The Midstates Consortium for Math and Science presents the

Undergraduate Research Symposium

Biological Sciences and Psychology

November 13 - 14, 2026
University of Chicago

Beloit College - Carleton College - Carthage College - Colorado College
Grinnell College - Gustavus Adolphus College - Hope College
Knox College - Lawrence University - Luther College
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 the University of Chicago		
November 13-14, 2026		
	Program Schedule	
Friday, November 13		
1:00 – 4:00 pm	Registration at The Study University of Chicago	
5:30 pm – 5:40 pm	WELCOME Navneet Bhasin Senior Instructional Professor Biological Sciences Collegiate Division University of Chicago Pamela Kittelson, Director Midstates Consortium for Math and Science Professor, Biology Gustavus Adolphus College	The Study Hotel
5:40 pm – 6:30 pm	KEYNOTE LECTURE Dr. Alexander Ruthenburg Associate Professor, University of Chicago	The Study Hotel
6:40 pm – 7:45 pm	Dinner Buffet	
8:00 pm – 8:40 pm	JANET ANDERSON AWARD LECTURE Dr. Laura Burrack Professor, Gustavus Adolphus College	The Study Hotel
Following lecture	Group Picture	

Saturday, November 14		
7:00 - 7:30 am	Check out. Walk to campus. If you need a ride, vehicles depart at 7:15. A secure room (GCIS 302E) is available for bags. Bring bags if flying. If driving, verify travel plan with chaperone.	The Study Hotel
7:15 - 8:15 am	Coffee and Breakfast at Venue	Gordon Center for Integrative Science (GCIS) Atrium
8:15 - 8:30 am	Set-up for Poster Session 1	
8:30 – 9:30 am	Session 1 Poster Presentations (n=24)	GCIS Atrium
9:30 – 9:45 am	Break. Remove Posters Check Set-up for Oral Presentation Session I	Coffee & tea in Atrium
9:45 – 10:45 am	Session I Oral Presentations (n= 4/session)	
	Session I.A: Moderator: Dr. Tony Smith	Kersten 101
	Session I.B: Moderator: Dr. Navneet Bhasin	Kersten 103
	Session I.C: Moderator: Dr. Kimberly Dickson	Kersten 105
10:45 - 11:00 am	Set-up posters for Session 2	Coffee & tea in Atrium
11:00 a.m. - 12:00 noon	Session 2 Poster Presentations (n=23)	GCIS Atrium
12:00 noon - 1:15 pm	Graduate Student Panel and Student Lunch	Kersten 301
12:00 noon - 1:15 pm	Faculty Social and Lunch	Kersten 303
1:15 – 1:30 pm	Set-up for Poster Session 3	GCIS Atrium
1:30 - 2:30 pm	Session 3 Poster Presentations (n=24)	Coffee & tea in Atrium
2:30 – 2:45 pm	Break. Remove Posters Load Session II Oral Presentations	
2:45 - 3:30 pm	Session II Oral Presentations (n=3/session)	
	Session II.E: Moderator: Dr. Kristina Blanke	Kersten101
	Session II.F: Moderator: Dr. Navneet Bhasin	Kersten 103
	Session II.G: Moderator: Dr. Tony Smith	Kersten 105
3:30 - 4:00 pm	Meeting Concludes. Remove Posters. Leave plastic name badges. Take Boxed Dinners. Complete Online Evaluations	GCIS Atrium

2026 Keynote Lecture

Journey to the center of the blob: what biochemical isolation of RNA polymerase condensates can tell you about how they work

Dr. Alexander Ruthenburg, Associate Professor
Division of Biological Sciences, University of Chicago



Abstract: I will detail our approach to understanding mysterious and controversial "transcriptional condensates" using a combination of classical biochemistry coupled to modern tools. Eukaryotic transcription is spatially organized into compartments which concentrate RNA polymerase II (Pol II), Mediator, and other components of the transcriptional machinery, termed "transcriptional condensates", "hubs", or "factories" by various groups in the field. These structures range from numerous small, short-lived species, to a handful of larger, stable bodies. Large condensates have been implicated in driving potent transcription of several super-enhancer regulated genes, yet the underlying mechanisms and the range of their client genes remain unclear. We have developed a biochemical approach called POCEMON, which combines density gradient centrifugation and affinity purification to partially purify large transcriptional condensates from nuclei, allowing systematic characterization of their nucleic acid components. We find that transcriptional condensate isolates engage thousands of gene promoters and harbor the nascent transcriptome, but do not stably co-purify with distal enhancers. Binding patterns of RNA polymerase II within condensates suggest these structures could facilitate promoter escape and promoter-proximal pause release. Together, our work supports a promoter-centric condensate organization and paves the way towards understanding the functional link between condensate architecture and nascent transcription.

About: Alex grew up in Portland, Maine, and attended Carleton College, majoring in chemistry. After graduating in 1999, Alex attended Harvard University where he earned his PhD in Chemical Biology and Organic Chemistry in 2005 in the Verdine lab supported by an NSF Predoctoral Graduate Research Fellowship. He then pursued postdoctoral training in the Allis Lab at Rockefeller University in Chromatin Biochemistry. In 2010, Alex started his own laboratory at the University of Chicago in the Departments of Molecular Genetics and Cell Biology as well as Biochemistry and Molecular Biology. Alex's research program spans traditional disciplines (discovery biochemistry, chemical biology, biophysics, technology development, quantitative genomics and cell biology) with the goal of developing fundamental mechanistic understanding of epigenetic information systems and transcription in cancer and early development. Alex was promoted to Associate Professor (2017), and his many honors include Kavli Fellow of the National Academy of Sciences and Harriet Manchester Quantrell Award for Excellence in Undergraduate Teaching (2025). Alex teaches Molecular Biology at the undergraduate and graduate levels, co-directs the Genetic Mechanisms in Evolution NIH training grant, and is the Director of Undergraduate Studies in Biology.

2026 Janet Andersen Award Lecture

How do fungal pathogens evolve resistance to antifungal drugs?

Dr. Laura Burrack, Professor
Department of Biology, Gustavus Adolphus College

Abstract: Fungal infections are a serious global health concern with invasive fungal infections killing at least 1.5 million people per year worldwide. One of the contributing factors to high mortality rates for fungal infections is treatment failure due to antifungal drug resistance and tolerance. Treatment with antifungal drugs is a strong evolutionary pressure that rapidly selects for changes in a cell's genome that allow for better growth of that cell and its progeny. In Candida albicans, the most common invasive fungal pathogen in the United States, the acquisition of aneuploidy (extra copies of chromosomes) is a common mechanism that promotes both drug resistance and tolerance. One significant driver of aneuploidy in C. albicans is the parasexual reproductive cycle. Using a random library of aneuploid C. albicans derived from parasexual reproduction, we found that diverse combinations of parasexual-derived aneuploidy karyotypes are sufficient to confer azole tolerance. We also found that parasexual recombination can also produce aneuploidy karyotypes with increased tolerance to the echinocandin class of antifungals. Some aneuploidy combinations also have specific drug interaction phenotypes with other medications prescribed in patients with candidemia, such as cyclosporin A. The aneuploidies that confer tolerance to azoles and echinocandins can be stably maintained during passaging even in the absence of antifungal drugs highlighting the importance of these aneuploidies as a reservoir for tolerance even when patients are not actively being treated.



About: Dr. Laura Burrack's expertise is microbiology and molecular genetics. She is a graduate of Macalester College and where she was a B. Goldwater Scholar. In addition to being a professor at Gustavus she has taught at Grinnell College. Laura earned a PhD from Harvard University where she used molecular biology, genetics and cell biology approaches to identify and characterize host cell factors required for intracellular infection by the bacterial pathogen *Listeria monocytogenes*. As a post-doc in Dr. Judith Berman's lab at the University of Minnesota she developed the yeast *Candida albicans* as a model system to understand chromosome segregation mechanisms. At Gustavus, her lab is focused on understanding how fungal pathogens, like *Candida albicans*' infections like thrush and candidemia, can evolve resistance and tolerance to antifungal drugs. She has mentored over 24 undergraduate researchers and their co-authored publications regularly appear in *Nature Microbiology*, *PLoS Pathogens* and *Genes*. Dr. Burrack Dr. Burrack also catalyzed development of college-wide Challenge courses modeled after a seminar titled, *The History of Eugenics and the Future of Genetic Testing.* Laura enjoys experimenting in the kitchen when she is not in the lab.

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. As a teacher and scholar, Janet was devoted to providing creative, high quality learning experiences for her students. As Consortium Director, she looked for ways to connect with and support 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.



Oral Session I Schedule

SESSION I.A: 9:45 - 10:30 a.m. Room: Kersten 101 Moderator: Dr. Tony Smith			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1	Will Li	Washington University in St. Louis	Proliferative Index and Disease Burden Predict CAR-T and Bispecific Outcomes in Multiple Myeloma
I.A.2	Nga Nguyen	Knox College	Context-Dependent Functions of the PI3K/AKT Pathway in IL-6-Independent Multiple Myeloma Cells
I.A.3	Kiran Simon	University of Chicago	Exploring Myeloid/T cell crosstalk in the Skin
I.A.4	Yixuan Liu	Washington University in St. Louis	HelQ Knockout Overcomes PARP Inhibitor Resistance and Enhances Chemosensitivity in BRCA-Mutant Cancer Cells

SESSION I.B: 9:45 - 10:45 a.m. Room: Kersten 103 Moderator: Dr. Navneet Bhasin			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1	Irmak Altinok	University of Chicago	Exploring how long-range physical interactions influence patterning in the developing *Drosophila retina*
I.B.2	Alex Zhang	University of Chicago	The Genetic Basis of Fin Expansion in a Walking Fish
I.B.3	Renee Mitchell	University of Chicago	Investigating the Role of Basement Membranes in Shaping the *Drosophila* Wing
I.B.4	Ava Lewin	University of Chicago	Genetic Redundancy in the Plant Drought Stress Response

WiFi: Visitors can access the wireless network via EduRoam or by selecting the chicago-guest network. The instructions for this are at the check-in table.

Oral Session I Schedule

SESSION I.C: 9:45 - 10:45 a.m. Room: Kersten 105 Moderator: Dr. Kimberly Dickson			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1	Serena Wang	Washington University in St. Louis	Impact of a Rare Neurodevelopmental Disorder on PKA Dynamics Across Sleep-Wake Cycle
I.C.2	Shelley Fernando	University of Chicago	Elucidating the Molecular Mechanisms of BRWD1-mediated B Cell Development
I.C.3	Sophia Xu	University of Chicago	NEDD4 and Degradation of Connexin 46
I.C.4	Yannik Leuz	University of Chicago	Mouse and Human Interferon Reactivity with Cross-Species Receptors, and Challenges in Protein Production

Oral Session II Schedule

SESSION II.D: 2:45 - 3:30 p.m. Room: Kersten 101 Moderator: Dr. Kristina Blanke			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1	Jay Kronbach	Knox College	Are Species-Specific Auditory Enrichment Methods Effective for Stress Reduction in Shelter Cats?
II.E.2	Giang Pham	Lawrence University	Structured Diagrams, Pretesting, and the Allocation of Visual Attention During Neuroscience Learning

SESSION II.E: 2:45 - 3:30 p.m. Room: Kersten 103 Moderator: Dr. Navneet Bhasin			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1	Paul Schroeder	Carthage College	Fighting Gram-Negative and Gram-Positive Bacteria: The Antibacterial Properties of an L-leucine-Based Surfactant
II.F.2	Ivana Wu	Macalester College	Investigating the Role of GelE during *Enterococcus faecalis* Recovery from Inhibition by *Streptococcus mutans*
II.F.3	Vinisha Tripathi	Washington University in St. Louis	The Impact of Molecular Xenomonitoring on Assessing the Efficacy of Moxidectin in Controlling Lymphatic Filariasis

SESSION II.F: 2:45 - 3:30 p.m. Room: Kersten 105 Moderator: Dr. Tony Smith			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.G.1	Kaden Goff	University of Chicago	Investigating *Papilio alphenor* Cell Types
II.G.2	Delaney Nguyen	Grinnell College	Nicotine-Induced α4β2 Nicotinic Receptors Upregulation Is Mediated in Golgi Satellites
II.G.3	Olivia Wiley	Hope College	Inflammatory Responses Following Brain Trauma Regulate Neurogenesis in the Olfactory Epithelium of Zebrafish

