The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

Oct. 31 - Nov. 1, 2025
Washington University in St. Louis

Beloit College - Carthage College - Colorado College
Grinnell College - Gustavus Adolphus College - Hope College Knox College - Lawrence University - Macalester College
St.Olaf College - University of Chicago
Washington University in St. Louis

Midstates Consortium for Math and Science Undergraduate Research Symposium for the Biological Sciences and Psychology at Washington University in St. Louis		
October 31 - November 1, 2025		
	Friday, October 31 Schedule	
2:00 – 5:20 pm	Lobby at Doubletree by Hilton Forest Park 4550 Forest Park Avenue St. Louis, MO 63108	Hotel Lobby
5:30 pm – 5:40 pm	WELCOME Dr. Pamela Kittelson, Director Midstates Consortium for Math and Science Professor of Biology Gustavus Adolphus College Dr. Anthony Smith Senior Lecturer and Coordinator of Undergraduate Research Experience Biological Sciences Collegiate Division Washington University	Eric P. Newman Event Center (EPNEC) Auditorium 320 S. Euclid Avenue St. Louis, MO
5:40 pm – 6:30 pm	KEYNOTE LECTURE *One step from chaos and it's all good* **Dr. Keith Hengen** Associate Professor, Washington University	EPNEC Auditorium
6:30 pm – 7:45 pm	Dinner	EPNEC Great Room A
8:00 pm – 8:40 pm	JANET ANDERSON AWARD LECTURE *A Transparent Window on Genetics and Gene Expression* **Dr. Elizabeth De Stasio** Raymond H. Herzog Professor of Science in the Biology Department and Biochemistry Program Lawrence University	EPNEC Auditorium
Following lecture	Group Picture	EPNEC Lobby

Saturday, November 1 Schedule		
Begins at 7:00 am Avoid 7:45 rush	Breakfast For those checking out, leave key cards at the desk and bring your luggage. EPNEC Loge is a secure room.	Doubletree Lobby
8:15-8:30 am	Walk to Eric P. Newman Event Center (EPNEC)	Coffee & Tea in Lobby
8:30-8:45 am	Set-up for poster session 1 Check set-up and load Session I oral presentations	Eric P. Newman Event Center (EPNEC) Great Room A
8:45 – 9:45 am	Session 1 Poster Presentations (n=20)	EPNEC Great Room A
9:45 – 10:00 am	Break. Remove posters Check set-up and load Session I oral presentations	Coffee & Tea in Lobby
10:00 -11:00 am	Session I Oral Presentations	
	Session I.A: Moderator: Dr. Tony Smith	Great Room B
	Session I.B: Moderator: Dr. Erin Weber	Seminar Room B
	Session I.C: Moderator: Dr. Elizabeth De Stasio	Seminar Room A
	Session I.D: Moderator: Dr. Elizabeth Danka	Room 301
11:00 am - 12:15 pm	Graduate Panels: Pick Up Lunch Order. Go to Preferred Program Session.	Great Room B: MD/PHD Seminar Room B: PhD Faculty: 301
12:15 – 12:30 pm	Set-up posters for Session 2 Check set-up and load Session II oral presentations	EPNEC Great Room A
12:30 – 1:30 pm	Session 2 Poster Presentations (n=20)	
1:30 – 1:45 pm	Break. Remove posters. Check set-up and load Session II oral presentations	Coffee & Tea in Lobby
1:45 – 2:30 pm	Session II Oral Presentations	
	Session II.E: Moderator: Dr. James Demas	Room 301
	Session II.F: Moderator: Dr. Tony Smith	Great Room B
	Session II.G: Moderator: Dr. Pamela Kittelson	Seminar Room A
	Session II.H: Moderator: Dr. Paul Fischer	Seminar Room B
2:30 -2:45 pm	Break. Set-up for Poster Session 3	
2:45 – 3:45 pm	Session 3 Poster Presentations (n=19)	EPNEC Great Room A
3:45 – 4:00 pm	Meeting Concludes. Remove posters. If leaving St Louis, take boxed dinners to go. Complete online evaluations.	

2025 Keynote Lecture

One step from chaos and it's all good

Dr. Keith Hengen
Associate Professor of Biology
Washington University in St. Louis

Abstract: A human brain contains 86 billion neurons, each connecting to thousands of others in a network more complex than the entire internet (by far). This biological computer can learn new skills, form memories, and adapt throughout your lifetime. How does it work? Why doesn't it overload or burn out? How can a brain work just as well in medieval Norway as it does in modern Tokyo? We think that the answer lies in a concept borrowed from physics called "criticality". This is the same mathematical principle that explains how water turns to steam and how avalanches spread down mountainsides. All of these systems suddenly become interesting when they're at a "tipping point", resting just on the edge of chaos. At criticality, the brain exhibits remarkable properties: it can process information across all time scales simultaneously, from split-second reflexes to long-term memories. Small changes can cascade through the network in patterns that look surprisingly similar to avalanches, forest fires, or earthquakes – all following the same mathematical rules that physicists have studied for decades.

In this talk, I'll explore how we study emergent computational properties (like criticality) using everything from tiny electrodes to brain scanners, and what happens when the brain drifts away from this optimal state. Our evidence suggests that criticality is necessary for learning, the purpose of sleep is to restore criticality, and many brain disorders – from Autism to Alzheimer's – are defined by departures from this regime.

Our work suggests that, despite their biological complexity, brains may follow surprisingly universal physical principles. Understanding these rules is transforming how we think about learning, sleep, and brain health across the lifespan.

About Dr. Keith Hengen: Dr. Hengen's laboratory uses a combination of neuroscience tools, theory, and molecular manipulations to shed light on why we sleep, how our brains support rich and diverse functions, and how disease impacts information moving through networks of neurons. If the brain is a biological computer, the goal of his lab is to understand the operating system and how computation emerges from biological systems. They address questions such as: How do billions of neurons generate robust cognition and behavior? Why do our brains need sleep to achieve robust computation? And can we use disease to shine a light on what's necessary for biological computation? To address these questions, they record thousands of neurons in the brains of freely behaving animals. They model and develop machine learning tools to find meaningful structure in complexity. Numerous grants including those to the NIH which fund his lab's research. He has earned an Outstanding Achievement Award in Alzheimer's Disease Research and been named Next Generation Leader by the Allen Institute for Brain Science. He has taught undergraduate courses such as *Principles of the Nervous System* to a graduate *Sleep and Circadian* Nanocourse.

2025 Janet Andersen Award Lecture

A Transparent Window on Genetics and Gene Expression

Dr. Elizabeth De Stasio
Raymond H. Herzog Professor of Science in the Biology Department and Biochemistry Program
Lawrence University

Description: In this lecture, we will look at how biological model systems allow us to answer research questions that help us understand how biological systems work. We'll then dive into how organisms that are transparent allow us to understand gene expression and organismal development, using gene expression in the *C. elegans* nervous system as an example.

About Professor De Stasio: Dr. Elizabeth De Stasio is the Raymond H. Herzog Professor of Science in the Biology Department and Biochemistry Program at Lawrence University. She was chosen as the Janet Andersen Awardee for her excellence in undergraduate teaching, research, and service to science education. Dr. De Stasio transformed courses including introductory biology, molecular biology and genetics, making them more active environments accessible to all students. She also incorporated contemporary topics with a research focus, providing students the scaffolding to communicate as scientists in writing and discussing the primary literature. Nationally, she pioneered the publication of educational primers for Genetics, the journal of the Genetic Society of America. The primers prepare students to read and critically evaluate research articles and help them learn about model genetic organisms. The primers introduce concepts clearly so that the literature becomes more tractable. Her excellence as an undergraduate mentor has been rewarded with numerous teaching awards. Dr. De Stasio repeatedly earned funding from HHMI, NSF-LSAMP, NSF-MRI and an NSF research grant, NIH research grants, and a Sherman-Fairchild instrumentation grant to the science programs. Much of her work was in support of underrepresented students in STEM. She developed a vibrant research lab, mentoring more than 120 students in original research related to neurobiology and genetics with 27 undergraduate co- authors. She also has published widely on the scholarship of teaching and learning, contributing many ideas for research-based activities in labs. Beth has served as an Associate Editor and now Senior Editor of the Primer section in Genetics and she served a term on their board, and in roles with the College Board and Pew dedicated to improving the way science is taught nationally at both the high school and undergraduate level. Lastly, Beth has co-created a partial credit course focused on career exploration and self-reflection for students considering careers in the health care and public health professions.

About the Janet Andersen Award Lecture: Professor Janet Andersen was a beloved faculty member in the Hope College Mathematics Department and served as the Midstates Consortium Director for five years before her life ended tragically in an automobile accident in 2005. As a teacher and scholar, Janet was devoted to providing creative, high quality learning experiences for her students, and she was always learning as she was teaching. As Consortium Director, she looked for ways to connect with and support natural science faculty, both new and experienced. To honor Janet's work in her teaching, research and service to the Consortium, the Janet Andersen Lecture Award was established in 2008. Each year, nominees from the Consortium are selected by the Executive Committee to present the Janet Andersen Lecture at the fall Undergraduate Research Symposia on a topic of his or her expertise.

WiFi: WUSM guest or Guest

Oral Session I Schedule for November 1, 2025

SESSION I.A: 10:00-11:00 a.m. Room: Great Room B Moderator: Dr. Tony Smith			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1	Alex Bittner	St. Olaf College	Defining a role for the proto-oncogene Vav1 in cancer cell metastasis
I.A.2	Rachel Zuckerman	University of Chicago	Differential Lysine Catabolism in Non-Small Cell Lung Cancer Cells in the Brain and Lung Microenvironments
I.A.3	Alexis Truta	University of Chicago	Assessing the Impact of BH3 Mimetics on Mitochondrial Dynamics in Activated Human T Lymphocytes
I.A.4	Isabel Voinescu	Grinnell College	Developing a 3D Model of Human Cardiac Fibrosis

SESSION I.B: 10:00-11:00 a.m. Room: Seminar Room B Moderator: Dr. Erin Weber			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1	Akanksha Varanasi	University of Chicago	Gene Expression and Immune Mechanism Profiles of Interferon-Treated Multiple Sclerosis Patients Across Subtypes
I.B.2	Felix Guo	Washington University	Discovering the Role of Immune-based Acceptance in Incompatible Plant Grafts
I.B.3	Ephraim Craddock	University of Chicago	An IL-2-TGF-β Fusion Protein Expands Tregs and Induces Tolerance of a Minor-mismatched Skin Graft
I.B.4	Ziyu Liu	Washington University	Development of LDLRAD3-Based Decoy to Block Venezuelan Equine Encephalitis Virus Infection

SESSION I.C: 10:00-11:00 a.m. Room: Seminar Room A Moderator: Dr. Elizabeth De Stasio			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1	Noah Kabbaj	Washington University	Uncovering Serotonergic Regulation of Plasticity Using All-optical Physiology
I.C.2	Emily Silva	Colorado College	The Role of Serotonin Receptors in Regulating Stability of Idiosyncratic Behavioral Preferences in *Drosophila melanogaster*
I.C.3	Vikram Karra	Washington University	Disease-Associated Microglial Activation in Response to White Matter Insult in a Mouse Model of Tauopathy
I.C.4	Tisya Goel	Knox College	Effect of *Bacopa monnieri* on Oxidative Stress in C6 Rat Glioma Cells

SESSION I.D: 10:00-11:00 a.m. Room: 301 Moderator: Dr. Elizabeth Danka			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.D.1	Shaza Ali	Washington University	Determining Impacts of PAR4 Polymorphism on Reactivity to β-arrestin 1/2 via CRISPR/Cas9 KOs
I.D.2	Vivian Khan	Lawrence University	Development of a Model to Assess Contributions of Receptor Endosomal Signaling to TRiM Efficacy
I.D.3	Prithi Srinivasan	University of Chicago	Critically Evaluating the Co-Binding of Cofilin and Importin 9 in Nuclear Actin Transport
I.D.4	Selene Chew Chien Huei	Knox College	Effects of *Bacopa monnieri* on Proliferation and Morphology of C6 Cells

Oral Session II Schedule for November 1, 2025

SESSION II.E: 1:45-2:30 p.m. Room: 301 Moderator: Dr. James Demas			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1	Dhara Greenberg	Macalester College	The Social Cipher Video Game as a Social Emotional Learning Intervention
II.E.2	Callil Tomei and Wiktoria Kowal	Grinnell College	The Effects of a Prior Bout of Exercise and Stimulus Presentation Rates on Visual Statistical Learning
II.E.3	Ian Smith	Knox College	Comparative Anatomy of Marine Vertebrates: Diaphragm Structure and Function in Mammals

SESSION II.F: 1:45-2:30 p.m. Room: Great Room B Moderator: Dr. Tony Smith			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1	Nathaniel John	Washington University	LRRC8C Deletion Enhances Angiogenesis and Accelerates Perfusion Recovery After Ischemic Injury
II.F.2	Alex Zhang	University of Chicago	Investigating Zebrafish Neural Crest Cell Fate Restriction by Imaging Transcription In Vivo
II.F.3	Ian Palanga	Macalester College	Investigating Controversy: Osteolytic Fibrosarcoma Only Sensitizes Small DRG Neurons

SESSION II.G: 1:45-2:30 p.m. Room: Seminar Room A Moderator: Dr. Pamela Kittelson			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.G.1	Jennifer Ong	Washington University	Quantification of Polyethylene Terephthalate in Patient Blood Samples and Its Implication on Health
II.G.2	Fionn Meehan	Knox College	Are Baseballs a Hidden Reservoir for MRSA? A Microbial Survey of Collegiate Sports Gear
II.G.3	Madeline Shirk	University of Chicago	Drinking Water Quality and Accessibility in Zambia

SESSION II.H: 1:45-2:30 p.m. Room: Seminar Room B Moderator: Dr. Paul Fischer			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.H.1	Katherine Hartmann	Hope College	Using LC/MS to Identify Post-translational Modifications on xCT and its Interactome
II.H.2	Jack Farah	Washington University	Investigation of Mechanisms of the Putative Amino Acid Transport 1 (AAT1) in *Plasmodium falciparum*
II.H.3	Aaron Tran	Washington University	Pangenome-based Allele-Specific Analysis Recovers Rare and Structural Variant-driven Epigenetic Variation

Poster Sessions Schedule for November 1, 2025

Poster Session P1: 8:45-9:45 a.m. Room: Great Room A and Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Selina Fan	Washington University	The Role of E3 Ubiquitin Ligase (UBR5) in MPNST Cell Survival
P1.02	Gabby Moon	University of Chicago	BNIP3-Dependent Muscle Atrophy in Cancer Cachexia Reflects Mitochondrial Remodeling and Metabolic Stress Signaling
P1.03	Bryn Bahnks	Washington University	ADAR1 and DHX9 Represent a Therapeutic Opportunity in p53-mutated Endometrial Cancer
P1.04	Christine Kwon	University of Chicago	Integrative Network Analysis of Molecular Subtypes in High-Grade Serous Ovarian Cancer
P1.05	Geneva Fackler	Gustavus Adolphus College	Quantitative Analysis of sRNA Binding Hierarchies: The Role of mRNA Accessibility in RyhB Target Selection
P1.06	Sophia Grocholski and Cambelle Jossart	St. Olaf College	RNAi Knockdown of Lipid Droplet Associated Proteins in *Tetrahymena thermophila*
P1.07	Preeti Arra	Knox College	Development and Optimization of Transfection Vector in *Stentor coeruleus*
P1.08	Mark Ma	Washington University	TRPV2: The Hidden Switch that Keeps STING in Check—Until It's Time to Strike
P1.09	Teagan McCarty	Gustavus Adolphus College	Phenotypic and Genomic Characterization of *Candida albicans* Strains Screened for Antifungal Drug Susceptibility
P1.10	Gongdao Lyu	St. Olaf College	Complementation of Yeast Seipin Knockouts with putative *Tetrahymena* Seipin TTHERM_00497200
P1.11	Esther Ineza	Colorado College	Centromeres of the budding yeast Cyberlindnera mrakii contain transposable elements and repeat sequences
P1.12	Cora Renning and Taylor Ruhl	Gustavus Adolphus College	Mutagenesis of sOlincRNA-encoded implicated in Plant Development and Abiotic Stress Response Using CRISPR/Cas9 in *Arabidopsis thaliana*
P1.13	Joshua Briley	Colorado College	*Liatris punctata* Physiological Response to 3-methyl-2(5H)-furanone and 2(5H)-furanone Mimicking low-grade Fire Resistance
P1.14	Logan Zakrajshek	Gustavus Adolphus College	Phenotypic Response of *Brassica rapa* to Increased Anthropogenic Temperature and Nitrogen Levels
P1.15	Ian Hauver-Radloff	Colorado College	The Effect of Warming on Arctic Plant Nectar Production

Poster Session P1: 8:45-9:45 a.m. Continued Great Room A and Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.16	Maddie Goss	Knox College	Phylogenetic Analysis of Argonaute proteins in Plants
P1.17	Jack Zielski	Lawrence University	Isolating Theta Activity for Action Guiding Content and Decision Guiding Context
P1.18	Lili Bednarek	Carthage College	Expression of c-Fos as a Marker for Neuronal Activity Following Signaled Lever Press Avoidance Training in Sprague-Dawley Rats
P1.19	Kimberly Maldonado	Hope College	Transcranial Temporal Interference Stimulation Modulates Spike Timing of Subthalamic Nucleus Neurons in a Computational Neuron Model
P1.20	Katie Craven	Colorado College	Differences in Stability of Idiosyncratic Behavioral Preferences between *Drosophila* Species

Poster Session P2: 12:30-1:30 p.m. Room: Great Room A and Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Katherine Hsieh	Washington University	*Pseudomonas, Stenotrophomonas,* and *Serratia* Species Are Present in Intensive Care Unit Sinks Despite Targeted Cleaning
P2.02	Shino Okamoto	Knox College	Assessing the Effects of *Bacopa monnieri* on Migration of C6 Glioma Cells
P2.03	Sarah Narula	Washington University	Repurposing SGLT2 Inhibitors for Cardiometabolic Liver Disease
P2.04	Rahaf Qarabsa	St. Olaf College	Optimizing a Co-Culture Model to Account for the Follicular Lymphoma Tumor Microenvironment in Treatment Response to Bispecific Antibodies
P2.05	Ethan Levy	Colorado College	Examining Modes of Interaction Between Inhibitor and SL-1 Hairpin of SARS-CoV-2
P2.06	Raksa Samnang	Hope College	Experimental Analysis of *Escherichia coli* Metabolism on D-serine
P2.07	Kaitlyn Sander	Carthage College	Screening *E. coli* for the Expression of PVY Activated – GFP (PA-GFP) for Detection of PVY
P2.08	Lara Sztamfater Chocolat	University of Chicago	Evolutionary Origins and Functions of Incomplete Cytokinesis
P2.09	Abby Kugler	Gustavus Adolphus College	Co-Purification of Ski7 with the Cytoplasmic Exosome in *Saccharomyces cerevisiae*
P2.10	Julia Gordan	University of Chicago	A Structural and Coevolutionary View of the Yeast J-domain Protein SIS1's Client-Docking Patterns
P2.11	Jessica Qi	University of Chicago	Cooperative RBMX-YTHDC1 Regulation of Nascent Transcription Sustains AML
P2.12	Elsa Johnson	Gustavus Adolphus College	Investigating Binding Site Accessibility in RhyB-mediated Target Hierarchies
P2.13	Annie Phan	Carthage College	Expression of Melanin-Concentrating Hormone (MCH) and Orexin Neurons in Mouse Models of Alzheimer's Disease
P2.14	Emersyn McCann	Hope College	Interneuron Development in an Animal Model of Bipolar Disorder
P2.15	Natasha Gibson	Lawrence University	Adolescent HDM Exposure Alters Anxiety, Lung, Hippocampal Inflammation, and HPA Axis Amygdala Gene Expression

