the behaviors a rat engages in during PMA. The current project seeks to understand which social interactions may facilitate or hinder the acquisition of social partner PMA. We will measure the time a rat spends near the barrier, distance between partners, and head orientation throughout the session to determine if these behaviors correlate with increased avoidance, freezing, or lever pressing. This research will lead to insights on how social behaviors influence how we learn about danger in our environment.

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112. PhoU homologs in *Staphylococcus aureus* form Homodimers

Sakib Mahmud[1], Nikolas Yackovich[1], Ryan Rodriguez[1], Katelyn Schmalz[1], Stewart Gardner[1]
[1]School of Sciences and Mathematics, Emporia State University, KS.

Staphylococcus aureus is a Gram-positive bacterium, a common human colonizer and pathogen. Infections range from skin and soft tissue to invasive ones such as pneumonia, osteomyelitis, and endocarditis. The broad spectrum of virulence factors, persister formation, and antibiotic resistance of this bacteria make the infection difficult to deal with and that's why it is our great concern now. In *S. aureus*, PhoU protein plays a role in the regulation of virulence factors, persister formation, and phosphate metabolism. Genome analysis revealed that *S. aureus* has two PhoU homologs, PhoU1 and PhoU2, located in the *pst* operon and *pit* operon, respectively. PhoU1 and PhoU2 have some overlapping functions but are not redundant. The PhoU protein from *Escherichia coli* interacts with PhoR, PstB, and metals to form a phosphate-signaling complex at the membrane. However, the number of PhoU homologs, functions, and quaternary structure of PhoU is species-specific. Among different bacterial species, PhoU monomer, dimer, trimer, and even hexamer structures have been reported. We hypothesized that the two PhoU homologs in *S. aureus* may function differently than in *E. coli*. In our study, we found that in *S. aureus* both PhoU1 and PhoU2 interact with themselves and form homodimers. Moreover, using size exclusion chromatography analysis, we found that PhoU1 and PhoU2 elute at the predicted dimer sizes. To further verify these findings and to identify which other proteins PhoUs bind with inside *S. aureus*, we plan to perform co-elution affinity chromatography followed by mass spectrometry to identify any interacting proteins. These results may help explain the molecular function of PhoU homologs in this important human pathogen.

113. Maternal heterozygosity in mice for the ciliary *Thm1* gene protects against cleft palate

Brittany M. Hufft-Martinez[1,2], Jeremy P. Goering[1], Sarah C. Wilson[1], An Tran[1], Dana N. Thalman[1], Michaella Rekowski,[3] Michael Washburn[3,4], Pamela V. Tran[1,5], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center,
[2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, [3]Department of Cancer Biology, University of Kansas Medical Center, [4]Kansas University Cancer Center,[5]Jared Grantham Kidney Institute, University of Kansas Medical Center

Craniofacial anomalies accompany a third of all birth defects, with cleft palate (CP) alone affecting 1/1200 newborns, either as an isolated phenotype or as part of a syndrome. We have found that autosomal dominant mutations in the cytoskeletal gene, *SPECC1L*, result in syndromic CP. In mice, *Specc1l*$^{\Delta CCD2/+}$ heterozygotes present with 18% CP. When combined with loss of one allele of a ciliary gene, *Thm1*$^{+/-}$, CP incidence in double-heterozygous embryos increased to 34%, indicating a novel genetic interaction between cytoskeletal *Specc1l* and ciliary *Thm1*. Surprisingly, this CP occurrence was observed only when *Specc1l*$^{\Delta CCD2/+}$ females were crossed with *Thm1*$^{+/-}$ males. When parental genotypes were reversed, CP was not observed in offspring of *Thm1*$^{+/-}$ mothers. Using control crosses, we determined that maternal *Thm1*$^{+/-}$ heterozygosity was protective against CP in the offspring. We propose that *Thm1* heterozygosity leads to changes in maternal uterine tissue that positively influence the fetus. To test this hypothesis, we performed proteomics analysis on uterine tissue, and showed that indeed *Thm1*$^{+/-}$ mothers have a different protein expression profile. Importantly, the top Gene Ontology categories associated with upregulated proteins were for Placenta Development and Response to Nutrients. Phospho-proteomics in uterine tissue from *Thm1*$^{+/-}$ mothers revealed changes in AKT and mTOR pathways that are known to affect both nutrient and placental signaling. To our knowledge, this is the first mouse model of a protective maternal genetic effect against a birth defect. These studies will generate novel insights into the role of maternal environment in the etiology of isolated CP complex disease.

114. Flow Cytometry Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory.

Peter R. McDonald [1], 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 and 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 ft^2 BSL-2 facility equipped with a BD FACSymphony™ S6 Cell Sorter, a BD FACSAria™ Fusion cell sorter, a Cytek™ Aurora Spectral Flow Cytometer, and other supplemental assay instrumentation. The Cytek™ Aurora full-spectrum flow cytometer enables tube-based and 96-well plate based spectral cytometry, with 5 lasers to allow analysis of 30+ colors. 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 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 FCC resources enable monitoring immune responses and activation status associated with infection, and measuring changes in cellular phenotypes in response to compound treatment. The FCC seeks to assist CBID collaborators in achieving their research goals.

Scientific Focus Area: Core Facility

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115. Targeted mutations of miRNA duplexes reveal asymmetries important for proper strand selection *in vivo*

Jeff Medley[1], Sumire Kurosu[1], Ganesh Panzade[2], Sarah Coffey[1], Will Sydzyik[1], Joel Sydzyik[1], Mira Bhandari[3] and Anna Zinovyeva[1]
[1]Division of Biology, Kansas State University
[2]Frederick National Laboratory for Cancer Research, National Institutes of Health
[3]Department of Molecular and Integrative Physiology, University of Michigan

Animal development relies on timely expression and inactivation of genes to achieve diverse cellular functions. microRNAs (miRNAs) are non-coding RNAs that play a central role in the regulation of eukaryotic gene expression, typically by repressing their target genes.
miRNAs are encoded as double-stranded molecules that are processed into a duplex comprising two functionally distinct strands. One dominant (guide) strand is loaded into an Argonaute (Ago) protein and is functional, while the other strand is degraded. As miRNAs target genes based on nucleotide base-pairing, the decision of which strand is loaded into Ago determines which genes are repressed by that miRNA. Previous studies have suggested that 5' nucleotide identity and thermodynamic asymmetry of duplex ends is sufficient to predict the miRNA guide strand in *vitro.* However, many mature miRNAs do not have sequence features favorable for Ago loading, suggesting additional factors may influence strand selection *in vivo*. Here, we mutated three *C. elegans* miRNAs to alter their duplex characteristics and examine how strand selection was affected. We show that strand selection of miRNAs can be reversed by introducing mutations that are highly unfavorable for Ago loading, supporting that duplex asymmetries influence strand selection *in vivo*. However, we found that some miR-58 mutations retained proper strand choice despite imbalances that should reverse strand selection. These findings suggest that additional factors are important for identifying which strand should be selected *in vivo*, possibly in a miRNA-dependent fashion. Collectively, these findings provide insights into how asymmetric miRNA strand selection is achieved *in vivo*.

116. Stroke and Neural Dynamics: Exploring the impact of focal ischemic infarcts in the latent space

Authors: Nishimoto, Matthew,[1] Federico Barban[2,3], Heather Hudson[4], Michela Chiappalone[2,3], Randolph J. Nudo[4,5], David J. Guggenmos[4]
[1]Department of Neurosurgery, University of Kansas Medical Center; [2]Department of Informatics, Bioengineering, Robotics System Engineering (DIBRIS), University of Genoa, Genoa, IT; [3]Rehab Technologies Lab, Istituto Italiano di Tecnologia, Genoa, IT; [4]Department of Physical Medicine and Rehabilitation, [5]Landon Center on Aging, University of Kansas Medical Center

Stroke is a leading cause of long-term disabilities worldwide. While stroke is a heterogenous injury, it often involves damage to primary motor cortex (M1). This leads to disruptions in descending motor signals and the integration of sensorimotor information, leading to motor deficits. Despite this, some spontaneous recovery of function can occur and is often enhanced through rehabilitative interventions. The underlying mechanisms for this recovery are still under investigation, but it is most likely driven by reorganization in spared premotor (PM) and somatosensory (S1) areas. It is therefore imperative to characterize the changing neural dynamics of PM and S1 following M1 injury to better understand the motor recovery process. To assess this, we used a within-animal design coupled with chronic microelectrode implants in PM and S1 to characterize changes in neural dynamics resulting from ischemic stroke in M1. We found that neither PM nor S1 showed injury-related differences in mean firing rate or local variation of refractoriness. However, Gaussian Factor Analysis (GFA) determined that the injury did disrupt the task-related population dynamics in PM and S1. Additionally, Canonical Correlation Analysis (CCA) showed a disruption in shared task-related activity between PM and S1 following injury. Collectively, M1 lesioning lead to a disruption in somatosensory-motor integration and task-related motor dynamics despite having little change in the underlying neuronal activity. Understanding how spared cortical regions functionally reorganize to execute motor commands will allow for the development of novel, targeted therapies for individuals with stroke and other acquired brain injuries.

117. Prescence of Porcine Endogenous Retrovirus Class C in Domestic pigs in selected areas in Kansas
Isaac Odoi, Eric T. Gillock, Fort Hays State University, Biology department

The study of Porcine endogenous retrovirus (PERV) is important in pig to human organ transplant. Xenotransplantation has great potential to be a significant approach to curb the shortage of human organ donors. Resorting to animals like pigs for organ transplant could be beneficial because of certain advantages like similarities between the anatomy and physiology of pigs and humans. However, the inclusion of the retrovirus genes in the genome of these pigs and their possible transfer to human organ recipients poses a risk and has to be properly checked. Previous studies have delineated different classes of the PERVs and have demonstrated PERV-A and PERV-B are present in all pig genome strains and can infect humans. Studies haven't proven yet whether the PERV-C infects humans, but recombinants between the PERV-A and PERV-C have been identified in the genome of pigs and can infect humans. In this study, 70 samples of domestically raised pig ear and tail biopsies were assayed. DNA extraction and conventional PCR techniques were used to determine the presence or absence of the PERV-C *env gene* in the samples. Only 14 of the samples possessed the PERV-C *env gene* by gel electrophoresis, representing 20% of the total samples. Future studies could include examining sequence variations in the PERV-C in various pig samples and breeds.

118. Unused

119. Unused

120. Unused

121. Effect of XPO1 inhibition on colorectal cancer tumorigenesis
Andrew E. Evans[1], Dan A. Dixon[1,2]
[1]Department of Molecular Biosciences, University of Kansas, Lawrence, KS, [2]University of Kansas Cancer Center, Kansas City, KS

Colorectal Cancer (CRC) is the second leading cause of cancer-related death in the U.S. A subset of individuals faces a notably higher likelihood of developing CRC within their lifetime. Hence, there is a compelling need for innovative chemopreventive treatments aimed at minimizing CRC tumorigenesis. Exportin 1 (XPO1; also referred to as CRM1) plays a pivotal role in transporting proteins from the nucleus to the cytoplasm. To counteract the overexpression of XPO1 in tumors, a novel class of drugs known as Selective Inhibitors of Nuclear Export (SINE) has been developed. Among these, Eltanexor (KPT-8602) has emerged as a promising therapeutic agent, demonstrating fewer side effects compared to its precursors. Using a genetic CRC model, $Apc^{min/+}$ mice, and a human CRC xenograft (HCT116 cells), we have shown that Eltanexor can significantly reduce tumor burden and tumor size, while exhibiting a noteworthy tolerability. To further ascertain Eltanexor's specificity for CRC tumors versus normal tissue, we conducted drug sensitivity assays using organoids derived from $Apc^{min/+}$ tumors and wild-type mice small intestinal tissue. We found that $Apc^{min/+}$ tumoroids have heightened sensitivity to Eltanexor-treatments when compared to wild-type organoids. In an endeavor to elucidate Eltanexor's potent *in vivo* tumorigenesis inhibitory effects, we conducted immunofluorescent assays, which revealed COX-2 protein expression reduction in $Apc^{min/+}$ Eltanexor-treated tumors. Our observations revealed that Eltanexor-treated CRC cells exhibit reduced COX-2 gene expression by inhibiting COX-2's promoter and COX-2's mRNA post-transcriptional stability. Collectively, our findings underscore XPO1 as a potent target for inhibiting CRC tumorigenesis.