Poster Sessions Schedule

Poster Session P1: 8:30 – 9:30 a.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Pallavi Baliyara	Grinnell College	Pharmacological Induction of Presynaptic Homeostatic Potentiation and Expansion Microscopy at the Neuromuscular Junction
P1.02	Jinwoo Chun	University of Chicago	Local Optogenetic Control Over Immune Stimuli in Zebrafish
P1.03	Tomás Avilés Tamariz	Lawrence University	Knockout of the Adra1a receptor in VIP neurons does not disrupt behavioral state-driven changes in visual cortex activity
P1.04	Owen Johnson Graves	Colorado College	Stability in Individual Behavioral Biases Differ between Drosophila Species and Serotonin Receptor Mutants
P1.05	Rebecca Reynolds	Lawrence University	Impacts of Human Activity on Parrotfish Wariness and Populations
P1.06	Imogen Riter	Beloit College	Active Goal Setting for Sleep: The Impact of Implementation Intentions on Sleep Quality & Cognition
P1.07	Blaine Soltwedel	Carthage College	Religions Mediation Effect on Disgust Sensitivity and Attitudes Toward Gay Men and Lesbian Women
P1.08	Anh Le and August Ngo	Grinnell College	The Influence of Cue Specificity on Retrieval-Induced Forgetting
P1.09	Jason Song	Washington University in St. Louis	Characterization of 2A Peptide-mediated Dual scFv Production in *S. boulardii* against Inflammatory Bowel Disease
P1.10	Monique Micallef	Knox College	The Effects of *Hericium erinaceus* on the Proliferation of C6 Glioma Cells
P1.11	Ruby Koo	Washington University in St. Louis	Regulation of Cell Adhesion Molecules after Stroke
P1.12	Lauren Moskal	University of Chicago	APOL1 Genotype and One-Year Kidney and Renal Outcomes: A Retrospective Cohort Study
P1.13	Ocean Fan	Carleton College	Investigating the Effects of Copper Elesclomol Treatment on GSDMD Palmitoylation Mediated Macrophage Pyroptosis
P1.14	Elliott Peter	Hope College	Effects of Antibiotic Timing and Combination on KP4-Antibiotic Synergy Against *Klebsiella pneumoniae*

P1.15	Amy Yang	Macalester College	Identifying Genes Required for *Enterococcus faecalis* Susceptibility to Inhibition by *Streptococcus mutans*
P1.16	Eleanor Burke	Hope College	How Different Culturing Conditions Change Strain-Level Competition in *Bacteroides thetaiotaomicron*
P1.17	Chenxin Xiang	Colorado College	Thermodynamic Analysis of Ion Binding to miR-184 RNA and DNA Constructs
P1.18	Marisen Turetzky	Gustavus Adolphus College	Elucidation of RyhB target prioritization in *E. coli*
P1.19	Urja Vohra	University of Chicago	SynCom15 Suppresses Excessive CKD Gut Tryptophan-to-Indole Flux, Limiting Indoxyl Sulfate Formation and Preserving AVF Patency
P1.20	Vishnu Srinivasan	Washington University in St. Louis	Identification of ERO1α-Selective Inhibitor Derivatives of M6766 as an Antithrombotic Strategy
P1.21	Noor Omar	Gustavus Adolphus College	Investigating the Role of p21+ Cells In Atherosclerotic Plaque Calcification
P1.22	Faith Frazier	Colorado College	Developing an In Vivo Prime Editing Gene Therapy Strategy for LCHAD Deficiency
P1.23	Dominic D'Ascenzo	Grinnell College	The Roots of Local Adaptation: Assessing Root Phenotypes In Differing Soil Textures And Hardnesses
P1.24	Sabrina Ng	Colorado College	Abiotic Effects on Nectar Production in Low Arctic Pollination Systems

Poster Session P2: 11:00 a.m. - Noon Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Adella Catanzaro	Grinnell College	Topography Matters, But Climate Rules an Annual Plant's Distribution in California
P2.02	Alice Lin and Dylan MacLehose	Carleton College	Microbes need Frenemies: Examination of Viral Influence on Deep-Sea Hydrothermal Vent Food Webs
P2.03	Mariah Mendez	Grinnell College	Adaptive Potential of Phenotypic Plasticity of UV Patterns in Monkeyflowers
P2.04	Chloe Pearl	Grinnell College	Phenotypic Plasticity of Monkeyflower Traits under Elevated CO2 and Temperature
P2.05	Raksa Samnang	Hope College	Experimental Analysis Of *Escherichia coli* on Carbon Sources
P2.06	Josefina Rodriguez Poggio	Colorado College	In Situ Carbon Transfer from Fungal Necromass into Soil during Decomposition
P2.07	Edie Hamilton	Carthage College	Use of Bioacoustics to Improve Estimates of Home Range Sizes of Cao-vit Gibbons (*Nomascus nasutus*)
P2.08	Almaz Turuspekov	Knox College	Tracking Intracellular Digestion and Waste Release in Stentor Coeruleus
P2.09	Danielle McConnell	University of Chicago	Enlightened By Excrements: An Investigation of Parabasalid Diversity in the Gut Microbiome
P2.10	Arya Jacobson	St. Olaf College	Optimization of Lipid Droplet Isolation Methods in *Tetrahymena*
P2.11	Sarah Yu	Washington University in St. Louis	Small Molecule Inhibition of SERPINB3 as an Anticancer Strategy in Cervical Cancer
P2.12	Peter Renwick	Colorado College	Analytical Optimization and Comparison of Titratable Acidity, Liquid Chromatography, and Enzymatic Methods for CAM Acid Quantification
P2.13	Amelia Lampi	Hope College	Replication Kinetics and Growth Parameters of the *Klebsiella pneumoniae* Lytic Bacteriophage KP4
P2.14	Jovana Urosevic	University of Chicago	Metabolic regulation of transcriptional plasticity in medullary thymic epithelial cells.
P2.15	Marina Seidl	Colorado College	SUP-26 and cytoskeletal mRNA regulation in C. elegans neuron morphology

Poster Session P2: 11:00 a.m. - Noon. Continued			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
~~P2.16~~			
P2.17	Arwen Baer	Gustavus Adolphus College	Suramin Inspires Next Generation Broad-Spectrum Antiviral Design
P2.18	Jay Patel	Washington University in St. Louis	Evaluating Propofol-Induced Changes in Sleep Spindle Density in Late-Life Treatment-Resistant Depression
P2.19	Betsy Hatlestad and Carson Muench	Gustavus Adolphus College	An Alternate Method of Analyzing Sprague-Dawley Rat Vaginal Cytology
P2.20	Tierney Johnson	Washington University in St. Louis	Investigating Divergent Mitochondrial Pathologies in Wolfram Syndrome
P2.21	Michelle Tung	Macalester College	Alzheimer's Disease and Sleep Deprivation: Neuroendocrine and Behavioral Assessment in APOE4 Female Mice
P2.22	Esme Colombel	University of Chicago	The Behavioral Responses of Goldfish (*Carassius auratus*) to Repeated Human Exposure
P2.23	Layne Rund	Carthage College	Match Demands and Workloads in NCAA DIII Women's Soccer

Poster Session P3: 1:30 - 2:30 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Andrew Zeng	Carleton College	An Information-Theoretic Analysis of Gene Expression Dynamics During Mus-musculus Prenatal Development
P3.02	Jimmy Zhang	Grinnell College	The Role of Vimentin in the Injury Response of the Zebrafish Heart
P3.03	Nhi Nguyen	Knox College	Cell Response To LPS And Echinacea
P3.04	Anna Peck	Colorado College	Leaf Morphology and Flower Coloration in *Ipomopsis aggregata*
P3.05	Jacob Caballero	Hope College	Exploring the Efficacy of Anticancer Plant Extracts on Slowing Down Cancer Development
P3.06	Lily Kaestner	Carthage College	Predicted Nitrogen Fixation Capability of a Novel Bacteria Isolated from *Kyphosus sydneyanus* Hindgut
P3.07	Dillon Beaudette	Colorado College	Centromere Evolution in Budding Yeast
P3.08	Gonzalo De Lorenzo	Gustavus Adolphus College	Targeting De Novo Pyrimidine Synthesis via CAD Inhibition Suppresses Hepatic Stellate Cell Activation and Liver Fibrosis
P3.09	Marisa Brashar	Colorado College	Synthesizing and Assaying Prodrug Inhibitors of *Pseudomonas aeruginosa* Biofilm Formation
P3.10	Jenna Swanlund	Lawrence University	Engineering Oxidative Resistance in Human Ribonuclease Inhibitor 1 (RNH1)
P3.11	Carly Orlins	University of Chicago	Temporal Activation of Adiponectin Receptor Signaling Pathways in B-Cell Acute Lymphoblastic Leukemia Following AdipoRon
P3.12	Nour Khayou	Macalester College	Assessment of Myelin Density And Axonal Degeneration In A Myrf Knockout Model Following DLK Inhibition
P3.13	George Naismith	Washington University in St. Louis	Anti-Myelin Oligodendrocyte Glycoprotein Antibodies in Neurodegenerative Diseases Across the Age Span
P3.14	Ryan Williamson	Washington University in St. Louis	Profiling the Differential Effects of Peptide MHCII CAR T Cells on the Blood-Brain Barrier
P3.15	Karishma Bhatara	Carthage College	A Comparative Study of Transthyretin Stabilizing Ligands Using Molecular Dynamics Simulations

Poster Session P3: 1:30- 2:30 p.m. Continued			
P3.16	Sydney Reed	Lawrence University	Creation of a CRISPR/Cas9 Teaching Lab That Incorporates Homology-Directed Repair
P3.17	Cameron Gruenberg	Carthage College	Using Molecular Dynamic Simulations to Characterize the Binding of Stabilizing Ligands to the Protein Transthyretin
P3.18	Samantha Anderson	Gustavus Adolphus College	Biochemical Characterization of Protein Kinase C Domains: Cloning to Activity
P3.19	Yann Cho	University of Chicago	EWAS of White Blood Cell Proportions with Long-Read Sequencing
P3.20	Anuva Yonzon	Grinnell College	Conformational Stability of the MTHFR Phe184Leu Variant Under Urea-Induced Denaturation Investigated via HDX-MS
P3.21	Zainab Syed	Gustavus Adolphus College	Influence of Caloric Restriction and Estrous State on Sucrose-seeking Behaviors
P3.22	Ella Meges	University of Chicago	Mothers' Experiences during Childbirth and Intrapartum Interventions
P3.23	Julia Gordan	University of Chicago	An Identity-Stress Model of Cancer-Related Cognitive Impairment for Preventive Psycho-Oncology
P3.24	Yukai Gu	Washington University in St. Louis	Exploring the Influence of Unpredictability in Event Perception and Duration Estimation

Abstracts for all Sessions
Biological and Psychological Sciences
MCMS Undergraduate Research Symposium University of Chicago
November 13-14, 2026

Presenter(s): Altinok, Irmak
School: University of Chicago
Session: I.B.1
Title: Exploring how long-range physical interactions influence patterning in the developing Drosophila retina
Co-Author(s):
Advisor(s): Ilaria Rebay

Abstract: Organ function depends on organizing different cell types into precise spatial patterns. While much is understood about the genetic pathways that determine cell fates, how physical interactions between cells influence their shapes and emerging tissue-scale patterns remains an open question. The developing Drosophila eye is an ideal model to address this gap. The retina is made of ~750 multicellular units called ommatidia, each consisting of core photoreceptors surrounded by supportive interommatidial pigment cells (IOPCs). During development, IOPCs arrange into a hexagonal lattice, forming a mechanically coupled network spanning the entire retina. Motivated by prior work in the Rebay lab showing that transmitted tensile forces within this network impact patterning, the goal of my project is to investigate the range at which such physical interactions influence ommatidial geometry. I hypothesize that mechanical interactions between cells propagate across the IOPC network to influence patterning at the tissue-scale. To test this, I use genetic tools to regionally perturb patterning and investigate how the differentially patterned regions influence each other. My results demonstrate that perturbed cells closer to wildtype regions exhibit recovery of the patterning defects across multiple rows of ommatidia, suggesting that physical interactions may play a long-range role in ommatidial patterning.

Presenter(s): Anderson, Samantha
School: Gustavus Adolphus College
Session: P3.18
Title: Biochemical Characterization of Protein Kinase C Domains: Cloning to Activity
Co-Author(s): Samuel Wyatt, Alan Penheiter, Anh T.Q. Cong, John R. Hawse, Matthew P. Goetz, Matthew J. Schellenberg
Advisor(s): Matthew J. Schellenberg

Abstract: Protein Kinase C (PKC) isozymes compose a family of ubiquitous serine/threonine kinases with key roles in regulating a variety of cellular pathways such as cell proliferation and apoptosis. PKC misregulation is tied to a variety of diseases, including cancer, cardiovascular disease, kidney disease, and neurodegeneration. Due to the innate similarities within the PKC family, many previous efforts to target PKCs have failed due to lack of drug-target binding specificity.Therefore, biochemical and structural characterization of the unique isozymes would greatly benefit the development of new therapeutics. This work aims to characterize the C-terminal kinase domains (CAT) of the PKC isozymes and compare structure and catalytic capacity amongst isozyme kinase domains and full-length proteins to further examine the role of N-terminal regulation and determine key differences between isozymes for use in PKC targeting efforts.