Poster Session P2: 12:30-1:30 p.m. Continued Great Room A and Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.16	Angelina Palmiotto	Gustavus Adolphus College	Investigating Inhibitory Controls of Sprague-Dawley Rats Using a Stop Signal Task
P2.17	Shuzheng Fang	Washington University	Effects of Juvenile Social Isolation on Activity of Nucleus Accumbens
P2.18	Milciades Gonzalez Medina and Nabina Rimal	Lawrence University	Understanding the Limits of Induced Awe: How Long Does it Last? Can it Increase Belongingness?
P2.19	Eleanor Wilson	Colorado College	Comparative Analysis of Innate Immune Responses to Abiotic Stressors Between Two *Caenorhabditis* Nematode Species
P2.20	Theo Ollier	Colorado College	Characterization of Fungal Endophytes from Native Colorado Flora

Poster Session P3: 2:45-3:45 p.m. Room: Great Room A and Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Trisha Gannu	Washington University	Evaluating VIT Chemotherapy Efficacy Across NF1-MPNST Subtypes
P3.02	Rutu Mungara	Knox College	Functional Gene Analysis in *Stentor coeruleus* Using RNA Interference
P3.03	Julia Coric	Washington University	PRDM1 Knockout Alters Tuft Cell Development and Reveals Peyer's Patch Immune Link
P3.04	Leslie Sauceda	Carthage College	Screening *E. coli* Expression Lines and Conditions for Production of a PVY-Activated GFP Reporter
P3.05	Ishita Aggarwal	Washington University	Analyzing the Efficacy of GM-CSF Zika Virus as an Oncolytic Therapy for Glioma
P3.06	Shelley Fernando	University of Chicago	Elucidating the Mechanisms of BRWD1-Mediated Chromatin Regulation of B Cell Development
P3.07	Ella Cerny	Washington University	Design, Synthesis, and Functional Evaluation of Intestinally-Selective Non-Isoxazole FXR Agonists
P3.08	Gabriel Simon	St. Olaf College	Media Lacking a Subset of Essential Amino Acids Signal Lipid Droplet Accumulation in *Tetrahymena thermophila*
P3.09	Samara Goltz	Gustavus Adolphus College	Investigating the Effect of Apolipoprotein C-III on Endothelial Lipase Activity
P3.10	Tanish Joshi-Apte	Washington University	Assessing Mitochondrial Dysfunction via Relative mtDNA Copy Number in TFAM-Knockout Müller Glial Cells
P3.11	Kate Rooker	Gustavus Adolphus College	Atrophy and Reduced Oxidative Capacity in Type-Identified Tibialis Anterior Muscle Fibers with Age
P3.12	Jayden Kratt	Macalester College	Relative to Females, Male Mice Exhibit a Greater Hypothermic Response Following Neurotensin Receptor 1 Activation
P3.13	Jocelyn Zacarias	University of Chicago	Associations Between Timing and Domain of Maternal Stress and Child Executive Function
P3.14	Toby Shaw	Hope College	Participants Show Motor Habit Preference and Loss Aversion in a Novel Iowa Gambling Task
P3.15	Ornela Gigolaj	Macalester College	Subcortical Sensitivity to Fearful, but not Sad, Facial Expressions in Humans

Poster Session P3: 2:45-3:45 p.m. Continued Great Room A and Lobby			
P3.16	Yael Smith	Washington University	Maternal Undernutrition Leads to Increased Risk for Offspring Steatotic Liver Disease (SLD)
P3.17	Siena Adwere-Boamah	Knox College	ADHD Moderates the Relationship Between Emotional Dysregulation and Problematic Internet Use
P3.18	Khoa Truong	Grinnell College	The Effect of Heat Stress Timing on Growth of *Arabidopsis* Seedlings
P3.19	Dasha Shyroka	Gustavus Adolphus College	Examining Pb Mobilization in Warming Peatland Ecosystems

Abstracts
Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, Washington University in St. Louis
November 1, 2025

All abstracts (poster and oral) are listed alphabetically by presenter last name.

Presenter(s): Adwere-Boamah, Siena
School: Knox College
Session: P3.17
Title: ADHD Moderates the Relationship Between Emotional Dysregulation and Problematic Internet Use
Co-Author(s):
Advisor(s): Dr. Heather Hoffmann, Knox College

Abstract: Technology use is rapidly increasing and as a result, so is the prevalence of excessive or unhealthy internet use. Problematic Internet Use (PIU) has been found to be positively associated with emotional dysfunction, as well as ADHD, and is more common in males than females. Because of this, past literature often proposes that because males typically have less emotional regulation than females, males with ADHD should be at the highest risk for PIU. However, there is a possibility that due to the interaction between biological sex and ADHD, females with ADHD may struggle more with emotional dysregulation and PIU than previously believed. The present study assessed the differences in emotional dysregulation and PIU across four groups (ADHD female, non-ADHD female, ADHD male, and non-ADHD male). Emotional dysregulation and PIU were positively associated in the overall sample. Females with ADHD scored the highest on PIU and emotional dysregulation measures out of the 4 groups, followed by males with ADHD, males without ADHD, and lastly, females without ADHD. Females with ADHD were found to have significantly higher emotional dysregulation and PIU compared to females without ADHD.

Presenter(s): Aggarwal, Ishita
School: Washington University in St. Louis
Session: P3.05
Title: Analyzing the efficacy of GM-CSF Zika Virus as an oncolytic therapy for glioma
Co-Author(s): Ashwani Kesarwani, Milan G. Chheda
Advisor(s): Milan G. Chheda, Washington University in St. Louis

Abstract: Glioblastoma (GBM) is the most lethal brain cancer with 5-year survival rate of 6.8%. Current therapies: surgery, radiation, and temozolomide fail to target glioblastoma stem cells (GSCs), which drive treatment resistance and recurrence (Lathia et. al, 2015). Our lab is developing Zika virus (ZIKV) as an oncolytic therapy, its selective tropism for GSCs and ability to recruit CD8+ T-cells (Zhu et al., 2017). Here, we engineered a GM-CSF-expressing ZIKV (GM-CSF-ZIKV) to enhance anti-tumor immunity and combined it with PD-1 checkpoint blockade. We hypothesize that GM-CSF-ZIKV and anti-PD-1 combination therapy will enhance long-term survival in mice bearing gliomas by improving dendritic cell-mediated T-cell priming and reversal of T-cell exhaustion in the tumor microenvironment (TME). To test this, we used syngeneic CT2A mouse glioma model, for treatment we used intratumoral GM-CSF-ZIKV and systemic anti-PD-1 and achieved 90% long-term survival, surpassing monotherapies

(GM-CSF-ZIKV: 66%; anti-PD-1: 25%) and no treatment controls (20%). By flow-cytometry combination-treated mice showed expanded cytotoxic CD8+ T-cells (CD44+, CD69+) and elevated effector molecules (granzymeB, perforin, IFN-γ, TNF-α). Notably, PD-1+, TOX+ exhausted T-cells were restored, suggesting immune checkpoint blockade enhanced viral-induced antigen presentation. Overall, this combination generated long-term survival and recruited cytotoxic T-cells to the TME, which may have caused tumor clearance.

Presenter(s): Ali,Shaza
School: Washington University in St. Louis
Session: I.D.1
Title: Determining impacts of PAR4 polymorphism on reactivity to β-arrestin 1/2 via CRISPR/Cas9 KOs
Co-Author(s):
Advisor(s): Robert Campbell, Washington University in St. Louis

Abstract: Arrestins recruit phosphatidylinositol-3 kinases (PI3K) to GPCRs and thrombin-stimulated platelets, which, in the presence of agonists of groups P2Y12 and Src kinases, result in a decrease of PAR4-dependent Akt phosphorylation and fibrinogen binding rates (Li, Dongjun, et al). Protease-activated receptor 4 (PAR4) has a functional dimorphism on the rs773902 SNP (expressing as A/G), which mutates residue 120, leading to two variants: Ala120 & Thr120. These variants exhibit varying levels of sensitivity to platelet agonists, with the Thr120 variant displaying hyperactivity in platelet activation, thereby promoting resistance to antiplatelet therapies (Tourdot, Stoveken, Trumbo, et al.). This variant of PAR4 occurs with greater frequency in Black individuals than in white individuals, suggesting that its incidence is in part due to racial difference, causing an increased risk of acute coronary events in Black subjects due to this SNP in the PAR4 gene, F2RL3 (Edelstein, Simon, Lindsay, et al.). The focus of this project is to determine the difference in β-arrestin 1 & 2 recruitment and sensitivity between the two variants, confirm a conformational change that occurs due to this polymorphism, and evaluate PAR4 as a mode of treatment against this polymorphism, bridging a treatment gap in cases of thrombosis and coronary heart disease.

Presenter(s): Arra, Preeti
School: Knox College
Session: P1.07
Title: Development and Optimization of Transfection Vector in *Stentor coeruleus*
Co-Author(s):
Advisor(s): Mark Slabodnick, Knox College

Abstract: *Stentor coeruleus* is a large, trumpet shaped unicellular organism with a sequenced genome. These aspects of the organism along with the development of new techniques such as RNA interference make it an emerging model system for morphogenesis, photosensation and regeneration. Unlike other models, there is no established technique for gene expression for this system. Here, we built a transfection vector, introduced mRNA into the cell via microinjection and monitored experimental conditions in an attempt to view transient expression of transgenic sequences in the cells.

Presenter(s): Bahnks, Bryn
School: Washington University in St. Louis
Session: P1.03
Title: ADAR1 and DHX9 Represent a Therapeutic Opportunity in p53-mutated Endometrial Cancer
Co-Author(s): Caleb L. Lines; Alex Mabry; Mitchell Bancks; Annalyn M. Welp; Leonard B. Maggi Jr; Jason D. Weber
Advisor(s): Jason D. Weber, Washington University in St. Louis

Abstract: The p53-mutated (p53mut) molecular classifier of endometrial cancer (EC) is associated with decreased survival and treatment resistance, underscoring the need for novel targets. p53mut EC shows elevated Type I interferon signaling, regulated by the dsRNA-binding enzymes ADAR1 and DHX9. High expression of both dsRNA enzymes is correlated with reduced survival. This study investigated the interactions between ADAR1/DHX9 in p53mut EC. Proximity ligation assay (PLA) and co-immunoprecipitation (IP) supported ADAR1–DHX9 interaction. ADAR1 and DHX9 were knocked down in six p53mut EC lines, with depletion verified by western blotting and EDU staining. ADAR1 loss reduced foci formation and DNA synthesis in most lines. Increased apoptosis (7–40%) was observed by Annexin V/7-AAD staining following ADAR1 loss, with only one cell line showing resistance. DHX9 loss consistently reduced growth across all lines by foci and EdU assays, with Annexin V/7-AAD staining pending. Overall, p53mut EC cells rely on ADAR1/DHX9 activity for survival and proliferation. These findings suggest that ADAR1 and DHX9 might be therapeutic targets, and provides a strong argument for the use of DHX9 inhibitors- already in Phase I trials for colorectal cancer- as an additional therapeutic option for EC treatment.

Presenter(s): Bednarek, Lili
School: Carthage College
Session: P1.18
Title: Expression of c-Fos as a Marker for Neuronal Activity Following Signaled Lever Press Avoidance Training in Sprague-Dawley Rats
Co-Author(s): Justin Miller, Paul Martino
Advisor(s): Sarah Terrill, Dan Miller. Carthage College

Abstract: Behaviorally inhibited (BI) temperament is identified as consistent cautiousness and sensitivity to unfamiliar situations. Sprague Dawley (SD) rats were chosen as a base model to measure BI and the neuronal areas affected by stress stimuli. SDs experienced designated intervals of signal lever press avoidance training, 1 day, 2 days, and homecage (no days). SD's brains were extracted and analyzed using immunohistological applications. CFos, the protein of interest, is expressed during neuronal activity and measured under nuclear fluorescence. The Bed Nucleus of Stria Terminalus (BNST), Paraventricular Nucleus (PVN), Amygdaloid regions, and the Periaqueductal Gray (PAG), were all selected for cFos analysis due to their contribution in stress response. CFos expression was significantly higher in groups 1 and 2 days than the homecage control in the BNST, PVN, and PAG, supporting that those areas are activated under stressful stimuli. In the amygdala, the 1 day group saw significantly higher expression than the 2 day group and homecage group, suggesting that acquisition is higher on day 1. These significant findings open doors for further exploration in BI, applications such as different stimuli, immuno stains, and animals/strains, particularly in the stress vulnerable Wistar-Kyoto rat that acquires leverpress avoidance more rapidly than SD rats.

Presenter(s): Bittner, Alex
School: St. Olaf College
Session: I.A.1
Title: Defining a role for the proto-oncogene Vav1 in cancer cell metastasis
Co-Author(s): Mustafa Emre Gedik, Omar Gutierrez Ruiz, Gina Razidlo
Advisor(s): Gina Razidlo, Mayo Clinic

Abstract: The proto-oncogene Vav1 is ectopically expressed in pancreatic ductal adenocarcinoma (PDAC). While its role as a guanine nucleotide exchange factor regulating Rac and Cdc42 is well established, its contribution to metabolic adaptation in PDAC remains unclear. PDAC cells undergo metabolic re-wiring under stress conditions, relying instead on glutamine as a critical energy source. Here, we investigate whether Vav1 regulates glutamine metabolism through effects on Glutaminase (GLS1) and its isoforms KGA and GAC. Using PDAC cell lines with Vav1 overexpression and knockdown, we assessed gene and protein expression by qPCR and western blot, and monitored cellular responses by microscopy. Interestingly, our data reveal an inverse relationship between KGA and GAC at both the transcriptional and translational levels. This study identifies, for the first time, Vav1 as a regulator of glutamine metabolism via GLS1 isoforms, highlighting its potential as a therapeutic target in PDAC.

Presenter(s): Briley, Joshua
School: Colorado College
Session: P1.13
Title: *Liatris punctata* Physiological Response to 3-methyl-2(5H)-furanone and 2(5H)-furanone Mimicking low-grade Fire Resistance
Co-Author(s): Shane Heschel
Advisor(s): Shane Heschel. Colorado College

Abstract: *Liatris punctata* (Asteraceae), a specific fire-resistant aster that is native to North America, Canada, and parts of northern Mexico, resides in ecosystems that are in danger of wildfires such as, the Colorado high montane, and the California chaparral. The establishment of this aster in stressful conditions has not been researched extensively. Despite this, *Liatris punctata* is needed for endangered butterfly species such as the skipper butterfly. In previous research, there was a relationship between butenolides (compounds in smoke and ash) and gibberellin (GA) which fostered a germination pathway promoting growth. In this study, we aim to measure germination frequency, biomass, and chlorophyll concentration in California-sourced *Liatris punctata* seeds to gather a better understanding of the establishment dynamics of plants in fire-prone systems. We asked the following questions: 1) How do heat-treated (70C) *Liatris punctata* seeds physiologically respond to butenolides? 2) What are the ideal concentrations and types of butenolide needed to promote germination?

Presenter(s): Callil Tomei, Helena
School: Grinnell College
Session: II.E.2
Title: The Effects of a Prior Bout of Exercise and Stimulus Presentation Rates on Visual Statistical Learning
Co-Author(s): Wiktoria Kowal, Paige Sargent, and Tanadanai Hawsatitam
Advisor(s): Christopher Conway, Grinnell College

Abstract: Statistical learning, a form of implicit learning based on pattern recognition, supports fundamental cognitive processes, including language acquisition, attention, and decision-making. Prior research suggests that factors such as physiological stress and stimulus speed can influence statistical learning performance. The present study examined the effects of acute exercise and stimulus presentation rate on visual statistical learning. Participants were randomly assigned to an exercise or no-exercise condition. Those in the exercise group completed 20 minutes of moderate-intensity cycling, whereas those in the no-exercise group remained seated for the same duration. Participants were then exposed to an artificial grammar sequence at a predetermined presentation rate before completing 24 two-alternative forced-choice test trials. Results indicated a trend toward an interaction between exercise and presentation rate, such that performance improved at faster presentation rates following exercise relative to the no-exercise condition. Additionally, within the exercise condition, higher average exercise habits were positively correlated with test performance, whereas no relationship emerged in the no-exercise condition. These findings suggest that both physiological states and individual differences in exercise behavior can shape the brain's capacity for implicit learning, highlighting potential applications for optimizing learning environments through exercise-based interventions.

Presenter(s): Cerny, Ella
School: Washington University in St. Louis
Session: P3.07
Title: Design, Synthesis, and Functional Evaluation of Intestinally-Selective Non-Isoxazole FXR Agonists
Co-Author(s): Bahaa Elgendy, Satyam Killari, Jacob DeRousse
Advisor(s): Bahaa Elgendy, Washington University in St. Louis

Abstract: Farnesoid X Receptor (FXR) is a nuclear receptor central to the regulation of bile acid, lipid, and glucose metabolism. Although FXR agonists have shown therapeutic potential for treating Non-Alcoholic Steatohepatitis (NASH) and related metabolic disorders, clinical development has been limited by adverse effects associated with systemic FXR activation. Gut-restricted FXR modulation offers a promising strategy to retain efficacy while minimizing toxicity. This project focuses on the design and synthesis of a novel series of non-isoxazole, nonsteroidal FXR agonists inspired by the gut-selective lead compound BE-2231. Compounds were designed to enhance enteric selectivity and reduce systemic exposure through targeted structural modifications. Functional evaluation is currently underway using ALPHA Screen-based coactivator recruitment assays to assess FXR activation and characterize ligand-induced receptor conformations. Preliminary structure–activity relationship (SAR) insights are informing ongoing chemical optimization. The synthesized series represents a new class of FXR ligands with potential utility in tissue-selective therapy for metabolic and inflammatory disease. This work integrates synthetic chemistry and planned high-throughput functional screening to address challenges in nuclear receptor drug discovery and lays a foundation for future studies of FXR signaling in gut–liver–immune and gut–brain communication.

Presenter(s): Chew Chien Huei, Selene
School: Knox College
Session: I.D.4

Title: Effects of *Bacopa monnieri* on Proliferation and Morphology of C6 Cells
Co-Author(s):
Advisor(s): Esther Penick, Knox College

Abstract: *Bacopa monnieri* (BM) is an Ayurvedic herb recently found to have neuroprotective effects against neurodegenerative diseases, antiproliferative properties against cancer cells, and can change neuronal morphology by increasing dendritic length and branching. However, it is unclear if low concentrations of BM have antiproliferative and morphological differentiation effects. Thus, *Bacopa's* properties were examined using C6 rat glioma cells as astrocyte models over a range of BM concentrations. With BM concentrations of 1, 3, 10, and 25 µg/mL, cell proliferation and death were quantified with MTT and LDH assays. Immunocytochemistry was conducted using the glial fibrillary acidic protein (GFAP) antibody to look at morphological differentiation. There was an increase in cell proliferation at a BM concentration of 3µg/mL with a decrease at 25µg/mL. The morphology of cells were also altered. This shows that BM can have a dose-dependent impact on cell proliferation and morphology. These effects may be related to their neuroprotective and antiproliferative properties.