122. "Pleiotropic Prioritization: Unraveling Shared Genetic Threads in Insomnia and Chronic Pain Through an Advanced Gene Prioritization Pipeline"
Morgan A. Ewald[1,2,3], Olivia J. Veatch[3], Erin E. Young[1]; University of Kansas Medical Center
[1]Department of Anesthesiology, University of Kansas Medical Center, Kansas City, KS
[2]Department of Integrative Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS
[3]Department of Psychiatry, University of Kansas Medical Center, Kansas City, KS

Many chronic pain patients report co-occurring sleep disturbances, like insomnia, which have been linked to chronic pain development and exacerbation. Though these two complex conditions frequently co-occur, it is unclear whether these are distinct conditions or whether a common mechanism may underlie development of both. Using a bioinformatics approach, we identified potential pleiotropic genes associated with both phenotypes. As a first step, we developed a pipeline to prioritize genes implicated via single nucleotide variants (SNVs) associated with both insomnia and chronic pain phenotypes in genome-wide association studies (GWAS). This search resulted in 8 SNVs located in or between 11 genes. Using the Functional Mapping and Annotation database, FUMA v1.5.6, we identified 29 genes associated with our phenotypes of interest and then mapped these to their mouse orthologs using the DRSC integrative ortholog prediction tool (DIOPT v9.0) resulting in a final list of 26 mouse genes. Using previously published whole genome-sequencing data generated from multiple inbred mouse strains, we identified 86 variants within our prioritized mouse genes. Leveraging differential expression data between closely related mouse sub-strains to narrow this list to 5 genes, *Mapt, Kansl1, Uqcc2, Grm4, and Dcc*, implicated in insomnia and chronic pain in humans that contained 47 variants differing between sub-strains warranting further investigation. This pipeline facilitates the generation of novel hypotheses centered around common genetic mechanisms of risk for both insomnia and chronic pain. Follow-up studies examining how these genes interact together or independently as well as potential for these genes to encode pharmaceutical targets are warranted.

123. Harnessing the power of *C. elegans* genetics to model neurodevelopmental disorder-associated *AGO1* and *AGO2* mutations.
Belén Gaete Humada[1], Ye Duan[2,3], Li Li[1], Ganesh Prabhakar Panzade[1], Sumire Kurosu[1], Amélie Piton[4], Victor Ambros[2], Anna Zinovyeva[1]
[1] Division of Biology, Kansas State University, Manhattan, KS; [2] Program of Molecular Medicine, University of Massachusetts Chan Medical School, Worcester, MA; [3] Department of Organismic and Evolutionary Biology, Museum of Comparative Zoology, Harvard University, Cambridge, MA; [4] Institute of Genetics and Molecular and Cellular Biology, Strasbourg University, France

Precise regulation of gene expression is essential for animal development and physiology. MicroRNAs (miRNA) are small, non-coding RNAs with important roles in gene regulation. Mature miRNAs associate with Argonaute (AGO) proteins to form the miRNA-induced silencing complex (miRISC) and silence target genes by mRNA degradation or translational repression. As AGO proteins are key contributors to miRNA biogenesis and function, impaired AGO activity affects miRNA-dependent gene regulation, negatively impacting development. Recently, several *de novo* coding variants in the human *AGO* genes *AGO1* and *AGO2* have been linked to neurodevelopmental disorders (NDD). Modeling NDD-associated *AGO* mutations in the *C. elegans* ortholog *alg-1* via genome editing has helped assess the effect of some of these variants on miRNA biogenesis and functionality. Modeled mutations in *C. elegans* appear to profoundly disrupt miRNA processing and target repression, leading to dysregulation of several genes, including those linked to NDD pathogenesis. Although the effects of these variants on the miRNA pathway have been described, it remains unclear whether neurological structure and function are affected in these mutants. Furthermore, only a fraction of the identified *AGO* variants have been modeled in *C. elegans*. Thus, my work continues the efforts of characterizing the effects of NDD-associated *AGO* mutations on post-transcriptional regulation and neurodevelopment. These efforts can deepen our understanding of AGO function and will be key to elucidating how pathogenic variants lead to NDD. Therefore, this project aims to expand the repertoire of modeled and characterized NDD-associated *AGO* mutations, exploring their effects on the miRNA pathway and nervous system.

124. Unraveling a novel role of DCLK1 in IBD and colon cancer

Kafayat Yusuf[1,2], Badal C. Roy[1,2], Shrikant Anant[2], Shahid Umar[1,2]
[1]Department of Surgery, University of Kansas Medical Center
[2]Department of Cancer Biology, University of Kansas Medical Center

Patients with Inflammatory Bowel Disease (IBD) face an elevated risk of colorectal cancer (CRC) due to chronic gut inflammation. Despite the increasing prevalence of IBD, understanding the mechanisms guiding its progression to colon cancer remains limited. DCLK1, with isoforms DCLK1-L and DCLK1-S, marks tuft cells that safeguard the gut by detecting and eliminating pathogens; DCLK1 also promotes colon cancer growth. Studies have revealed that hypermethylation in the DCLK-1α promoter in colorectal cancer leads to a shift to the DCLK1-S isoform that promotes invasive tumor development. In the lab, we observed a marked elevation of DCLK1-S in patients with IBD tissue samples. We also recently discovered in two different murine models of colitis that DCLK1-S is predominantly expressed in Ly6G; MHCII- neutrophils, which coincide with elevated levels of inflammation and tissue damage in the colon. To further understand the role of DCLK1 isoforms in the progression of colitis to colon cancer, we crossed Dclk1fl/fl mice with MRP8-Cre-ires/GFP mice to create Dclk1fl/fl;MRP8-Cre+/- mice that eliminate DCLK1-L upon tamoxifen injection, resulting in sustained expression of DCLK1-S in neutrophils. MRP8;Dclk1-/- mice developed more severe colitis when infected with *Citrobacter rodentium* (CR) than MRP8;Dclk1+/- or WT mice. Similarly, MRP8;Dclk1-/- animals developed tumors throughout the colon in response to AOM/DSS treatment. Research is being conducted to unravel the molecular processes of inflammation and tumor formation in MRP8;Dclk1-/- mice. These findings are crucial to understanding how DCLK1-S acts as a sentinel to link neutrophils to the progression of colitis to colon cancer.

125. A novel method based on field-amplified sample injection coupled with electrokinetic supercharging for the sensitivity detection of glyphosate in flow-gated capillary electrophoresis

Ying Gong, Maojun Gong
Department of Chemistry and Biochemistry, Wichita State University, Kansas

Glyphosate (GlyP) is a non-selective herbicide widely employed for weed control or for harvest preparation, its worldwide application has been over one million tons annually. The concern about its cancerous risk is persistent although no solid evidence has been obtained. GlyP and its major degradation product, aminomethylphosphonic acid (AMPA) have been detected in numerous foodstuffs and environmental water sources, and thus are also present in bodies of animals and humans, therefore, it is urgent for us to develop simple and sensitive techniques to detect them. This study developed a sensitive and reliable technique for the quantitative determination of glyphosate and AMPA residues in the surface water system with flow-gated capillary electrophoresis (CE). Surface Water samples were first fluorogentically derivatized with 4-Fluoro-7-nitrobenzofurazan (NBD-F) in a low-conductivity buffer at room temperature. The sample mixture was injected and the analytes were preconcentrated in separation capillary based on the field-amplified sample injection coupled with electrokinetic supercharging. The detection sensitivity was improved by 296, 444, and 861 folds for glufosinate (GluF), AMPA, and GlyP, respectively. This study provides an effective method for sensitive detection of herbicide residues in water samples. After appropriate sample preparation (solid phase extraction), the method can also be applied to the analysis of other samples including biological liquids and plant products.

126. Iridium Containing Artificial Dye-decolorizing Peroxidases with Non-canonical Axial Ligand for Catalysis of Unnatural Chemical Reactions

Samiksha Khadka, Chao An and Ping Li
Department of Chemistry, Kansas State University, Manhattan, KS, 66502

Dye-decolorizing peroxidases (DyPs) are versatile biocatalysts due to their ability to catalyze hydrogen peroxide-dependent oxidation of various substrates. They have shown promising potentials in lignin degradation, dye decolorization, and wastewater treatment. DyP from *Thermonospora curvata* (*Tc*DyP) belongs to an A-class DyP and has displayed high activities against anthraquinone- and azo-based industrial dyes such as reactive blue 19 and reactive black 5 with high redox potentials. The heme iron and axial histidine in heme peroxidases are known to play important roles in the enzyme function. In our work, we modulated the cofactor metal and the axial ligand to investigate the enzyme's efficiency in catalysis of previously unknown chemical reactions. By changing the iron with iridium and replacing the histidine ligand with the N-methyl histidine, we aim to get a better understanding of their roles as well as develop a robust enzyme with new functions and catalytic efficiency.

127. CRISPR-Mediated Endogenous NTMT1 Tagging for NTMT1 PROTAC Characterization, Design, and Optimization

Wei Wu, Chao An, and Ping Li
Department of Chemistry, Kansas State University, Manhattan, Kansas

Although dysregulation of N-terminal methyltransferase 1 (NTMT1) has been linked to many diseases such as colorectal, lung and brain cancers, and malignant melanoma, its biological roles remain elusive due to substrate complexity and inaccessibility to an effective cellular probe. Our research addresses this gap by developing NTMT1 degraders based on proteolysis targeting chimera (PROTAC). The initial generation of NTMT1 PROTACs has demonstrated potential as a chemical probe in cellular studies; however, further optimizations are essential for enhancing their efficiency. In this study, NanoBIT-tagged endogenous NTMT1 is constructed via CRISPR-mediated gene knock-in, enabling real-time continuous monitoring of NTMT1 degradation. This approach allows for the precise characterization of PROTACs compared to traditional western blotting, providing insights into their dynamics and efficacy. Simultaneously, NanoBIT-tagged NTMT1 serves as a valuable tool for evaluating PROTAC cell permeability, NTMT1-E3 ligase interactions, and ubiquitination processes, offering crucial information for the design and optimization of PROTACs.

128. Gestational Choline Modulates Adolescent Cognitive Outcomes in a Maternal Immune Activation Model of Neurodevelopmental Disorders

Cole King[1,2], Bethany Plakke[2]
[1]Master of Public Health Program, Kansas State University
[2]Department of Psychological Sciences, Kansas State University

Maternal Immune Activation (MIA) during pregnancy is a risk factor for neurodevelopmental disorders like autism and schizophrenia. To induce MIA in pregnant rats, dams were given a single intraperitoneal injection of high molecular weight poly(I:C) on gestational day 15, which corresponds to the second trimester of human pregnancy (n=5 saline dams, n=13 poly(I:C) dams). Six of the poly(I:C) dams also received 5% dietary choline chloride supplementation throughout pregnancy and lactation. Offspring were tested early and middle adolescence (postnatal days 28 and 50, respectively) in the novel object recognition task and the rotarod motor coordination test (n=152). Postnatal day 50 offspring were also tested on reversal learning (n=66). At postnatal day (PND 28), MIA females were impaired on novel object discrimination (p=0.035) compared to controls, performing no differently from chance. At PND 50, however, MIA animals of both sexes discriminated above chance while controls did not, and the male maternal choline-supplemented group discriminated far better than both the MIA and control groups (p=0.0015). On the rotarod, MIA females at PND 50 achieved much higher maximum latency to fall off the rod (p=0.012), suggesting improved acquisition of repetitive motor behavior. On reversal learning, MIA males at PND 50, regardless of maternal choline, exhibited a deficit in initial reversal learning compared to controls (p=0.031), and non-choline males tended toward increased regressive errors on reversal phases (p=0.0524). Together, these results replicate prior findings in the MIA model and suggest that maternal choline supplementation during pregnancy may partially ameliorate behavioral deficits from MIA in adolescence.

129. Nociceptor sensory neurons promote pneumonic sepsis during carbapenem-resistant *Klebsiella pneumoniae* lung infection

Prabhu R. Joshi[1], Pankaj Baral*[1]
*Corresponding author
[1]Section of Microbiology and Immunology, Division of Biology, Kansas State University, Manhattan, KS, USA, 66506.

Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is a leading cause of Gram-negative pneumonia and pneumonic sepsis for which limited therapeutic options are available. The lungs are densely innervated by nociceptive sensory neurons (nociceptors), which mediate breathing, cough, and bronchoconstriction. However, the role of these neurons in host defense against CRKP-induced pneumonic sepsis is unknown. We found that nociceptors play a host deleterious role in promoting pneumonic sepsis. Using a conditional *Cre-LoxP* genetic strategy to deplete the nociceptors in mice, we observed that the nociceptor-ablated mice showed an enhanced survival and bacterial clearance after CRKP lung infection. Furthermore, nociceptors ablation resulted in the increased influx of neutrophils and Ly6C^{hi} monocytes and cytokine induction. Depletion of Ly6C^{hi} monocytes, but not of neutrophils, impaired lung bacterial clearance and bacterial dissemination in nociceptor- ablated mice, indicating that Ly6C^{hi} monocytes are a critical cellular population downstream of nociceptors to regulate pneumonic sepsis. Moreover, nociceptive neuropeptide calcitonin gene-related peptide suppressed induction of reactive oxygen species and intracellular bacterial killing. Collectively, our data suggest that the nociceptor neuronal signaling could be a therapeutic target for treating multidrug-resistant CRKP lung infections and pneumonic sepsis.