Presenter(s): Avilés Tamariz, Tomás
School: Lawrence University
Session: P1.03
Title: Knockout of the Adra1a receptor in VIP neurons does not disrupt behavioral state-driven changes in visual cortex activity
Co-Author(s): Kyle Jenks, Mriganka Sur
Advisor(s): Kyle Jenks

Abstract: Internal and behavioral states profoundly modulate visual processing in the cerebral cortex. Previous research indicates that states of locomotion and arousal enhance neuronal firing rates, pairwise correlations, and the signal-to-noise ratio of visual responses. Neuromodulators may drive these changes in cortical activity, with norepinephrine release closely tracking pupil dilation events that signal arousal. However, the mechanisms linking norepinephrine release to behaviorally-evoked changes in neuronal activity remain unclear. Disinhibitory Vasointestinal Polypeptide (VIP)-expressing interneurons may be key players in this process, with abundant expression of Adra1a adrenergic receptors and responsiveness to pupil dilation and locomotion. We hypothesized that knocking out Adra1a from VIP interneurons would disrupt their correlation to state and subsequent disinhibition of excitatory neurons. We compared neuronal activity in V1 VIP and putative excitatory cells during spontaneously-evoked changes in internal/behavioral states between VIP-Cre and VIP-Cre x Adra1a-floxed mice. We found that neuronal activity across both groups and cell types changes during locomotion and vigilance; VIP and excitatory cell activity becomes more correlated, and the orientation selectivity of excitatory cells increases. Because these effects are observed in both experimental groups, we conclude that Adra1a receptor knockout does not impair the ability of VIP cells to respond to state-dependent changes.

Presenter(s): Baer, Arwen
School: Gustavus Adolphus College
Session: P2.17
Title: Suramin Inspires Next Generation Broad-Spectrum Antiviral Design
Co-Author(s): Ge Yang, Fan Bu, Bin Liu
Advisor(s): Bin Liu

Abstract: Many medically important viruses store their genetic material as RNA and rely on RNA dependent RNA polymerases (RdRps) for genome replication and transcription. RdRps share a conserved right-handed structure with fingers, palm and thumb subdomains connected by channels that play a major role in the entry of nucleotide triphosphates (NTPs) and template RNA into the active site1. This remarkable structural conservation has made viral polymerases attractive targets for broad-spectrum antiviral development. To date, however, most clinically approved RdRp inhibitors are nucleoside analogues that target the catalytic center. Although highly successful, these inhibitors remain susceptible to resistance mutations, require intracellular metabolic activation, and exploit only a limited portion of the polymerase surface. Conserved non-catalytic RNA-binding channels therefore represent an underexplored opportunity for developing orthogonal antiviral mechanisms that complement catalytic-site inhibition while potentially reducing the impact of resistance.

Presenter(s): Baliyara, Pallavi
School: Grinnell College
Session: P1.01
Title: Pharmacological Induction of Presynaptic Homeostatic Potentiation and Expansion

Microscopy at the Neuromuscular Junction
Co-Author(s):
Advisor(s): Clark Lindgren

Abstract: Presynaptic Homeostatic Potentiation (PHP) is a form of synaptic plasticity at the neuromuscular junction (NMJ) that stabilizes neurotransmitter release following postsynaptic receptor blockade. This study investigates the pharmacological induction of PHP and the underlying structural organization of the mouse neuromuscular junction. Using ex-vivo electrophysiological recordings, we evaluated the effects of two nicotinic acetylcholine receptor (nAChR) blockers on transmitter release. We demonstrate that the nAChR antagonist mecamylamine induces PHP, whereas the partial agonist succinylcholine fails to elicit this compensatory increase in acetylcholine release. Building on these findings, we hypothesize that Acid-Sensing Ion Channels (ASICs) may act as key mediators in the retrograde signaling cascade of PHP. To resolve sub-synaptic architecture beyond standard diffraction limits, we attempted to optimize Expansion Microscopy (ExM) for mouse NMJ tissue. Standard confocal fluorescence microscopy effectively labeled pre- and post-synaptic markers, including synaptotagmin and α-bungarotoxin. While post-digestion ExM gels successfully retained marker fluorescence, physical hydrogel expansion produced structural distortions that currently require further protocol refinement. Together, these results clarify the distinct pharmacological triggers required for PHP and highlight both the promise and technical challenges of adapting expansion microscopy techniques to mammalian muscle tissue.

Presenter(s): Beaudette, Dillon
School: Colorado College
Session: P3.07
Title: Centromere Evolution in Budding Yeast
Co-Author(s): Sara Hanson, Pearl Peterson
Advisor(s): Sara J. Hanson

Abstract: A key aspect of cell division is the equal segregation of DNA content between the cells that are produced. Centromeres are DNA sequences found on each chromosome that are recognized by a protein complex called the kinetochore to ensure proper segregation. Despite their importance in this biological process, centromeres have changed rapidly in sequence and structure over evolutionary time. In budding yeast, a transition from epigenetically-defined centromeres that are several thousand base pairs in length to short (<200 bp), genetically-defined point centromeres has occurred. To better understand this key transition, our work focuses on Phaffomycetales budding yeast, which diverged prior to the evolution of point centromeres. We performed long-read genome sequencing and assembly for *Starmera stellimalicola* and *Cyberlindnera jadinii* to identify and characterize their centromeres. We show evidence of conserved synteny for centromere location and potential centromere motifs in both species. Future research will examine the evolution of centromere structure in this clade, coevolution of kinetochore proteins, and confirm centromere function.

Presenter(s): Bhatara, Karishma V.
School: Carthage College
Session: P3.15
Title: A Comparative Study of Transthyretin Stabilizing Ligands Using Molecular Dynamics Simulations
Co-Author(s):

Advisor(s): Kevin Morris

Abstract: This project investigated the binding of small molecules to the protein transthyretin (TTR). TTR transports thyroid hormones in the bloodstream. The protein is a tetramer with each monomer containing 127 amino acids. Point mutations can cause TTR tetramers to dissociate and aggregate into amyloid fibrils that then deposit around the heart. These fibrils build up in the cardiac muscle and can cause diastolic dysfunction and eventually heart failure. The destabilizing Valine-122 to Isoleucine-122 mutation was studied here. This point mutation is present in 3% of the African American community. This study used molecular dynamics (MD) simulations to investigate the binding of small molecule ligands to TTR. The molecules investigated have been shown to stabilize the tetramer and prevent TTR dissociation and aggregation. The goal of the study was to characterize the intermolecular interactions between the ligands and the TTR protein. These insights can then be used to design more effective stabilizing ligands. Hydrogen-bonding and hydrophobic interactions between the ligands and TTR, along with structures of the TTR: ligand complexes will be presented.

Presenter(s): Brashar, Marisa
School: Colorado College
Session: P3.09
Title: Synthesizing and Assaying Prodrug Inhibitors of *Pseudomonas aeruginosa* Biofilm Formation
Co-Author(s): Amy Dounay; Olivia Hatton
Advisor(s): Amy Dounay; Olivia Hatton

Abstract: Antimicrobial resistant bacteria pose a serious threat to public health, being listed by the World Health Organization as one of the top global health and development threats, and responsible for 1.27 million deaths in 2019. Antimicrobial resistant *Pseudomonas aeruginosa* is of interest to this study as it poses one of the highest global bacterial threats to life. *P. aeruginosa's* strong antibiotic resistance is attributed in part to its ability to form biofilms: a matrix generated to surround the bacteria and protect from extreme conditions, including the host's immune system and antibiotic treatment. Focusing antibiotic research on compounds which can disrupt biofilms, is therefore of extreme importance. 3,4-Difluorinated-phenylalanine (3,4-FPhe) has been shown to effectively inhibit biofilm formation in *P. aeruginosa*, but may also be disruptive and toxic in animal and human biological systems. A targeted prodrug approach to delivering the fluorinated antibiotic can reduce harm to the host and has the potential to stabilize the antibiotic cargo until in contact with select enzymes synthesized by *P. aeruginosa*. This study modifies a previously designed prodrug to utilize 3,4-FPhe, and to test the efficacy of a shortened linker.

Presenter(s): Burke, Eleanor
School: Hope College
Session: P1.16
Title: How Different Culturing Conditions Change Strain-Level Competition in *Bacteroides thetaiotaomicron*
Co-Author(s):
Advisor(s):

Abstract: A disrupted gut microbiota is correlated with inflammatory bowel disease (IBD). Although IBD patients have effective therapies, they often have side effects that cause severe

patient burden. Engineering probiotics to modulate the microbiome may lessen this burden. However, it is unknown how to effectively engraft bacteria into inflamed environments. *Bacteroides thetaiotaomicron* (Bt) is a common commensal gut microbiota inhabitant and is used as a model organism. Conventionally, these bacteria are grown under static conditions, however this may not be representative of the physiology within the human gut, due to peristaltic movement. Using Bt, we examined how different culturing conditions and media formulations affected strain-level competition; reflective of different nutrient niche landscapes encountered in vivo. We inoculated strains in four different carbon sources in vitro, under static or agitated growing conditions to determine if relative abundance changes between conditions. We found more stable competition in agitated conditions than static and saw striking differences in strain outcome based on the type of media used. By better understanding these in vitro phenotypes and mechanisms of niche establishment we will be able to expand the therapeutic potential of engineered microbes by guiding design of therapeutics aimed at stable engraftment and competition in vivo.

Presenter(s): Caballero-Heuker, Jacob
School: Hope College
Session: P3.05
Title: Exploring the Efficacy of Anticancer Plant Extracts on Slowing Down Cancer Development
Co-Author(s): Jaclyn Decker, Maxwell McCormick, Jaden Johnson, Jianhua Li
Advisor(s): Jianhua Li

Abstract: Cancer develops from unregulated cell growth, with risks in specific tissues correlating strongly with stem cell division rates and advancing age. This study explores whether water based extracts from known anticancer plants can effectively inhibit cell division and growth at low, non toxic concentrations, thereby delaying cancer development. Tissues from eight plant species, including *Asimina triloba, Taxus brevifolia*, and *Caulophyllum thalictroides*, were dried at sixty degrees Celsius and processed using a Soxhlet apparatus to isolate their chemical components in water. To test their efficacy, *Allium fistulosum* root primordia were immersed in varying extract concentrations for five days under constant light. Pure water and the anticancer drug methotrexate served as negative and positive controls respectively. Statistical analyses evaluated differences in root number, root length, and plant height as proxies for cellular proliferation. While root quantities did not differ significantly across treatments, extracts from six of the tested plants demonstrated significant efficacy in slowing cell division and elongation at higher concentrations. This impact was notably more evident on root length than on overall plant height. Ultimately, these preliminary results support the hypothesis that low doses of botanical extracts offer a promising strategy for proactive cancer prevention.

Presenter(s): Catanzaro, Adella
School: Grinnell College
Session: P2.01
Title: Topography Matters, But Climate Rules an Annual Plant's Distribution in California
Co-Author(s): Vincent M. Eckhart
Advisor(s): Vincent M. Eckhart

Abstract: Species distribution models (SDMs) are tools for determining the environmental features that shape geographic range and predicting possible range shifts with climate change. Hierarchical SDMs specify factors operating at different spatial scales, which may improve

predictive performance. We developed and compared regional-scale, landscape-scale, and hierarchical SDMs for the California annual plant *Clarkia xantiana* ssp. *xantiana*. Population presence locations of 217 populations within a ca. 50 x 60 km region came from previous field surveys, supplemented by iNaturalist records. We used the Maxent method to generate and compare three kinds of SDMs: (1) models including only climate predictors, at 100-meter resolution; (2) landscape-scale models using topographic predictors, at 10- and 25-meter resolutions; and (3) hierarchical models at fine-scales that included the output of the climate model as a predictor, along with topographic variables. The best climate model, based on seasonal precipitation variables, had high predictive performance. The best landscape-scale model determined that steep, north- and east-facing predict presence, but predictive power was low. Hierarchical models performed marginally better than the regional-scale climate model. Climate variables filter the distribution of *Clarkia xantiana* ssp. *xantiana* at large scales, while topography affects habitat suitability within regions of appropriate climate.