Presenter(s): Coric, Julia
School: Washington University in St. Louis
Session: P3.03
Title: PRDM1 Knockout Alters Tuft Cell Development and Reveals Peyer's Patch Immune Link
Co-Author(s): Kaelyn Sumigray, Anderson Santos, Linh Buu
Advisor(s): Kaelyn Sumigray, Washington University in St. Louis

Abstract: The small intestine's epithelium undergoes highly regulated postnatal maturation through processes such as crypt–villus morphogenesis and lineage specification. The PRDM1 gene acts as a transcriptional repressor that delays this process. Epithelial knockout (KO) mice display accelerated crypt development, altered nutrient uptake, and increased mortality. Prior work has shown premature Paneth cell differentiation in PRDM1 KO intestinal epithelium, but the impact on tuft cell specification and immune maturation is less understood. Tuft cells are rare chemosensory epithelial cells that emerge later in development and are enriched near Peyer's patches, specialized immune structures in the intestine. We hypothesized that PRDM1 KO accelerates tuft cell specification. Using immunofluorescence imaging of wild-type and KO samples across postnatal days (P0–P12), we observed tuft cells at all ages in KO mice, while only appearing at P12 in controls. Notably, in P4 KO samples, tuft cells were dramatically enriched around Peyer's patches compared to the more diffuse distribution in controls. This study provides the first evidence that PRDM1 may regulate not only epithelial maturation but also epithelial–immune interactions, potentially influencing the timing of tuft cell–mediated immune signaling. Future work should investigate whether PRDM1 KO alters Peyer's patch development or immune readiness, raising broader questions about how intestinal maturation genes coordinate epithelial–immune cross-talk.

Presenter(s): Craddock, Ephraim
School: University of Chicago
Session: I.B.3
Title: An IL-2-TGF-β Fusion Protein Expands Tregs and Induces Tolerance of a Minor-mismatched Skin Graft
Co-Author(s): Alexandra Cassano, Luqui Chen, Richard DiPaolo, Maria-Luisia Alegre

Advisor(s): Maria-Luisa Alegre, University of Chicago

Abstract: Transplanted organs are recognized as foreign by the host's immune system which, in the absence of continuous immunosuppression, rapidly rejects the grafts. Lifelong immunosuppression of the host, however, carries the risk of severe side effects and leaves the recipient susceptible to infections and cancers. Developing short-term therapies that can reprogram the immune system to tolerate the grafts is a key goal in transplantation to avoid these complications. Regulatory T cells (Tregs) are a subset of white blood cells that can suppress the immune system, and the cytokines TGF-β and IL-2 promote their development and expansion. We hypothesized that combining these cytokines may induce tolerance. We tested a novel IL-2/TGF-β fusion protein, engineered to preferentially expand Tregs over graft-rejecting effector cells. Three injections of IL-2/TGF-β significantly increased circulating Treg percentages and led to permanent acceptance of minor-mismatched skin grafts without any other treatment. Furthermore, these mice spontaneously accepted a second donor-matched graft a month later in the absence of any therapy, demonstrating that the hosts have developed true tolerance. We conclude that IL-2/TGF-β therapy can induce tolerance to minor-mismatched grafts. Ongoing studies are investigating the specific effects of this short-term treatment on graft-reactive Tregs and effector cells.

Presenter(s): Craven, Katie
School: Colorado College
Session: P1.20
Title: Differences in stability of idiosyncratic behavioral preferences between *Drosophila* species
Co-Author(s):
Advisor(s): Ryan Maloney, Colorado College

Abstract: Animals show individuality in their behaviors, even when genetic and environmental conditions are held constant. To explore how this individuality varies across species and environments, we measured behavioral consistency in multiple *Drosophila* species using a Y-maze assay. Behavior was recorded over two-hour sessions across three consecutive days. In one experiment, we tested non-melanogaster species obtained from laboratory populations. In a separate experiment, we tested wild-caught *Drosophila* collected from the Colorado Springs area to compare species sharing the same natural environment. We see robust differences between different populations of flies, though further research is required to test if these differences can be attributable to differences between species . These findings provide insight into the potential mechanisms underlying individuality and its regulation, and contribute to a broader understanding of how different species use behavioral variability to optimize survival in unpredictable environments.

Presenter(s): Fackler, Geneva
School: Gustavus Adolphus College
Session: P1.05
Title: Quantitative Analysis of sRNA Binding Hierarchies: The Role of mRNA Accessibility in RyhB Target Selection
Co-Author(s): Janie Frandsen, Joseph Ream
Advisor(s): Janie Frandsen, Gustavus Adolphus College

Abstract: *Escherichia coli*, a commonly found bacteria within the human microbiome, relies on regulatory mechanisms to maintain homeostasis. One of these mechanisms is non-coding RNAs, called small RNAs (sRNA), that are involved in regulating gene expression of a cell. A single sRNA binds with multiple messenger RNAs (mRNAs), collectively called a targetome, manipulating their expression to help maintain homeostasis. Due to the large targetome, scientists wonder if prioritization of targets occurs, and if so, what features dictate this prioritization. For the targetome of the sRNA SgrS, a regulatory hierarchy has been identified; this is assumed to be true for other sRNAs. Still unknown are the features that dictate this hierarchy. Accessibility describes how available the mRNA binding site is to interact with the sRNA. Our research focuses on how the accessibility of sRNA binding sites in mRNAs affects prioritization. We hypothesize that binding sites that are more accessible will be bound at low concentrations of sRNA, while binding sites that are very inaccessible will be bound at high concentrations of sRNA. We are using a pull-down assay to determine the order in which the sRNA RyhB binds to the mRNAs in its targetome. We are manipulating the concentration of RyhB using differing amounts of the inducer, arabinose, to distinguish high-priority and low-priority targets. When sRNA levels are low, high-priority target mRNAs will be regulated. Only once sRNA levels increase can low-priority targets be regulated. To determine which targets are bound to RyhB at each concentration, we are using qRT-PCR. qRT-PCR uses fluorescence to quantitatively measure the amount of mRNA bound at different sRNA concentrations. With the results from the qRT-PCR analysis, we are able to determine which mRNAs are low-priority and which are high-priority for the cell. Combining our data with another project in our lab, we can assess if sRNA binding site accessibility is a determining feature that dictates the prioritization of the mRNA targetome. Understanding the regulatory mechanisms of *E. coli* enables us to infer the regulatory mechanisms of other organisms, like humans.

Presenter(s): Fan, Selina
School: Washington University in St. Louis
Session: P1.01
Title: The Role of E3 Ubiquitin Ligase (UBR5) in MPNST Cell Survival
Co-Author(s): Diana Odhiambo, Angela C. Hirbe
Advisor(s): Angela C. Hirbe, Washington University School of Medicine

Abstract: Neurofibromatosis type 1 (NF1) is a cancer predisposition syndrome caused by germline NF1 mutations. Malignant peripheral nerve sheath tumors (MPNST), an aggressive soft tissue sarcoma, are the leading cause of premature death in NF1 patients. The current standard of care is surgical resection with negative margins; however, the prognosis remains poor with most patients dying within 5 years of diagnosis, underscoring the need for new therapies. Previous work from our lab demonstrated that chromosome 8q gain is a frequent event in NF1-MPNST, and a CRISPR screen identified UBR5 as one of the significantly amplified genes within chr8q that is essential for MPNST survival. My project investigated the role of UBR5 in MPNST progression using a murine MPNST cell line. UBR5 knockdown was achieved via shRNA, with efficiency confirmed by qPCR and Western blot. Cell proliferation and wound-healing assays were monitored by IncuCyte live-cell imaging. Genetic knockdown of UBR5 resulted in reduced proliferation in murine MPNST cells and increased migratory capacity. These data suggest that UBR5 is important for the survival and progression of MPNST. It could potentially provide new therapeutic avenues in MPNST management that could ultimately improve outcomes and quality of life for individuals with NF1-driven MPNST.

Presenter(s): Fang, Shuzhe
School: Washington University in St. Louis
Session: P2.17
Title: Effects of Juvenile Social Isolation on Activity of Nucleus Accumbens
Co-Author(s): Masatoshi Inoue, Dominic Polsinelli
Advisor(s): Masatoshi Inoue, Washington University School of Medicine in St. Louis

Abstract: Social interactions are critical for mammalian development, and disruption during sensitive periods can lead to long-lasting consequences. Juvenile social isolation (JSI) has been linked to altered reward processing, yet the circuit mechanisms remain unclear. We focused on the ventral tegmental area (VTA) and nucleus accumbens (NAc), as this mesolimbic pathway is central to reward processing and social motivation. Mice were housed individually (JSI) or in groups (controls) from weaning to adulthood, followed by behavioral assays and fiber photometry. Fiber photometry enabled real-time monitoring of neural activity during social behavior. Behaviorally, JSI mice showed reduced preference for social targets compared to controls, indicating impaired social approach. Chemogenetic activation of the VTA reduced social interaction in both groups, though this result may reflect surgical mistargeting and requires further validation. Future work will selectively target the dopaminergic VTA–NAc circuit to clarify its causal role. Neural recordings revealed a trend toward elevated dopamine activity in the NAc of JSI mice prior to regrouping, an effect absent after reintroduction to social housing. Together, these findings indicate that JSI alters both social behavior and mesolimbic dopamine dynamics, highlighting the complexity of circuit-level mechanisms mediating social motivation.

Presenter(s): Farah, Jack
School: Washington University in St. Louis
Session: II.H.2
Title: Investigation of Mechanisms of the Putative Amino Acid Transport 1 (AAT1) in *Plasmodium falciparum*
Co-Author(s): Alvee Hasan, Eva Istvan, Daniel Goldberg
Advisor(s): Daniel Goldberg, Washington University in St. Louis

Abstract: *Plasmodium falciparum* is the deadliest of the malaria parasites capable of infecting humans, a parasitic infection that is difficult to contain due to its fast-developing resistance towards drugs such as chloroquine (CQ). Mutations in CQ resistant parasites have been found in genes including the chloroquine resistance transporter (CRT), and amino acid transporter 1 (PfAAT1, PF3D7_0629500), the focus of this investigation. CRT, a digestive vacuole (DV) membrane localized protein, transports chloroquine out of the DV when mutated, at the cost of the impairment of peptide transport. Mutations in drug resistant parasites over the past 30 years have suggested a haplotypic relationship and possibly a functional relationship between CRT and AAT1. By creating a conditional knockdown system complemented with different AAT1 alleles derived from field isolates, we have tested the growth phenotypes of different mutations in vitro. The data has supported the idea that CRT and AAT1 assist each other's functions and CRT mutants have an increased dependence on AAT1. This project is part of a larger ongoing study into *P. falciparum's* resistance mechanisms.

Presenter(s): Fernando, Shelley
School: University of Chicago

Session: P3.06
Title: Elucidating the Mechanisms of BRWD1-Mediated Chromatin Regulation of B Cell Development
Co-Author(s): Margaret Veselits, Malay Mandal, Marcus Clark
Advisor(s): Marcus Clark, University of Chicago

Abstract: Epigenetic reader, bromodomain and WD repeat-containing protein 1 (BRWD1) plays numerous roles in mammalian pathophysiological processes including neurogenetic disorders, infertility, lymphocyte development and humoral immune response. Recent works have demonstrated that BRWD1 is functionally associated with global chromatin remodeling via nucleosome positioning, developmental and lineage restricted enhancer silencing or activation, enhancer-promoter interactions, formation and activation of dynamic cohesion complex essential for loop extrusion and many others. However, the molecular mechanisms underlying these biological functions are elusive. It is hypothesized that BRWD1 does so by interacting with chromatin remodeling or associated complexes responsible for nucleosome positioning and transcription machinery. Recently, four mutations in human BRWD1, namely, G65S, H175Y, L339S and Q1844L were reported to be associated with infertility. Further study of these mutations provides insight into the molecular mechanisms by which BRWD1 regulates the pathophysiology mentioned. Here, I aim to clone and express different domains of BRWD1 with and without mutations in mammalian cell lines to identify binding partners of BRWD1 through immunoprecipitation and mass spectrophotometry. Broadly, this work aims to contribute to our understanding of the molecular mechanisms of BRWD1 mediated chromatin regulation during lymphocyte development and insights into disease mechanisms.

Presenter(s): Gannu, Trisha
School: Washington University in St. Louis
Session: P3.01
Title: Evaluating VIT Chemotherapy Efficacy Across NF1-MPNST Subtypes
Co-Author(s): Kangwen Xiao, Angela C. Hirbe
Advisor(s): Angela C. Hirbe, Washington University in St. Louis

Abstract: Neurofibromatosis type 1 (NF1) is a genetic disorder caused by germline NF1 mutations, which encode neurofibromin, a regulator of cell growth. Approximately 8–13% of NF1 patients develop malignant peripheral nerve sheath tumors (MPNSTs), aggressive sarcomas derived from Schwann cell precursors. While biallelic NF1 loss is required for tumor formation, additional events such as loss of CDKN2A and mutations in TP53, SUZ12, and EGFR drive malignant transformation. Chromosome 8q (Chr8q) gain is a near-universal event in NF1-MPNST and is associated with poor overall survival across multiple sarcoma types. Prior work in our lab identified 55 critical genes on Chr8, including oncogenes such as MYC, FGFR1, UBR5, and PTK2, that contribute to MPNST cell survival. RNA-seq-based unsupervised clustering of these genes defined two MPNST subtypes: Chr8 Cluster A and Chr8 Cluster B, which differ in prognosis and predicted therapeutic sensitivity. Therapeutic responses in Cluster A were evaluated using the cell lines JH2-002 and WU-356. Cells were treated with VIT chemotherapy (vincristine, irinotecan, temozolomide) or the MEK inhibitor Mirdametinib, and proliferation and cell death were monitored using IncuCyte live-cell imaging. Both Cluster A cell lines exhibited similar responses, supporting the potential for Chr8q-based precision medicine strategies to improve outcomes for patients with NF1-MPNST.

Presenter(s): Gibson, Natasha
School: Lawrence University
Session: P2.15
Title: Adolescent HDM Exposure Alters Anxiety, Lung, Hippocampal Inflammation, and HPA Axis Amygdala Gene Expression
Co-Author(s): Anisa Phillip, Lydia Meres, Sanjana Velu, Sonia Cavigelli, Helen Kamens, William Horton
Advisor(s): Sonia Cavigelli, Pennsylvania State University

Abstract: Asthma is a chronic respiratory disease affecting 10% of U.S. adolescents and is associated with a 23% increased risk of anxiety. This study aims to better understand the mechanisms of asthma-associated anxiety using a mouse model. Mice exposed to house dust mites (HDM) can develop lung inflammation that resembles asthma-like pathophysiology. Here, we examined whether HDM can lead to anxiety-like behaviors, an altered HPA axis, and neuroinflammation-related gene expression in BALB/cJ mice. Male and female adolescent mice received intranasal treatments of saline or HDM (1, 2, or 4 μg/μL) three times weekly for seven weeks. Anxiety was assessed in adulthood using the elevated plus maze and light-dark test. Gene expression was measured by qPCR in the lungs (IL-4, IL-5, IL-13), amygdala for HPA-axis genes (CRHR1, CRHR2, FKBP5), and ventral hippocampus for neuroinflammatory cytokines (IL-6, IL-1β, TNFα). Results demonstrated an HDM dose-dependent increase in anxiety behaviors and lung inflammation in females. Preliminary gene expression analyses indicate HDM exposure increases expression of multiple genes associated with lung inflammation, HPA-axis activation, and ventral hippocampus inflammation. These findings are consistent with a biobehavioral connection between adolescent asthma and anxiety and suggest that a mouse model can yield insights into this association.

Presenter(s): Gigolaj, Ornela
School: Macalester College
Session: P3.15
Title: Subcortical Sensitivity to Fearful, but not Sad, Facial Expressions in Humans
Co-Author(s): Karyna E. Steele, Ram Guruprasad, Silas C. Benevento Zahner, Moura Saad, E. Darcy Burgund
Advisor(s): E. Darcy Burgund, Macalester College

Abstract: Research on facial recognition has identified a network of cortical regions involved in facial processing. Recent studies revealed that facial perception is modulated by specific brain structures at the subcortical level as well. These subcortical structures have been shown to be more sensitive to face identities than to non-human objects. The present research investigated whether these subcortical regions are sensitive only to facial identities or also to facial expressions. Taking advantage of the fact that cells in subcortical structures are monocular, these structures were assessed by presenting faces with the same or different identities and expressions to the same or different eye. For sad faces, response times were faster for same-eye than different-eye presentations regardless of expression, indicating that subcortical systems are not sensitive to the difference between sad and neutral expressions. For fearful faces, response times were faster for same-eye than different-eye presentations when the expression was the same, but not when it was different, indicating that subcortical systems are sensitive to the difference between fearful and neutral expressions. This finding implies that subcortical structures are sensitive to certain facial expressions (fearful) but not

others (sad).

Presenter(s): Goel, Tisya
School: Knox College
Session: I.C.4
Title: Effect of *Bacopa monnieri* on Oxidative Stress in C6 Rat Glioma Cells
Co-Author(s):
Advisor(s): Esther Penick, Knox College

Abstract: With an ongoing incline the average age of the world's population, maintaining and improving cognitive health for healthy aging is more prevalent. With age, it becomes harder for neural cells to differentiate due to many factors, one of them being oxidative stress**.** Oxidative stress is a significant cause for cell and tissue damage, and is implicated in the progression of neurodegenerative disorders like Alzheimer's by damaging brain cells. Research has shown *Bacopa monnieri* to reverse the effects of oxidative stress by enhancing enzyme activity, and directly scavenging for free radicals. The effects of *Bacopa* as a natural remedy is significant in the field of biology. Despite the fact that it has been studied for several decades, the amount of research on the topic is limited, and requires more investigation into its mechanism, appropriate dosage, and effectiveness. This study aims to investigate the effects of *Bacopa* on oxidative stress in C6 rat glioma cells, which is a model for astrocytes. By using hydrogen peroxide to induce oxidative stress in cells, the effect of *Bacopa* on oxidative stress will be established.

Presenter(s): Goltz, Samara
School: Gustavus Adolphus College
Session: P3.09
Title: Investigating the Effect of Apolipoprotein C-III on Endothelial Lipase Activity
Co-Author(s):
Advisor(s): Brandon Davies, University of Iowa

Abstract: Lipoproteins are lipid-protein complexes that deliver fats and cholesterol throughout the bloodstream. Proper regulation of lipoproteins by enzymes such as endothelial lipase (EL) and lipoprotein lipase (LPL) is crucial for cardiovascular health. EL primarily hydrolyzes phospholipids on high-density lipoproteins (HDL) to release fatty acids, but EL can also hydrolyze triglycerides in triglyceride-rich lipoproteins (chylomicrons and very low-density lipoproteins, VLDL). Apolipoprotein C-III (ApoC3) is a surface protein of lipoproteins, mainly VLDL and HDL, that is known to inhibit LPL. LPL, like EL, aids in triglyceride clearance by hydrolyzing triglycerides in triglyceride-rich lipoproteins. Because LPL deficiency impairs triglyceride clearance and promotes cardiovascular disease, blocking its inhibitors, such as ApoC3, has become a major focus; however, ApoC3's effect on EL remains unknown. ApoC3 has been shown to block triglyceride clearance in LPL-dependent and independent pathways, and we hypothesize that ApoC3 inhibits EL to hinder triglyceride clearance. Through EL and LPL activity assays, our findings show that unbound ApoC3 is not sufficient to inhibit LPL or EL. Furthermore, HDL can be incorporated into LPL and EL assays, but ApoC3 incubation with HDL does not lead to LPL inhibition. Identifying the conditions in which ApoC3 inhibits LPL is vital to understanding whether it regulates EL.

Presenter(s): Gonzalez Medina, Milciades
School: Lawrence University
Session: P2.18
Title: Understanding the limits of induced awe: How long does it last? Can it increase belongingness?
Co-Author(s): Nabina Rimal
Advisor(s): Lori M. Hilt, Lawrence University

Abstract: Awe is a mixed-valence emotion associated with positive psychological outcomes. Experimentally induced awe heightens willingness to learn, lowers inflammatory cytokines, and triggers a diminished sense of self, which leads to increased pro-social tendencies (i.e., generosity, helping behaviors) that promote enhancements in social connectedness. A question remains regarding how durable these laboratory effects are, as they are typically measured only immediately post-induction. Additionally, it is unclear whether the prosociality effects would help individuals with a thwarted sense of belongingness, which is a risk factor for suicide. The present study seeks to address these gaps in the literature. College student participants (N = 25) will complete questionnaires online prior to a single laboratory session where they will watch both neutral and awe-evoking immersive virtual reality videos. State affect, belongingness, and feelings of awe will be assessed immediately prior to and following each video. Feelings of awe will continue to be assessed for 20 minutes following the awe video. Understanding the durability of induced awe will help inform brief interventions that may improve college students' belongingness, which could have impacts on retention as well as mental and physical health.