Key words: Nociceptor neurons, Neuroimmune, CRKP pneumonia, Pneumonic sepsis.

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130. Assessing the Incidence of Methicillin-Resistant (MRSA) and Methicillin-Susceptible Staphylococcus aureus (MSSA) in Pigs at the FHSU Animal Farm's Swine Unit

Kofi Addo Okyere-Addo[1], Dr. Claudia Da Silva Carvalho[1]
[1]Department of Biological Sciences, Fort Hays State University, Hays, Kansas.

Staphylococcus aureus is a bacterium that naturally exists in both our bodies and the environment. While typically harmless, it can become opportunistic and cause infections in humans and animals. The misuse of antimicrobial therapy has worsened this issue, leading to Methicillin-Sensitive *Staphylococcus aureus* (MSSA) to mutate into Methicillin-Resistant *Staphylococcus aureus* (MRSA) strains. MRSA is particularly concerning as it is pathogenic and resistant to multiple antibiotics used for treating associated diseases. To address this, proactive surveillance and investigation of potential MRSA sources are essential. In this study, my objectives were to assess the occurrence of livestock-associated MRSA in the pig herd at the FHSU animal farm and determine its source to prevent transmission from animals to individuals who come into direct contact with them. Preliminary results from the phenotypic detection using chromogenic mannitol salt agar and CHROMagar MRSA II media showed positive results for the presence of staphylococcus sp. and suspected MRSA, respectively. Further confirmation of *S. aureus* detection was obtained through biochemical tests, including a catalase test. To confirm the presence of MRSA, genotypic identification is currently underway using PCR to detect the *mec-A* gene and other resistance genes. The study aims to provide novel insights into the epidemiology of MRSA at the FHSU animal farm. Given the farm's low biosecurity levels, the potential colonization of MRSA in pigs is highly likely. By understanding the prevalence and sources of MRSA, necessary measures can be implemented to mitigate its spread and protect both human and animal health.

131. Lung-innervating Nociceptor Sensory Neurons augment lung defense against *Aspergillus fumigatus* Pneumonia

Chinemerem Onah,[1] Michael Bartkoski,[1] and Pankaj Baral[1]
[1]Kansas State University Division of Biology, Manhattan, Kansas.

The incidence of invasive pulmonary aspergillosis (IPA) is currently on the rise owing to an increasing proportion of immunocompromised and chronic lung disease patients. These individuals experience IPA and lethal pneumonia caused by *Aspergillus fumigatus*, leading to altered immune cell responses and rapid destruction of airway barrier permeability. The lungs are heavily innervated by nociceptive sensory neurons which secrete neuropeptide calcitonin-gene-related peptide (CGRP). This neuronal subset and their secreted CGRP mediate pain production and the maintenance of lung homeostasis. Innate immune cells, macrophages, monocytes, and neutrophils are critical for host protection against *A. fumigatus*. This study aims to understand the interactions between lung-innervating nociceptor neurons and the immune system to identify novel anti-fungal therapeutic target(s) through their signaling. We intranasally infected nociceptor neuron-ablated and non-ablated littermate control mice with *A. fumigatus* conidia and found an increased fungal burden, immune cell infiltration, and inflammatory cytokines among the nociceptor neuron-ablated mice. In addition, flow cytometry analyses of bronchoalveolar lavage after *A. fumigatus* lung infection demonstrated an increased abundance of neutrophils and alveolar macrophages in nociceptor-ablated mice. Further, follow-up *in vitro* and *ex vivo* experiments showed that CGRP enhances the anti-fungal innate immune response by acting through the RAMP1 signaling pathway to increase phagocytosis and killing of conidia by macrophages, monocytes, and neutrophils. Altogether, our data suggest that the lung nociceptor neuron-immune crosstalk as a potential therapeutic avenue to treat IPA.

Keywords: *Aspergillus fumigatus*; Invasive aspergillosis; CGRP; Nociceptor neurons

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132. optima: an open-source R package for the Tapestri platform for integrative single cell multiomics data analysis

Dong Pei 1,2, Rachel Griffard 1, Nanda Kumar Yellapu 1,2, Emily Nissen 1, Devin C. Koestler 1,2
1 Department of Biostatistics & Data Science, University of Kansas Medical Center, KS, Kansas City, USA. 2 The University of Kansas Cancer Center, Kansas City, KS, USA.

The Tapestri platform offers DNA and protein analysis at the single cell level. Integrating both types of data is beneficial for studying multiple cell populations in heterogeneous microenvironments, such as tumor tissues. Here, we present *optima*, an R package for the processing and analysis of data generated from the Tapestri platform. This package provides streamlined functionality for raw data filtering, integration, normalization, transformation, and visualization. Insights gained from the *optima* package help users to identify unique cell populations and uncover surface protein expression patterns. The results generated by *optima* help researchers elucidate dynamic changes at the single cell level in heterogeneous microenvironments. This package is available in Github: https://github.com/rachelgriffard/optima

133. The Synthetic Chemical Biology Core (SCB): A Resource for Research in Chemical Biology

Chamani T. Perera[1]

[1]*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 encompasses the Purification and Analysis Laboratory (PAL) that provides purification, analysis and quality control of compounds via LC/MS. The SCB core also provides MALDI-TOF analysis of biomolecules.

134. Musashi1 affects intestinal epithelium growth by regulating mTORC1 pathway

Bikash Pokhrel[1], Dr Kristi Neufeld[1]
[1] Department of Molecular Biosciences, University of Kansas, Lawrence, USA

Intestine is the only organ in the body that regenerates its entire surface/lining every five to seven days. It is important to understand how it maintains cell growth, proliferation, and differentiation because errors can lead to many diseases, most notably cancer. We study the role of Masashi, a key regulator of proliferation and differentiation, in maintaining homeostasis/equilibrium in the intestine. RNAsequencing data from Musashi overexpressed mice model showed that mRNAs involved in mTOR pathway (rragd, tm4sf5, SLC transporters) were highly downregulated. Gene ontology analysis showed processes such as lipid synthesis, ion transporter activity downregulated whereas hydrolases, endopeptidases (involved in autophagy) upregulated. These processes are directly affected by mTOR pathway. Also, immunohistochemistry study showed that enterocytes and KI67 positive cells were fewer in Musashi overexpressing mice compared to wild type. These data from our lab hinted that mRNAs of mTOR pathway activators are targets of Musashi translational regulation. Downregulated mTOR causes decrease in number of cells in the intestinal epithelium. We aim to determine if Musashi directly binds to and inhibits translation of the mTOR pathway activators. Also, to determine if processes directly influenced by mTOR pathway are affected by Musashi overexpression.

135. The Hepatic-Brain Axis in Obesity Related Hypertension Development
Michael E. Ponte[1], John C. Prom[1], Jane A. Ibude[1], and E. Matthew Morris[1]
[1]Dept. Cell Biology and Physiology, University of Kansas Medical Center

Obesity stands as a primary risk factor for cardiovascular disease, with its induced sympathetic nervous system activation contributing to systemic hypertension. However, the precise mechanisms behind heightened sympathetic activity due to a chronic high-fat diet remains incompletely understood. Recent research indicates that reduced liver ATP, seen in obese conditions, leads to diminished hepatocyte membrane potential, consequently lowering vagus nerve afferent firing rates. In our investigation, we aimed to understand how altered peripheral vagal afferent signals from the liver influence the development of obesity-induced hypertension resulting from a chronic high-fat diet. Previous observations in (LPGC1a+/-; liver-specific, PGC1a heterozygous) mice revealed that impaired hepatocyte mitochondrial energy metabolism led to increased short-term weight gain on a high-fat diet. PGC1a, crucial for mitochondrial biogenesis, is diminished in obesity. Male LPGC1a+/- mice on a chronic high-fat diet exhibited elevated blood pressure compared to wild-type counterparts, accompanied by heightened neural activity (c-Fos+ cells) in the nucleus of the solitary tract, indicating maladaptive sensory integration. Intriguingly, female LPGC1a+/- mice displayed reduced blood pressure compared to their wild-type counterparts. These findings imply that impaired hepatocyte mitochondrial energy metabolism yields sex-specific disparities in high-fat diet-induced hypertension, potentially through dysfunctional integration of peripheral sensory signals. Future research will delve into identifying the specific hepatic neurons contributing to the observed blood pressure differences. Additionally, we will investigate neural activity in the paraventricular nucleus of the hypothalamus, a critical regulator of blood pressure.

136. Extracellular Vesicle MicroRNAs as Novel Biomarkers in Asthma Pathobiology
Chandrashekhar Prasad[1], Santhosh Kumar Duraisamy[1], Alexander Alsup[2], Rachel Griffard[2], Dong Pei[2], Navneet Dhillon[1], Mario Castro[1], Isaac Kirubakaran Sundar[1]
[1]Department of Internal Medicine, Division of Pulmonary, Critical Care and Sleep Medicine, [2]Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, KS, USA

Extracellular vesicles (EVs) are membranous nanovesicles that are essential to maintaining cellular communication and homeostasis within the lung. EVs contain proteins, lipids, nucleic acids, and membrane receptors of the cells from which they originate. We hypothesized that circulating EVs as novel biomarkers from healthy controls (HC), non-severe asthmatics (NS), and severe asthmatics (SA) would possess uniquely enriched small RNAs (miRNA) that correlated with their clinical phenotypes. Human plasma-derived EVs from HC (n=15), NS (n=10), and SA (n=10) individuals were isolated and phenotypically characterized. Total RNA from plasma-derived EVs was used for small RNA sequencing (RNA-seq) followed by bioinformatics analysis. Plasma-derived EVs (~150-200 nm) were significantly more numerous in SA compared to HC or NS; and no significant differences were observed in the expression of EV-related surface marker (MACSPlex Exosome Kit) from the pairwise comparisons (HC vs. NS; HC vs. SA; NS vs. SA). A total of 12 miRNAs were differentially expressed (DE) among the 3 different pairwise comparisons. DIANA-mirPath analysis of DE miRNAs revealed enriched KEGG pathways such as adherens junction, NF-kB signaling, TNF signaling, and apoptosis that support their role in asthma pathobiology. Unique DE miRNA signatures show promise as potential biomarkers in defining the clinical phenotypes of asthma; future research will validate these results using a larger cohort. ***Funding*****:** K-INBRE P20 GM103418, R01 HL142543, *and KUMC School of Medicine, Internal Medicine Start-up Funds (IKS).*

137. Reduced Hepatic Mitochondrial Energy Metabolism Decreases Food Intake Inhibition by Oral Preloads in Mice.
John C. Prom[1], Michael E. Ponte[1], Jane A. Ibude[1], and E. Matthew Morris[1]
[1]Dept. Cell Biology and Physiology, University of Kansas Medical Center

Satiation describes within-meal signaling to elicit meal termination in response to energy homeostasis cues from different nutrient, hormonal, and neural signals. Many of these signals come from afferent vagal nerves initiating in the stomach and intestines that terminally synapse in higher-order brain structures. Our lab has previously observed differences in feeding behavior in a mouse model of reduced hepatocyte mitochondrial energy metabolism (LPGC1a). To assess whether impaired satiation signaling was involved in the observed feeding behaviors of LPGC1a mice, we utilized oral pre-loads to assess the dose-dependent effect of gastric delivery of nutrients on subsequent food intake. Mice were fasted for 2 hours prior to gavage of mixed macronutrients (Ensure®) or sham. Additionally, mice were injected IP with receptor antagonists for peripheral neuroendocrine satiation signals 30 mins before the oral gavage. During sham gavage, LPGC1a mice tended to eat fewer, larger, and longer meals. Oral gavage of 3 doses of Ensure resulted in reduced inhibition of acute food intake in LPGC1a mice compared to control. Further, the oral preloads exaggerated the larger and longer meal behaviors of the LPGC1a mice. Also, IP delivery of peripheral satiation signal (serotonin, cholecystokinin, and glucagon-like peptide-1) receptor antagonists failed to increase food intake following the oral preload in LPGC1a mice compared to control. These findings indicate that the liver mitochondrial energy metabolism plays a role in the modulation of satiation signaling, and further suggests that the liver is innervated by vagal afferent fibers.