Presenter(s): Cho, Yeonwoo
School: University of Chicago
Session: P3.19
Title: EWAS of White Blood Cell Proportions with Long-Read Sequencing
Co-Author(s): Ava K. L. Krause, James L. Li, Niyati Jain, Sarbani Thakur, Brandon L. Pierce
Advisor(s): Brandon L. Pierce

Abstract: Background: The proportions of circulating white blood cells (WBCs) may serve as biomarkers for various conditions. Prior studies examined the relationship between WBC proportions and patterns of DNA methylation (DNAm), but such studies remained limited due to the lack of available electronic health record (EHR) data for participants who also have DNAm data. Methods: We performed an epigenome-wide association study (EWAS) of white blood cell type proportions utilizing 6.3-7.3K participants in the AoU study with measured leukocyte proportions, who also had long-read whole genome sequencing (lrWGS) data. We then tested the association between each of 5 leukocyte proportions and DNAm at approximately 25 million CpG sites using linear regression, adjusting for covariates. Results: At the genome-wide level, our EWAS identified 269785 CpGs associated with neutrophils and 662731 with lymphocytes, corresponding to the two major WBC types by abundance. Notably, the EWAS of both of these major WBC types showed marked genomic inflation ($\lambda = 1.4$ and 1.6, respectively). Top CpG hits were located in locations that suggest these hits may play a role in gene regulation and influence 3D chromatin structure. Conclusion: This study highlights many epigenetic changes are associated with the proportions of major WBC types.

Presenter(s): Chun, Yiwoo
School: University of Chicago
Session: P1.09
Title: Local Optogenetic Control Over Immune Stimuli in Zebrafish
Co-Author(s):
Advisor(s): Elizabeth Jerison

Abstract: Tissues are constantly bombarded with time varying stimuli that the immune system must rapidly react to mitigate infection and/or tissue damage; ultimately maintaining long term organismal homeostasis. To enable this response, tissues and the immune system use tightly controlled signaling to recognize and relay perturbations to homeostasis. IL1-β signaling is a key axis in the early immune response to perturbation, however how signaling is propagated through

different tissues is poorly understood owing to a difficulty in initiating and tracking IL-1β signaling dynamics in living organisms. To bypass this limitation, we leveraged the optical transparency of the larval Zebrafish, whose immune system is largely conserved to humans, to develop a novel transgenic system of IL-1β under precise spatiotemporal control in living zebrafish using custom infrared optics. This system also enables tracking of subsequent signaling live via super-resolution confocal microscopy(iSIM) in a living organism.

Presenter(s): Colombel, Esme
School: University of Chicago
Session: P2.17
Title: The Behavioral Responses of Goldfish (*Carassius auratus*) to Repeated Human Exposure
Co-Author(s):
Advisor(s): Melina Hale

Abstract: Animals may change their behavior in response to repeated exposure to humans, yet the extent to which these behavioral changes occur remains understudied in aquatic species. This study investigates whether repeated human interaction affects the behavior of goldfish (*Carassius auratus*) over time, and explores whether these changes are consistent with increasing habituation to human presence. Goldfish prove to be a useful model in demonstrating behavioral plasticity due to their demonstrated capacity to learn and adapt to new environmental stimuli. By observing the changes in goldfish interactions with humans and their environment over an extended period, this study demonstrates how repeated human exposure can lead to increased comfort and positive behavioral responses, including anticipatory behavior.

Presenter(s): D'Ascenzo, Dominic
School: Grinnell College
Session: P1.23
Title: The Roots of Local Adaptation: Assessing Root Phenotypes In Differing Soil Textures And Hardnesses
Co-Author(s): Vincent M. Eckhart
Advisor(s): Vincent M. Eckhart

Abstract: Local adaptation, superior fitness of geographically distinct populations in their home locations, is common in plants. Understanding the evolution of local adaptation requires identifying the environmental drivers of natural selection that vary geographically, as well as learning what traits evolve as populations adapt to those drivers. Recent studies of crop plants show that certain root traits improve performance in compacted, fine-textured soils. Whether geographic variation in these traits underlies local adaptation to soil texture and compaction in wild species is not known. We compared root biomass allocation and root-tip sharpness in populations of the California annual plant *Clarkia xantiana* ssp. *xantiana*. In this species, most populations occupy soft, coarse-textured soils derived from igneous rocks, while others occupy harder, finer-textured soils formed from metasedimentary rocks. Root allocation differed among populations but not by soil type. Root-tips of seedlings were sharper (i.e., more pointed) in populations native to more compacted, finer soil. As sharper root tips are expected to increase penetration of hard, fine soil, variation in root-tip shape may contribute to local adaptation to this species and others that experience soil variation across their geographic ranges.

Presenter(s): De Lorenzo, Vicente
School: Gustavus Adolphus College

Session: P3.08
Title: Targeting De Novo Pyrimidine Synthesis via CAD Inhibition Suppresses Hepatic Stellate Cell Activation and Liver Fibrosis
Co-Author(s): Alexander Washington, Zeba Firdaus, Enis Kostallari
Advisor(s): Enis Kostallari

Abstract: Chronic liver injury leads to fibrosis and cirrhosis, a leading cause of death worldwide, and is driven by hepatic stellate cell (HSC) activation, characterized by proliferation and collagen deposition. HSC activation, when stimulated by platelet-derived growth factor (PDGF), has been demonstrated to involve increased glycolysis, but the involvement of other metabolic pathways remains elusive. Pyrimidine metabolism from glutamine (de novo) or recycled nucleic bases (salvage) generates nitrogenous bases required for DNA/RNA synthesis. How de novo drives HSC activation and subsequent liver fibrosis remains unknown and is the focus of the study. Here, we pharmacologically inhibited the Carbamoyl-phosphate synthetase 2, Aspartate transcarbamoylase, and Dihydroorotase complex (CAD) in primary human HSCs in vitro and patient-derived precision-cut liver slices ex vivo. In vitro, PDGF increased HSC proliferation compared to vehicle as measured by uptake of 5-Ethynyl-2'-deoxyuridine, which was abrogated by sparfosic acid, a CAD inhibitor. Ex vivo, PDGF increased collagen deposition compared to vehicle in human PCLS, which was attenuated by sparfosic acid. Collagen deposition was assessed by total collagen staining via picrosirius red and collagen 1 expression via Western blot. Collectively, these findings demonstrate that pyrimidine from de novo synthesis promotes HSC proliferation and fibrosis, presenting a novel therapeutic target.

Presenter(s): Fan, Ocean
School: Carleton College
Session: P1.13
Title: Investigating the Effects of Copper Elesclomol Treatment on GSDMD Palmitoylation Mediated Macrophage Pyroptosis
Co-Author(s): Norah Dillner, Melissa Rachofsky, Christina Song, Lauren Tittel, and Angel Solis
Advisor(s): Angel Solis

Abstract: Cuproptosis is a recently characterized form of regulated cell death in which copper binds to lipoylated proteins of the tricarboxylic acid cycle, resulting in proteotoxic stress and cell death. However, how copper-induced cellular stress interacts with inflammatory cell death pathways such as pyroptosis remains unclear. Here, we investigated how copper–elesclomol (Cu+E) treatment influences pyroptosis in RAW264.7 macrophages, with a particular focus on gasdermin D (GSDMD) and its palmitoylation. Cell viability and cytotoxicity were evaluated using MTT and LDH assays, while inflammatory responses and GSDMD activation were assessed using cytokine measurements, Western blotting, and immunofluorescence. Our results suggest that Cu+E treatment may influence pyroptotic responses. These findings provide a foundation for further investigating the molecular relationship between copper-induced cellular stress, GSDMD regulation, and macrophage inflammatory cell death.

Presenter(s): Fernando, Shelley
School: University of Chicago
Session: I.C.1
Title: Elucidating the Molecular Mechanisms of BRWD1-mediated B Cell Development
Co-Author(s): Margaret Veselits, Malay Mandal, Marcus Clark
Advisor(s): Margaret Veselits

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 developmental and lineage restricted enhancer silencing or activation, and modulation of enhancer-promoter interactions. 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 the assembly of transcription machinery. Here, I clone and purify different domains of BRWD1 from bacterial cultures, then use these purified proteins to conduct immunoprecipitation experiments with bacterial lysates overexpressing chromatin regulatory proteins, aiming to identify direct binding partners of BRWD1. 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): Frazier, Faith
School: Colorado College
Session: P1.22
Title: Developing an In Vivo Prime Editing Gene Therapy Strategy for LCHAD Deficiency
Co-Author(s): Stephanie Blackwood, Vi Pham, Kiran Musunuru, Rebecca Ahrens-Nicklas
Advisor(s): Rebecca Ahrens-Nicklas, Darrell Killian

Abstract: LCHADD, or Long Chain 3-HydroxyAcyl CoA Dehydrogenase Deficiency is a genetic metabolic disorder that impairs long-chain fatty acid β-oxidation, preventing normal energy production. Patients are at high risk for acute metabolic decompensation as well as chronic symptoms such as liver and heart failure, peripheral neuropathy, and retinopathy. Current treatments for LCHADD patients focus on dietary management in order to prevent metabolic decompensation episodes. Because most patients with LCHADD share the same c.1528 G>C variant in the HADHA gene, gene editing is a promising treatment option. We investigated a prime editing strategy to precisely correct this variant, screening various prime editing guide RNAs (pegRNAs) and nicking guide RNAs (ngRNAs) in a cell line carrying the HADHA variant. These pegRNAs were designed with the help of a new machine learning program, OptiPrime, developed by David Liu. Increased editing was observed in pegRNAs with reverse transcriptase template (RTT) sequences of 40-42 base pairs in length. Additionally, one of the ngRNAs that we tested was determined to be more effective compared to the other. Once further optimization is achieved, testing in a LCHADD mouse model will help determine if this prime editing strategy could eventually be used as a treatment for LCHADD.

Presenter(s): Goff, Kaden
School: University of Chicago
Session: II.G.1
Title: Investigating *Papilio alphenor* Cell Types
Co-Author(s):
Advisor(s):

Abstract: Several species of swallowtail butterflies have evolved female-limited mimicry that causes them to resemble certain inedible butterfly species to avoid predation. This includes the species *Papilio alphenor*. Females can develop multiple wing patterns, with some females

resembling the nonmimetic males, and others mimicking the distantly related poisonous species *Pachilopta aristolochiae*. The switch between female morphs is controlled by alternate alleles of doublesex (dsx). The wing pattern is made up of tiny, individually colored scales. dsxH expression during pupal development changes how and where the different scale types form in the wing to produce the mimetic pattern. While the scales are what ultimately show the color pattern, other cell types in the wing cooperate to establish the pattern. To gain a better understanding of the cellular makeup of the wing, I used previously generated single nuclei RNA-seq data to identify the major cell types present in the pupal wings, then identified and validated cell-type specific marker genes using Hybridization Chain Reaction. My results included the identification of a tracheal-cell subtype and existence of an interstitial cell type and membrane in the wings that were undocumented in lepidoptera literature in addition to other cells that make up the wing.

Presenter(s): Gordan, Julia
School: University of Chicago
Session: P3.23
Title: An Identity-Stress Model of Cancer-Related Cognitive Impairment for Preventive Psycho-Oncology
Co-Author(s):
Advisor(s): Gilberto Rodrigues

Abstract: Objective: Cancer-related cognitive impairment (CRCI) is prevalent during and after cancer treatment, with widely varying prevalence estimates by cancer type, assessment method, and timing. Biological injury from cancer therapy does not fully explain why some patients develop persistent cognitive symptoms while others with similar treatment exposures do not. We propose an identity-stress model integrating neurobiological vulnerability with psychosocial stress, role disruption, loneliness, and cancer-related identity change, and translates it into a testable preventive psycho-oncology research agenda. Methods: We conducted a theory-generating narrative review using a PRISMA-style evidence map, prioritizing systematic reviews, meta-analyses, randomized trials, consensus recommendations, and cancer-specific qualitative studies from PubMed/MEDLINE, Cochrane, PsycINFO, CINAHL, Embase, and Web of Science. Results: CRCI prevalence is heterogeneous. Anxiety, symptom burden, fatigue, sleep disruption, loneliness, and role loss may amplify perceived cognitive dysfunction through stress, inflammatory, attentional, and behavioral pathways. Direct evidence that identity disruption causes objective CRCI is limited, but cancer-identity and role-change studies support its plausibility as an undermeasured exposure. Conclusions: CRCI should be understood as a multidetermined syndrome with distinct but related objective and patient-reported dimensions. The identity-stress model positions CRCI as a bidirectional process linking treatment-related neurotoxicity, social-context disruption, self-aspect threat, stress biology, and cognitive symptoms.

Presenter(s): Graves, Owen
School: Colorado College
Session: P1.04
Title: Stability in Individual Behavioral Biases Differ between *Drosophila* Species and Serotonin Receptor Mutants
Co-Author(s): Asher Porad, Mia Predmore, Payton Bell, Kwon Lazarus
Advisor(s): Ryan Maloney

Abstract: Individuals across a wide range of species show individual behavioral preferences even

when controlling for environment and genotype. This may serve an evolutionary bet-hedging function to ensure that a fraction of the population is suited for unpredictable environment. Theoretical work has shown that the stability of these preferences within an individual's life may serve an important role in driving variation within a population, particularly for behaviors subject to selective pressures that fluctuate within an animal's lifespan. We provide empirical evidence for this hypothesis by testing the stability of individual locomotor handedness across different species of Drosophila. We show differences between species with differing lifespans in the stability of their preferences over time, consistent with theoretical predictions for optimal bet-hedging strategies. We furthermore investigate potential mechanisms by which the stability of individual preferences could be maintained, and show that knocking out each of the five serotonin receptors in Drosophila melanogaster decreases the stability of individual behavioral preferences to differing degrees. Together these results provide a deeper insight into the potential ecological significance of individuality and how it may change over time, as well as provide a mechanistic substrate by which this evolutionary strategy can be implemented.