Presenter(s): Gordan, Julia
School: University of Chicago
Session: P2.10
Title: A Structural and Coevolutionary View of the Yeast J-domain Protein SIS1's Client-Docking Patterns
Co-Author(s):
Advisor(s): David Pincus, University of Chicago

Abstract: Protein homeostasis relies on molecular chaperones that recognize and stabilize substrates or orphan proteins—newly synthesized proteins that are not associated with their stoichiometric binding partner(s) and are at risk of misfolding—preventing their aberrant aggregation. The Hsp40 co-chaperone SIS1 plays a role in this process by selectively binding to orphan-protein substrates and facilitating their folding or delivery to the Hsp70 machinery. We investigate the molecular interactions between SIS1 and a panel of substrate proteins, including CCT3, RPS3, TUB2, SUP35, RNQ1, TUB1, ACT1, UBC9, and RPL26A, essential for cellular functions and prone to forming condensates when unchaperoned. Using AlphaFold Multimer, we modeled protein-protein complexes between SIS1 and these substrates to predict binding interfaces and structural determinants of chaperone-substrate recognition. Our in-silico assays reveal a pattern of substrate-specific binding modes, suggesting that SIS1 adopts conformational flexibility to accommodate a diverse range of client proteins. Despite this diverse range of bindable substrates, our models find that SIS1 frequently occupies the same molecular interface as the substrate's native binding partner. These findings provide structural insights into SIS1's role as a first-line defense against protein aggregation and offer a foundation for future engineering of targeted chaperone variants to mitigate proteotoxic stress

in disease models.

Presenter(s): Goss, Madelyn
School: Knox College
Session: P1.16
Title: Phylogenetic Analysis of Argonaute Proteins in Plants
Co-Author(s):
Advisor(s): Matthew Jones-Rhoades, Knox College

Abstract: Since the initial identification of 10 unique argonaute (AGO) protein families in *Arabidopsis thaliana* (Vaucheret, 2008), several studies have been published characterizing the diversification and conservation of AGO proteins in land plants (Li et al, 2022; Wang et al, 2021; Feng et al, 2024; Belanger, 2023). However, few studies have focused on characterizing AGO proteins from algae in these analyses. Therefore, this study attempts to identify and create a phylogeny of plant AGO proteins to further characterize the phylogenetic relationships of chlorophyte and streptophyte algae in relation to those found in land plants using AGO protein sequences from *Arabidopsis thaliana* from *Oryza sativa*, *Physcomitrella patens, Chara braunii, Zygnema cylindricum, Klebsormidium nitens, Chlorella vulgaris,* and *Chlamydomonas reinhardtii*. It was found that streptophyte algae contained numerous diverse sequences of AGO proteins. It was also found that both *Klebsormidium* and *Chara* contained sequences belonging to or closely related to Arabidopsis AGO clades. This may indicate the last common ancestor of streptophyte algae and land plants contained a diverse set of AGO proteins ancestral to those found in land plants. As more algae proteomes are sequenced, further analysis will be valuable in better characterizing and understanding the diversity of algal AGO proteins.

Presenter(s): Greenberg, Dhara
School: Macalester College
Session: II.E.1
Title: The Social Cipher Video Game as a Social Emotional Learning Intervention
Co-Author(s):
Advisor(s): Alexa Matlack, The University of Washington

Abstract: Social Cipher is a video game designed by and for those with Autism Spectrum Disorder (ASD). The game teaches Social Emotional Learning (SEL) skills through the main character avatar of Ava. This experiment investigated the connection between the Social Cipher intervention and the participants' senses of belonging. Seventeen participants were selected through the APEX Summer Treatment Program at the University of Washington. Participants played Social Cipher for four weeks and were given questionnaires on their self awareness and self regulation skills. Preliminary results will be presented and future work will test the generalizability of the intervention.

Presenter(s): Grocholski, Sophia
School: St. Olaf College
Session: P1.06
Title: RNAi Knockdown of Lipid Droplet Associated Proteins in *Tetrahymena thermophila*
Co-Author(s): Cambelle Jossart; Gracia Wallace
Advisor(s): Jean Porterfield**,** St. Olaf

Abstract: Lipid droplets are essential organelles found in all eukaryotic cells, and are involved in fat storage and metabolism. Lipid droplets utilize the functions of multiple proteins to regulate these processes, but the proteins vary across different species. A former proteomic screen found that *Tetrahymena thermophila*, a ciliated single-celled eukaryotic organism, has many lipid-droplet associated proteins, including some that do not have any close homologs in other species. One of these proteins, called lipid droplet protein 10 (LDP10) has its own set of putative homologs within the *T. thermophila* genome. Neither LDP10 nor any of its homologs have been characterized in their role in the association with lipid droplets. In order to better understand and characterize these proteins, we have been developing RNA interference (RNAi) plasmids to knockdown expression of these proteins. To build the plasmids with each gene of interest, we used a previously developed RNAi plasmid called pREC8i. We cut out the pREC8i gene sequence excerpts, and replaced them with our gene excerpts. The resulting RNAi plasmid is linearized and introduced into *T. thermophila* using biolistic transformation. The concentration of cycloheximide (CHX), a drug used to select for the RNAi construct, is increased to select for high expression because *T. thermophila* divides amitotically and randomly distributes their genes among offspring. Cadmium is added to induce the RNAi pathway, and fluorescent microscopy is utilized to analyze the difference in phenotypic results. Currently, five genes are in this workflow: seipin, LDP10 and two of its homologs, as well as a different lipid-droplet associated protein called LDP2. Preliminary microscopy has begun with the LDP2 and LDP10 proteins, and RNAi plasmids are being developed for two additional LDP10 homologs.

Presenter(s): Guo, Felix
School: Washington University in St. Louis
Session: I.B.2
Title: Discovering the role of immune-based acceptance in incompatible plant grafts
Co-Author(s): Sam Yanders, Margaret Hannah Frank
Advisor(s): Kevin Cox, Jr., Washington University in St. Louis

Abstract: Current agricultural technologies, such as conventional breeding, can introduce resistance to abiotic and biotic stresses, but take years to develop and be approved. Grafting provides these benefits at a more efficient rate. Grafting is a technique where the apical portion of one plant (scion) is connected to the root system (rootstock) of another plant. To create a successful graft, the species must reform vascular connections between the root and scion. However, little is known about the molecular basis of graft incompatibility when vascular reconnection does not occur. Interestingly, studies in our lab of incompatible tomato:pepper grafts found over 1000 upregulated genes involved in defense-related processes, indicating a possible immune response. In this study, we seek to determine whether graft incompatibility is caused by immune response. We used tomato mutants with knockouts of disease regulatory pathways to study the effect of loss-of-function in disease pathways on graft compatibility in compatible tomato:tomato and incompatible tomato:pepper grafts. By characterizing mutant graft phenotypes with a novel flash-staining method, we can determine the functional role of disease regulatory networks in graft compatibility. We observed a change in graft compatibility in disease mutant lines, providing experimental evidence of disease response in graft compatibility.

Presenter(s): Hartmann, Katherine
School: Hope College
Session: II.H.1
Title: Using LC/MS to Identify Post-translational Modifications on xCT and its Interactome
Co-Author(s): Katherine McCain, Leah Chase
Advisor(s): Leah Chase, Hope College

Abstract: System xc- is a membrane transporter containing subunits 4F2HC and xCT. The transporter regulates oxidative stress through exchange of intracellular glutamate for extracellular cystine to create the antioxidant glutathione which reduces oxidative stress and limits cell death. The goal of this project is to study the regulation of xCT using liquid chromatography mass spectroscopy (LC/MS) to answer two questions: 1) where is xCT post-translationally modified? (PTM) and 2) which proteins associate with xCT? These questions will be answered using bottom-up proteomics through immunoprecipitation of xCT and digestion of xCT and associated proteins (interactome) with Trypsin/LysC or Elastase coupled with LC/MS analysis. We have optimized these procedures and have identified several proteins in the xCT interactome. We are also sending our samples for analysis on a nano-LC/MS in the Cologna lab at UIC which has increased sensitivity for identifying peptides to improve our PTM and interactome analysis.

Presenter(s): Hauver-Radloff**,** Ian
School: Colorado College
Session: P1.15
Title: The Effect of Warming on Arctic Plant Nectar Production
Co-Author(s):
Advisor(s): Roxaneh S. Khorsand, Colorado College

Abstract: Warming is disproportionately affecting the Arctic, making it a proxy for near-future climate change. Many studies have documented plant phenological and growth responses to warming, but few have studied the effects on floral nectar production, which is of key importance as a food source to pollinators. Research at northern latitudes remains limited, and no studies have examined nectar responses in the Arctic species *Arctous alpina* (bearberry), *Vaccinium uliginosum* (bog blueberry), and *Vaccinium vitis-idaea* (lingonberry). We investigated the effect of short- and long-term warming on nectar rewards, answering the question: What is the effect of experimental warming on nectar quantity and quality? We measured nectar volume and Brix (sucrose concentration) from these three species using microcapillary tubes and handheld refractometers. Data were collected in June and July of 2025, building on data collected in 2019 on one of the species. Preliminary findings suggest that warming increases volume with no effect on sucrose concentration, but this response varies among species. These results align with current literature showing increased nectar volume and species-specific responses in sugar concentration under experimental warming. Changes in the total nectar rewards and the timing of floral rewards over a season have important implications for Arctic plant-pollinator networks.

Presenter(s): Hsieh, Katherine
School: Washington University in St. Louis
Session: P2.01

Title: *Pseudomonas, Stenotrophomonas*, and *Serratia* Species Are Present in Intensive Care Unit Sinks Despite Targeted Cleaning
Co-Author(s): Emily Benedict, Carrie O'Neil, Tiffany Hink, Meghan Wallace, Candice Cass, David McDonald, Lucy Vogt, Alyssa Valencia, Kevin Jolani, Carleigh Samuels, Jennie H. Kwon, Gautam Dantas
Advisor(s): Gautam Dantas, Washington University in St. Louis

Abstract: Healthcare-associated infections (HAIs) from antimicrobial resistant organisms (AROs) pose a significant concern for medically vulnerable and immunocompromised patients in hospital intensive care units (ICUs). Previous work revealed that ARO burden in ICU sink drains can be reduced through implementation of a two-part sink-targeted cleaning intervention, and the goal of this work was to expand this intervention for generalizability. We implemented the same sink cleaning protocol at 2x/week intervals in 8 St. Louis medical intensive care unit (MICU) sink drains and maintained 4 untreated (0x/week) MICU sinks. We sampled all sink drains during baseline, 3 intervention, and 3 post-intervention periods across 46 weeks and performed short-read whole genome sequencing on 423 isolate samples. *Pseudomonas aeruginosa, Stenotrophomonas maltophilia*, and *Serratia neve*i were identified multiple times in the same and across MICU rooms, suggesting that these sink drains contain persistent reservoirs of these species or consistent reseeding occurs. Notably, *Pseudomonas, Stenotrophomonas*, and *Serratia* species were present even in MICU sinks that received the cleaning intervention. Strain-level analysis of these consistently appearing species may reveal the extent of their persistence and potential effects on sink drain ecology.

Presenter(s): Ineza, Esther
School: Colorado College
Session: P1.11
Title: Centromeres of the Budding Yeast *Cyberlindnera mrakii* Contain Transposable Elements and Repeat Sequences
Co-Author(s): Marin Snyder, Sara Hanson
Advisor(s): Sara Hanson, Colorado College

Abstract: Centromeres ensure accurate segregation of chromosomes during cell division and DNA replication by providing a site for assembly of the kinetochore. Investigations into different species of yeast have revealed that there is immense diversity when it comes to centromere structure and location.There has been a dramatic evolutionary shift from regional, epigenetically defined centromeres to short, genetically defined point centromeres, which is still not fully understood. Recent hypotheses suggest the existence of an intermediate centromere type, characterized by transposable elements and repetitive sequences that may represent a transitional form. This study explores the budding yeast, *Cyberlindnera mrakii*, for the presence of these elements in order to investigate this trend further. Using long-read sequencing and detailed genome annotation, we generated a high-quality genome assembly and identified candidate centromere regions. These regions exhibit features such as repetitive sequences and Ty5l transposable element enrichment, suggesting a centromere architecture distinct from both classical point and regional types. Our findings contribute to a deeper understanding of centromere evolution in budding yeast and support the potential existence of structural intermediates between point and regional centromeres.

Presenter(s): John, Nathaniel
School: Washington University in St. Louis
Session: II.F.1
Title: LRRC8C Deletion Enhances Angiogenesis and Accelerates Perfusion Recovery After Ischemic Injury
Co-Author(s): Qiujin Yu, Mehran Rahimi, Rajan Sah
Advisor(s): Rajan Sah, Washington University in St. Louis

Abstract: Angiogenesis, the growth of new blood vessels, is driven by endothelial cell (EC) proliferation, migration, and network formation. Impaired angiogenesis hinders tissue repair and contributes to worse outcomes in cardiovascular diseases, including coronary and peripheral artery disease. We previously reported that Leucine-Rich Repeat-Containing 8A (LRRC8A) forms the core subunit of the EC volume-regulated anion channel (VRAC) and regulates EC alignment to flow and blood pressure via Akt-endothelial nitric oxide synthase (eNOS) signaling. Here, we identified the EC VRAC as an LRRC8A/B/C heteromer and investigated how these subunits affect angiogenesis. In human umbilical vein endothelial cells (HUVECs), LRRC8C knockdown (KD) led to significantly greater tube formation in invasion assays and enhanced migration in scratch wound assays. To extend these findings in vivo, we performed femoral artery ligation on global LRRC8C knockout (gLRRC8C KO) and wild-type mice. Global LRRC8C KO mice demonstrated accelerated perfusion recovery in the ischemic distal limb as measured by laser doppler perfusion imaging. Hematoxylin-eosin (H&E) staining of gastrocnemius muscle revealed more centrally located myonuclei in gLRRC8C KO mice, suggesting increased muscular regeneration secondary to improved angiogenesis. These results reveal that LRRC8C modulates angiogenesis and may provide a novel therapeutic target to accelerate vascular recovery after ischemic injury.

Presenter(s): Johnson, Elsa
School: Gustavus Adolphus College
Session: P2.12
Title: Investigating Binding Site Accessibility in RhyB-mediated Target Hierarchies
Co-Author(s):
Advisor(s): Jane K. Frandsen, Gustavus Adolphus College

Abstract: Small RNAs (sRNAs) are post-transcriptional regulatory factors that allow bacteria, like Escherichia coli, to respond to environmental changes by binding to mRNA targets and altering their gene expression. While individual sRNAs can regulate multiple targets, they do not regulate all targets equally; instead, sRNAs establish a regulatory hierarchy, prioritizing certain targets over others. We sought to understand whether variability in the accessibility of sRNA binding sites within target mRNAs helps determine regulatory hierarchy. Our focus is RhyB, which has a well-characterized targetome with varying binding site accessibility. To investigate this, we use a two-plasmid assay: one plasmid expresses RhyB under a Tet promoter, while the other expresses a target fused to green fluorescent protein (GFP) under a Lac promoter. By measuring GFP fluorescence in E. coli exposed to varying inducer concentrations, we can quantify the extent of RhyB-mediated repression and identify high- or low-priority targets depending on their changes in expression at different RhyB levels. Our work focused on optimizing this assay using a single mRNA from the RhyB targetome, sodB. Expanding the project to include additional targets may provide insight into the role of binding site accessibility in sRNA target prioritization and improve our understanding of

sRNA-mediated post-transcriptional regulation.

Presenter(s): Joshi-Apte, Tanish
School: Washington University in St. Louis
Session: P3.10
Title: Assessing Mitochondrial Dysfunction via Relative mtDNA Copy Number in TFAM-Knockout Müller Glial Cells
Co-Author(s):
Advisor(s): Poonam Naik, Rajendra S. Apte

Abstract: Mitochondrial dysfunction is a key contributor to retinal disease. Mitochondrial transcription factor A (TFAM), is essential for mitochondrial DNA (mtDNA) replication and transcription, with its disruption leading to mitochondrial dysfunction. Simultaneously, Müller glial cells play an essential role in maintaining overall retinal homeostasis. Thus, investigating TFAM down-regulation and mtDNA integrity in Müller cells is relevant to understanding mitochondrial contributions to retinal ocular diseases. MIO-M1 cell line (immortalized Müller glial cells) were transduced with sgRNAs targeting TFAM control constructs. TFAM transcript levels were quantified using RT-qPCR, with GAPDH as housekeeping gene. Relative mtDNA copy number was measured by qPCR using ND1 and ND6, normalized to 18S rRNA. Relative TFAM downregulation was 85% and 89% observed in sgRNA 1 and sgRNA 2, respectively. Compared to MIOM1 sample 1, sgRNA 1+2 showed a 72.1% decrease in relative mtDNA copy number and sgRNA 2 showed a 49.7% decrease. In MIOM1 sample 2, sgRNA 1+2 showed a 84.9% decrease in relative mtDNA copy number and a 72.7% decrease in relative copy number for sgRNA 2. These findings demonstrate that TFAM knockdown in MIO-M1 cells reduces both TFAM expression and relative mtDNA copy numbers, highlighting the critical role of TFAM in maintaining Müller glial mitochondrial integrity.

Presenter(s): Jossart, Cambelle
School: St. Olaf College
Session: P1.06
Title: RNAi Knockdown of Lipid Droplet Associated Proteins in *Tetrahymena thermophila*
Co-Author(s): Sophia Grocholski
Advisor(s): Kim Kandl, St. Olaf College

Abstract: Lipid droplets are essential organelles found in all eukaryotic cells, and are involved in fat storage and metabolism. Lipid droplets utilize the functions of multiple proteins to regulate these processes, but the proteins vary across different species. A former proteomic screen found that *Tetrahymena thermophila*, a ciliated single-celled eukaryotic organism, has many lipid-droplet associated proteins, including some that do not have any close homologs in other species. One of these proteins, called lipid droplet protein 10 (LDP10) has its own set of putative homologs within the *T. thermophila* genome. Neither LDP10 nor any of its homologs have been characterized in their role in the association with lipid droplets. In order to better understand and characterize these proteins, we have been developing RNA interference (RNAi) plasmids to knockdown expression of these proteins. To build the plasmids with each gene of interest, we used a previously developed RNAi plasmid called pREC8i. We cut out the pREC8i gene sequence excerpts, and replaced them with our gene excerpts. The resulting RNAi plasmid is linearized and introduced into *T. thermophila* using biolistic transformation. The concentration of cycloheximide (CHX), a drug used to select for the RNAi construct, is

increased to select for high expression because *T. thermophila* divides amitotically and randomly distributes their genes among offspring. Cadmium is added to induce the RNAi pathway, and fluorescent microscopy is utilized to analyze the difference in phenotypic results. Currently, five genes are in this workflow: seipin, LDP10 and two of its homologs, as well as a different lipid-droplet associated protein called LDP2. Preliminary microscopy has begun with the LDP2 and LDP10 proteins, and RNAi plasmids are being developed for two additional LDP10 homologs.