138. Gene expression of oncolytic virus receptors in human head and neck squamous cell carcinomas
Silas Rosiere, Sara Akhtar, Christopher Simmons, and Phillip Harries
Department of Biology, Pittsburg State University

Head and neck squamous cell carcinoma (HNSCC) is the 6th most common cancer worldwide. HNSCC affects 600,000 new patients every year with over 250,000 annual deaths attributed to the disease. Oncolytic viruses are those that kill cancer cells and they have been increasingly utilized as an adjuvant therapy paired with more traditional forms of treatment to attack a wide array of cancers. Although a handful of studies have tested oncolytic viruses on HNSCC, there is relatively little known about which viruses may be most effective for this specific type of cancer. In order for any oncolytic virus to kill cells, it must first initiate an infection by binding to and entering the host cell. This initial interaction is generally mediated by binding of a protein on the surface of the virus particle with a receptor on the surface of the host cell. In this study, we compare gene expression patterns of known oncolytic virus receptors in HNSCC compared to a healthy control. We further examine the potential role of cytosine methylation in such patterns. The overall goal of this work is to identify oncolytic viruses that might have the best chance of infecting HNSCC compared to normal health tissue.

139. Active avoidance is acquired more rapidly when learned through observation compared to direct experience in rats.
Authors: Shannon Ruble, Cassandra Kramer, Lexe West, Ivy Auletti, Maria M. Diehl
Affiliation: Department of Psychological Sciences, Kansas State University, Manhattan, Kansas, USA

Learning to actively avoid danger can occur through direct or indirect experience. Indirect learning allows individuals to avoid danger without direct harm. Individuals can learn about danger by observing another individual directly experiencing harm, and this has been reported in conditioned fear and some avoidance tasks. However, it is unknown whether decision-based, clinically relevant forms of active avoidance can be learned through observation, which is the main question of this study. Our lab uses a rodent model of platform-mediated avoidance (PMA) in which rats learn to avoid a tone-signaled shock by stepping onto a safe platform, which comes at the cost of a sucrose reward. During Observational PMA, Observers witnessed a Demonstrator perform PMA, followed by a test session of direct PMA training. Observers witnessed one of three timepoints during PMA training: day 1 (D1; n=18), days 2 through 9 (D2-9; n=17), or day 10 (D10; n=20). D1 Observers Exhibited the lowest levels of avoidance during the test session compared to D2-9 and D10 Observers. Interestingly, D2-9 and D10 Observers showed similar levels of avoidance, suggesting that witnessing a single session performed by a well-trained Demonstrator provides equal benefit as witnessing multiple sessions. Although all Observers avoided less at the beginning of their test session compared to rats who learned PMA directly, all Observers acquired avoidance more rapidly across the test session than direct learners. Ongoing studies are examining neural activation in prefrontal cortex to determine the neural correlates of observational PMA.

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140. The cellular behavior and molecular regulation of neural cells in response to electrical signals
Audrey Scherrman, Li Yao
Department of Biological Sciences, Wichita State University

Various studies have observed the function of electric fields on nervous system development and tissue wounding. It was reported that endogenous electric fields are widespread in developing and regenerating tissues. During embryonic development, endogenous electrical signals have been detected at the neural plate and neural fold stages. The electrical vectors are aligned with the major embryonic axes. In vitro studies revealed that the electric signal can guide the migration of various cell types including epithelial cells and neurons. Directed cell migration depends on the establishment of cell polarity, and cells are polarized dynamically in response to extracellular signals. We recently reported that the glial cells and glioma cell migration can be guided by electrical stimulation. However, it is not clear if the same stimulation strength can affect the cell viability. In this study, we investigated the cellular and molecular response of PC12 cells that is rat pheochromocytoma to an applied electric field. The time-lapse recording demonstrated that the cell migration can be directed to the cathode by electrical stimulation. We also measured the cell viability and cell cycle for the cells treated with electrical stimulation. The study showed the significant effect of electrical stimulation on cell migration. However, the same stimulation strength and duration did not affect cell viability and cell cycle. PC12 cell can serve as a model to study the molecular mechanism of cell polarization and direction cell migration in further investigations.
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141. EWS is upregulated in Ewing sarcoma and a potentially targetable dependency
Evan Schulz, Harsha Hapugaswatta, Mizuki Azuma – University of Kansas

Ewing sarcoma (ES) is the second most common adolescent bone cancer, and has no available targeted chemotherapies. To develop targeted chemotherapies, the role of ES-specific events in tumor development and chemosensitivities must be understood. The hallmark tumor-specific event of ES is the t(11:22) chromosomal translocation, generating two aberrations of the EWS protein: the loss of an EWS allele and expression of EWS/FLI1. EWS/FLI1 and EWS knockdown have been shown to be embryonically lethal and cytotoxic *in vitro*. Our previous work demonstrated both EWS/FLI1 expression and EWS knockdown to impair EWS functionality. We hypothesized that cells adaptively upregulate EWS to compensate for t(11:22) EWS aberrations during tumor development. Analysis by western blotting, immunohistochemistry, and NCBI RNA-seq bioinformatics showed that **EWS is *upregulated* in ES** cells compared to other sarcomas, carcinomas, and normal bone tissues. We also hypothesized that EWS aberration impaired EWS functionality sensitizes ES to chemotherapies that target EWS-dependent mitotic pathways. Since EWS is required for proper mitotic Aurora B (AuB) activity and spindle formation, we investigated whether EWS/FLI1 expression and EWS knockdown sensitize cells to microtubule disruptors (MtDs) or AuB inhibitors (AuBis). Analysis of drug sensitivity data in the DepMap Portal database showed that ES is significantly more dependent on EWS ($p<0.0001$) and sensitive to MtDs ($p=0.014$) and AuBis ($p=0.0001$) than all other tumor types in the database. Cell viability and apoptotic marker assays with MtD (nocodazole) and AuBi (ZM447439) were congruent with database findings and demonstrated **induction of t(11:22) EWS aberrations sensitizes DLD-1 cells to nocodazole** ($p<0.01$, $p<0.05$).

142. Enhancing the immune response during chronic virus infection using an autoimmunity-associated allele of PTPN22
Shaikh, Anam F,* Bevis, Alec, Jenna Barnes, Schwarting, Nancy, Cockerham, Tammy, and Orozco, Robin C**
Department of Molecular Biosciences, University of Kansas, Lawrence, KS
*Presenting author
**Corresponding author

Dysfunctional dendritic cell (DC) function can lead to inadequate T cell activation resulting in persistent virus infection. Conversely, enhancement of DC function could improve T cell activation, thus clearing virus infection. We have previously found that mice that express the autoimmunity associated allele of PTPN22 (PEP-619WW in mice) successfully cleared LCMV-cl13 infection. This is paired with a more immune stimulatory DC phenotype and improved T cell function. We hypothesized that PEP-619WW impacts the DC function, ultimately leading to improved T cell function and early virus clearance in PEP-619WW mice. To elucidate the specific impact of PEP-619WW on DCs during LCMV cl13 infection, we assessed the infectivity of bone marrow-derived dendritic cells (BMDCs) from PEP-WT and PEP-619WW mice in culture. Additionally, we examined DC population in-vivo using flow cytometry and RNA-seq following infection in PEP-WT and PEP-619WW mice, focusing on changes in DC subsets. and looked specifically at the change in DC subsets. Furthermore, we interrogated the impact of PEP-619WW on CD8 T cell function. Our results demonstrated that while PEP-619WW did not significantly affect major LCMV cl13 epitope, it did enhance T cell function against minor epitope. Collectively, our study sheds light on how PEP-619WW augments the functions of both DCs and T cells, potentially influencing broader antiviral immune response.

143. The Kansas State University KINBRE Data Science Core
Teresa Shippy
KSU Data Science Center, Division of Biology, Kansas State University

The KINBRE Data Science Core (formerly Bioinformatics Core) has branches at KSU, KU-L and KUMC, with services available to the entire KINBRE community. The core at Kansas State University focuses primarily on genomic and multiomic data, with a particular emphasis on insects and non-model systems. We assist with experimental design, data analysis and interpretation of omics projects and provide data science training opportunities to KINBRE researchers. The KSU Data Science Core provides custom workshops based on KINBRE project needs. Faculty at Primarily Undergraduate Institutions (PUIs) are encouraged to apply for KINBRE Data Science Core – PUI grants, which provide funds for a collaborative 1-year data science-focused research project.

144. Role of Malvolio, the *Drosophila* ortholog of human NRAMP2 metal ion transporter, in salivary gland morphogenesis
Contributors:
Mary Short[1] (Presenting Author), Srihitha Akula[2], Aditi Kulkarni[2], Tony Zou[2], Rika Maruyama[2], Deborah Andrew[2], Raj Logan[1]
Institution: 1. Department of Biological Sciences, Wichita State University, KS 67260; 2. Department of Cell Biology, Johns Hopkins University, Baltimore, MD 21205.

Malvolio (Mvl) is the Drosophila ortholog of the mammalian Solute Carrier Protein Slc11a2, which transports divalent metals, including iron. Mvl shows Fkh-dependent expression during embryonic salivary gland (SG) morphogenesis. *Mvl* zygotic loss has no effect on viability although a developmental delay was observed in $Mvl^{exc1}/Df(Mvl)$, with adults eclosing 48 – 72 hours later than their balancer-carrying siblings. Zygotic loss of *Mvl* also resulted in mild SG abnormalities and occasional small gaps in the denticles. Combined maternal and zygotic loss led to pronounced defects in SG morphology and high frequency denticle gaps. We also observed a loose assemblage of CrebA+ embryonic cells in the anterior region of the *Mvl* homozygotes that may be crystal cells (a subpopulation of Drosophila immune cells). Collectively, these results demonstrate varying degrees of developmental defects with the loss of *Mvl* during embryogenesis. Imaging of *Mvl* null embryos revealed that although the levels and localization of the adherens junction protein E-cadherin and polarity marker Bazooka were comparable to wild-type SGs, the levels of the apical polarity determinant Crumbs were notably decreased. To learn where Mvl localizes in SG cells and is likely to function, we generated Mvl antiserum and costained SGs with anti-Mvl in combination with several organelle-specific markers. These experiments revealed Mvl localization to Golgi, early, and late endosomes. We are testing a working hypothesis that the cell morphogenetic defects in *Mvl* loss-of-function are linked to defective endomembrane trafficking that affects Crb localization and recycling at the sub-apical domain. We are currently assaying the requirements for iron versus proton transport in *Mvl* function.

145. Methylation Patterns Across Tissue Type and Time in *Peromyscus leucopus*: A Targeted Museum Study
Smith, Loryn[1], Nicholas Stewart[2], Alexandra DeCandia[3], Lorelei Patrick[1]
[1]Department of Biology at Fort Hays State University, [2]Department of Biology at Southern Oregon University, [3]Department of Biology at Georgetown University

Museum specimens are a vital data source for many types of studies. One relatively new use includes studying methylation patterns. Methylation patterns are a form of epigenetics or how gene expression changes without alteration of the genetic code. These patterns have been examined in many mammals. However, the focus has previously been on overall epigenetic patterns. Few studies have investigated whether methylation patterns differ across tissue types, time, or preservation method. In this study, I compared methylation patterns in muscle, liver, toe pads, and nasal bones from *Peromyscus leucopus* (white-footed mouse) museum specimens collected in 2022, 2018, 2014, and 2008 using reduced-representation bisulfite sequencing. I found methylation patterns were most similar within an individual and there was little to no clustering of methylation patterns based on tissue type or collection year. Additionally, tissue preservation in ethanol had no effect on methylation patterns. This study illuminates the role of tissue type and preservation method in methylation patterns of *P. leucopus*, and thereby provides an important resource for researchers seeking to study DNA methylation in museum specimens.