Presenter(s): Gruenberg, Cameron
School: Carthage College
Session: P3.17
Title: Using Molecular Dynamic Simulations to Characterize the Binding of Stabilizing Ligands to the Protein Transthyretin
Co-Author(s): Kevin Morris
Advisor(s): Kevin Morris

Abstract: Transthyretin (TTR) is a tetrameric protein produced in the liver that transports thyroid hormones throughout the body. In some individuals, a V122I point mutation destabilizes the tetramer, causing it to dissociate, misfold, and aggregate into amyloid deposits in cardiac tissue. These deposits cause the disease Familial Amyloid Cardiomyopathy (FAC). FAC is treated by administering stabilizing drugs that bind to TTR, stabilize the tetramer, and prevent dissociation. Recently, a new group of stabilizers were discovered that interact simultaneously with both of TTR's binding pockets. Molecular dynamics (MD) simulations were used to investigate and identify the atomic-scale interactions between TTR and these new stabilizing ligands. These insights could potentially lead to the development of even more potent stabilizers. Hydrogen bonding interactions between the stabilizing ligands and TTR amino acid residues were analyzed. The results showed that the ligands formed strong hydrogen bonds and electrostatic interactions with TTR Lys-15 residues. Hydrophobic interactions between the stabilizers and TTR residues Leu-17 and Leu-110 also occurred. All of these interactions likely enhance the stability of the tetramer. Results from the hydrogen-bonding analyses and structures from the MD simulations showing the interactions discussed above will be presented.

Presenter(s): Gu, Yukai
School: Washington University in St. Louis
Session: P3.24
Title: Exploring the Influence of Unpredictability in Event Perception and Duration Estimation
Co-Author(s): Yining Ding, Jeff Zacks
Advisor(s):

Abstract: Duration judgments are often reconstructed from memory. Past studies have found that these judgments depend on both objective elapsed time and event structure, but little is known about how unpredictability changes the perceived structure of an event and its remembered

duration. We therefore examine whether unpredictable events are perceived and remembered differently from routine experience. Two separate experiments were conducted using matched videos of everyday activities with predictable and unpredictable versions differing in a single critical action that either conform to or violate schematic knowledge. In the first experiment (N = 37), participants watched videos while pressing a key whenever they perceived a boundary between two events. They identified significantly more boundaries in unpredictable videos, with the increase localized around the interval containing the unexpected action. In the second experiment (pilot n = 16), participants mentally replayed the video immediately after watching it, and then reported the events they recalled from the video. We found unpredictable videos tended to be replayed longer, and the unexpected actions were more likely to be recalled compared with the predictable video. Together, these findings suggest that unpredictability may influence both how continuous experience is perceived and reconstructed from memory.

Presenter(s): Hamilton, Edie
School: Carthage College
Session: P2.07
Title: Use of Bioacoustics to Improve Estimates of Home Range Sizes of Cao-vit Gibbons (*Nomascus nasutus*)
Co-Author(s):
Advisor(s): Angela Dassow

Abstract: The application of bioacoustics has become an increasingly important tool in addressing conservation challenges of rare and endangered species, such as the cao-vit gibbon (*Nomascus nasutus*) in northern Vietnam. The cao-vit gibbon was thought to be extinct until the early 2000s, but a population of approximately 70 individuals was recently rediscovered, highlighting the need for a conservation plan. Using synchronized autonomous recording devices, we recorded over 7,000 hours of audio between May 2022-January 2026 and then acoustically localized family groups of this critically endangered primate. Results from this work discovered larger home ranges than previously identified using manual methods. Future work will combine these new home range maps with individual vocal identification in order to examine how each gibbon moves throughout their home range. Home range size and individual movement information will be used by conservation officers in developing plans for habitat restoration and corridor development.

Presenter(s): Hatlestad, Elizabeth
School: Gustavus Adolphus College
Session: P2.19
Title: An Alternate Method of Analyzing Sprague-Dawley Rat Vaginal Cytology
Co-Author(s): Carson Muench
Advisor(s): Kelle Nett

Abstract: Cell suspension is a common approach to collecting vaginal cytology samples in Sprague-Dawley rats, though there is minimal literature on the method. The traditional method relies on smear preparation and staining. Using a cell suspension decreases the processing time and the errors that can occur when staining a sample. It increases the number of cells in the sample and also enables visualization of live cells, whereas stained samples are fixed. Though cell suspension samples are unable to be archived in the way that smeared samples are, microscope images were collected to refine suspension technique and to track estrus. We used this method to examine vaginal samples and characterize them based on the main cell types present to determine

which stage of the estrus cycle they were in. Proestrus samples were predominantly composed of nucleated epithelial cells, while estrus was dominated by keratinized (cornified) epithelial cells. Metestrus showed a mixture, including nucleated epithelial cells, cornified epithelial cells, and leukocytes, while diestrus was characterized by sparse cellularity, primarily leukocytes. Overall, the cell suspension provided clear, reproducible cytology profiles. It represents a practical and efficient method for estrus cycle analysis in Sprague-Dawley rats.

Presenter(s): Jacobson, Arya
School: St. Olaf College
Session: P2.10
Title: Optimization of lipid droplet isolation methods in *Tetrahymena*
Co-Author(s):
Advisor(s): Laura Listenberger

Abstract: Lipid droplets are dynamic structures that are present in nearly all cells. They serve as storage depots for energy rich neutral lipids and hold precursors for signaling molecules and membrane lipids. The proteins on the surface of lipid droplets influence which functions are prioritized. Thus, identification of the proteins found on lipid droplets is essential to understanding how they direct the function of the organelle and allow an organism's metabolism to respond to different conditions. Our experiments aim to expand the identification of lipid droplet proteins to the single celled organism *Tetrahymena thermophila*. We have developed a method for isolating lipid droplets from starved *Tetrahymena* and for screening these fractions for contamination by other organelles. By separating lipid droplets from other cellular structures, we will be able to pursue the identification of associated proteins. This will support future research on how these proteins respond to varying external and internal challenges.

Presenter(s): Johnson, Tierney
School: Washington University in St. Louis
Session: P2.20
Title: Investigating Divergent Mitochondrial Pathologies in Wolfram Syndrome
Co-Author(s): Brianna Carman, Ghazaleh Ashrafi
Advisor(s): Ghazaleh Ashrafi

Abstract: Wolfram syndrome (WS) is a rare neurodegenerative disease, caused by recessive inheritance of loss-of-function WFS1 gene variants. Loss of WFS1 results in ER stress, disrupted ER calcium management, and reduced ER-mitochondria contact sites causing secondary mitochondrial dysfunction. Prior rodent models link WFS1 loss to impaired ER-mitochondria calcium transfer, which disrupts mitochondrial function and trafficking. However, the mechanism connecting calcium dysregulation to mitochondrial motility remains ill-defined and findings in human disease-relevant models are limited. This project characterizes axonal mitochondrial morphology and motility in WS patient-derived induced pluripotent stem cell derived neurons. Visualizing with hSyn-mito-dsRed, we found that WS axonal mitochondria exhibit reduced size, coverage, and increased motility compared to isogenic controls. Stabilizing cardiolipin restored mitochondrial morphology and coverage yet failed to rescue mitochondrial motility, indicating that the aberrant motility phenotype is independent of overall mitochondrial integrity. Actin is a known regulator of mitochondrial anchoring and movement and previously unstudied in WS. Moving forward, we plan to probe whether mitochondrial motility is driven by reduced actin polymerization by employing Fis1-LifeAct-GFP to quantify mitochondria that are in-contact with polymerized actin. These results may indicate separate mitochondrial mechanisms that are

dysregulated in WS, guiding future therapeutic approaches.

Presenter(s): Kaestner, Lily
School: Carthage College
Session: P3.06
Title: Predicted Nitrogen Fixation Capability of a Novel Bacteria Isolated from *Kyphosus sydneyanus* Hindgut
Co-Author(s): Madeline Huff, Emily M. Wollmuth
Advisor(s): Emily M. Wollmuth

Abstract: Nitrogen fixation is an essential process for converting nitrogen from the environment into usable forms. Organisms require nitrogen to be used in processes such as the synthesis of amino acids. However, not all organisms are capable of fixing their own nitrogen. Herbivorous animals often rely on their gut microbiota to provide them with usable nitrogen. Isolate 38 is a Rikenellaceae bacterium isolated from the gut of Kyphosus sydneyanus, a herbivorous fish. The sequenced genome of Isolate 38 was annotated using BlastKOALA to identify the presence of genes related to nitrogen fixation. Previous studies have found that bacteria must have the genes nifHDKB at minimum to independently fix nitrogen. The annotation of Isolate 38's genome identified the presence of not only the essential nifHDKB genes, but also the presence of additional genes associated with the nitrogen fixation process, nifENV. The same nitrogen fixation associated genes were similarly annotated in Isolate 38's genome using the separate tool SnapGene, further supporting that Isolate 38 has the metabolic potential to independently fix nitrogen. Continued research into the nitrogen fixation capabilities of fish hindgut bacteria will increase understanding of the symbiotic relationships between marine hosts and their microbiota.

Presenter(s): Khayou, Nour
School: Macalester College
Session: P3.12
Title: Assessment of Myelin Density And Axonal Degeneration In A Myrf Knockout Model Following DLK Inhibition
Co-Author(s): Inaya Laubach, Mohammed Mashal, Greg Duncan
Advisor(s): Greg Duncan

Abstract: Myrf is a transcription factor required for myelination. Previous research demonstrated that remyelination failure in Myrf-deficient mice is associated with increased neuronal apoptosis and DLK signalling, a neuronal stress-response kinase. Inhibiting DLK is associated with reduced apoptosis in the optic nerve and retina. It's unclear whether DLK inhibition affects myelin density and axonal degeneration outside the optic nerve and retina. Therefore, we examined the effects of DLK inhibition on the spinal cord of mice with Myrf knockout. Wild-type (WT; n = 8) and Myrf knockout (KO; n = 10) were treated with either a vehicle or DLK inhibition. Immunohistochemistry was performed to stain for Myelin Basic Protein (MBP) and Neurofilament Degenotag (NFL-DegenoTag) to assess for myelin density and axonal degeneration, respectively. Myelin density and axonal degeneration were quantified as the percentage of MBP-positive and NFL-DegenoTag-positive areas respectively using HALO image analysis. Genotype, treatment, and genotype-by-treatment effects were assessed using two-way ANOVA. KO mice exhibited significantly lower MBP-positive area and greater NFL-Degenotag-positive area compared to WT mice. DLK inhibition did not produce a significant change in either MBP-positive area or NFL-Degenotag-positive area, and there was no significant genotype-treatment interaction. This suggests that the DLK inhibition does not

significantly impact myelin loss or axonal degeneration in the spinal cord.

Presenter(s): Koo, Ruby
School: Washington University in St. Louis
Session: P1.11
Title: Regulation of Cell Adhesion Molecules after Stroke
Co-Author(s): Rose León-Alvarado, Sofía Angulo-Lopera, Asher J. Albertson
Advisor(s): Asher J. Albertson

Abstract: Cell adhesion molecules (CAMs) are integral to synapse formation, stabilization, and plasticity, but their role in post-stroke recovery remains poorly understood. We examined four CAMs: β-catenin, N-cadherin, Neurexin-1β, and Neuroligin-1, following experimental stroke and heterozygous forebrain β-catenin knockout to better understand their regulation. β-catenin and N-cadherin expression were quantified by Western blotting in the cortex, thalamus, and hippocampus of heterozygous β-catenin knockout mice and wild-type controls (n=6/group). Neurexin-1β and Neuroligin-1 were quantified in ipsilesional cortical tissue one week after photothrombotic stroke and compared with sham controls (n=6/group). β-catenin expression was significantly decreased in the thalamus of knockout mice, with no significant differences in the cortex or hippocampus. N-cadherin expression did not significantly differ in any region. Following stroke, Neuroligin-1 showed a trend toward increased expression in the ipsilesional cortex but did not reach statistical significance ($p=0.0622$). Neurexin-1β showed no significant difference. Thus, CAM expression appears to be regionally and contextually regulated in a circuit- and protein-specific manner, suggesting that changes occur within specific circuits rather than homogeneously across the brain. Ongoing work will examine additional time points and brain regions, with the ultimate goal of identifying targetable pathways to improve post-stroke recovery.