Presenter(s): Kabbaj, Noah
School: Washington University in St. Louis
Session: I.C.1
Title: Uncovering serotonergic regulation of plasticity using all-optical physiology
Co-Author(s): Adrienne Kashay, Susan Hong, Navid Ghazi, Hafsa Amin, Linlin Z. Fan
Advisor(s): Linlin Z. Fan, Massachusetts Institute of Technology

Abstract: Neuromodulators like serotonin have been implicated in hippocampal learning, yet it remains unclear how they regulate physiology and modulate plasticity. We hypothesize that serotonin encodes salience via projections from the median raphe (MR), providing a modulatory signal that regulates hippocampal plasticity and learning. Using all-optical physiology to simultaneously manipulate and record membrane voltage during behavior, we can induce place cells in the CA1 region of the hippocampus at select locations through behavioral timescale plasticity. To determine endogenous patterns of hippocampal serotonin, we optogenetically activated serotonergic neurons from the MR and observed induced serotonin dynamics in the CA1. The duration of this effect was extended with fluoxetine, a selective serotonin reuptake inhibitor. To evaluate hippocampal serotonin dynamics in response to a salient stimulus, we subjected mice to air-puff delivery, which induced serotonin dynamics in the CA1. Additionally, we found exposure to a novel environment, a salient but neutrally valenced stimulus, increased activity in MR serotonergic neurons. When non-projection-defined MR serotonergic neurons were stimulated, twitch-like motion ensued; however, projection-defined MR to CA1 serotonergic neuron stimulation did not impact animal motion. These results support the hypothesis that serotonin may be involved in encoding salience to the hippocampus, regulating aspects of learning and memory.

Presenter(s): Karra, Vikram
School: Washington University in St. Louis
Session: I.C.3
Title: Disease-Associated Microglial Activation in Response to White Matter Insult in a Mouse Model of Tauopathy
Co-Author(s):
Advisor(s): Qingyun (Tristan) Li, Washington University in St. Louis

Abstract: Microglia, the brain's innate immune cells, are critical for maintaining homeostasis and have been intensely studied for their contributions to neurodegenerative disease. Their remarkable plasticity allows them to respond to diverse environmental cues by reshaping their transcriptional profiles. We focused on the activation of disease-associated microglia (DAMs), a distinct subpopulation of microglia, in a mouse model of tauopathy, a hallmark of Alzheimer's disease closely linked to cognitive decline. Using a Clec7a reporter line to track DAMs, we found that their activation emerged by seven months of age, following the appearance of tau

fibrillary tangles at five months. Interestingly, DAMs not only localized to tau tangles, but also accumulated along white matter tracts devoid of tau, suggesting that microglial activation is driven in part by white matter injury rather than tau pathology alone. Electron microscopy confirmed myelin abnormalities, while immunohistochemistry further revealed the phagocytosis of damaged oligodendrocytes. DAMs in these regions upregulated MHC-II, implicating their interaction with adaptive immune cells, such as T-Cells. Together, these findings uncover an underappreciated aspect of pathology in the tau model, highlighting white matter injury as a driver of microglial activation. Future studies will assess the functional significance of these microglia with respect to T-cell infiltration and their role in modulating myelin damage.

Presenter(s): Khan, Vivian
School: Lawrence University
Session: I.D.2
Title: Development of a Model to Assess Contributions of Receptor Endosomal Signaling to TRiM Efficacy
Co-Author(s): Destiny Schultz, Daniel Braas, Brian Davies, Ted Tseng, Mariah McNamer, David Katzmann
Advisor(s): Eric Lewellyn, Lawrence University

Abstract: Arrowhead Pharmaceuticals utilizes targeted RNA interference molecule (TRiMTM) technology to silence mRNA as a therapeutic strategy. Targeted knockdown (KD) by TRiMTM depends on receptor-mediated uptake into the target cell type, escape into the cytosol, and loading into Ago2/RISC for productive mRNA silencing. Mechanism(s) of TRiMTM escape from the endosomal lumen to the cytosol are unknown but appear to be dependent on the receptor; some receptors lead to cytoplasmic TRiMTM access while others do not. As a first pass to understanding what makes ASGR1 a productive receptor for delivery of siRNA therapeutics, mutant forms were generated that were defective for effector recruitment. ASGR1 wild type and mutant receptors were all expressed at indistinguishable levels and afforded comparable TRiMTM uptake but failed to support TRiMTM –mediated knock-down (KD). A noted decrease in targeting ligand cleavage from TRiMTM was also observed. Robust KD activity seen in hepatocytes correlates with cleavage of targeting ligand; ligand cleavage isn't observed in heterologous cell lines. Cell lines lack expression of N-acylethanolamine acid amidase (NAAA), thus limiting the ability to cleave ligand from TRiMTM. Introduction of NAAA or identification of another cell line with NAAA expression will be necessary to dissect contributions of ASGR1 effectors to productive KD. Identification of a link between ASGR1 effectors and TRiMTM activity will provide new insight into how TRiMTM escape occurs and allow for identification of potential receptors to target during therapeutic platform development.

Presenter(s): Kowal, Wiktoria
School: Grinnell College
Session: II.E.2
Title: The Effects of a Prior Bout of Exercise and Stimulus Presentation Rates on Visual Statistical Learning
Co-Author(s): Helena Callil Tomei, Paige Sargent, Tanadanai Hawsatitam
Advisor(s): Christopher Conway, Grinnell College

Abstract: Statistical learning, a form of implicit learning based on pattern recognition, supports fundamental cognitive processes, including language acquisition, attention, and

decision-making. Prior research suggests that factors such as physiological stress and stimulus speed can influence statistical learning performance. The present study examined the effects of acute exercise and stimulus presentation rate on visual statistical learning. Participants were randomly assigned to an exercise or no-exercise condition. Those in the exercise group completed 20 minutes of moderate-intensity cycling, whereas those in the no-exercise group remained seated for the same duration. Participants were then exposed to an artificial grammar sequence at a predetermined presentation rate before completing 24 two-alternative forced-choice test trials. Results indicated a trend toward an interaction between exercise and presentation rate, such that performance improved at faster presentation rates following exercise relative to the no-exercise condition. Additionally, within the exercise condition, higher average exercise habits were positively correlated with test performance, whereas no relationship emerged in the no-exercise condition. These findings suggest that both physiological states and individual differences in exercise behavior can shape the brain's capacity for implicit learning, highlighting potential applications for optimizing learning environments through exercise-based interventions.

Presenter(s): Kratt, Jayden
School: Macalester College
Session: P3.12
Title: Relative to Females, Male Mice Exhibit a Greater Hypothermic Response Following Neurotensin Receptor 1 Activation
Co-Author(s):
Advisor(s): Lauren M. Slosky, University of Minnesota

Abstract: Neurotensin receptor 1 (NTSR1) is a G protein-coupled receptor that regulates diverse physiological functions and a promising therapeutic target for multiple indications, including neuroprotection and substance use disorders. PD149163, a metabolically stable analogue of the endogenous ligand neurotensin, induces hypothermia. While this hypothermia may be beneficial for treating fever and ischemic injury, it is an unwanted effect in the context of psychiatric disease management. Differences in the neurotensin system exist between males and females. Understanding sex differences in response to PD149163 will facilitate therapeutic development. This study evaluated whether PD149163-induced hypothermia differed with sex in C57BL/6J mice. Single doses of PD149163 (0.075 or 0.15 mg/kg, i.p.) caused more transient hypothermia in females than males. In a multi-day dosing protocol (0.15 mg/kg i.p. once daily for five days), both sexes developed tolerance with no sex difference by day 5. After a 14-day washout, males exhibited a more complete loss of tolerance compared to females. These findings indicate female mice show reduced hypothermic responses and retain tolerance longer than males. This highlights the need to study NTSR1 ligands in both sexes to design therapies that either exploit or avoid hypothermia. Future research aims to elucidate the biological mechanisms underlying these sex differences.

Presenter(s): Kugler, Abby
School: Gustavus Adolphus College
Session: P2.09
Title: Co-Purification of Ski7 with the Cytoplasmic Exosome in *Saccharomyces cerevisiae*
Co-Author(s):
Advisor(s): Jeff Dahlseid, Gustavus Adolphus College

Abstract: The cytoplasmic exosome of *Saccharomyces cerevisiae* is a multi-subunit complex that degrades RNA in the 3′→5′ direction and maintains mRNA quality. Efficient cytoplasmic decay requires adaptor proteins, including the Ski complex (Ski2, Ski3, Ski8) and Ski7, which bridges these factors to the exosome. While the structural features of the core exosome are well defined, the nature of Ski7 association with the cytoplasmic exosome is less clear. This project focused on purifying Ski7 and testing whether exosome subunits co-purify under different buffer conditions. Yeast strains expressing His-tagged Ski7 were prepared, and protein extracts were subjected to affinity chromatography using an AKTA Pure FPLC system. Fractions were collected based on UV absorbance and analyzed by Bradford assays and SDS-PAGE to evaluate protein content and recovery. Preliminary results showed Ski7 in both flow-through and elution fractions, suggesting incomplete binding or salt-dependent disruption of interactions. Future work includes repeating purifications at higher salt concentrations and performing Western blotting to confirm Ski7 and associated exosome subunits. This study provides a foundation for dissecting Ski7–exosome interactions and demonstrates experimental approaches for investigating RNA decay mechanisms in yeast and other eukaryotic systems.

Presenter(s): Kwon, Christine
School: University of Chicago
Session: P1.04
Title: Integrative Network Analysis of Molecular Subtypes in High-Grade Serous Ovarian Cancer
Co-Author(s): Viola Fanfani
Advisor(s): John Quackenbush, Harvard T.H. Chan School of Public Health

Abstract: High-grade serous ovarian carcinoma (HGSOC) is the most lethal gynecologic malignancy. Previous work has characterized four molecular subtypes of HGSOC—immunoreactive, differentiated, mesenchymal, and proliferative—but many aspects of disease progression and regulation remain elusive. We applied gene regulatory network methods from the netZoo suite to TCGA DNA methylation and gene-expression data to investigate how epigenetic and transcriptional regulation contribute to subtype-specific behavior. We used DRAGON to compute multi-omic partial correlation networks between promoter methylation and gene expression, and identified subtype-specific silencing of oncogenic transcription factors including STAT5A, WT1, and NFIB, as well as coordinated epigenetic and transcriptional programs distinguishing subtypes. We then used PANDA to infer transcription factor-gene regulatory networks and ALPACA to detect sub-networks with differential modularity. In comparing the least aggressive immunoreactive subtype to the others, we found endocrine-linked modules involving reproductive hormone signaling in the differentiated subtype and cell-cycle and DNA-repair modules in the proliferative subtype. These regulatory differences provide insight into mechanistic factors differentiating ovarian cancer subtypes that could lead to subtype-specific therapeutic interventions and suggest that reproductive hormone-linked programs and cell-cycle control are key axes of HGSOC development and progression.

Presenter(s): Levy, Ethan
School: Colorado College
Session: P2.05
Title: Examining Modes of Interaction Between Inhibitor and SL-1 Hairpin of SARS-CoV-2

Co-Author(s): Sophie Gaspel, Neena Grover
Advisor(s): Neena Grover, Colorado College

Abstract: Over 7 million people have died of SARS-CoV-2 since its emergence. SARS-CoV-2 is a positive sense RNA virus containing five stem loops in its 5'-UTR. Stem-loop 1 (SL-1) is critical for binding of the virus to nonstructural protein 1 (nsp1) and plays a significant part in viral replication. Our laboratory had designed an inhibitor to bind to SL-1 to prevent SL-1 from binding to nsp1. This project was aimed at examining the mode of binding between nsp-1 and DNA corresponding to SL-1. Circular dichroism (CD) shows a duplex-like signature when tested across multiple different pH, temperature, and buffer conditions such as high salt concentrations. RNA structure also predicts a stable duplex structure between the inhibitor strand and hairpin RNA. We investigated well-established triplex structures to examine signatures of triplex strand formation using CD. Using isothermal titration calorimetry (ITC), we determined full triplex formation near 100% is possible in acidic and high-salt conditions, though not under physiological conditions. Our experiments indicate that binding of the short inhibitor strand is likely to form an alternate duplex rather than a triplex between the SL-1 hairpin and the inhibitor strand.

Presenter(s): Liu, Ziyu
School: Washington University in St. Louis
Session: I.B.4
Title: Development of LDLRAD3-Based Decoy to Block Venezuelan Equine Encephalitis Virus Infection
Co-Author(s): Hongming Ma
Advisor(s): Michael Diamond, Washington University in St. Louis

Abstract: Venezuelan equine encephalitis virus (VEEV) is an alphavirus responsible for recurrent outbreaks in humans and equines across Central and South America, causing symptoms that range from self-limiting febrile illness to severe neurological complications. A genome-wide screen previously identified low-density lipoprotein receptor class A domain-containing protein 3 (LDLRAD3) as the primary entry receptor for VEEV. Subsequent structural studies mapped the viral binding domain to domain 1 (D1) of LDLRAD3 and identified key amino acids mediating this interaction. Guided by these findings, we introduced mutations at residue 41 of the N-terminus (wild-type arginine) to identify D1 variants with enhanced affinity for VEEV. We found that substitution of R41 with acidic or long aliphatic side-chain residues greatly increased the capacity of D1-Fc fusion proteins to neutralize VEEV infection. Surface plasmon resonance (SPR) measurements confirmed higher affinities of R41E and R41I mutants compared to wild-type D1. Furthermore, to improve the potency of soluble D1-Fc decoys, we optimized the linker length between the D1 and Fc fragments, resulting in significant increase in neutralization capacity. Overall, these results provide critical insights into the structure and function of LDLARD3 and lay the groundwork for developing potent therapeutics against VEEV infection.

Presenter(s): Lyu, Gongdao
School: St. Olaf College
Session: P1.10
Title: Complementation of Yeast Seipin Knockouts with putative *Tetrahymena* Seipin TTHERM_00497200

Co-Author(s): Gracia Wallace, Kim Kandl
Advisor(s): Kim Kandl, St. Olaf College

Abstract: Lipid droplets are essential organelles in eukaryotic cells, responsible for fat storage and metabolism. Seipin, a conserved transmembrane protein, is critical for their formation. Without seipin, lipids fail to detach from the endoplasmic reticulum, forming a single aggregated clot instead of normal individual droplets. It is thought that all cells have seipin; however, seipin protein has not been identified in *Tetrahymena thermophila*, a ciliated single-celled eukaryotic model organism. Using DOMAIN-BLAST, a seipin domain was identified in the gene TTHERM_00497200, aligning with other eukaryotic seipins. Molecular modeling also suggests structural similarity to *Saccharomyces cerevisiae* (yeast) seipin and human seipin. This research explores whether TTHERM_00497200 functions as seipin in Tetrahymena through a complementation study by transforming the putative *Tetrahymena* seipin gene into yeast seipin knockout (sei1Δ) cells to determine whether lipid droplet formation is restored, as indicated by a significant increase in lipid droplet number. We constructed plasmids by codon-optimizing the putative seipin gene and ligating it into yeast plasmids (pRS405/415/425) with a leucine-selectable marker, the yeast TEF1 promoter, and the CYC1 terminator. The resulting recombinant plasmids were transformed into sei1Δ yeast. Currently, fluorescence microscopy and data analysis are ongoing to evaluate plasmid-mediated rescue of lipid droplet formation in sei1Δ yeast.

Presenter(s): Ma, Mark
School: Washington University in St. Louis
Session: P1.08
Title: TRPV2: The Hidden Switch that Keeps STING in Check—Until It's Time to Strike
Co-Author(s):
Advisor(s): Zhongsheng You, Washington University in St. Louis

Abstract: cGAS–STING innate immune pathway is central to cellular detection of cytosolic DNA (cytoDNA) arising from viral infection, genotoxic stress, or mitochondrial defects. While robust activation of this pathway is vital for host defense and antitumor immunity, inappropriate activity drives autoimmunity and chronic inflammation. How cGAS–STING maintains dormancy yet enables rapid activation remains incompletely defined. Here, we identify the Ca^{2+} channel TRPV2 as a bidirectional regulator that enforces STING quiescence and facilitates its activation. In the absence of cytoDNA, TRPV2 physically associates with STING at the endoplasmic reticulum (ER), restraining spontaneous signaling. Upon cytoDNA generation, cGAS-derived cGAMP triggers TRPV2 dissociation from STING, unleashing TRPV2-dependent ER Ca^{2+} release. The resulting rise in intracellular Ca^{2+} promotes STING ER-to-Golgi translocation and subsequent phosphorylation, culminating in type I interferon induction. Functionally, TRPV2 thereby governs STING-driven immune effector outcomes, including enhanced natural killer (NK) cell–mediated cytotoxicity. To further dissect the complexity of the cGAS-STING pathway, our future work aims to investigate how STING can be activated independently of upstream cGAS/cGAMP signals. My current project focuses on identifying and characterizing self-activating STING mutants, which may provide key insights into the intrinsic regulation of this pathway and its broader implications in immunity and disease.

Presenter(s): Maldonado, Kimberly
School: Hope College
Session: P1.19
Title: Transcranial temporal interference stimulation modulates spike timing of subthalamic nucleus neurons in a computational neuron model
Co-Author(s):
Advisor(s): Daniel Dorman, Hope College

Abstract: The established treatment for Parkinson's disease is deep brain stimulation (DBS), an effective but invasive procedure requiring surgical implantation of electrodes. Transcranial temporal interference stimulation (tTIS) is a novel, noninvasive technique with potential to target deep brain regions. It applies two high-frequency currents with a slight offset through scalp electrodes, producing a low-frequency envelope that may modulate neuronal activity where the fields overlap. The subthalamic nucleus (STN) is the favored DBS target in advanced Parkinson's disease. While tTIS has been studied in humans, animals, and generic neuron models, no work has examined tTIS on optimized models of STN neurons. We simulated tTIS on STN neurons to identify parameters for effective modulation. Using NEURON, we implemented an anatomically and biophysically realistic STN model and designed a tTIS model with optimized frequency, amplitude, and gradient. Two sinusoidal electric fields with slightly offset frequencies were applied via the extracellular mechanism, producing a low-frequency envelope. The gradient was optimized to depict current distribution across neuronal compartments. STN analysis reflected expected patterns: tTIS entrained and enhanced firing activity, with a noticeable phase shift in spike timing. These results indicate tTIS can noninvasively influence STN activity, supporting its potential as a therapeutic tool for Parkinson's disease.

Presenter(s): McCann, Emersyn
School: Hope College
Session: P2.14
Title: Interneuron Development in an Animal Model of Bipolar Disorder
Co-Author(s): Natalie Olander, Eden Comer, and Leah Chase
Advisor(s): Leah Chase, Hope College

Abstract: Bipolar disorder (BD), a neuropsychological disorder featuring cyclical periods of depressive and manic behaviors. The Chase lab aims to establish the face validity of a novel animal model for BD by assessing its behavioral and morphological traits. So we can better understand the pathophysiology of the disorder, others have shown that BD results in a decrease in interneurons within the prefrontal cortex and hippocampus. We are currently using immunocytochemistry to measure the number of parvalbumin (PV) and somatostatin (SST) interneurons in the hippocampus and prefrontal cortex in our animal model relative to controls. Preliminary results indicate no change in the number of PV interneurons, and an increase in SST interneurons in the hippocampus of the animal model. Ultimately, this study will allow us to determine whether shifts in manic/depressive behaviors are associated with changes in the total number of PV and SST GABAergic interneurons in the hippocampus/prefrontal cortex.

Presenter(s): McCarty, Teagan
School: Gustavus Adolphus College
Session: P1.09

Title: Phenotypic and Genomic Characterization of *Candida albicans* Strains Screened for Antifungal Drug Susceptibility
Co-Author(s): Kade Copple, Laura Burrack
Advisor(s): Laura Burrack, Gustavus Adolphus College

Abstract: *Candida albicans* is an opportunistic fungal pathogen that can develop into a deadly systemic bloodstream infection, particularly in immunocompromised individuals. These infections are notoriously difficult to treat because *C. albicans* populations may develop resistance and tolerance to the limited antifungal medications available. Studies have linked aneuploid strains (possessing an irregular number of copies of one or more chromosomes) to higher rates of resistance and tolerance against several drugs. Aneuploidies can arise as a result of drug exposure or concerted chromosome loss (CCL), a meiosis-like process that is part of the parasexual reproduction process observed in *C. albicans*. However, the impact of aneuploidies specifically arising from CCL on the emergence of drug resistance and tolerance is not well understood. This project's goal is to determine the frequency, range, and stability of aneuploidies acquired via CCL that contribute to drug tolerance and resistance. Here, we randomly selected several strains that did not pass a screening for resistance or tolerance, then performed several tests to understand why they were omitted–including minimum inhibitory concentration assays, growth curves conducted in the presence/absence of drug, and whole genome sequencing and mapping to identify variation in ploidy–then compared their characteristics to the resistant and tolerant strains.