146. Leukemia inhibitory factor signaling in human trophoblast stem cells
Savannah L. Speckhart[1], Khursheed Iqbal[1], Ayelen Moreno-Irusta[1], Marija Kuna[1], Regan L. Scott[1], and Michael J. Soares[1,2,3]
[1]Institute for Reproductive and Developmental Sciences, Department of Pathology and Laboratory Medicine, [2]Department of Obstetrics and Gynecology, University of Kansas Medical Center, Kansas City, KS, [3]Center for Perinatal Research, Children's Research Institute, Children's Mercy, Kansas City, MO

In the early stages of human pregnancy, cells from the developing placenta, termed extravillous trophoblast (EVT) cells, enter the uterus to remodel spiral arteries. Dysregulation of the molecular controllers responsible for this remodeling can lead to several pregnancy complications. Previously, a cytokine called leukemia inhibitory factor (LIF) was implicated as a candidate regulator of early placentation in the mouse. In the present study, we performed in-situ hybridization, RT-qPCR, and bulk RNA-sequencing. In situ hybridization revealed EVT cell columns were positive for *LIFR*, and its downstream signaling partners, janus kinase 1 (*JAK1*) and signal transducer and activator of transcription 3 (*STAT3*). Human TS cells were differentiated into EVTs. *LIFR* transcript levels increased approximately 10-fold as TS cells transitioned to the EVT cell state. Although, LIF expression was not prominent in human TS cells or their differentiated products, LIF is a known ligand produced by the uterus. We also examined the effects of recombinant human LIF on human TS cells. Acute exposure to LIF resulted in an increase in phosphorylated STAT3. In addition, bulk RNA-sequencing demonstrated that LIF treatment during EVT cell differentiation resulted in a downregulation of EVT cell associated transcripts, whereas several stem state markers were upregulated. In summary, LIF-LIFR signaling has prominent restraining effects on development of the EVT cell phenotype. This may reflect a pathway utilized by the uterine compartment to restrain excessive intrauterine EVT cell invasion and a regulatory mechanism susceptible to dysregulation in disease states characterized by abnormalities in intrauterine EVT cell invasion.

Key words: Sympathetic neuron, Albuterol, β_2-adrenergic, RSV, Immune cell

147. NMR insights into the structural/functional differences of *Manduca sexta* pro-moricin-6 and moricin-6

Andy Su[1], Aprajita Jha[1], Nitin Mishra[1], Tomohiro Kimura[1,2], Chunxiang Hou[3], Haobo Jiang[3] and Om Prakash[1]
[1]Department of Biochemistry and Mol. Biophysics, Kansas State University, Manhattan, KS [2]Department of Chemistry, Kansas State University, Manhattan, KS
[3]Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK

Insects produce a variety of antimicrobial peptides (AMPs) to kill invading microbes during immune responses. Among them, moricins have a pre-pro-structure, that is, a signal peptide for secretion, a 2 or 4-residue pro-region, and a mature peptide predicted to form an amphipathic α-helix that disrupts bacterial cell membrane. In the tobacco hornworm *Manduca sexta*, six genes encode moricin-1 through -6. We hypothesize that the pro-moricin becomes fully active after their $(Xaa\text{-}Pro)_{1-2}$ is removed by a proline-specific dipeptidyl peptidase-4 (DPP4). Two peptides were chemically synthesized: 1) pro-moricin-6, APEPGRLSAIKKGGKIIKKGLGVISAAGTAHEVYSHVKNRRN (42-mer); 2) moricin-6, GRLSAIKKGGKII KKGLGVISAAGTAHEVYSHVKNRRN (38-mer). There was a substantial increase in bactericidal activity after the N-terminal tetrapeptide APEP was cleaved. We have initiated structural and dynamics studies on pro-moricin-6 and moricin-6 using NMR spectroscopy to understand structural differences in the two structures, which may account for the increase in the AMP activity.

148. Characterization of polymorphic mitochondrial tRNA fragments that correlate with severity of metastasis

Katy L. Swancutt[1], Adam D. Scheid[1], Christian Foster[1], Raymond E. Preston[2], Sydney P. Quijano[1], Emily Nissen[3], Devin C. Koestler[3], Tony Vanden Bush[1], Isidore Rigoutsos[4], Danny R. Welch[1]
[1]Department of Cancer Biology, University of Kansas Medical Center, Kansas City, KS, [2]Parker B. Francis Summer Research Fellowship, University of Missouri Columbia, Columbia, MO, [3]Department of Biostatistics, University of Kansas Medical Center, Kansas City, KS, [4]Computational Medicine Center, Sidney Kimmel Medical College, Thomas Jefferson University, Philadelphia, PA

To investigate potential contributions of the mitochondrial genome (mtDNA) to metastasis we developed mitochondrial nuclear-exchange (MNX) mice in which the mitochondrial genome of one inbred strain is combined with the nuclear genome of another strain. In MNX mouse crosses with transgenic mice possessing oncogenic drivers, we found that the mitochondrial genome contains at least one quantitative trait locus that alters efficiency of tumorigenicity and metastasis. A polymorphic region in the mitochondrial tRNA for arginine (MT-TR) correlated with differential regulation of epigenetic marks and gene expression in the nuclear genome, metabolism, gut microbiota composition, and immune profiles. Preliminary data show that MT-TR produces tRNA-derived fragments (tRF), also seen with nuclear genome-encoded tRNA. We hypothesize that MT-TR-derived tRF act as signaling molecules whose actions lead to the observed phenotypic alterations. We aimed to characterize MT-TR-derived tRF nucleotide sequences and expression across tissues with the ultimate goal of elucidating signaling pathways and key potential targets regulating the severity of metastasis. The work proposed herein will establish a foundation allowing us to functionalize mt-tRF, focusing on their ability to modulate tumorigenicity, metastasis, and the expression of nuclear DNA-encoded genes.

149. Loss of *Specc1l* causes disorganization of Blood-CSF Barrier resulting in Congenital Hydrocephalus

Dana Thalman[1], Brittany M. Hufft-Martinez[1,2], Jeremy Goering[1], Luke Wenger[1], An Tran[1], Zaid Umar[1], Benjamin Kelm[1], Sarah C. Wilson[1], Marta Stetsiv[1], Irfan Saadi[1,2]
[1]Department of Cell Biology and Physiology, University of Kansas Medical Center, Kansas City, KS, [2]Institute for Reproductive and Developmental Sciences, University of Kansas Medical Center, Kansas City KS

Congenital hydrocephalus is a genetically heterogeneous condition affecting 1/2000 live-births. Cerebrospinal fluid (CSF) accumulates in brain ventricles, resulting in skull expansion, brain compression, and impaired brain function. *SPECC1L* is a cytoskeletal scaffolding protein that interacts with actin, microtubules, and junctional proteins. Patients with autosomal-dominant *SPECC1L* mutations mainly develop craniofacial anomalies, but some also manifest ventriculomegaly. On both C57BL6/J and FVB/NJ genetic backgrounds, homozygous *Specc1l* null mouse mutants showed perinatal lethality with midgestational edema along the developing cranium and spine. However, on C57BL/6J;FVB/NJ F1 (50:50) mixed background, homozygous *Specc1l* mutants survived postnatally and developed hydrocephalus. This confirms a novel role for *Specc1l* deficiency in the etiology of congenital hydrocephalus, and indicates genetic modulation of *Specc1l* deficient phenotype by the F1 mixed background. Lateral ventricles were enlarged two-fold in mutants at embryonic day (E) 16.5, suggesting an early defect in CSF production, ciliary flow, or CSF drainage. On homogeneous FVB/NJ or C57BL/6J background, E16.5 mutant choroid plexus in the lateral ventricles was structurally disorganized, with abnormal branching and vacuolization of ependymal-endothelial interface. The mutant ependymal cells also showed abnormal localization for b-catenin (adherens junctions) and ZO-1 (tight junctions), consistent with a blood-CSF barrier defect. The ependymal cell motile cilia showed increased length and number per cell in mutants, which could result in abnormal CSF flow. Our studies using F1 mixed background-based *Specc1l* mutants will serve to identify which aspects of *Specc1l* mutant dysfunction are ameliorated, and thus determine genetic modulation in the etiology of the human condition of ventriculomegaly and congenital hydrocephalus.

150. Presence of Porcine Endogenous Retrovirus C in Domestic Pig Populations

Welton, Avery[1], Eric Gillock[1]
[1]Department of Biological Sciences, Fort Hays State University

There is currently a shortage of organs avaliable to perform allotransplants in humans. To help alleviate some of this pressure, xenotransplantation has been increasingly studied as an alternative. Xenotransplantation is the transplantation of living tissues between different species. Porcine tissues are being highly considered for xenotransplantation for many reasons. However, there are some major concerns for cross species transmission. More specifically, there is concern for transmission of Porcine Endogenous Retroviruses (PERVs) when considering this type of xenotransplantation. These are retroviruses that have infected germ-line cells of pigs and become permanently integrated into the host cell's DNA, leading to vertical transmission of the virus. This is of note because two of the three subtypes of the PERVs, A and B, are infectious to humans and can recombine with the third subtype, C. The purpose of this study is to determine the presence of PERV-C in the domestic population of pigs at the FHSU university farm. In total, 23 positives have been identified out of 68 samples (34% positives).

151. Mitochondrial ATPase ClpB is essential for neutrophil differentiation of myeloid precursor cells
Tomasz Wenta, Guanpeng Wang, Lexi Ziolo, Michal Zolkiewski, Anna Zolkiewska
Department of Biochemistry and Molecular Biophysics, Kansas State University

Biallelic or monoallelic mutations in the human *CLPB* gene result in congenital neutropenia, an inborn disorder of granulopoiesis characterized by a low count of mature neutrophils in the blood. In severe cases, *CLPB* mutations lead to life threatening infections and death in the first weeks or months of life. *CLPB* encodes an ATPase that is exclusively localized to the intermembrane space in the mitochondria, but its function during neutrophil differentiation is currently unknown. We show that CRISPR-Cas9-mediated ClpB knockout in murine myeloblastic 32D cell line using two different guide RNAs leads to decreased mitochondrial membrane potential and accumulation of the shortest isoform of optic atrophy type 1 (OPA1), which is indicative of a mitochondrial stress and altered mitochondrial dynamics. Stimulation of 32D cell differentiation using granulocytic colony stimulating factor (G-CSF) increased cell apoptosis in ClpB-deficient 32D cells, as determined by Apotracker Green staining, followed by flow cytometry, and by detecting cleaved caspase 3 by Western blotting. Using the MitoSOX Red indicator of superoxide in the mitochondria of live cells, we detected elevated superoxide levels in ClpB-deficient cells incubated with G-CSF, as compared to control 32D cells. Collectively, these results suggest that ClpB plays an important role in promoting the survival of myeloid cells during granulocytic differentiation induced by G-CSF.

152. Investigating medium-chain fatty acid production in developing fruits of Chinese elm.
P A D B Vinusha Wickramasinghe, Ruth Welti
Division of Biology, Kansas State University

Medium-chain fatty acids (MCFAs) are straight-chain mono-carboxylic acids containing 6 – 12 carbons. Among their many commercial applications, MCFAs are directly used as flavorants and antimicrobials. Triglycerides (triacylglycerols) with medium-chain fatty acids as the main components can be used biofuels with minimal processing and without derivatization. MCFAs also have many uses in the chemical industry, and it is predicted that their market value will increase continuously.

Ulmus parvifolia (common name: Chinese elm) fruits produce primarily capric acid, also known as decanoic acid, a saturated MCFA with 10 carbons, as high as about fifty weight percent of total lipid content. Our preliminary studies using gas chromatography and triple quadrupole mass spectrometry confirmed the presence of high levels of capric acid in elm fruit and identified caprylic acid (i.e., an 8-carbon fatty acid, octanoic acid) as the second most common fatty acid. Additionally, targeted analysis on developing fruits of *U. parvifolia* shows that capric acid levels generally increase during development.

153. A Novel Role for the 'Migraine Molecule' Calcitonin Gene-Related Peptide in Neurogenic Bowel Pain and Dysfunction
Adam Willits[1], Leena Kader[1], Olivia Eller[2], Kyle Baumbauer[2], Erin Young[1]
[1]Department of Anesthesiology, University of Kansas Medical Center
[2]Department of Cell Biology and Physiology, University of Kansas Medical Center

Neurogenic bowel (NB) affects 60% of people with spinal cord injury (SCI) and is characterized by slow colonic transit, constipation, and chronic abdominal pain. NB rarely resolves and tends to worsen over time, making it a long-term challenge. The knowledge gap surrounding NB mechanisms after SCI means that interventions are primarily symptom-focused and largely ineffective. Identifying the mechanism(s) that initiate and maintain NB after SCI is critically important to the development of evidence-based, novel therapeutic options for NB after SCI. We employed tissue-specific, multi-omics approaches in a T8-10 mouse model of contusion SCI to characterize NB pathogenesis. Preliminary analyses indicate a rapid and persistent increase in expression of the inflammatory mediator, calcitonin gene-related peptide (CGRP), suggestive of neurogenic inflammation engaged by SCI. Intrarectal antagonism of CGRP activity significantly prevents NB-like phenotypes including colonic dysmotility, neoplastic lymphoid hyperplasias, and other structural defects of the colon. Interestingly, the effect of gut microbial dysbiosis including primary afferent hyperresponsiveness to fecal supernatants was also prevented by CGRP antagonism. This suggests that CGRP overexpression not only precedes microbiome dysbiosis but also that dysbiosis can be prevented by targeting CGRP at the time of injury. These data support the role for CGRP as a biological substrate for NB after SCI and a potential novel therapeutic target for the prevention of maladaptive colonic inflammation and gut dysbiosis in NB.