Presenter(s): Kronbach, Jay
School: Knox College
Session: II.E.1
Title: Are Species-Specific Auditory Enrichment Methods Effective for Stress Reduction in Shelter Cats?
Co-Author(s): Jennifer Templeton
Advisor(s): Jennifer Templeton

Abstract: Cats are one of the most common pets in the world, and make up over half of shelter populations. Animal welfare is a primary concern for animal shelters, boarding facilities, veterinary offices, and individual owners. Stress is an animal welfare concern due to short and long term effects on the animals and humans in the environment. Chronic stress seriously affects a cat's quality of life, and often leads to problematic behaviors like aggression or destruction, which cause cats to be surrendered and not re-adopted. In order to mitigate stress for shelter cats and improve animal welfare, cat-specific stress management is necessary. There is evidence that audio stimuli/enrichment can be beneficial for mitigating stress in cats by providing mental stimulation through species-specific stimuli. I exposed a sample of shelter cats to a set of auditory stimuli to determine if the cats show an increase in relaxed behaviors as a response. I used cat-formulated music and an audio of purring as audio stimulus treatments in one experiment. The auditory enrichment used in this experiment did not result in any difference in the shelter cats' behaviors, informing future cat welfare decisions to improve the lives and adoptability of shelter cats.

Presenter(s): Lampi, Amelia

School: Hope College
Session: P2.13
Title: Replication Kinetics and Growth Parameters of the *Klebsiella pneumoniae* Lytic Bacteriophage KP4
Co-Author(s): Christian Kooistra, Elliott Peter, Yang Yu
Advisor(s): Yang Yu

Abstract: *Klebsiella pneumoniae* is a clinically important pathogen associated with antimicrobial resistance for which alternative antimicrobial strategies are needed. Bacteriophages offer a promising approach because of their ability to selectively infect and lyse bacterial pathogens. We previously isolated two lytic phages, KP1 and KP4, against *K. pneumoniae* ATCC 132 and identified KP4 as a member of the genus Webervirus within the family Drexlerviridae. Here, we assessed KP4 stability across temperature, pH, and chloroform conditions and determined the MOI for optimal KP4 propagation to support further evaluation against diverse *K. pneumoniae* strains. KP4 retained substantial infectivity between 4-50°C, with PFU counts decreasing by 12% at 4°C and by 25% at 50°C compared with the control at 37°C. In contrast, exposure to 80°C for 1 h eliminated detectable infectivity. KP4 exhibited maximal stability at pH 7 and retained infectivity under moderately acidic conditions, with PFU counts decreasing by 19% at pH 5. Infectivity decreased by 30% and 49% at pH 9 and 11, respectively, while exposure to pH 3 resulted in a 98% reduction in PFU. KP4 also exhibited high tolerance of chloroform exposure. Approximately 58% of phage infectivity remained after treatment with 80% chloroform for 1 h. PFU recovery increased by 133%, 108%, and 108% following treatment with 10%, 20%, and 40% chloroform, respectively, indicating that these treatments did not reduce recoverable infectivity. Phage production was considerably enhanced at low MOI. An MOI of 0.0001 produced the highest phage yield, approximately 6.6×10^9 PFU. Further decreasing the MOI to 0.00001 reduced the yield to 3.7×10^9 PFU, while increasing the MOI to 0.1 and 1 resulted in lower yields of 1.4×10^9 and 1.5×10^8 PFU, respectively. Thus, the optimal low MOI of 0.0001 resulted in approximately 44-fold higher phage yield than an MOI of 1. Together, these results demonstrate that KP4 retains infectivity across a broad range of temperature and pH conditions and shows strong tolerance to chloroform exposure, while low MOI enhances phage production. These findings establish key stability and propagation parameters for KP4 and provide a foundation for future evaluation of its infectivity against diverse, including antibiotic-resistant, *K. pneumoniae* strains.

Presenter(s): Le, Anh
School: Grinnell College
Session: P1.08
Title: The Influence of Cue Specificity on Retrieval-Induced Forgetting
Co-Author(s): Anh Le, Khanh Ngo, Orestis Papaioannou
Advisor(s): Ngo, Khanh

Abstract: The retrieval of a subset of items can influence the possibilities of the others to be forgotten, a phenomenon that is coined retrieval-induced forgetting (RIF) by Anderson et al. (1994). In this study, we were interested in how the hierarchical nature of the retrieval cue during the final memory testing influences retrieval-induced forgetting. 36 Grinnell College undergraduates first studied a list of category–word pairs with narrow category cues. Participants then completed a retrieval-practice task involving a subset of the studied words, with half of the practiced items presented with broad cues and half with narrow cues. Finally, after a distractor task, participants completed a memory test for all studied items. Our result indicated that items

tested with narrow cues were recalled more successfully than items tested with broad cues. However, we did not find evidence of retrieval-induced forgetting, as recall did not significantly differ among practiced, related-but-unpracticed, and unpracticed items. These findings suggest that cue specificity is important for memory in general, but might not be relevant for RIF specifically.

Presenter(s): Leuz, Yannik
School: University of Chicago
Session: I.C.4
Title: Mouse and Human Interferon Reactivity with Cross-Species Receptors, and Challenges in Protein Production
Co-Author(s): Jillian Bonilla, Haley Hardtke
Advisor(s): Juan Mendoza

Abstract: Interferons are a signaling molecule, functioning as an alarm system for the human body. They are released in response to infection and signal cells in the surrounding area to put up barriers or perform apoptosis, as well as recruit the immune system to the site of infection. The mouse model is frequently used to study human phenomena such as interferon behavior, however there is uncertainty whether mouse interferons interact with their receptors in the same way that human ones do. Thus, we lack confidence in claiming that mouse observations translate well to humans. This project aims to resolve this inconsistency by examining the cross-reactivity of mouse and human interferons with each other's receptors. To do so, Monolith binding assays will be performed, to measure the binding affinity between each receptor-ligand combination. These assays work by measuring the changing wavelength of a fluorophore, as its structure changes due to ligand binding. Unfortunately, however, significant difficulties arose during the protein production and purification process, the results of which will be presented here. While extensive improvements to the purification procedure were already explored, various avenues still exist for the completion of this project, which will be attempted in the coming year.

Presenter(s): Lewin, Ava
School: University of Chicago
Session: I.B.4
Title: Genetic Redundancy in the Plant Drought Stress Response
Co-Author(s): Ava Lewin, Ernesto Gagarin, Ronan O'Malley
Advisor(s): Ronan O'Malley

Abstract: The global population currently comprises 8.3 billion individuals and is expected to exceed 10 billion by 2060. Supplying food for this global population will become increasingly difficult, not only because of population growth but also due to the effects of climate change. In particular, climate change will result in longer and more severe droughts, significantly reducing crop yields. One potential solution to this issue is the development of more drought-tolerant crops through genetic modification. Achieving this goal, however, requires a better understanding of the genetic mechanisms underlying the plant drought stress response. In particular, determining the level of functional overlap between genes involved in this response, or genetic redundancy, will be essential for effective genetic modification. For this reason, I investigated genetic redundancy in the drought stress response of the model plant *Arabidopsis thaliana*. My project focuses on interactions among six key transcription factors in the basic leucine zipper (bZIP) transcription factor family, a group of master regulators involved in coordinating the plant drought stress response.

Presenter(s): Li, William
School: Washington University in St. Louis
Session: I.A.1
Title: Proliferative Index and Disease Burden Predict CAR-T and Bispecific Outcomes in Multiple Myeloma
Co-Author(s): Shaji Kumar, Jiahuai Kang, Prashant Kapoor, Angela Dispenzieri, Francis Buadi, David Dingli, Saurabh Zanwar, Dragan Jevremovic, Suzanne Hayman, Nelson Leung, Joselle Cook, Nadine Abdallah, Moritz Binder, Eli Muchtar, Rahma Warsame, Taxiarchis Kourelis, Ronald Go, Yi Hwa, Miriam Hobbs, Amie Fonder, Yi Lin, Morie Gertz, S. Vincent Rajkumar, Wilson Gonsalves
Advisor(s): Wilson Gonsalves

Abstract: Comprising approximately 10% of all hematological malignancies, Multiple Myeloma affects over 20,000 people in the U.S. annually. Novel immunotherapies such as CAR-T and T-cell-engaging bispecifics have demonstrated success in the clinic, prompting widespread adoption in the field. However, high risk Myeloma patients frequently experience poorer clinical outcomes from treatment, as their disease biology is more complicated. This retrospective study examines whether baseline bone marrow disease burden and plasma-cell-proliferative-index (S-phase%) predict response outcomes to T-cell immunotherapies in relapsed/refractory multiple myeloma. We compared three patient cohorts treated at our institution: 47 on teclistamab (anti-BCMA), 47 on talquetamab (anti-GPRC5D), and 176 on ciltacel-autoleucel (anti-BCMA CAR-T). All groups had similar prior treatment intensity (median 4 prior LOTs) and prevalence of high-risk cytogenetics. Primary resistance occurred more often with teclistamab (43%) than talquetamab (21%), and was not a common outcome in CAR-T (2%). For teclistamab only, primary resistance was significantly linked to higher bone-marrow-plasma-cell (BMPC% ≥50%) burden and higher proliferative index (S-phase% ≥ 5%). In CAR-T, higher S-phase% and BMPC% were both correlated to shortened progression-free-survival as well as overall-survival time. These findings ultimately suggest both high disease burden and high S-phase% are predictive in undermining the efficacy of anti-BCMA directed immunotherapies.

Presenter(s): Lin, Alice
School: Carleton College
Session: P2.02
Title: Microbes need Frenemies: Examination of Viral Influence on Deep-Sea Hydrothermal Vent Food Webs
Co-Author(s): Dylan MacLehose, Rika Anderson
Advisor(s): Rika Anderson

Abstract: Deep-sea hydrothermal vents are unique biogeochemical environments where reduced, metal-enriched water emerges from the seafloor at temperatures up to 400˚C. These habitats host specialized communities of prokaryotes (bacteria and archaea), eukaryotes (protists), and viruses forming around these vents, creating complex interconnected relationships. The microbes living in the marine subseafloor at these vents play a significant role in marine carbon cycling in the deep-sea through their role as the principal primary producers and decomposers in the deep-sea food web. The project examines metagenomic samples taken from hydrothermal vents and their plumes at the Mid-Cayman Rise in the Caribbean Sea to better understand how interactions between microbes and viruses impact the deep-sea food web. Variation in viral lifestyles and diversity are of particular interest, which have implications for how viruses can manipulate

microbial metabolism. We show that viruses disproportionately infect autotrophic microbes compared to heterotrophic microbes, which could have large impacts on the marine carbon cycle. Moreover, we show that lysogenic viruses, which have the ability to incorporate their viral genome into a microbial host, are found to be highly abundant in deep-sea hydrothermal environments compared to background deep seawater. This is significant because these lysogenic viruses are able to manipulate microbial evolution through integration and expression of viral genes within microbial genomes. By looking at transposase abundance and infection patterns across microbial metabolic pathways, we can gain deeper insights into the ecology and evolution of vent communities.

Presenter(s): Liu, Yixuan
School: Washington University in St. Louis
Session: I.A.4
Title: HelQ Knockout Overcomes PARP Inhibitor Resistance and Enhances Chemosensitivity in BRCA-Mutant Cancer Cells
Co-Author(s): Vladislav Sviderskiy, Andrew Olson, Alessandro Vindigni
Advisor(s): Alessandro Vindigni

Abstract: Hereditary BRCA1 mutations increase the risk of breast and ovarian cancers. BRCA1-mutant tumors have defective DNA double-strand break repair, creating a therapeutic vulnerability to PARP inhibitors (PARPi). While PARPi have shown clinical promise, resistance development limits their long-term effectiveness. Using a CRISPR screen targeting DNA repair proteins, our lab identified HELQ, a normally non-essential DNA helicase, as a candidate for overcoming PARPi resistance. We hypothesize that HELQ knockout will overcome PARPi resistance specifically in BRCA1-deficient cancer cells and sensitize them to additional DNA-damaging chemotherapeutic agents. We used CRISPR-Cas9 to knock out a control target or HELQ in PARPi-resistant BRCA1-mutant ovarian cancer cells and confirmed HelQ loss by Western blot. CellTiter-Glo viability assays were used to assess sensitivity to PARPi and other chemotherapeutic agents: cisplatin, mitomycin C, RAD51 inhibitors, and WEE1 inhibitors. PARPi treatment had minimal effect on control cells' viability, whereas HELQ loss significantly reduced cell viability after PARPi treatment. HELQ-depleted cells also showed increased sensitivity specifically to cisplatin and mitomycin C. Our results suggest that HELQ loss overcomes PARPi resistance and sensitizes BRCA1-mutant cancer cells to certain chemotherapeutic agents. Ongoing studies will determine whether this effect is selective for BRCA1-deficient cells, potentially establishing a therapeutic window for targeting HELQ.