Presenter(s): Meehan, Fionn
School: Knox College
Session: II.G.2
Title: Are Baseballs a Hidden Reservoir for MRSA? A Microbial Survey of Collegiate Sports Gear
Co-Author(s):
Advisor(s): Matthew Jones-Rhoades, Knox College

Abstract: Methicillin-resistant *Staphylococcus aureus* (MRSA) is an antibiotic-resistant bacterium that poses serious health concerns in both athletic and clinical settings. It is often found in high-contact sports, such as football and wrestling, where skin-to-skin contact and shared equipment increase the transmission of bacteria. However, little research has been done on the presence of MRSA in lower-contact sports like baseball and softball. This study analyzed the presence of MRSA and related bacteria on 10 collegiate baseballs and 10 collegiate softballs. This was accomplished by swabbing and culturing the samples on Mannitol Salt Agar to promote the growth and identification of Staphylococcus colonies. Many isolated samples showed characteristics consistent with Staphylococcus, including mannitol fermentation, gram-positive staining, cocci morphology, and rDNA sequencing. However, all isolates tested negative for coagulase activity, indicating none were S. aureus, and none of the *Staphylococcus* isolates had antibiotic resistance profiles consistent with being MRSA. Thus, while the majority of sampled baseballs and softballs contained *Staphylococcus* isolates, none were observed to harbor *S.aureus* or MRSA. Ongoing testing comparing high-contact surfaces on campus will help to assess the broader presence of MRSA in community environments.

Presenter(s): Moon, Gabrielle
School: University of Chicago

Session: P1.02
Title: BNIP3-Dependent Muscle Atrophy in Cancer Cachexia Reflects Mitochondrial Remodeling and Metabolic Stress Signaling
Co-Author(s): Alexandra S. Ware, Elizabeth CS Foster, Jason Kwon, Alexis Demonbreun, Addison Barber, Ioanna Karras, Ishan Roy, Kay F. Macleod
Advisor(s): Kay Macleod, University of Chicago

Abstract: Cancer cachexia is a debilitating effect of human cancers, including pancreatic ductal adenocarcinoma (PDAC), resulting in rapid bodyweight loss through skeletal muscle atrophy and heightened chemotherapy toxicity risk. We suggest a role for the mitochondrial cargo receptor BNIP3 in driving skeletal muscle atrophy during PDAC-associated cachexia, using novel genetically engineered mouse models. Muscle-specific BNIP3 deletion in the autochthonous PDAC mouse model inhibited muscle atrophy such that skeletal muscle exhibited increased weight, increased myofiber cross-sectional area, and decreased expression of muscle atrogenes MuRF1 and Atrogin1, compared to skeletal muscle BNIP3-containing PDAC mice. We further hypothesized BNIP3 drives cachectic muscle loss by preventing mTORC1 (a central regulator of cell metabolism) activation by the Rheb GTPase, weakening cellular protein and lipid biosynthesis. Because AMP-activated protein kinase (AMPK), a nucleotide synthesis suppressor, also negatively regulates mTORC1 activity, we investigated whether BNIP3 influences metabolic pathways downstream of AMPK. Steady-state metabolomics revealed downregulated purines in muscle and plasma of cachectic mice, suggesting BNIP3-dependent mitophagy in muscle limits 1C metabolism, which occurs in mitochondria. Western blots across the quadriceps, gastrocnemius, and tibialis anterior muscles revealed tumor-burden–dependent increases in BNIP3, differential Rheb expression, and bimodal AMPK activation, further linking BNIP3 to mTORC1 and nucleotide biosynthesis.

Presenter(s): Mungara, Rutu
School: Knox College
Session: P3.02
Title: Functional Gene Analysis in *Stentor coeruleus* Using RNA Interference
Co-Author(s):
Advisor(s): Mark Slabodnick**,** Knox College

Abstract: My summer research focused on exploring gene function in the single-celled organism called *Stentor coeruleus*, which is known for its remarkable ability to regenerate the lost structures. Using RNA interference (RNAi), I attempted to knock down candidate genes (13572, 24560, 24902, PP2A, and LF4 [control]) and observe phenotypic changes related to cell morphology and regeneration. Through this project, I gained experience with RNAi injections, microscopy, and surgical techniques such as bisecting cells into head and tail halves to test their regenerative capacity. While most candidate gene knockdowns (13572, 24560, 24902) did not result in visible phenotypic changes, PP2A consistently showed structural degradation and eventual cell death, supporting its critical role in maintaining viability. These results highlight both the promise and the challenges of genetic studies in Stentor, where verifying RNAi efficiency and developing additional molecular tools remain important future steps. This project not only strengthened my technical skills in molecular biology but also deepened my curiosity about regeneration at the cellular level. Overall, my work

contributes to the ongoing effort in our lab to expand genetic tools for *Stentor* by a very small degree and helps me to better understand the molecular basis of single-cell regeneration.

Presenter(s): Narula, Sarah
School: Washington University in St Louis
Session: P2.03
Title: Repurposing SGLT2 Inhibitors for Cardiometabolic Liver Disease
Co-Author(s): Kim Liss, Daniel Ferguson, Tan Nguyen, Brian Finck, Justin Berger
Advisor(s): Justin Berger, Washington University in St Louis

Abstract: Sodium glucose co-transporter 2 inhibitors (SGLT2i) were designed as glucose-lowering diabetes medications but also have powerful cardioprotective effects. Accordingly, we hypothesized that SGLT2i provides therapeutic effects in metabolic liver disease. Metabolic dysfunction-associated steatohepatitis (MASH) is characterized by fat accumulation in the liver resulting in inflammation, hepatocyte damage, fibrosis, and eventually liver failure. We tested effects of genetic and pharmacologic SGLT2 inhibition on insulin resistance, diet-induced obesity (DIO), hepatic steatosis, and liver damage in a mouse model of MASH. Cohorts of 8-week-old MASH mice were subjected to two forms of systemic SGLT2 inhibition: global SGLT2 knockout (gKO) mice and SGLT2i empagliflozin treatment. After 8 weeks, wild-type (WT) and gKO mice were randomized to treatment with or without empagliflozin. At 16 weeks, the mice underwent body composition analysis (echoMRI) and glucose tolerance testing. At 20 weeks, endpoints were measured including body weight, glucosuria, and liver histology. Genetic and pharmacologic SGLT2 inhibition had significant metabolic benefits including protection from DIO, decreased fat mass, and improved insulin resistance. SGLT2 inhibition also decreased plasma AST and ALT concentrations, reduced hepatomegaly, and diminished expression of fibrotic and inflammatory markers. These pre-clinical data suggest that SGLT2i is a promising therapeutic treatment for MASH via an SGLT2-dependent mechanism.

Presenter(s): Okamoto, Shino
School: Knox College
Session: P2.02
Title: Assessing the Effects of *Bacopa monnieri* on Migration of C6 Glioma Cells
Co-Author(s):
Advisor(s): Esther Penick, Knox College

Abstract: *Bacopa monnieri* is a plant that has been used in Ayurvedic Medicine. It has been suggested to have positive effects on several diseases, including Parkinson's disease and diabetes. According to recent studies, it may also have anti-cancer effects. Generally, high doses of certain chemicals can lead to cell death by increasing cell stress. In contrast, a previous study demonstrated that *Bacopa monnieri* arrests colon cancer cells at the G0/G1 phase, but does not induce cell death. Since it is an herb that can be used daily, it might be a novel substance for cancer treatment. However, the effects and the mechanism have not been fully examined. In this study, the effects of *Bacopa* on C6 glioma cells were investigated using the wound healing assay, which has been correlated to cancer metastasis. Cells were seeded into plates, and *Bacopa* solution (50, 100, 150, 200, 300 µg/ml) was added. After 2 hours of treatment, scratches were made and left to heal. The next day pictures were taken to measure the wound closure. There was a significant dose-dependent decrease in wound healing,

suggesting that it negatively regulates cell migration, which has potential anti-cancer effects. Additional study is needed to determine its mechanism.

Presenter(s): Ollier, Theo
School: Colorado College
Session: P2.20
Title: Characterization of Fungal Endophytes from Native Colorado Flora
Co-Author(s): Miles Katzen, Jesús F. Peña
Advisor(s): Jesús F. Peña, Colorado College

Abstract: Fungal endophytes are an understudied group of fungi that exist in all land plants, primarily as mutualists. Endophytes have a wide range of effects on their host plants, including but not limited to the ability to reduce fungal pathogen infection, promote plant growth, and reduce the effects of abiotic stressors. As many parts of the world are experiencing reduced water availability as a result of climate change, finding new ways to reduce the water needs of agricultural crops will be crucial. This study hopes to demonstrate the efficacy of arid-adapted endophytes at reducing drought stress in a maize, a model crop. This study characterizes the above and below-ground fungal endophyte communities of three native Colorado plants: C. imbricatus, O. polyacantha, and Y. glauca. Fungal DNA sequences were obtained from the plants sampled in June 2025 using the internal transcribed spacer region (ITS) and large subunit (LSU) of fungal ribosomal DNA (rDNA) with fungal-specific primers. Beyond identifying these plants' endophytic counterparts, the next step for this study is to carry out a drought experiment in which maize seedlings will be inoculated with selected endophytes and grown under varying levels of drought stress.

Presenter(s): Ong, Jennifer
School: Washington University in St. Louis
Session: II.G1
Title: Quantification of Polyethylene Terephthalate in Patient Blood Samples and Its Implication on Health
Co-Author(s):
Advisor(s): Christopher Farnsworth, Washington University in St. Louis

Abstract: The integration of plastics into daily life has led to severe plastic pollution in the environment. Over time, these plastics are susceptible to biodegradation, producing microplastics and nanoplastics. Recently, these particles have been detected in the human body--embedding themselves in blood, tissue, and organs. Studies suggest relationships between microplastic exposure and inflammatory, metabolic, endocrine, and immunotoxic pathways, raising concerns about their long-term health effects. To fully understand how the presence of microplastics in the body affects health, social determinants of health (SDOH) must also be investigated to understand individual and community level exposure risks. However, with the costs and limitations of the current technology needed to quantify microplastics, the widespread implementation of efficient microplastic testing is difficult. Thus, we developed a method to quantify the concentration of polyethylene terephthalate (PET), the most common microplastic, in remnant blood samples using UV spectrometry. Then, we conducted a retrospective chart review to examine possible associations between PET exposure and health outcomes as well as identify possible mechanisms for their embodiment

into the body's makeup. This will lay a foundation for the next steps in combatting health risks of microplastic exposure by enabling efficient, yet accurate detection methods.

Presenter(s): Palanga,Ian
School: Macalester College
Session: II.F.3
Title: Investigating Controversy: Osteolytic Fibrosarcoma Only Sensitizes Small DRG Neurons
Co-Author(s): Viatcheslav Viatchenko-Karpinski, Iryna Khasabova, Sergey Khasabov, Malcolm Johns, Phoebe Thomas, Donald A. Simone
Advisor(s): Donald Simone, University of Minnesota School of Dentistry

Abstract: Bone cancer pain is driven by a combination of neuropathic and inflammatory mechanisms initiated by tumor cells, and nerve and bone damage. Simultaneously, nerve endings at tumor sites are in low-oxygen, acidic, high-calcium environments that strongly promote nociceptor sensitization. Such extreme environments may be capable of sensitizing not only primary nociceptors (pain-signaling cells) but non-nociceptive sensory neurons as well, and that crosstalk between neurons in the DRG (dorsal root ganglia) may also sensitize such cells. By measuring electrical properties of small nociceptive DRG neurons that innervate skin overlying an osteolytic fibrosarcoma tumor in the mouse paw (identified by fluorescent retrograde tracer DiI), we previously showed that they become more excitable in tumor-bearing mice with increased behavioral responses to painful stimuli on the plantar surface of the tumor-bearing paw. To test whether non-nociceptive neurons, which are distinctively larger than primary nociceptors, also experience electrophysiological changes in our model, we measured their properties using the same whole-cell patch clamping protocol, and observed no biophysical alterations between labelled or unlabeled neurons, as compared to neurons from naïve mice, suggesting that neither the tumor environment, nor crosstalk, sensitizes large DRG neurons. This reinforces small DRG neurons as drivers of peripheral nociception during bone cancer.

Presenter(s): Palmiotto,Angelina
School: Gustavus Adolphus College
Session: P2.16
Title: Investigating Inhibitory Controls of Sprague-Dawley Rats Using a Stop Signal Task
Co-Author(s): Nicole Post
Advisor(s): Kelle Nett, Gustavus Adolphus College

Abstract: The ability to inhibit a behavior is vital for an organism's survival. Specifically, the ability to inhibit an in-progress behavior is particularly important, especially when presented with new information (e.g., a songbird pausing a mating call to avoid attracting a nearby predator). The Stop Signal Reaction Time (SSRT) task provides a standard metric of inhibitory control over initiated behaviors. We trained Sprague-Dawley rats (n=16) on this two-part, lever-pressing task. First, rats learned to press a "seeking" lever to gain access to a "taking" lever, which delivered a food reward when pressed. Once rats could rapidly perform this sequence, an auditory cue was introduced that signaled to the rat that it must withhold the final "taking" lever press to receive the reward. This auditory cue becomes the signal for the rats to inhibit the initiated behavior. Our experiment showed that some rats successfully learned to withhold the final lever press when prompted by the inhibitory cue. This demonstrates a reliable method for measuring their impulse control. Future research will use this training

protocol followed by a specific probe test to calculate each rat's SSRT under varying conditions to investigate factors that impair inhibitory control, such as prolonged drug use.

Presenter(s): Phan, Annie
School: Carthage College
Session: P2.13
Title: Expression of Melanin-Concentrating Hormone (MCH) and Orexin Neurons in Mouse Models of Alzheimer's Disease
Co-Author(s): Sarah J. Terrill
Advisor(s): Sarah J. Terrill, Carthage College

Abstract: Neurodegenerative diseases such as Alzheimer's Disease are often associated with changes in appetite and taste preferences. We explored whether two neuropeptides that play a role in regulating sleep-wake cycles and energy homeostasis, melanin-concentrating hormone (MCH) and orexin (OX), show altered expression in two distinct mouse models of AD: hTau and 3xtg. Coronal forebrain sections containing the lateral-hypothalamus and zona-incerta were slide-mounted for MCH and OX staining using fluorescent immunohistochemistry. Labeled sections were imaged using a confocal microscope for neuronal quantification. We found that MCH neurons are particularly vulnerable to tau-related pathology, while orexin neurons appear relatively resilient. That's important because MCH is linked to sleep and appetite, which are two things that are commonly disrupted in Alzheimer's disease. These findings highlight MCH as a potential target for understanding and treating sleep and appetite disturbances in AD.

Presenter(s): Qarabsa, Rahaf
School: St. Olaf College
Session: P2.04
Title: Optimizing a Co-Culture Model to Account for the Follicular Lymphoma Tumor Microenvironment in Treatment Response to Bispecific Antibodies
Co-Author(s): Sophie Zhu, Emily Sumpena, Ioulia Vogiatzi, Mark Murakami
Advisor(s): Mark Murakami, Harvard University - Dana-Farber Cancer Institute

Abstract: Follicular lymphoma (FL) is an indolent non-Hodgkin lymphoma (NHL), accounting for ~20% of all NHL. It is characterized by frequent relapses and potential transformation to diffuse large B-cell lymphoma, making it less responsive to novel treatments such as bispecific antibodies (BsAbs). BsAbs, specifically the effector cell engager type, recruit T-cells via CD3 on one end, while the other end recognizes the tumor-associated antigen CD20 on B-cells, bringing those cells into close proximity, facilitating cytotoxic tumor cell killing. Despite being a promising therapeutic approach, the efficacy can be dampened by the FL tumor microenvironment (TME). The TME is characterized by a large number of myeloid cells, primarily tumor-associated macrophages (TAMs), which directly and indirectly exhaust the T-cells. Our goal is to employ an assay for testing tumor response to BsAb therapy. To better study this immunosuppressive context, our goal is to establish a co-culture system that accurately models the TME. This system will be used to reproduce key features of T-cell exhaustion driven by TAMs, provide a platform for testing tumor responses to BsAb therapy, and enable mechanistic insights into T-cell dynamics.

Presenter(s): Qi, Jessica
School: University of Chicago
Session: P2.11
Title: Cooperative RBMX-YTHDC1 Regulation of Nascent Transcription Sustains AML
Co-Author(s): Michael Kharas, Xuejing Yang, Isaac Wakiro, Emily Batchelor
Advisor(s): Michael Kharas, Memorial Sloan Kettering Cancer Center

Abstract: RNA binding proteins (RBPs) play key roles in post-transcriptional regulation and are found to be dysregulated in hematological malignancies. Here, we investigate how two RBPs, RBMX and the nuclear m6A reader YTHDC1, cooperate to sustain acute myeloid leukemia (AML). We previously found that RBMX is overexpressed and essential in AML by regulating the rate of nascent transcription. YTHDC1 is similarly aberrantly expressed and required, and it forms nuclear condensates on m6A-modified transcripts that shield them from PAXT-mediated degradation. Loss of either RBP delays leukemia development. More recently, we found that RBMX not only co-localizes with YTHDC1, but they also physically interact. Here, we show that YTHDC1 regulates RBMX targets. In line with this, loss of YTHDC1 results in reduced protein levels of RBMX targets. Consistent with this, ectopic expression of YTHDC1 increases protein levels of these targets. Acute RBMX depletion via dTAG reduces CBX5 with compensatory YTHDC1 upregulation, consistent with coordinated control of nascent transcription and RNA fate. Finally, we demonstrate that METTL3 knockout in MEFs provides a platform to test whether RBMX condensates require m6A. Together, our data support a model in which RBMX and YTHDC1 collectively regulate nascent transcription in leukemia, revealing joint therapeutic opportunities.

Presenter(s): Renning, Cora
School: Gustavus Adolphus College
Session: P1.12
Title: Mutagenesis of sOlincRNA-encoded implicated in Plant Development and Abiotic Stress Response Using CRISPR/Cas9 in *Arabidopsis thaliana*
Co-Author(s): Taylor Ruhl; Anna Imdieke
Advisor(s): Katherine Leehy, Gustavus Adolphus College

Abstract: As climate change intensifies, abiotic stressors such as drought, extreme temperatures, and salinity are becoming more frequent and severe, threatening crop productivity and global food security. We are investigating how specific short open reading frame-encoded peptides (SEPs) encoded in the *Arabidopsis thaliana* genome influence plant development and responses to environmental stress. These SEPs are difficult to identify due to limited structural similarities. Collaborators in the Nelson lab recently identified over 160 long intergenic non-coding RNAs (lincRNAs) in *A. thaliana* that are translated and responsive to stress. While many corresponding genes have mutant lines available, 20 identified sORFs do not. To study them, we are designing guide RNAs that target Cas9 to induce mutations in each sORF. Constructs containing 1–5 gRNAs, Cas9, and GFP under a seed-specific promoter are transformed into *A. thaliana* and screened via seed fluorescence. We have generated constructs targeting 9 genes and are screening plant lines for successful mutagenesis. Once mutants are confirmed, we will use high-throughput phenotyping and molecular analyses to determine the role of each SEP in growth and stress responses. This work will identify potential gene editing targets to enhance crop resilience under climate stress, contributing to the development of more sustainable agricultural systems.