154. Infectious Disease Assay Development Core: High Throughput Screening Laboratory at the University of Kansas
Anuradha Roy, PhD
IDAD-HTS Laboratory, University of Kansas, Lawrence, KS, USA

The overall goal of the IDAD Core is to provide expertise, facilities, services, and training in the area of HTS assay design, development, validation, small and large-scale screening for whole cell based or biochemical infectious disease targets. The IDAD core is an extension of the University of Kansas High Throughput Screening Laboratory which is a fee-for-service, state-of-the-art facility dedicated to providing academia, not-for-profit institutions, biotech, and pharmaceutical industries with exceptional assay development, high throughput screening and data mining 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. The laboratories are equipped with cutting-edge liquid handling and signal detection instrumentation for increasing throughput and precision of screening campaigns. Clients have the option of using our collection of 395,000 compounds and/or a client's own chemical library. KU-IDAD/HTS 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.

Symposium Participants

#	Name	Institution	Identifier/Title	Email
1	Abdine, Yara	Wichita State University	Undergraduate student	yhabdine@shockers.wichita.edu
2	Abraham, Kj	Langston University	Associate Professor and Campus Coordinator	kj.abraham@langston.edu
3	Accilien, Kervens	University of Kansas - Lawrence	Graduate student	kerv.acc@ku.edu
4	Ackley, Brian	University of Kansas - Lawrence	Associate Professor and Campus Coordinator	bdackley@ku.edu
5	Adamson, Summer	Kansas State University	Undergraduate student	summer22@ksu.edu
6	Adefuye, Ifelayo	Fort Hays State University	Assistant Professor	iiadefuye@fhsu.edu
7	Adem, Seid	Washburn University	Professor	seid.adem@washburn.edu
8	Adhikari, Sandeep	Kansas State University	Graduate student	sadhikari@ksu.edu
9	Agah, Arvin	University of Kansas - Lawrence	University Administrator	agah@ku.edu
10	Aikin, Tatum	University of Kansas - Lawrence	Undergraduate student	tatum.aikin@gmail.com
11	Akhtar, Sara	Pittsburg State University	Undergraduate student	sara.akhtar@gus.pittstate.edu
12	Alaribe, Oluchi	Kansas State University	Graduate student	olualaribe@ksu.edu
13	Allen, Blake	Kansas State University	Undergraduate student	bmikester123@gmail.com
14	Allphin, Braden	Fort Hays State University	Undergraduate student	b_allphin@mail.fhsu.edu
15	An, Chao	Kansas State University	Graduate student	chaoan@ksu.edu
16	Anchondo, Maya	Kansas State University	Undergraduate student	mayaiza@ksu.edu
17	Apprill, Lauren	Kansas State University	Undergraduate student	lapprill03@gmail.com
18	Arria, Blake	Kansas State University	Undergraduate student	arria32@ksu.edu
19	Auletti, Ivy	Kansas State University	Undergraduate student	ivya@ksu.edu
20	Azuma, Yoshiaki	University of Kansas - Lawrence	Professor	azumay@ku.edu
21	Bachtel, Taylor	Kansas State University	Graduate student	tbachtel2@gmail.com
22	Balthazor, James	Fort Hays State University	Associate Professor and Campus Coordinator	jrbalthazor@fhsu.edu
23	Bann, James	Wichita State University	Associate Professor	jim.bann@wichita.edu
24	Barnes, Jenna	University of Kansas - Lawrence	Undergraduate student	jenna.barnes@ku.edu
25	Bartkoski, Michael	Kansas State University	Undergraduate student	michaelb145@ksu.edu
26	Baumbauer, Kyle	University of Kansas Medical Center	Assistant Professor	kbaumbauer@kumc.edu
27	Becerra, Jesus	Kansas State University	Undergraduate student	Jbecerra837@ksu.edu
28	Beck, Moriah	Wichita State University	Professor	moriah.beck@wichita.edu
29	Bevis, Alec	University of Kansas - Lawrence	Graduate student	ambevis@ku.edu
30	Bhusal, Kiran	Kansas State University	Graduate student	Kbhusal@ksu.edu
31	Bjerke, Susan	Washburn University	Associate Professor	susan.bjerke@washburn.edu
32	Blake, Caden	Kansas State University	Undergraduate student	ccblake@ksu.edu
33	Blanco, Gustavo	University of Kansas Medical Center	Professor and Chair	gblanco@kumc.edu
34	Blecha, Frank	Kansas State University	University Distinguished Professor	blecha@vet.ksu.edu
35	Blocker, Erin	Emporia State University	Assistant Professor	eblocker@emporia.edu
36	Bolick, Abby	Pittsburg State University	Undergraduate student	abolick@gus.pittstate.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
37	Bousfield, George	Wichita State University	Professor	george.bousfield@wichita.edu
38	Boydston, Paige	Pittsburg State University	Assistant Professor	paigeboydston@pittstate.edu
39	Braasch-Turi, Maggi	Fort Hays State University	Assistant Professor	mmbraaschturi@fhsu.edu
40	Bremer, Keith	Fort Hays State University	Director of Graduate School	kabremer@fhsu.edu
41	Brodsky, Christine	Pittsburg State University	Associate Professor and Campus Coordinator	cbrodsky@pittstate.edu
42	Brown, Susan	Kansas State University	Professor and K-INBRE Core Director	sjbrown@ksu.edu
43	Burnett, Tim	Emporia State University	Dean, Associate Professor, K-INBRE Core Director	tburnett@emporia.edu
44	Camper, Sally	University of Michigan	K-INBRE External Advisory Board Member	scamper@umich.edu
45	Cantu, Kayla	Wichita State University	Undergraduate student	kacantu@shockers.wichita.edu
46	Carreon, Eldric	University of Kansas - Lawrence	Graduate student	ejtcarreon96@ku.edu
47	Carrico, Levi	Pittsburg State University	Graduate student	lcarrico@gus.pittstate.edu
48	Carrier, Camille	Kansas State University	Undergraduate student	ccarrier@ksu.edu
49	Carte, Meris	Wichita State University	Research Lab Manager	meris.carte@wichita.edu
50	Cashell, Meghan	Emporia State University	Graduate student	mcashell@g.emporia.edu
51	Casillas-Vallejo, Oscar	Langston University	Undergraduate student	oscasil@langston.edu
52	Cesur, Robin	Fort Hays State University	Graduate student	r_cesur@mail.fhsu.edu
53	Chahine, Kamar	University of Kansas - Lawrence	Undergraduate student	chahinekamar3@ku.edu
54	Chan, Tiffany	University of Kansas - Lawrence	Undergraduate student	tchan@ku.edu
55	Chapes, Stephen	Kansas State University	K-INBRE Emeritus	skcbiol@ksu.edu
56	Chapin, Bridgett	Haskell Indian Nations University	Professor and Campus Coordinator	bchapin@haskell.edu
57	Chapman, Heiata	University of Kansas Medical Center	K-INBRE Assistant Director	hchapman@kumc.edu
58	Chen, Keying (Kelly)	Fort Hays State University	Undergraduate student	k_chen9@mail.fhsu.edu
59	Cheng, Nikki	University of Kansas Medical Center	Professor, Graduate School Representative	ncheng@kumc.edu
60	Chintapalli, Sree	University of Arkansas for Medical Sciences	Assistant Professor	svchintapalli@uams.edu
61	Chitanavong, Pearly	Wichita State University	Undergraduate student	pchit45@gmail.com
62	Choi, Jae Young	University of Kansas - Lawrence	Assistant Professor	jaeyoung.choi@ku.edu
63	Chung, Peter	Pittsburg State University	Professor	pchung@pittstate.edu
64	Claar, Ben	Piestar, Inc.	Vendor (Piestar)	ben@piestar.com
65	Claridge, David	Emporia State University	Undergraduate student	dclaridg@g.emporia.edu
66	Coffman, Lauren	Wichita State University	Undergraduate student	lgcoffman@shockers.wichita.edu
67	Conners, Ethan	Washburn University	Undergraduate student	ethan.conners@washburn.edu
68	Consani, Angela	Bioscience Core Skills Institute	Vendor (Bioscience Core Skills Institute)	angela@coreskillsinstitute.com
69	Cooper, Nasya	Langston University	Undergraduate student	nasya.cooper402@gmail.com
70	Covert Miller, Laura	Pittsburg State University	Professor	lcovert@pittstate.edu
71	Cuellar, Evelyn	University of Kansas - Lawrence	Undergraduate student	e696c433@ku.edu
72	Da Silva Carvalho, Claudia	Fort Hays State University	Assistant Professor	cmdasilvacarvalho@fhsu.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
73	Dasgupta, Ayushee	Pittsburg State University	Undergraduate student	adasgupta@gus.pittstate.edu
74	Dasgupta, Debolina	University of Kansas Medical Center	Graduate student	ddasgupta@kumc.edu
75	Davido, David	University of Kansas - Lawrence	Professor	ddavido@ku.edu
76	Davies, Griffin	Fort Hays State University	Undergraduate student	gwdavies@mail.fhsu.edu
77	Davis, Lindsay	Langston University	Assistant Professor	dalin@langston.edu
78	Davis, Myles	Haskell Indian Nations University	Undergraduate student	myles.davis@haskell.edu
79	Davison, Dinah	Kansas State University	Postdoc	dinahdavison@ksu.edu
80	Dean, Tara	Piestar, Inc.	Vendor (Piestar)	tara@piestar.com
81	DeVader, Sarah	Kansas State University	Graduate student	sdevader05@ksu.edu
82	Devkota, Surya	Kansas State University	Graduate student	devkotasp@ksu.edu
83	Diaz-Rocha, Ashley	University of Kansas Medical Center	Undergraduate student	ashleydiaz0706@gmail.com
84	Diehl, Maria	Kansas State University	Assistant Professor	mmdiehl@ksu.edu
85	Ding, Jing	Kansas State University	Postdoc	jingd@ksu.edu
86	Dixon, Dan	University of Kansas - Lawrence	Professor	dan_dixon@ku.edu
87	Dogan, Duru	Kansas State University	Undergraduate student	duru@ksu.edu
88	Duraisamy, Santhosh Kumar	University of Kansas Medical Center	Postdoc	sduraisamy@kumc.edu
89	Eichhorn, David	Wichita State University	University Administrator	david.eichhorn@wichita.edu
90	Ensley, Ian	University of Kansas Medical Center	Undergraduate student	iensley1@jh.edu
91	Evans, Andrew	University of Kansas - Lawrence	Graduate student	andrewevans@ku.edu
92	Ewald, Morgan	University of Kansas Medical Center	Graduate student	m465r355@kumc.edu
93	Fan, Scott	Kansas State University	Professor	skfan@ksu.edu
94	Feist, Dylan	Kansas State University	Undergraduate student	dbfeist@ksu.edu
95	Ferguson, Jonathan	Fort Hays State University	Undergraduate student	jrferguson2@mail.fhsu.edu
96	Ferkul, Anna	University of Kansas - Lawrence	Undergraduate student	annaferkul@ku.edu
97	Fernandez, Meagan	Emporia State University	Undergraduate student	mfernan3@g.emporia.edu
98	Fette, Abigail	Washburn University	Undergraduate student	abigail.fette@washburn.edu
99	Fields, Stephen	Emporia State University	Associate Professor and Campus Coordinator	sfields1@emporia.edu
100	Fleming, Sherry	Kansas State University	Professor and Campus Coordinator	sdflemin@ksu.edu
101	Frantz, Clare	University of Kansas Medical Center	K-INBRE Program Coordinator	cfrantz2@kumc.edu
102	Freedman, Abegel	Wichita State University	Postdoc	abegel.freedman@wichita.edu
103	Gaete Humada, Belen	Kansas State University	Graduate student	bgaete@ksu.edu
104	Gagnon, Carly	University of Kansas Medical Center	Undergraduate student	chopegagnon@gmail.com
105	Gardner, Jamie	Emporia State University	Academic Advisor	jgardne7@emporia.edu
106	Gardner, Stewart	Emporia State University	Assistant Professor	sgardne4@emporia.edu
107	Gardner, Ziyyah	Langston University	Undergraduate student	Ziyyah.gardner@langston.edu
108	Gates, Charles	Langston University	Undergraduate student	Charles.Gates@langston.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
109	Gaudreault, Natasha	Kansas State University	Research Assistant Professor	nng5757@vet.k-state.edu
110	Geisbrecht, Erika	Kansas State University	Professor	geisbrechte@ksu.edu
111	Ghosh, Anuradha	Pittsburg State University	Associate Professor	aghosh@pittstate.edu
112	Gillock, Eric	Fort Hays State University	Professor	egillock@fhsu.edu
113	Ginsberg, Paul	University of Kansas - Lawrence	Postdoc	pginsberg@ku.edu
114	Glover, Logan	Kansas State University	Undergraduate student	lglover@ksu.edu
115	Gong, Ying	Wichita State University	Graduate student	yxgong2@shockers.wichita.edu
116	Gress, Joanna	Emporia State University	Faculty	jgress@emporia.edu
117	Greving, Camryn	Fort Hays State University	Undergraduate student	cfgreving2@mail.fhsu.edu
118	Grigsby, Ryan	University of Kansas - Lawrence	Facility Director	ryan.grigsby@ku.edu
119	Gruenstaeudl, Michael	Fort Hays State University	Assistant Professor	m_gruenstaeudl@fhsu.edu
120	Hackett, Jennifer	University of Kansas - Lawrence	Core Facility Director	jhackett@ku.edu
121	Hale, Joseph	Kansas State University	Undergraduate student	jhale24@ksu.edu
122	Hallacy, Makayla	Emporia State University	Undergraduate student	mhallacy@g.emporia.edu
123	Hammond, Sydnee	Emporia State University	Undergraduate student	shammon1@g.emporia.edu
124	Harries, Phillip	Pittsburg State University	Professor	pharries@pittstate.edu
125	Hefty, P. Scott	University of Kansas - Lawrence	Professor and Director of CBID CoBRE	pshefty@ku.edu
126	Hendry, Bill	Wichita State University	Professor and Campus Coordinator	william.hendry@wichita.edu
127	Henry, Sebastian	Pittsburg State University	Undergraduate student	smhenry@gus.pittstate.edu
128	Hickman, Catherine	Kansas State University	COBRE Program / Project Manager	catherineh@vet.k-state.edu
129	Hiszczynskyj, Hannah	Emporia State University	Undergraduate student	hiszczynskyjh@gmail.com
130	Ho, Kuan-Lun	Kansas State University	Graduate student	kuanlun@ksu.edu
131	Honeycutt, Drew	University of Kansas - Lawrence	Undergraduate student	drhoneycutt@ku.edu
132	Ibude, Jane	University of Kansas Medical Center	Graduate student	jibude@kumc.edu
133	Interiano, Jennifer	University of Kansas Medical Center	Undergraduate student	jenniferinteriano2021@hotmail.com
134	Isaac, Daysha	Langston University	Undergraduate student	daysha.isaac@langston.edu
135	Izard, Tariq	Wichita State University	Undergraduate student	tariqizard@gmail.com
136	Jabara, Selena	University of Kansas Medical Center	Assistant Photographer	sjabara@kumc.edu
137	James, Anika	University of Kansas - Lawrence	Graduate student	anika.james@ku.edu
138	Jesudoss Chelladurai, Jeba	Kansas State University	Assistant Professor	jebaj@vet.k-state.edu
139	Ji, Yan	Kansas State University	Staff	yanj@ksu.edu