Presenter(s): MacLehose, Dylan
School: Carleton College
Session: P2.02
Title: Microbes need Frenemies: Examination of Viral Influence on Deep-Sea Hydrothermal Vent Food Webs
Co-Author(s): Lin, Alice
Advisor(s): Rika Anderson

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deep-sea through their role as the principal primary producers and decomposers in the deep-sea food web. The project examines metagenomic samples taken from hydrothermal vents and their plumes at the Mid-Cayman Rise in the Caribbean Sea to better understand how interactions between microbes and viruses impact the deep-sea food web. Variation in viral lifestyles and diversity are of particular interest, which have implications for how viruses can manipulate microbial metabolism. We show that viruses disproportionately infect autotrophic microbes compared to heterotrophic microbes, which could have large impacts on the marine carbon cycle. Moreover, we show that lysogenic viruses, which have the ability to incorporate their viral genome into a microbial host, are found to be highly abundant in deep-sea hydrothermal environments compared to background deep seawater. This is significant because these lysogenic viruses are able to manipulate microbial evolution through integration and expression of viral genes within microbial genomes. By looking at transposase abundance and infection patterns across microbial metabolic pathways, we can gain deeper insights into the ecology and evolution of vent communities.

Presenter(s): McConnell, Danielle
School: University of Chicago
Session: P2.09
Title: Enlightened By Excrements: An Investigation of Parabasalid Diversity in the Gut Microbiome
Co-Author(s): Elias Gerrick
Advisor(s): Elias Gerrick

Abstract: Within our gastrointestinal tract, a community of bacteria, archaea, viruses and protists work in tandem to digest nutrients, influence inflammation, and maintain overall health. However, despite protists' fundamental role in this biological ecosystem, they remain sorely understudied. As protists disappear from industrialized microbiomes, the need to study these microbes' mushrooms. Aiming to spearhead this eukaryotic blackbox, my project focuses on isolating novel protists from the Parabasalia phylum to expand a budding biobank. Importantly, although parabasalid protists have been lost in some populations, research has shown that human-associated parabasalid species are also found in animals such as nonhuman primates and ungulates. In collaboration with the Lincoln Park Zoo and The University of Illinois Chicago, we are isolating human-associated protists to establish a pure culture for downstream analysis. In addition to isolating novel protists, I am elucidating three characteristics: who are they, what do they eat, and how do they look. By identifying preferred carbon sources, I delve into what these organisms are consuming within the gut. Using *Tetratrichomonas buttreyi*, I performed growth curves in four unique medias and found that pectin is the preferred carbon source for these microbes. With continued carbon utilization research, I can further characterize the niches found in the order. To investigate morphology, I am performing immunofluorescence microscopy to highlight intracellular and extracellular features within the genus. After DNA extraction and 18s PCR sequencing, I identified a *T. buttreyi* as a commensal protist in Baboons. The phylogenetic tree elucidates this species is also found in pigs. I aim to continue molecular identification, thus growing the biobank and phylogenetic tree. Protists are fundamental to the world around us and the world of microbes within us; understanding them advances medicine, infectious diseases, and ecology.

Presenter(s): Meges, Eleanor
School: University of Chicago
Session: P3.22

Title: Mothers' Experiences during Childbirth and Intrapartum Interventions
Co-Author(s): Sara Franic, Magdelena Kurbanovic, Branka Mrzic, Irena Zakarija-Grkovic
Advisor(s): Irena Zakarija-Grkovic

Abstract: Croatian maternity care lacks standardized clinical guidelines, leaving care decisions to individual providers and enabling continued use of practices unsupported by evidence. Obstetric interventions such as episiotomies, fundal pressure, and oxytocin augmentation appear to occur at high rates in Croatian hospitals, despite WHO recommendations against their routine use. Reliable data on these practices is scarce: the most comprehensive source is self-selected online surveys, while national public health reporting remains limited. Beyond the epidemiological gap, there is a lack of research capturing women's own perspectives on these interventions, or examining associations between intrapartum interventions and early postpartum outcomes, such as pain, mobility, breastfeeding initiation, skin-to-skin contact, bladder and bowel function, and perceived sense of control during birth, which are outcomes that have implications for both maternal wellbeing and infant health. This study aims to address these gaps by using a questionnaire to document intervention frequency among women giving birth in Split, explore their experiences, and investigate links between intrapartum interventions and postpartum outcomes.

Presenter(s): Mendez, Mariah
School: Grinnell College
Session: P2.03
Title: Adaptive Potential of Phenotypic Plasticity of UV Patterns in Monkeyflowers
Co-Author(s): Kathleen G. Ferris, Juj Sullivan, Caroline M. Dong
Advisor(s): Caroline M. Dong

Abstract: Phenotypic plasticity can facilitate adaptation to heterogeneous environments by allowing organisms to modify traits in response to local conditions. We investigated habitat-dependent plasticity in floral ultraviolet (UV) pigmentation using recombinant inbred lines derived from hybrids between *Mimulus guttatus* and *M. laciniatus* in a reciprocal transplant experiment between meadow and granite habitats. Relative UV patch size was quantified from ultraviolet photographs of flowers that bloomed in the field. Although habitat had no overall effect on relative UV patch size, its effect depended significantly on UV morph. Bullseye flowers produced smaller relative UV patches in meadow habitats than in granite habitats, whereas runway flowers exhibited the opposite trend, producing larger relative UV patches in meadow habitats. These contrasting habitat responses indicate that the relationship between environment and floral UV pigmentation differs among UV morphs. Our results suggest that adaptive responses to contrasting habitats depend on floral UV morph, highlighting morph-specific phenotypic plasticity as a potential mechanism contributing to habitat adaptation

Presenter(s): Micallef, Monique
School: Knox College
Session: P1.10
Title: The Effects of *Hericium erinaceus* on the Proliferation of C6 Glioma Cells
Co-Author(s):
Advisor(s): Esther Penick

Abstract: *Hericium erinaceus* is a fungus with various medicinal properties, including neuroprotective, neuroregenerative, and anticancer effects. These neurotrophic effects have been

extensively studied; however, the anticancer effects of *H. erinaceus* remain underexplored. Gliomas are among the most common and aggressive brain tumors, associated with a poor prognosis and limited treatment advancement. Based on the literature on its anticancer effects on different cancer cell lines, we expect *H. erinaceus* to reduce cell proliferation in C6 glioma cells. To investigate this, active components of *H. erinaceus* were extracted in water. Filtered extracts were dried, and the pellet was resuspended in media. Different concentrations of the extract were added to cultured C6 glioma cells for 24 hours, and cell proliferation was measured using a crystal violet assay. Our findings suggest that there is some reduction of cell proliferation in the presence of *H. erinaceus*. When comparing the differing properties of *H. erinaceus* (fruiting body vs mycelium), we found that mycelium did not have any statistically significant effect on cell proliferation, whereas the fruiting body property did. This suggests that *H. erinaceus* could be used as a novel treatment for gliomas. Further experimentation is being conducted to understand the mechanism of action fully.

Presenter(s): Mitchell, Renee
School: University of Chicago
Session: I.B.3
Title: Investigating the Role of Basement Membranes in Shaping the Drosophila Wing
Co-Author(s): Carol Dilts, Ilaria Rebay
Advisor(s): Ilaria Rebay

Abstract:
Basement membranes (BMs) contribute to the establishment and maintenance of 3D tissue shapes by coupling the extracellular environment to the intracellular cytoskeleton through interactions with integrin receptors. I study this process in the Drosophila wing, whose 3D architecture is defined by cell-type-specific basal adhesion between two epithelial sheets – nonvein cells adhere to each other basally, while vein cells do not. My working hypothesis is that these differences in basal adhesion result from differential expression of BM components and their integrin receptors. To test this, I used GFP-tagged alleles of BM proteins and integrins to visualize their expression patterns. My results reveal expression of LamininB1, a fibrous BM component, in both vein and nonvein regions, with only nonvein cells expressing integrins. This suggests that LamininB1-integrin interactions in nonvein regions are necessary for nonvein basal adhesion. To test this, I drove knockdowns of LamininB1 in vein and nonvein cells individually. While vein-specific knockdowns did not perturb wing structure, nonvein-specific lamininB1 knockdowns produced severe wing blisters, a phenotype consistent with loss of basal adhesion. Together, my data suggest that nonvein cells secrete lamininB1 and express its integrin receptor, thereby promoting adhesion between nonvein regions to produce the flat tissue morphology essential for flight.

Presenter(s): Moskal, Lauren
School: University of Chicago
Session: P1.12
Title: APOL1 Genotype and One-Year Kidney and Renal Outcomes: A Retrospective Cohort Study
Co-Author(s): Arlene B. Chapman, Mohammed A. Rafey
Advisor(s): Arlene B. Chapman, Mohammed A. Rafey

Abstract: Background: APOL-1 high risk genotypes are associated with kidney disease.

However, blood pressure and treatment trajectories following clinical genetic testing are less characterized. This study examines the association between APOL1 genotype, blood pressure control, antihypertensive treatments, and kidney function over a year. Methods: This is a single-centre retrospective cohort study at the University of Chicago Medical center, June 2024. Participants are classified as high-risk, carrying two risk alleles, intermediate risk, carrying one risk allele, or low risk, carrying no risk alleles. Electronic health records will provide data such as blood pressure, eGFR, proteinuria, and medication data at baseline, sex months, and one year. Analyses will compare blood pressure control, antihypertensive medication intensification, and renal outcomes between genotype groups. Hypothesis: Identification of an APOL1 high-risk genotype would prompt greater intensification of antihypertensive therapy, resulting in improved blood pressure control and better preservation of kidney function over twelve months compared with patients carrying zero or one risk allele. Significance: This study will provide exploratory evidence on genotype-associated clinical trajectories and support future longitudinal research.

Presenter(s): Muench, Carson
School: Gustavus Adolphus College
Session: P2.19
Title: An Alternate Method of Analyzing Sprague-Dawley Rat Vaginal Cytology
Co-Author(s): Elizabeth Hatlestad
Advisor(s): Kelle Nett

Abstract: Cell suspension is a common approach to collecting vaginal cytology samples in Sprague-Dawley rats, though there is minimal literature on the method. The traditional method relies on smear preparation and staining. Using a cell suspension decreases the processing time and the errors that can occur when staining a sample. It increases the number of cells in the sample and also enables visualization of live cells, whereas stained samples are fixed. Though cell suspension samples are unable to be archived in the way that smeared samples are, microscope images were collected to refine suspension technique and to track estrus. We used this method to examine vaginal samples and characterize them based on the main cell types present to determine which stage of the estrus cycle they were in. Proestrus samples were predominantly composed of nucleated epithelial cells, while estrus was dominated by keratinized (cornified) epithelial cells. Metestrus showed a mixture, including nucleated epithelial cells, cornified epithelial cells, and leukocytes, while diestrus was characterized by sparse cellularity, primarily leukocytes. Overall, the cell suspension provided clear, reproducible cytology profiles. It represents a practical and efficient method for estrus cycle analysis in Sprague-Dawley rats.

Presenter(s): Naismith, George
School: Washington University in St. Louis
Session: P3.13
Title: Anti-Myelin Oligodendrocyte Glycoprotein Antibodies in Neurodegenerative Diseases Across the Age Span
Co-Author(s): Angela S. Archambault, Clarice Pavlak, Gregory F. Wu
Advisor(s): Gregory F. Wu

Abstract: Anti-Myelin oligodendrocyte glycoprotein (MOG) antibody-associated disease (MOGAD) is an immune-mediated demyelinating disease characterized by the presence of anti-MOG immunoglobulins. Studies have reported anti-MOG IgG in a variety of neurological diseases, such as multiple sclerosis. Since these antibodies are not specific to MOGAD, their detection in neurological diseases can confuse diagnosis while altering prognostication and

therapeutic decision-making. This study aimed to determine the prevalence of anti-MOG antibodies in Alzheimer's Disease (AD) and Down Syndrome (DS), two neurodegenerative diseases examined based on age-dependent factors in anti-MOG antibody prevalence. To determine the prevalence of anti-MOG IgG and IgA in these diseases, serum was obtained from patients with AD or DS and used in a cell-based assay in which cells stably transduced to express MOG were incubated with the serum. This was followed by incubation with secondary antibodies tagged to fluorescent molecules and flow cytometric analysis based on gating of MOG-expressing and antibody-binding cells. There was significant anti-MOG binding in both diseases, AD having a prevalence of 4%, while DS had 3% prevalence. These findings suggest that anti-MOG antibodies may be present in neurodegenerative diseases widely independent of age, presenting the opportunity for investigations to define the clinical and pathological implication of anti-myelin antibodies.