Presenter(s): Rimal, Nabina
School: Lawrence University
Session: P2.18
Title: Understanding The Limits Of Induced Awe How Long It Lasts And Can It Increase Belongingness?
Co-Author(s): Miliciades Gonzalez- Medina, Savannah E. Mujkanovic
Advisor(s): Lori M. Hilt, Lawrence University

Abstract: Awe is a mixed-valence emotion associated with positive psychological outcomes. Experimentally induced awe heightens willingness to learn, lowers inflammatory cytokines, and triggers a diminished sense of self, which leads to increased pro-social tendencies (i.e., generosity, helping behaviors) that promote enhancements in social connectedness. [LMH1] A question remains regarding how durable these laboratory effects are, as they are typically measured only immediately post-induction. Additionally, it is unclear whether the prosociality effects would help individuals with a thwarted sense of belongingness, which is a risk factor for suicide. The present study seeks to address these gaps in the literature. College student participants (N = 25) will complete questionnaires online prior to a single laboratory session where they will watch both neutral and awe-evoking immersive virtual reality videos. State affect, belongingness, and feelings of awe will be assessed immediately prior to and following each video. Feelings of awe will continue to be assessed for 20 minutes following the awe video. Understanding the durability of induced awe will help inform brief interventions that may improve college students' belongingness, which could have impacts on retention as well as mental and physical health.

Presenter(s): Rooker, Kate
School: Gustavus Adolphus College
Session: P3.11
Title: Atrophy and Reduced Oxidative Capacity in Type-Identified Tibialis Anterior Muscle Fibers with Age
Co-Author(s): Genesis Hernandez, Gary Sieck, Matthew Fogarty
Advisor(s): Matthew Fogarty, Mayo Clinic College of Biomedical Sciences

Abstract: Lumbar nerves innervate the tibialis anterior (TA), a limb muscle in control of dorsiflexion and inversion of the foot. As people age, the TA weakens, making the muscle prone to sarcopenia, the age-associated weakness and atrophy of muscles. The TA comprises four muscle fiber types: Fatigue-resistant (I and IIa) fibers, utilized for endurance; and the more fatigable (IIx and IIb) muscle fibers, involved in explosive behaviors. From previous studies of the diaphragm muscle, type I/IIa fibers are resistant to sarcopenia, whereas type IIx/b fibers are sensitive. Vulnerability to sarcopenia is characterized as a reduction in cross-sectional area and specific force of the IIx/b muscle fibers with age. Applying the same principles when studying the TA, the degeneration of motor units was assessed in accordance with their metabolic properties (SDHmax activity) and the cross-sectional area of the muscle, in young and old rats. We hypothesized that type IIx/b fibers would exhibit characteristics of sarcopenia, like the atrophy represented by reduced specific force and reduced SDHmax activity. Results show a decrease in cross-sectional area of type IIx/b fibers and a decrease in mitochondrial activity in only 24-month-old Fischer 344 rats.

Presenter(s): Ruhl, Taylor
School: Gustavus Adolphus College
Session: P1.12
Title: Mutagenesis of sOlincRNA-encoded implicated in Plant Development and Abiotic Stress Response Using CRISPR/Cas9 in *Arabidopsis thaliana*
Co-Author(s): Cora Renning; Anna Imdieke
Advisor(s): Katherine Leehy, Gustavus Adolphus College

Abstract: As climate change intensifies, abiotic stressors such as drought, extreme temperatures, and salinity are becoming more frequent and severe, threatening crop productivity and global food security. We are investigating how specific short open reading frame-encoded peptides (SEPs) encoded in the Arabidopsis thaliana genome influence plant development and responses to environmental stress. These SEPs are difficult to identify due to limited structural similarities. Collaborators in the Nelson lab recently identified over 160 long intergenic non-coding RNAs (lincRNAs) in *A. thaliana* that are translated and responsive to stress. While many corresponding genes have mutant lines available, 20 identified sORFs do not. To study them, we are designing guide RNAs that target Cas9 to induce mutations in each sORF. Constructs containing 1–5 gRNAs, Cas9, and GFP under a seed-specific promoter are transformed into *A. thaliana* and screened via seed fluorescence. We have generated constructs targeting 9 genes and are screening plant lines for successful mutagenesis. Once mutants are confirmed, we will use high-throughput phenotyping and molecular analyses to determine the role of each SEP in growth and stress responses. This work will identify potential gene editing targets to enhance crop resilience under climate stress, contributing to the development of more sustainable agricultural systems.

Presenter(s): Samnang, Raksa
School: Hope College
Session: P2.06
Title: Experimental Analysis of *Escherichia coli* Metabolism on D-serine
Co-Author(s): Marian G. Diaz, Annika K. Sytsma, Jacquelin D. D'Lamater, Frederick T. Melges
Advisor(s): Clayton Piehl, Lauren Cribbs, Natalie Huisman, Brent Krueger, Aaron Best, Michael Pikaart, Hope College

Abstract: *Escherichia coli* strains play an important role in a variety of habitats, including open aquatic environments. Using data collected from the local Macatawa Watershed, we isolated 10,000 and sequenced over 500 water-derived *E. coli* strains, generating a genome-scale metabolic model for each. Past lab members utilized Biolog PM1 and PM2a plates to analyze metabolic behavior of 32 watershed strains and one reference strain (*E. coli* MG1655) on 190 possible carbon-based substrates. A noticeable discrepancy was noted between metabolic model predictions and actual growth on a number of substrates. In particular, the substrate D-serine produced only eight growing *E. coli* strains compared to the 31 predicted to grow by the model. The D-serine operon is found to be a vital component of *E. coli* strains that can metabolize D-serine. In fact, any missing operon components inhibit strains' abilities to grow on D-serine. Retesting on minimal media agar plates supplemented with D-serine was done on a variety of *E. coli* strains to further confirm growth patterns. On the minimal supplemented plates, one strain grew unexpectedly on the D-serine when it was predicted not to. Additionally,

at least two strains tested appear to exhibit unexpected “breakthrough” colonies after 72 hours of incubation.

Presenter(s): Sander, Kaitlyn
School: Carthage College
Session: P2.07
Title: Screening *E. coli* for the Expression of PVY Activated – GFP (PA-GFP) for Detection of PVY
Co-Author(s): Erin Weber, Leslie Sauceda
Advisor(s): Erin Weber, Carthage College

Abstract: The spread of Potato virus Y (PVY) through its host is not well characterized, due to inefficient early detection methods. For this reason, the development of a PVY-activated dark-to-bright reporter utilizing green fluorescent protein (PA-GFP) may prove useful in the investigation of PVY spread through its host. Fluorescence of GFP can be quenched via the Influenza M2 transmembrane helix through a PVY cleavable linker. The presence of PVY is indicated by the appearance of GFP signal after cleavage and release of the quenching peptide. The expression of PA-GFP was previously attempted using BL21 *E. coli*, but the resulting recombinant protein was not soluble. We screened alternative expression strains and induction conditions to improve PA-GFP expression. We found that PA-GFP expresses best in Lemo21 *E. coli* strain using autoinduction media induced at 16 °C. However, the recombinant protein was largely insoluble. Screening of additional induction conditions is ongoing. Plans include testing the PA-GFP design as a PVY substrate. Once optimized, the PA-GFP reporter may provide an advantageous tool in the study and real-time identification of PVY.

Presenter(s): Sauceda, Leslie
School: Carthage College
Session: P3.04
Title: Screening *E. coli* Expression Lines and Conditions for Production of a PVY-Activated GFP Reporter
Co-Author(s): Erin Weber**,** Kaitlyn Sander
Advisor(s): Erin Weber, Carthage College

Abstract: Potato virus Y (PVY) is one of the biggest threats to potato production, as the infection can lower tuber yield and quality. Visual symptoms are unreliable for identification due to inconsistent symptoms across strains and cultivars. Early identification and removal are key to combat PVY. Currently the most reliable method for PVY screening is Enzyme-Linked Immunosorbent Assay (ELISA). However, ELISA requires a high viral titer, multiple days to complete, and specialized equipment. This work aims to develop PVY-activated dark-to-bright Green Fluorescent Protein (GFP) reporters as a simpler, cheaper, and faster method to detect PVY, even at low titer of infection. The fluorescence of GFP is quenched by a polyglycine linker attached to a PVY cleavable sequence. GFP signal is detected when the polyglycine linker and PVY cleavable sequence is removed. This work describes the screening of E. coli strains and conditions to identify optimal conditions for producing soluble PA-6G-GFP. The best expression of PA-6G-GFP was observed from the Lemo21 E. coli strain after short induction; however, the expressed protein was insoluble. Future work aims to optimize conditions for PA-6G-GFP solubility.

Presenter(s): Shaw, Toby
School: Hope College
Session: P3.14
Title: Participants Show Motor Habit Preference and Loss Aversion in a Novel Iowa Gambling Task
Co-Author(s): Therea Kratt, Daniel Dorman
Advisor(s): Daniel Dorman, Hope College

Abstract: Difficulty in controlling and changing habitual and impulsive behaviors is a common feature of psychiatric disorders. To better understand how people modify their habits in a variable reward-driven environment, we designed a novel Iowa Gambling Task (IGT). The original IGT is an accepted experimental task that assesses risk-taking in participants, specifically in a static hidden expected value situation. Our task changes between two distinct blocks, where participants must distinguish between the block where they must make decisions based on the positioning of certain options (selected through directional keypresses), or the labeling of said options. By analyzing their decisions between blocks, the amount of weight participants give to habitual responses compared to goal-based decision making can be compared. 17 undergraduate students completed the modified IGT, and habitual responses were found to make up the majority of the decisions. Results indicated that participants switch position-based strategies (but not label-based strategies) depending on the block, and that participants' choices across the entire experiment were more position-based than label-based. Participants also avoided options with frequent losses regardless of expected value, showing a degree of loss aversiveness. Overall, these results suggest that in a changing environment, people default to safe, motorized habitual decision making.

Presenter(s): Shirk, Madeline
School: Hope College
Session: II.G.3
Title: Drinking Water Quality and Accessibility in Zambia
Co-Author(s): Emma G. Smith, Jacquelin D. D'Lameter, Emma J. Koeman
Advisor(s): Lauren M. Cribbs, Brent P. Krueger, Virginia Beard, and Aaron Best, Hope College

Abstract: Poetice is a non-profit organization leading interventions to improve drinking water quality and access in Choma, Zambia. The Global Water Research Institute (GWRI) worked with Poetice to evaluate water access and quality across existing water sources, with a goal of identifying potential improvements brought about by recently installed boreholes. Poetice and GWRI designed a survey to gather information about household demographics, water collection and usage, cost, health, economic factors, and security. We also collected 59 water samples from three different site-types: shallow wells, taps and boreholes. Samples were tested for heavy metals, VOCs, *E. coli*, and total coliforms. *E. coli* was found in 42% of sampled sites; 88% had total coliforms present. Seventy-five percent of sampled sites were free from detectable metal and VOC contaminants. These results guide Poetice's work to increase regular, affordable access to safe drinking water for community members in Choma.

Presenter(s): Shyroka, Dasha
School: Gustavus Adolphus College
Session: P3.19
Title: Examining Pb mobilization in warming peatland ecosystems

Co-Author(s): Jeff Jeremiason
Advisor(s): Jeff Jeremiason, Gustavus Adolphus College

Abstract: Ombrotrophic bogs are special ecosystems that get all their nutrients from the atmosphere, rather than from groundwater or surrounding soil. They also store large amounts of carbon. About 30% of the world's soil carbon is found in peatlands, which include these types of bogs. Peatland ecosystems have been studied at the USDA Forest Service Marcell Experimental Forest (MEF), located about 40 kilometers north of Grand Rapids, Minnesota. The site is located at the southern margin of the boreal peatland forest. This climate change experiment is called SPRUCE (Spruce and Peatland Responses Under Changing Environments).The SPRUCE experiment is the primary component of the Terrestrial Ecosystem Science Scientific Focus Area at ORNL focused on terrestrial ecosystems and the mechanisms that underlie their responses to environmental change. In this experiment, researchers built large enclosures where temperature and carbon dioxide (CO_2) levels are varied. The goal is to find out how northern peatlands respond to warmer temperatures and higher CO_2, especially whether they might start releasing the massive amounts of carbon they currently store. Responses to warming and interactions with increased atmospheric CO_2 concentration are anticipated to have important feedback on Earth's carbon cycle because of the high carbon stocks harbored by such ecosystems.

Presenter(s): Silva, Emily
School: Colorado College
Session: I.C.2
Title: The role of serotonin receptors in regulating stability of idiosyncratic behavioral preferences in *Drosophila melanogaster*
Co-Author(s):
Advisor(s): Ryan Maloney, Colorado College

Abstract: Animals often display individuality in their behavior, even when genetic and environmental conditions are held constant. Previous studies suggest serotonin plays a key role in regulating this behavioral variability, but it remains unclear which serotonin receptors are most influential. To investigate this, we compared control *Drosophila melanogaster* with serotonin-deficient mutants lacking each of the five known Drosophila serotonin receptors. We measured individual handedness in a Y-maze assay over two-hour sessions across three days. Mutants for 5HT1A, 5HT1B, 5HT2B, and 5HT7 receptors exhibited decreased consistency in turning preference over time, indicating greater behavioral drift. These findings suggest that multiple serotonin receptor subtypes contribute to maintaining stable behavioral phenotypes, providing insight into how neuromodulatory signaling supports individuality in animal behavior.

Presenter(s): Simon, Gabriel
School: St. Olaf College
Session: P3.08
Title: Media Lacking a Subset of Essential Amino Acids Signal Lipid Droplet Accumulation in *Tetrahymena thermophila*
Co-Author(s): Alex Bittner, Brenna Lindeen, Jonas Geere, Jessica Schmidt, Emily Nuttall, Ian Holtz-Hazeltine, Kim Kandl, Laura Listenberger
Advisor(s): Kim Kandl, St. Olaf College

Abstract: Lipid droplets are important and dynamic organelles in all cells. Work in our lab has expanded the study of lipid droplets to *Tetrahymena thermophila*, a single-celled freshwater ciliate. *Tetrahymena* are evolutionarily distant from better studied model organisms, but similarly to them, *Tetrahymena* accumulate lipid droplets in response to nutrient deprivation. Previous work in our lab demonstrated lipid droplet accumulation in *Tetrahymena* when cells were moved from a nutrient rich Neff media (0.25% proteose peptone, 0.25% yeast extract, 0.5% glucose, 33 μM FeCl3) to 10 mM Tris buffer, a media lacking multiple nutrients. However, the specific trigger for lipid droplet accumulation in *Tetrahymena* remains unknown. Thus, our lab investigated which missing nutrient in Tris is responsible for initiating lipid droplet synthesis. Our results show that when certain amino acids, including arginine, histidine, isoleucine, leucine, lysine, methionine, valine, tryptophan, threonine, phenylalanine, and serine, are dropped out of a synthetic complete media, we observe an increase in lipid droplet formation, triglyceride accumulation and inhibition of cell division.

Presenter(s): Smith, Ian
School: Knox College
Session: II.E.3
Title: Comparative anatomy of marine vertebrates: Diaphragm structure and function in mammals
Co-Author(s): Alyssa Stringer, Emily McParland, Nicholas Gidmark
Advisor(s): Nicholas Gidmark, Knox College

Abstract: Ventilation is a vital part of the respiratory process for all mammals. The diaphragm is the primary muscle responsible for ventilation. It flattens during inhalation, creating negative pressure in the lungs, drawing air in, then flexing upwards during exhalation, emptying air from the lungs. In terrestrial mammals, oxygen is readily available, whereas marine mammals have diaphragms that are adapted to compensate for an environment where they can only ventilate for a brief period. Adaptations in some species include collagen reinforcement of the diaphragm in cetaceans, the evolution of separated hemidiaphragms in manatees, and the collapse of the diaphragm when diving. However, the diaphragms of marine mammals have not been studied extensively with respect to the diaphragms of terrestrial mammals. By examining the differences, we can gain further insight into ventilation across species and how it is adapted for diverse environments. This study demonstrates that facultatively and obligately aquatic species have diaphragms with longer muscle fiber lengths and higher masses, indicating an increase in power when ventilating. They also have larger ratios of the size of their diaphragms as compared to their torsos, which is an indicator of speed and overall strength to ventilate more explosively in an aquatic environment.

Presenter(s): Smith,Yael
School: Washington University in St. Louis
Session: P3.16
Title: Maternal Undernutrition Leads to Increased Risk for Offspring Steatotic Liver Disease (SLD)
Co-Author(s): Holly Hinrichs, Monica Young, Michael D. Thompson
Advisor(s): Michael D. Thompson, Washington University in St. Louis

Abstract: Maternal undernutrition is a global concern that may impact offspring health long-term. Studies show that the weaning period (2-4 weeks of age) in mice is critical for immune system development. Additionally, maternal overnutrition via a high fat, fructose, and cholesterol (HFFC) diet exacerbates hepatic injury in mouse offspring. We hypothesize that maternal undernutrition (UN) similarly worsens liver disease in offspring weaned to HFFC and may disrupt the weaning reaction. Starting day 12.5 of pregnancy, dams were randomly assigned either a 50% food-restricted UN or ad libitum CHOW diet. Offspring tissues were either collected at 2 or 3 weeks to test the weaning reaction or weaned to HFFC for 10 weeks; all samples underwent qPCR and staining. In the HFFC model, UN offspring showed elevated lipid metabolism regulators (PPARa, FASN) and fibrotic markers (Col1a1, Col3a1, a-SMA.) H&E staining identified increased steatosis in the UN offspring. In the weaning experiment, UN offspring at 3 weeks had elevated ileum pro-inflammatory cytokines (TNFa, IFNg.) Though preliminary, these results may indicate disrupted immune system development, but further research is needed to conclude. Maternal undernutrition may also predispose offspring to liver disease marked by steatosis and early-stage fibrosis.

Presenter(s): Srinivasan, Prithi
School: University of Chicago
Session: I.D.3
Title: Critically Evaluating the Co-Binding of Cofilin and Importin 9 in Nuclear Actin Transport
Co-Author(s): Amanda J. Keplinger, Alexander J. Ruthenburg
Advisor(s): Alexander Ruthenburg, University of Chicago

Abstract: In addition to its canonical cytoskeletal role, actin plays an essential role in the nucleus, interacting with RNA polymerases, chromatin-remodeling complexes, and DNA damage-repair machinery to modulate genomic architecture and stability. As a result, it is critical to understand the factors underlying actin's entry into the nucleus. Cell-based measurements have contributed to a widely accepted model in which the nuclear import chaperone Importin 9 (IPO9) works in concert with the actin filament-severing protein cofilin to mediate actin's entry into the nucleus. In striking contradiction to this model, we demonstrate with surface plasmon resonance and actin polymerization assays that IPO9 directly binds monomeric actin with high affinity at the actin target-binding cleft. Furthermore, we identify that in vitro, cofilin does not mediate actin•IPO9 binding, but acts conversely – competitively inhibiting actin•IPO9 binding. These findings strongly contradict the established model for actin's import, suggesting a dynamic system dictating nuclear actin transport through 1) the formation of monomeric actin via cofilin's filament-severing activity, 2) the dissociation of cofilin from actin monomers, and 3) the subsequent binding of these actin monomers by IPO9 for nuclear import.