140	Jones, Jessica	Pittsburg State University	Undergraduate student	jessica.jones@gus.pittstate.edu
141	Joshi, Prabhu	Kansas State University	Graduate student	prjoshi@ksu.edu
142	Judd, Abigail	Kansas State University	Undergraduate student	abigai21@ksu.edu
143	Kader, Leena	University of Kansas Medical Center	Graduate student	lkader@kumc.edu
144	Kennemer, Brandon	Fort Hays State University	Undergraduate student	blkennemer@mail.fhsu.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
145	Khadka, Sahadev	Kansas State University	Graduate student	skhadka2353@ksu.edu
146	Khadka, Samiksha	Kansas State University	Graduate student	samiksha@ksu.edu
147	Khan, Yousaf	Wichita State University	Undergraduate student	ymkhan@shockers.wichita.edu
148	King, Cole	Kansas State University	Graduate student	coleking227@ksu.edu
149	Knotts, Genevieve	Haskell Indian Nations University	Undergraduate student	genevieve.knotts@haskell.edu
150	Koestler, Devin	University of Kansas Medical Center	Professor and K-INBRE Satellite Core Director	dkoestler@kumc.edu
151	Korte, Genevieve	Kansas State University	Undergraduate student	genkorte2002@gmail.com
152	Kramer, Cassandra	Kansas State University	Research Assistant	casskramer@ksu.edu
153	Kumari, Roshan	University of Kansas Medical Center	Postdoc	rkumari@kumc.edu
154	Kurosu Moriya, Sumire Carolina	Kansas State University	Undergraduate student	sumirek@ksu.edu
155	Kusi-Appiah, Alfred	Fort Hays State University	Graduate student	a_kusiappiah@mail.fhsu.edu
156	Lee, Yongkuk	Wichita State University	Assistant professor	yongkuk.lee@wichita.edu
157	Letterman, Brayden	Pittsburg State University	Graduate student	bletterman@gus.pittstate.edu
158	Leung, Sam	Washburn University	Professor and Campus Coordinator	sam.leung@washburn.edu
159	Lewis, Sharon	Langston University	Associate Professor	lewissa@langston.edu
160	Li, Ping	Kansas State University	Associate Professor	pli@ksu.edu
161	Lim, Samuel	University of Kansas - Lawrence	Graduate student	lim@ku.edu
162	Logan, Raj	Wichita State University	Assistant Professor	raj.logan@wichita.edu
163	Lopez Vazquez, Lidia	Kansas State University	Undergraduate student	LidiaL30V@gmail.com
164	Lovell, Scott	University of Kansas - Lawrence	Director and Invited Speaker	swlovell@ku.edu
165	Lundquist, Erik	University of Kansas - Lawrence	Professor, Associate Vice Chancellor for Research	erikl@ku.edu
166	Lunte, Susan	University of Kansas - Lawrence	Distinguished Professor	slunte@ku.edu
167	Macdonald, Stuart	University of Kansas - Lawrence	Professor and K-INBRE Satellite Core Director	sjmac@ku.edu
168	Mackey, Les	Fort Hays State University	Graduate School Representative	lwmackey@fhsu.edu
169	Madduru, Kushala	University of Kansas Medical Center	Undergraduate student	kmadduru@icloud.com
170	Magstadt, Alexa	University of Kansas - Lawrence	Undergraduate student	alexamagstadt@ku.edu
171	Mahmud, Sakib	Emporia State University	Graduate student	sakibnishan@gmail.com
172	Markiewicz, Mary	University of Kansas Medical Center	Associate Professor	mmarkiewicz@kumc.edu
173	Marriage, Tara	University of Kansas - Lawrence	Assistant Teaching Professor	tmarria@ku.edu
174	Martin, Eleanor	Kansas State University	Undergraduate student	eleanor3martin@ksu.edu
175	Martinez, Brittany	University of Kansas Medical Center	Postdoc	bmartinez3@kumc.edu
176	Martinez, Michael	Wichita State University	Undergraduate student	u755k249@wichita.edu
177	Mattick, Paige	Fort Hays State University	Undergraduate student	pemattick@mail.fhsu.edu
178	McCullough, Courtney	Fort Hays State University	Undergraduate student	courtney.mccullough@trojans.colbycc.edu
179	McDonald, Brianna	Langston University	Undergraduate student	brianna.mcdonald@langston.edu
180	McDonald, Jocelyn	Kansas State University	Associate Professor	jmcdona@ksu.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
181	McDonald, Peter	University of Kansas - Lawrence	Core Manager (Staff)	petemcd@ku.edu
182	McGann, Alexa	Emporia State University	Undergraduate student	amcgann@g.emporia.edu
183	McGinty, Hande Kucuk	Kansas State University	Assistant Professor	hande@ksu.edu
184	Medley, Jeffrey	Kansas State University	Postdoc	jcmedley@ksu.edu
185	Meuli, Rose	Wichita State University	Undergraduate student	rmmeuli@shockers.wichita.edu
186	Michaelis, Alia	Wichita State University	Undergraduate student	aliamichaelis@gmail.com
187	Monroe, Elissa	University of Kansas Medical Center	Photographer	emonroe@kumc.edu
188	Montelone, Beth	Kansas State University	University Administrator	bethmont@ksu.edu
189	Moore, Lauren	Langston University	Undergraduate student	lauren.moore10@langston.edu
190	Morris, E. Matthew	University of Kansas Medical Center	Assistant Professor	emorris2@kumc.edu
191	Mull, Olivia	Fort Hays State University	Undergraduate student	okmull@mail.fhsu.edu
192	Munsell, Keetan	Washburn University	Undergraduate student	keetan.munsell@washburn.edu
193	Murphy, Dusty	Haskell Indian Nations University	Undergraduate student	dustymurphy@gmail.com
194	Muthineni, Nikhitha	University of Kansas Medical Center	Undergraduate student	nsm63@georgetown.edu
195	Ness, Halle	Kansas State University	Undergraduate student	hness@ksu.edu
196	Neufeld, Kristi	University of Kansas - Lawrence	Professor	klneuf@ku.edu
197	Nguyen, Hoang Long	Washburn University	Assistant Professor	hoang.nguyen@washburn.edu
198	Nguyen, Ngoc Huan	University of Kansas - Lawrence	Graduate student	huannguyen@ku.edu
199	Nickols, Edgar	Haskell Indian Nations University	Undergraduate student	edgar.nickols@haskell.edu
200	Nishimoto, Matthew	University of Kansas Medical Center	Graduate student	m311n289@kumc.edu
201	Odoi, Isaac	Fort Hays State University	Graduate student	iyodoi@mail.fhsu.edu
202	Ogunbase, Joshua	Langston University	Undergraduate student	jlogunbase@gmail.com
203	Okyere-Addo, Kofi	Fort Hays State University	Graduate student	k_okyereaddo@mail.fhsu.edu
204	Olson, Bradley	Kansas State University	Associate Professor and K-INBRE Core Director	bjsco@ksu.edu
205	Onah, Chinemerem	Kansas State University	Graduate student	chinemeonah@ksu.edu
206	Panter, Halle	Pittsburg State University	Undergraduate student	hpanter@gus.pittstate.edu
207	Park, Albert	University of Kansas - Lawrence	Undergraduate student	abpark02@ku.edu
208	Patrick, Lorelei	Fort Hays State University	Assistant Professor	lepatrick@fhsu.edu
209	Paudyal, Girish	Washburn University	Undergraduate student	girish.paudyal@washburn.edu
210	Payne, Carlie	Pittsburg State University	Undergraduate student	cjpayne@gus.pittstate.edu
211	Pei, Dong	University of Kansas Medical Center	Research Assistant Professor	dpei@kumc.edu
212	Perera, Chamani	University of Kansas - Lawrence	Core Director	chamani@ku.edu
213	Perlmutter, Jessamyn	University of Kansas - Lawrence	Postdoc	jessamyn.perlmutter@ku.edu
214	Peterson, Alonzo	Langston University	Interim Vice President for Academic Affairs	alonzo.peterson@langston.edu
215	Petrescu, Claudia	Kansas State University	Dean and Vice Provost	cpetrescu@ksu.edu
216	Phelps-Durr, Tara	Fort Hays State University	Professor and Chair	tlphelpsdurr@fhsu.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
217	Plakke, Bethany	Kansas State University	Assistant Professor	bplakke@ksu.edu
218	Pokhrel, Bikash	University of Kansas - Lawrence	Graduate student	bikashpokhrel@ku.edu
219	Ponte, Michael	University of Kansas Medical Center	Graduate student	mponte@kumc.edu
220	Prakash, Om	Kansas State University	Professor	omp@ksu.edu
221	Prasad, Chandrashekhar	University of Kansas Medical Center	Postdoc	cprasad@kumc.edu
222	Prétôt, Laurent	Pittsburg State University	Assistant Professor	lpretot@pittstate.edu
223	Prieto, Diego	University of Kansas - Lawrence	Undergraduate student	diego.prieto@ku.edu
224	Pritchard, Michelle	University of Kansas Medical Center	Associate Professor, Graduate School Rep	mpritchard@kumc.edu
225	Proctor, Emily	University of Kansas - Lawrence	Undergraduate student	emilyproctorr@ku.edu
226	Prom, John	University of Kansas Medical Center	Graduate student	jprom@kumc.edu
227	Pugh, Coleen	Wichita State University	Professor, Dean, Vice Provost for Research	coleen.pugh@wichita.edu
228	Quintana, Theresa	Kansas State University	Graduate student	taq@ksu.edu
229	Rafferty, Ryan	Kansas State University	Associate Professor	rjraff@ksu.edu
230	Rance, Shane	Pittsburg State University	Undergraduate student	srance@gus.pittstate.edu
231	Rastogi, Trisha	Blue Valley High School	High School Night at the Lab Winner	trastogi@bluevalleyk12.net
232	Rastogi, Varun	Blue Valley High School	High School Night at the Lab Winner	vrastogi@bluevalleyk12.net
233	Reagor, McKinley	Langston University	Undergraduate student	Mcreagor.13@gmail.com
234	Reed, Aliyana	Langston University	Undergraduate student	aliyana.reed@langston.edu
235	Reh, Shelley	Piestar, Inc.	Vendor (Piestar)	shelley@piestar.com
236	Rice, Paige	University of Kansas Medical Center	University Administrator	price3@kumc.edu
237	Richardson, Kaysey	Wichita State University	Marketing and Communicaitons Coordinator	kaysey.richardson@wichita.edu
238	Richt, Juergen	Kansas State University	Regents Distinguished Professor	jricht@vet.k-state.edu
239	Richter, Kimber	University of Kansas Medical Center	Professor and Director	krichter@kumc.edu
240	Rips-Goodwin, Audrey	University of Kansas - Lawrence	Undergraduate student	audrey.rips@ku.edu
241	Robinson, Alexandra	Pittsburg State University	Undergraduate student	anrobinson@gus.pittstate.edu
242	Rockley, Jillian	Kansas State University	Undergraduate student	jnrockley@gmail.com
243	Rodriguez, Ryan	Emporia State University	Undergraduate student	12927.ryan@gmail.com
244	Rojas, Jianna	Fort Hays State University	Undergraduate student	jmrojas@mail.fhsu.edu
245	Rorstrom, Carl	Washburn University	Undergraduate student	carl.rorstrom@washburn.edu
246	Rosiere, Silas	Pittsburg State University	Graduate student	srosiere@gus.pittstate.edu
247	Rosowsky, David	Kansas State University	Vice President for Research	rosowsky@ksu.edu
248	Roy, Anuradha	University of Kansas - Lawrence	Core Director (Staff)	anuroy@ku.edu
249	Ruble, Shannon	Kansas State University	Graduate student	shannonruble@ksu.edu
250	Rueschhoff, Gabriella	Fort Hays State University	Undergraduate student	gjrueschhoff@mail.fhsu.edu
251	Rymer, Audrey	Fort Hays State University	Undergraduate student	amrymer@mail.fhsu.edu
252	Rymer, Garret	Fort Hays State University	Undergraduate student	gdrymer@mail.fhsu.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
253	Saadi, Irfan	University of Kansas Medical Center	Associate Professor	isaadi@kumc.edu
254	Sanderson, Brian	University of Kansas - Lawrence	Research Staff	brian.sanderson@ku.edu
255	Sandoval, Alexander	University of Kansas - Lawrence	Research Assistant	a406s688@ku.edu
256	Sandoval, Allie	Kansas State University	Undergraduate student	allierosesand@gmail.com
257	Sanneman, Joel	Kansas State University	Core Facility Manager (Staff)	jsanneman@vet.k-state.edu
258	Scherrman, Audrey	Wichita State University	Graduate student	arscherrman@shockers.wichita.edu
259	Schieferecke, Grace	Kansas State University	Undergraduate student	gschief@ksu.edu
260	Schmidt, Shaun	Washburn University	Professor and Chair	shaun.schmidt@washburn.edu
261	Schrick, Kathrin	Kansas State University	Associate Professor	kschrick@ksu.edu
262	Schulte, Emily	Fort Hays State University	Undergraduate student	easchulte@mail.fhsu.edu
263	Schulz, Evan	University of Kansas - Lawrence	Graduate student	evanschulz@ku.edu
264	Seiler, Madelyn	Kansas State University	Undergraduate student	mrseiler@ksu.edu
265	Sekavec, Jeffrey	Fort Hays State University	Professor	jgsekavec@mail.fhsu.edu
266	Self, Adrian	Kansas State University	Operations Research Analyst (Staff)	amself@ksu.edu
267	Shaikh, Anam	University of Kansas - Lawrence	Graduate student	anamshaikh@ku.edu
268	Sharma, Madhulika	University of Kansas Medical Center	Assistant Professor	msharma3@kumc.edu
269	Shi, Michael	University of Kansas Medical Center	Undergraduate student	michaelshi2142@gmail.com
270	Shippy, Teresa	Kansas State University	Bioinformatics Center Staff	tshippy@ksu.edu
271	Short, Mary	Wichita State University	Research Technician	shortmarym@gmail.com
272	Siddique, Ariana	University of Kansas - Lawrence	Undergraduate student	Asiddique@ku.edu
273	Simmons, Christopher	Pittsburg State University	Undergraduate student	Christopher.Simmons@gus.pittstate.edu
274	Simmons, Juliane	Langston University	Undergraduate student	juliane.simmons@langston.edu
275	Singh, Navya	University of Kansas - Lawrence	Undergraduate student	navyasinghgrad@gmail.com
276	Sivayokan, Bhavana	Kansas State University	Graduate student	bhavana@ksu.edu
277	Smith, Howard	Pittsburg State University	University Administrator	hwsmith@pittstate.edu
278	Smith, Kayla	Langston University	Undergraduate student	Kayla.smith15@langston.edu
279	Smith, Loryn	Fort Hays State University	Graduate student	lmsmith0998@gmail.com
280	Snow, Neil	Pittsburg State University	Professor	nsnow@pittstate.edu
281	Snowden, Nathan	Kansas State University	Undergraduate student	ndsnowden@ksu.edu
282	Soares, Michael	University of Kansas Medical Center	University Distinguished Professor	msoares@kumc.edu
283	Souza-Neto, Jayme	Kansas State University	Assistant Professor	jsouzaneto@vet.k-state.edu
284	Spaulding, Zachary	Kansas State University	Graduate student	jdspauld@ksu.edu
285	Speckhart, Savannah	University of Kansas Medical Center	Postdoc	sspeckhart@kumc.edu
286	Speer, Timothy	Washburn University	Undergraduate student	timothy.speer@washburn.edu
287	Stanford, John	University of Kansas Medical Center	Professor and K-INBRE Program Director	jstanford@kumc.edu
288	Stanley, Carter	Kansas State University	Undergraduate student	carterstanley@k-state.edu