Presenter(s): Sztamfater Chocolat, Lara
School: University of Chicago
Session: P2.08
Title: Evolutionary Origins and Functions of Incomplete Cytokinesis
Co-Author(s): Michael Glotzer
Advisor(s): Michael Glotzer, University of Chicago

Abstract: Centralspindlin, a protein complex composed of two subunits of each Kif23 and CYK-4, oligomerizes at the spindle midzone and the adjacent cortex to control cytokinesis with

high spatiotemporal precision, enabling outcomes such as asymmetric cell division and incomplete cytokinesis. This heterotetramer's structure and key domains are highly conserved across metazoans. It has, therefore, been postulated that the refinement of centralspindlin supported the emergence of clonal multicellularity, cell specialization, and germline cysts, all characteristics dependent on regulated cytokinesis and ubiquitous across metazoans. Most choanoflagellates, metazoan's closest living relatives, lack centralspindlin-like complexes. Salpingoeca rosetta, however, encodes Kif23 and CYK-4 homologs predicted to heterotetramerize, and notably forms colonies via incomplete cytokinesis. Developing antibodies against these proteins would allow localization of this putative centralspindlin-like complex at intercellular bridges to be assessed. Further experimentation with genetic knockdowns could test the complex's role in regulated cytokinesis and clarify whether the last common ancestor of choanoflagellates and metazoans encoded a centralspindlin-like complex, providing great insight into the origin of metazoans. To this end, expression and purification of S. rosetta CYK-4 and Kif23 have been optimized and achieved. Current efforts and short-term goals include upscaling protein purification and development of synthetic antigen binders via phage display.

Presenter(s): Tran, Aaron
School: Washington University in St. Louis
Session: II.H.3
Title: Pangenome-based Allele-Specific Analysis Recovers Rare and Structural Variant-driven Epigenetic Variation
Co-Author(s):
Advisor(s): Juan Macias-Velasco, Washington University in St. Louis

Abstract: The control of the context and level of gene expression via variation in chromatin structure is critical in modulating RNA and protein. One of the main drivers of chromatin variation is genetic variation. Studying chromatin variation induced by genetic variation requires controlling for environmental factors that induce chromatin variation. One method is allele-specific analysis (ASE), which compares genetic variants on each genome copy, controlling for environmental factors within the same cells. However, because ASE compares rare genetic variants, ASE requires the robust recovery of low-frequency alleles. These alleles are difficult to map to the human reference genome, because it does not capture much genetic diversity. I introduce an ASE pipeline utilizing the human pangenome, a reference genome that contains multiple human genomes in parallel, thus enabling mapping to capture variants in people not previously represented in the reference. I show that pangenomic pipelines capture more variants than a traditional linear reference pipeline, and that the newly captured variants are disproportionately structural variants. I further show that these structural variants are more likely to cause chromatin variation than small variants. Thus, pangenomic methods are critical for capturing human diversity and improving analyses of genetic and chromatin variation.

Presenter(s): Truong, Khoa
School: Grinnell College
Session: P3.18
Title: The Effect of Heat Stress Timing on Growth of *Arabidopsis* Seedlings
Co-Author(s): Joey Stock, Lindsey Schultz
Advisor(s): Dr. DeRidder, Grinnell College

Abstract: Heat stress presents an increasing obstacle to plant growth and agricultural productivity, particularly as climate change intensifies. To better understand plant acclimation, we investigated the timing of heat stress exposure during early development using the model organism *Arabidopsis thaliana*. Extended mild heat stress triggers thermomorphogenesis, a process characterized by altered growth patterns such as elongated hypocotyls, thinner leaves, and reduced root length. These morphological adjustments help plants regulate normal functions during heat stress but often come at the expense of overall growth and yield. Our objective was to determine which period during the first week of growth is most detrimental for seedlings exposed to heat stress. In a pilot study, we found that 32 ºC was the most effective stress condition. In the main experiment, seedlings were exposed to 32 ºC for two-day increments within the first six days of growth. Our results revealed plants exposed to heat stress during the earliest developmental stages exhibited the most severe growth inhibition, while seedlings stressed during days 5–6 showed higher chlorophyll levels, longer root length, and greater fresh weight. These findings suggest that delaying heat exposure improves early seedling resilience, offering insight into strategies for mitigating heat stress impacts on crop yields.

Presenter(s): Truta, Alexis
School: University of Chicago
Session: I.A.3
Title: Assessing the Impact of BH3 Mimetics on Mitochondrial Dynamics in Activated Human T Lymphocytes
Co-Author(s): Jocelyn Hsu, James LaBelle
Advisor(s): James LaBelle, University of Chicago

Abstract: The BCL-2 family of proteins regulates intrinsic apoptosis and mitochondrial dynamics. BH3 mimetics are small-molecule inhibitors that engage anti-apoptotic BCL-2 family members to induce apoptosis in malignant cells at the level of the mitochondrion. However, little is known about how these drugs affect healthy immune cells, which contain the same family of proteins but can be resistant to BH3 mimetics. We investigated how BH3 mimetics alter mitochondrial morphology and function in human T cells expanded and activated ex vivo in the presence of these compounds. Confocal microscopy revealed that inhibition of BCL-2 with venetoclax or NW-123 promoted mitochondrial fission, whereas inhibition of MCL-1 with S63845 induced mitochondrial fusion. Flow cytometry analysis further showed that treatment of $CD8^+$ T cells with venetoclax or S63845 at sublethal doses (IC20) for two days increased both mitochondrial mass and membrane potential. Future work will test whether these morphological changes are mediated through Drp-1 phosphorylation and translocation, and whether distinct BH3 mimetics alter protein-protein interactions between BCL-2 family members and mitochondrial dynamics regulators such as Drp-1, MFN2, and Opa1. This work will uncover how BH3 mimetics alter mitochondrial structure in immune cells, shedding light on their non-apoptotic immunomodulatory potential.

Presenter(s): Varanasi, Akanksha
School: University of Chicago
Session: I.B.1
Title: Gene Expression and Immune Mechanism Profiles of Interferon-Treated Multiple Sclerosis Patients Across Subtypes
Co-Author(s): Anthony T. Reder, Xuan Feng

Advisor(s): Anthony T. Reder, University of Chicago

Abstract: Multiple sclerosis (MS) is a chronic disease resulting from nerve damage that causes increased inflammation in the central nervous system. MS affects two important immune cell pathways: Th1 (pro-inflammatory) and Th2 (anti-inflammatory). A balance between the two is necessary to control the disease. Interferon-β (IFN-β) treatment for MS targets gene expression in specific immune cells and pathways to reduce inflammation. The observed effects of IFN-β treatment on Th1/Th2 pathways have differed throughout scientific literature, and Th1/Th2 gene expression and immune activity have not been explored thoroughly in different subtypes of MS. In this study, we aim to fill that gap by looking at IFN-β effects on Th1/Th2 pathways in two different subtypes—relapsing-remitting MS (RRMS) and secondary-progressive MS (SPMS). Each MS subtype has distinct Th1/Th2 pathway activity, and thus both will be differently affected by IFN-β. We have already determined that there are subtype differences in the progression of Th1/Th2 gene expression in interferon-treated MS patients over time. Further research into the effects of IFN-β on Th1/Th2 pathways across subtypes will ultimately advance our knowledge of the IFN-β treatment response in MS patients in different stages of disease.

Presenter(s): Voinescu, Isabel
School: Grinnell College
Session: I.A.4
Title: Developing a 3D Model of Human Cardiac Fibrosis
Co-Author(s): I. C. W. Heathershaw, J. H. Whalen, J. T. Roddey, J. T. Maxwell
Advisor(s): J. T. Maxwell, Wake Forest University

Abstract: Cardiovascular Diseases (CVD), including Heart Failure (HF), are the leading cause of death worldwide. Cardiac fibrosis, the excessive buildup of scar tissue in the heart, is a common consequence of various CVDs and a significant contributor to HF. Despite its prevalence, there are no curative treatments available. In this study, we aimed to develop and characterize a three-dimensional human in vitro organoid model that accurately represents the fibrotic heart microenvironment using three distinct cardiac cell types. Fibrotic conditions were induced by adding Transforming Growth Factor Beta 1 (TGF-β1), a well-established pro-fibrotic signaling molecule. Organoids treated with TGF-β1 were compared to untreated age-matched controls. Functional analysis was performed by measuring beats per minute, contraction velocity, relaxation velocity, and contractility. The model was characterized using bright field imaging to compare organoid areas. Our results demonstrated significantly reduced contractility and relaxation velocity in the +TGF-β1 fibrotic model indicating impaired contractility. Additionally, we observed a significantly smaller area in the TGF-β1-treated organoids. Our model can represent the examined structural and functional effects of cardiac fibrosis on the human heart. Future work will focus on evaluating therapeutic potentials of stem cell–based interventions on our model to develop viable therapies or prevention of cardiac fibrosis.

Presenter(s): Wilson, Eleanor
School: Colorado College
Session: P2.19
Title: Comparative analysis of innate immune responses to abiotic stressors between two *Caenorhabditis* nematode species

Co-Author(s): Rachel Ganz and Spencer Gang
Advisor(s): Spencer Gang, Colorado College

Abstract: Microsporidia are obligate intracellular pathogens that infect many animals, including humans. The nematode *Caenorhabditis elegans* is a convenient model for studying immune responses to microsporidia infection. The Intracellular Pathogen Response (IPR) program in *C. elegans* encompasses around 80 genes that are upregulated after microsporidia infection, including most of the pals gene family, which have unknown functions. Recent studies have shown that the IPR is also induced upon exposure to specific abiotic stressors. However, the degree of conservation of this immune program in other species is unclear. To investigate this, we used the nematode *Caenorhabditis briggsae* as a comparative model. We assessed *C. briggsae* responses to three abiotic triggers known to activate the *C. elegans* IPR: prolonged heat stress, cadmium-induced heavy metal stress, and proteasome inhibition. Using a combination of GFP transcriptional reporter analysis and endogenous gene expression analysis via qPCR, we found all three stressors induced varying degrees of pals gene expression in *C. briggsae*, with proteasome inhibition producing the strongest response and heat stress inducing the weakest response. To gain a deeper understanding of the response to abiotic stressors in *C. briggsae*, samples for each stress treatment will be sent for whole-transcriptome RNA sequencing.

Presenter(s): Zacarias, Jocelyn
School: University of Chicago
Session: P3.13
Title: Associations Between Timing and Domain of Maternal Stress and Child Executive Function
Co-Author(s): Ji Young Song, Sonya V. Troller-Renfree
Advisor(s): Sonya V. Troller-Renfree, Columbia University

Abstract: Growing research links maternal stress to children’s developmental outcomes. This association has been particularly true for child executive functioning (EF)—the skills children use to complete goals. Previous research has found that early EF is associated with broader longitudinal outcomes, including academic performance, social interaction, employment, and criminal involvement. Understanding how maternal stress impacts child EF development is important, as maternal stress may be modifiable through intervention. However, stress is a complex phenomenon, varying across multiple dimensions, including timing and domain. This research examines two dimensions of maternal stress: (1) timing—when in a mother's lifespan stress occurred, and (2) domains—what kinds of stressors are most associated with children’s EF skills in preschool. Using a semi-structured maternal stress interview and play-based EF assessment, findings suggest stressors experienced during a mother’s adulthood, particularly within the past 12 months, were most strongly associated with lower child EF. Significant domains included interpersonal loss, physical danger, treatment/health, and life-threatening experiences. These results underscore the importance of considering stress timing and domain when promoting healthy child EF development.

Presenter(s): Zakrajshek, Logan
School: Gustavus Adolphus College
Session: P1.14

Title: Phenotypic response of *Brassica rapa* to increased anthropogenic temperature and nitrogen levels
Co-Author(s): Aidra Johnson, Naomi Rushing
Advisor(s): Naomi Rushing, Gustavus Adolphus College

Abstract: Commercial agriculture practices have led to increased amounts of nitrogen entering and acidifying the soil through nitrogen deposition and nutrient runoff. This, coupled with rising temperatures due to increased carbon emissions, could create new selective pressures on plant fitness and population structure over the average plant's growing season. Using controlled growth chambers at varying temperatures (23 ℃ and 26.5 ℃, based on RCP4.5 2080 Midwest temperature predictions), this research analyzed the interacting effects of rising temperature and nitrogen levels on a short-lived annual fieldside plant, *Brassica rapa*, in order to understand and address the effects of these anthropogenic factors. Only temperature, not nitrogen levels, significantly affected specific leaf area (SLA) and total biomass of the plants, with the control temperature treatments having greater SLA and biomass than the warm temperature treatments. The average flower production differed significantly only in the control temperature and nitrogen treatment, suggesting less total flower production at lower temperatures and fertilization levels. These results suggested overall negative impacts on *Brassica rapa* fitness if temperatures continue to rise, which could have cascading effects on ecosystem interactions and services. The exact impacts of nitrogen were less clear and require future study.

Presenter(s): Zhang, Alex
School: University of Chicago
Session: II.F.2
Title: Investigating Zebrafish Neural Crest Cell Fate Restriction by Imaging Transcription In Vivo
Co-Author(s): Michael Wen, Victoria Prince
Advisor(s): Victoria Prince, University of Chicago

Abstract: The neural crest (NC) is a multipotent cell population in vertebrate embryos that generates diverse derivatives including craniofacial cartilage, neurons, glia, and cardiomyocytes. While NCCs have been well-studied over the past several decades, the mechanism by which they adopt a single fate is still unclear. In 2021, Robert Kelsh proposed the cyclical fate restriction (CFR) model, which posits that NCCs cycle through different 'substates,' each primed towards specification signals for a single fate. If the relevant signals are present at sufficient strength and duration, the NCC may adopt that fate; otherwise, it will switch into a different substrate. Switching between substates is proposed to depend on transcription factors necessary for differentiation into certain fates (e.g., sox10 for neuronal fates, foxd3 for glial fates). To test CFR, I am applying the MS2/PP7 RNA-labeling system to enable live imaging of transcription dynamics for sox10 and foxd3 in individual NCCs. I have generated transgenic zebrafish lines expressing fluorescently labeled MS2 and PP7 coat proteins. Crossing these fish with a transgenic line labeling sox10 and foxd3 with MS2 and PP7 stem loops will allow me to quantify their transcription activity and test for cycling, in accordance with the cycling substates of the CFR model.

Presenter(s): Zielski, Jack
School: Lawrence University

Session: P1.17
Title: Isolating theta activity for action guiding content and decision guiding context
Co-Author(s): Dennis Boakye, Eitan Price, Jake Watkins, Kaylee Wu, Jack Zielski
Advisor(s): Chunyue Teng, Lawrence University

Abstract: Working memory (WM) allows us to flexibly maintain representations that can be used to guide different types of behavior depending on task demands. WM content can directly support action (e.g., recalling a specific feature) or serve as a context to guide how other representations are used. Prior work suggests that theta oscillations play a key role in prioritizing WM representations (e.g., Pomper & Ansorge, 2019), but it remains unclear whether theta preferentially supports action guiding content versus decision guiding context. To address this question, we designed an EEG experiment in which both content and context were presented laterally on the screen and had to be memorized in WM. At test, participants were probed to either report the feature of the memorized content or a rotated version of it, depending on the accompanying context information. In this way, the context determined how the content representation was reported. Our initial findings show that ping elicited neural responses in posterior visual regions were biased toward the processing of WM content compared to WM context. These results provide preliminary evidence that theta dynamics may preferentially support action guiding content representations over decision guiding context.

Presenter(s): Zuckerman, Rachel
School: University of Chicago
Session: I.A.2
Title: Differential Lysine Catabolism in Non-Small Cell Lung Cancer Cells in the Brain and Lung Microenvironments
Co-Author(s):
Advisor(s): Brandon Faubert, University of Chicago

Abstract: Non-small cell lung cancer (NSCLC) is the leading cause of cancer-related death, in part due to its high propensity to metastasize to the brain. The mechanisms underlying successful metastasis and adaptation to distant tissues remain poorly understood. However, one constant of this transition is metabolic reprogramming of cancer cells, including significant shifts in amino acid metabolism. Amino acids support tumor growth and survival, and notable changes in amino acid metabolites have been observed following metastasis to the brain. Critically, the specific metabolic differences between primary NSCLC tumor cells and brain-metastatic NSCLC tumor cells remain unknown, including in lysine. Using techniques such as 15N tracing and Western blotting, this project aims to characterize differential lysine metabolism in NSCLC cells under conditions that model the primary lung tumor microenvironment versus the brain microenvironment. Elucidating why and how brain metastases catabolize lysine may yield new insights into the biology of this aggressive disease to treat a lethal aspect of NSCLC progression.

Students Presenting at
MCMS Undergraduate Research Symposium, Washington University in St. Louis
Biological and Psychological Sciences
October 31 - November 1, 2025

Carthage College: Liliana Bednarek, Annie Phan, Kaitlyn Sander, Leslie Sauceda

Colorado College: Joshua Briley, Katie Craven, Ian Haver-Radloff, Ester Ineza, Ethan Levy, Theo Ollier, Emily Silva, Eleanor Wilson

Grinnell College: Helena Callil Tomei, Wiktoria Kowal, Khoa Truong, Isabel Voinescu

Gustavus Adolphus College: Geneva Fackler, Samara Goltz, Elsa Johnson, Abby Kugler, Teagan McCarty, Angelina Palmiotto, Kathyryn Rooker, Taylor Ruhl, Cora Renning, Daria Shyroka, Logan Zakrajshek

Hope College: Katherine Hartmann, Kimberly Maldonado, Raksa Samnang, Emersyn McCann, Toby Shaw, Madeline Shirk

Knox College: Siena Adwere-Boama, Preeti Arra, Tisya Goel, Madelyn Goss, Selene Chew Chien Huei, Fionn Meehan, Rutu Mungara, Shino Okamoto, Ian Smith

Lawrence University: Natasha Gibson, Milciades Gonzalez, VIvian Khan, Nabina Rimal, Jack Zielski

Macalester College: Ornela Gigolaj, Dhara Greenberg, Jayden Kratt, Ian Palanga

St Olaf College: Alex Bittner, Sophia Grocholski, Campbell Jossart, Gongdao Lyu, Rahaf Qarabsa, Gabriel Simon

University of Chicago: Ephraim Craddock, Shelley Fernando, Julia Gordan, Christine Kwon, Gabrielle Moon, Prithi Srinivasan, Jessica Qi, Alexis Truta, Akanksha Varanasi, Jocelyn Zacarias, Alex Zhang, Rachel Zuckerman

Washington University in St. Louis: Ishita Aggarwal, Shaza Ali, Bryn Bahnks, Ella Cerny, Julia Coric, Jack Farah, Selina Fan, Trisha Gannu, Felix Guo, Katherine Hsieh, Tanish Joshi-Apte, Nathaniel John, Noah Kabbaj, Vikram Karra, Ziyu Liu, Mark Ma, Sarah Narula, Jennifer Ong, Fang Shu, Yael Smith, Aaron Tran

Participating Faculty and Graduate Students
MCMS Undergraduate Research Symposium, Washington University in St. Louis
Biological and Psychological Sciences
October 31 - November 1, 2025

Aboonabi, Anahita. University of Chicago, Post-doctoral Research Associate, Division of Biological Sciences.

Conway, Christopher. Grinnell College, Associate Professor of Psychology.

Clayton, Tom. Knox College, Professor of Chemistry.

Danka, Elizabeth. Gustavus Adolphus College, Assistant Professor of Biology.

Demas, James. St. Olaf College, Associate Professor of Biology and Physics.

De Stasio, Elizabeth. Lawrence University, Raymond H. Herzog Professor of Science in the Biology Department and Biochemistry Program.

Fischer, Paul. Macalester College, Professor of Chemistry.

Heschel, Shane. Colorado College, Professor of Organismal Biology and Ecology.

Leahy, Andrew. Knox College, Professor of Mathematics.

Smith, Anthony. Washington University, St. Louis, Senior Lecturer and Coordinator of Undergraduate Research Experiences.

Weber, Erin. Carthage College, Assistant Professor of Chemistry.

Yu, Yang. Hope College, Assistant Professor of Biology Instruction.

Washington University Graduate Student and Post-Doc Panel

Brian Gallagher, PhD
Christina Fu
Maya Olcer
Ilana Olin
Morgan Timm