Symposium Participants

#	Name	Institution	Identifier/Title	Email
289	Stark, William	Fort Hays State University	Professor	wjstark@fhsu.edu
290	Steigner, Sofia	Emporia State University	Undergraduate student	ssteigne@g.emporia.edu
291	Strating, Hunter	Kansas State University	Undergraduate student	hunter45@ksu.edu
292	Sturm, Belinda	University of Kansas - Lawrence	Interim Vice Chancellor for Research	bmcswain@ku.edu
293	Su, Andy	Kansas State University	Graduate student	suandy2639@ksu.edu
294	Sundar, Isaac Kirubakaran	University of Kansas Medical Center	Associate Professor	isundar@kumc.edu
295	Swancutt, Katy	University of Kansas Medical Center	Postdoc	kswancutt@kumc.edu
296	Swedlund-Hall, Shae	BioKansas	Poster Judge	shae@biokansas.org
297	Sweger, James	Langston University	Undergraduate student	james.sweger@langston.edu
298	Swider, Patrick	Emporia State University	Undergraduate student	pswider@g.emporia.edu
299	Sydzyik, Will	Kansas State University	Undergraduate student	wsydzyik@ksu.edu
300	Talebibarmi, Pouria	Kansas State University	Graduate student	pouria@ksu.edu
301	Tamura, Masaaki	Kansas State University	Professor	mtamura@vet.ksu.edu
302	Tank, Guilherme	Kansas State University	Graduate student	wtank@ksu.edu
303	Thalman, Dana	University of Kansas Medical Center	Graduate student	dthalman@kumc.edu
304	Thomas, Brent	Emporia State University	University Administrator	rthomas2@emporia.edu
305	Thompson, Mia	Kansas State University	Undergraduate student	miathomp@ksu.edu
306	Tiwari, Prabhat	Kansas State University	Postdoc	tiwari.prabhat@gmail.com
307	To, Bao Nhu	Wichita State University	Undergraduate student	bnto@shockers.wichita.edu
308	Todd, Richard	Kansas State University	Associate Professor	rbtodd@ksu.edu
309	Tolbert, Emily	Kansas State University	Undergraduate student	etolbert@ksu.edu
310	Tran, Julie	Wichita State University	Undergraduate student	jxtran8@shockers.wichita.edu
311	Tran, Pamela	University of Kansas Medical Center	Associate Professor	ptran@kumc.edu
312	Trout, Kaye	Piestar, Inc.	Vendor (Piestar)	dkayetrout@cox.net
313	Unckless, Robert	University of Kansas - Lawrence	Associate Professor	unckless@ku.edu
314	Veith, Sabrina	Kansas State University	Undergraduate student	sabrinann22@ksu.edu
315	Velasquez, Sarah	University of Kansas Medical Center	K-INBRE Core Director	svelasquez@kumc.edu
316	Vijayakumar, Saranya	Kansas State University	Postdoc	saranya@ksu.edu
317	Walker, Greyson	Kansas State University	Undergraduate student	gjwalker21@ksu.edu
318	Wall, Hannah	Langston University	Undergraduate student	hannah.wall@langston.edu
319	Wallace, Nick	Kansas State University	Associate Professor	nwallac@ksu.edu
320	Wang, Guanpeng	Kansas State University	Graduate student	guanpenw@ksu.edu
321	Ward, Christopher	Pittsburg State University	Assistant Instructional Professor	christopherward@pittstate.edu
322	Watanabe, Masakatsu	Fort Hays State University	Assistant Professor	M_watanabe@fhsu.edu
323	Watson, Jack	Emporia State University	Undergraduate student	jwatson9@g.emporia.edu
324	Wedman, Clarissa	Pittsburg State University	Undergraduate student	clarissa.wedman@gmail.com

Symposium Participants

#	Name	Institution	Identifier/Title	Email
325	Welch, Danny	University of Kansas Medical Center	Professor	dwelch@kumc.edu
326	Welti, Ruth	Kansas State University	Professor	welti@ksu.edu
327	Welton, Avery	Fort Hays State University	Graduate student	averywelton21@gmail.com
328	Wendel, Sebastian	Kansas State University	Postdoc	sw87@ksu.edu
329	Wenta, Tomasz	Kansas State University	Postdoc	twenta19@ksu.edu
330	Wickramasinghe, P A D B Vinusha	Kansas State University	Graduate student	vinuwickram@ksu.edu
331	Wildeman, Kameron	Kansas State University	Undergraduate student	krwilde@ksu.edu
332	Willits, Adam	University of Kansas Medical Center	Graduate student	awillits@kumc.edu
333	Wolf, Jaylynn	Wichita State University	Undergraduate student	jnwolf@shockers.wichita.edu
334	Woolf, Marshall	Fort Hays State University	Undergraduate student	m_woolf@mail.fhsu.edu
335	Wright, Doug	University of Kansas Medical Center	Professor and K-INBRE Principal Investigator	dwright@kumc.edu
336	Wright, Jeff	Piestar, Inc.	Vendor (Piestar)	wright@piestar.com
337	Wrixon, Liam	Haskell Indian Nations University	Undergraduate student	liamwrixon@gmail.com
338	Wu, Wei	Kansas State University	Graduate student	gisswu@ksu.edu
339	Yackovich, Nikolas	Emporia State University	Undergraduate student	nyackovi@g.emporia.edu
340	Yang, Shang-You	Wichita State University	Associate Professor	shang-you.yang@wichita.edu
341	Yao, Li	Wichita State University	Associate Professor	li.yao@wichita.edu
342	Yessin, Wael	Wichita State University	Undergraduate student	wael.yessin@gmail.com
343	Young, Erin	University of Kansas Medical Center	Assistant Professor	eyoung6@kumc.edu
344	Yusuf, Kafayat	University of Kansas Medical Center	Graduate student	kyusuf@kumc.edu
345	Zhang, Qiyang	Emporia State University	Associate Professor	qzhang2@emporia.edu
346	Ziolo, Lexi	Kansas State University	Undergraduate student	lexiziolo@ksu.edu
347	Zolkiewska, Anna	Kansas State University	Professor	zolkiea@ksu.edu
348	Zolkiewski, Michal	Kansas State University	Professor and Department Head	michalz@ksu.edu
349	Zoong Lwe, Zolian	Kansas State University	Graduate student	zolian@ksu.edu
350	Zurek, Daniel	Pittsburg State University	Professor	dzurek@pittstate.edu

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