Presenter(s): Ng, Sabrina
School: Colorado College
Session: P1.24
Title: Abiotic Effects on Nectar Production in Low Arctic Pollination Systems
Co-Author(s):
Advisor(s): Roxaneh Khorsand

Abstract: Nectar is a vital floral reward for pollinators, providing a critical food source for insects and offering an incentive for pollination. Arctic ecosystems are warming rapidly, yet little is known about how floral reward production will respond to abiotic shifts in the Low Arctic. We used open top chambers to simulate warming in two tundra plant community types on the North Slope of Alaska and measured nectar volume and percent sucrose in three focal species throughout the growing season, alongside monitoring abiotic factors including soil moisture and soil temperature. Prior findings show warming increases nectar volume without changing sucrose concentration. This work builds on these findings by identifying species-specific responses to warming, as well as quantifying the relationship between soil moisture and nectar production. By providing critical data for the understudied Low Arctic, this research can inform predictions of shifting pollinator foraging patterns and plant-pollinator interactions under continued warming.

Presenter(s): Ngo, Khanh
School: Grinnell College
Session: P1.08
Title: The Influence of Cue Specificity on Retrieval-Induced Forgetting
Co-Author(s): Anh Le, Khanh Ngo, Orestis Papaioannou
Advisor(s): Orestis Papaioannou

Abstract: The retrieval of a subset of items can influence the possibilities of the others to be forgotten, a phenomenon that is coined retrieval-induced forgetting (RIF) by Anderson et al. (1994). In this study, we were interested in how the hierarchical nature of the retrieval cue during the final memory testing influences retrieval-induced forgetting. 36 Grinnell College undergraduates first studied a list of category–word pairs with narrow category cues. Participants then completed a retrieval-practice task involving a subset of the studied words, with half of the practiced items presented with broad cues and half with narrow cues. Finally, after a distractor task, participants completed a memory test for all studied items. Our result indicated that items tested with narrow cues were recalled more successfully than items tested with broad cues.

However, we did not find evidence of retrieval-induced forgetting, as recall did not significantly differ among practiced, related-but-unpracticed, and unpracticed items. These findings suggest that cue specificity is important for memory in general, but might not be relevant for RIF specifically.

Presenter(s): Nguyen, Delaney
School: Grinnell College
Session: II.G.2
Title: Nicotine-Induced α4β2 Nicotinic Receptors Upregulation is Mediated in Golgi Satellites
Co-Author(s): Anitha P. Govind, William N.Green
Advisor(s): Anitha P. Govind, William N.Green

Abstract: Nicotine addiction is one of the most common substance-use disorders, and chronic nicotine exposure continues to pose a health threat. A well-documented effect of long-term nicotine exposure is the upregulation of α4β2 nicotinic receptors (α4β2Rs), including an increased number of high-affinity ligand-binding sites and enhanced receptor function. However, the mechanism underlying this upregulation remained unclear. Here, we show that Golgi satellites (GSats) mediate α4β2R upregulation. Using a fluorescence probe, we found that high-affinity ligand-binding sites formed during chronic nicotine treatment colocalize in space and time with GSats, consistent with upregulation-inducing modifications as receptors traffic through this compartment. Chronic nicotine exposure furthermore induces a post-translational modification of complex glycosylation of the receptor as it traffics through GSats. Notably, an independent low-temperature incubation produces the same effect as chronic nicotine exposure, suggesting that these two conditions converge on a common upregulation pathway. Furthermore, introducing a human β2 mutation associated with poison-frog toxin resistance eliminated the upregulation effect of both nicotine and low-temperature incubation. Together, these results identify GSats as the site where α4β2R upregulation occurs, both high-affinity binding-site formation and receptor complex glycosylation. This work establishes a model for studying nicotine addiction in which nicotine causes long-term receptor changes through Golgi structures.

Presenter(s): Nguyen, Nga
School: Knox College
Session: I.A.2
Title: Context-Dependent Functions of the PI3K/AKT Pathway in IL-6-Independent Multiple Myeloma Cells
Co-Author(s): Janet E. Kirkley
Advisor(s): Janet E. Kirkley

Abstract: Multiple myeloma is a plasma cell neoplasm that frequently progresses due to cytokine independence, specifically from interleukin-6 (IL-6) signaling. In this study, we examined whether constitutive activation of the PI3K/AKT pathway contributes to survival and proliferation of IL-6-independent MOPC315 myeloma cells. Across a serum gradient (0-10% FCS), phospho-AKT (Ser473) was highest when cells were serum-deprived and decreased as serum increased, whereas PTEN, a suppressor of the PI3K/AKT signaling pathway, exhibited an inverse trend. Secretion of IgA, an effector function of these cells, exhibited a threshold effect rather than a linear dose-response pattern, with a significant increase observed only at 2% and 10% FCS ($p = 0.0034$). Treatment with the pharmacological AKT inhibitor MK-2206 resulted in an approximately 30% reduction in viable cell yield at 10% FCS, whereas little difference was observed at 0% and 1% FCS. These findings suggest that AKT may have context-dependent

functions in MOPC315 cells, supporting baseline survival under serum deprivation while also contributing to cell proliferation in the presence of serum. This model points toward future isoform-specific investigation of AKT1, AKT2, and AKT3.

Presenter(s): Nguyen, Thuy Yen Nhi
School: Knox College
Session: P3.03
Title: Cell Response to LPS and *Echinacea*
Co-Author(s):
Advisor(s): Janet Kirkley

Abstract: *Echinacea* is a herbal supplement that helps to regulate the immune system. This project observed LPS-stimulated macrophages' response to tea-based Echinacea extracts. After J774A.1 macrophage cells were exposed to *Echinacea* extracts with or without chloroform and LPS, inducible nitric oxide synthase (iNOS) produced more nitric oxide (NO) measured indirectly from the concentration of nitrite. Cells also produced more cytokines such as TNF-α and IL-6 to fight against the external antigen. The results show that the concentrations of nitrite, TNF-α, and IL-6 were present a lot more compared to when cells were only exposed to either LPS or Echinacea only. To understand how *Echinacea* extract regulates the immune response, the Griess assay, ELISA, and Western Blotting will be conducted and analyzed to observe concentration changes in these substances. Additionally, high concentrations of *Echinacea* could cause a lot of stress on cells, resulting in cell death.

Presenter(s): Omar, Noor
School: Gustavus Adolphus College
Session: P1.21
Title: Investigating the Role of p21+ Cells In Atherosclerotic Plaque Calcification
Co-Author(s): Bennett Childs, Karthikbabu Jeganathan, Darren Baker
Advisor(s): Darren Baker

Abstract: Cardiovascular disease is the second leading cause of death in this country (1). The primary preventative treatment option (statins) has ~20-30% reduction in major adverse cardiovascular events. Atherosclerosis is a chronic inflammatory disease characterized by accumulation of lipid-laden plaques in the arterial wall (2). As plaques advance and in response to statins, many undergo calcification, which, depending on morphology, can be beneficial or detrimental to plaque stability. Recent studies showed that plaque calcification is associated with a decrease in active vascular inflammation (3). In prior work, we established a model of dyslipidemia reversal calcification. Here, Ldlr-/- mice fed a high fat diet (HFD) for 12.5 weeks to establish intermediate atherosclerotic plaques respond to subsequent low fat diet (LFD) for 9 weeks with significant improvements in circulating lipid levels and concordant increased plaque calcification and chondrocyte accumulation. Collectively, this suggests altering circulating lipid profile drives significant remodeling. Although vascular calcification has historically been thought of as a passive degenerative process, recent research indicates that it may be similar to bone development. Cells expressing p21 have been recently implicated as inhibiting mineralization in bone fracture callus (4). To investigate the role of p21 cells in this process, diet-switched Ldlr-/- /p21-ATTAC/+ treated with AP mice were utilized to eliminate p21 expressing cells to determine whether these cells are required for plaque calcification. As $p21^+$ cells have been shown to inhibit bone repair, we hypothesized that $p21^+$ cells analogously blunt plaque calcification after lowering lipid levels in Ldlr-/- mice. By en face measurement, we found

no difference in plaque burden with AP or vehicle treatment. Consistent with an inhibitory role of p21+ cells in plaque calcification, Alizarin red-staining showed a tendency towards an increase in calcification in both sexes. Finally, western blotting of arch plaque lysate for CDKi's including p21 suggested that AP-treated Ldlr-/- /p21-ATTAC/+ showed less p21 compared to vehicle, but interpretation was complicated by limiting amounts of material, long required exposure, and uneven loading. In conclusion, this pilot study suggests an inhibitory role for p21+ cells in plaque calcification, however, additional follow-up validation of p21+ cell clearance and examination of calcification in larger cohorts is required to obtain firm conclusions.

Presenter(s): Orlins, Carly
School: University of Chicago
Session: P3.11
Title: Temporal Activation of Adiponectin Receptor Signaling Pathways in B-Cell Acute Lymphoblastic Leukemia Following AdipoRon and Vincristine Treatment
Co-Author(s): Janane Rahbani, Emmy Villela
Advisor(s): Janane Rahbani

Abstract: Obesity is associated with poorer outcomes in B-cell acute lymphoblastic leukemia (B-ALL), including reduced chemotherapy response and increased relapse risk. Adiponectin, a hormone reduced in obesity, is hypothesized to enhance chemosensitivity through AMPK activation and modulation of downstream survival pathways including ERK and AKT. AdipoRon, a small molecule adiponectin receptor agonist, represents a pharmacologic strategy to activate this signaling axis in obese hosts. Prior experiments showed that 1-hour AdipoRon treatment produced no detectable AMPK phosphorylation, suggesting adiponectin receptor signaling requires a longer activation window. To address this, I designed a time course experiment using 8093 B-ALL cells treated with AdipoRon (2μM) and vincristine (3nM), with sample collection at 4, 6, and 12 hours. AMPK pathway activation was assessed by western blot using p-ACC and p-AMPK as primary readouts, with p-ERK and p-AKT as downstream markers. Inconsistent protein normalization limited interpretation at 6 hours, highlighting the need for protocol optimization. However, robust pERK elevation was observed at 12 hours, and trace p-ACC activation provided preliminary evidence of AMPK engagement. These findings suggest adiponectin receptor signaling operates on a delayed timescale in B-ALL cells. Future work will refine this time course and integrate findings into broader studies examining bone marrow adipocyte-mediated chemosensitivity.

Presenter(s): Patel, Jay
School: Washington University in St. Louis
Session: P2.18
Title: Evaluating Propofol-Induced Changes in Sleep Spindle Density in Late-Life Treatment-Resistant Depression
Co-Author(s): Nathaniel Gunter, Robby Greenspan, Millie Gyawali, Brendan P. Lucey, Charles F. Reynolds, III, Eric J. Lenze, Ben Julian A. Palanca
Advisor(s): Ben Julian A. Palanca

Abstract: Sleep spindles are thalamocortical oscillations that mark stage N2 sleep and support sleep stability and synaptic plasticity. Aging and neuropsychiatric illness reduce spindle expression. Propofol, a GABAergic anesthetic, induces spindle-like oscillations and slow-wave dynamics, suggesting it may modulate these circuits. The SWIPED I trial (ClinicalTrials.gov NCT04680910) used propofol as a mechanistic probe to enhance slow-wave expression in adults

with late-life treatment-resistant depression. We examined whether propofol altered spindle density and whether such changes related to antidepressant effects. Fifteen adults aged 60 and older received two propofol infusions titrated to maximize slow-wave expression, with overnight polysomnography at baseline and each infusion night. Spindles were quantified from N2 sleep using a personalized semi-automatic spindle detection algorithm, and density was calculated as spindles per minute. Depressive severity was assessed via the Montgomery-Asberg Depression Rating Scale. Total propofol dose correlated with increases in N2 spindle density ($r=0.62$, $p=0.015$), while frequency, amplitude, and duration were unchanged. Increased density correlated with reduced depressive severity at one week ($r=-0.61$, $p=0.016$) and three weeks ($r=-0.60$, $p=0.018$), but not ten weeks post-infusion. These dose-dependent findings suggest spindle density may mark or mediate propofol's antidepressant response, motivating an ongoing Phase II RCT.

Presenter(s): Pearl, Chloe
School: Grinnell College
Session: P2.04
Title: Phenotypic Plasticity of Monkeyflower Traits under Elevated CO2 and Temperature
Co-Author(s): Caroline M. Dong
Advisor(s): Caroline M. Dong

Abstract: Climate change exposes plants to multiple environmental stressors, yet the combined effects of elevated atmospheric CO2 and temperature on phenotypic plasticity remain poorly understood. We investigated individual and combined effects of elevated CO2 (750 ppm) and temperature (27°C) on floral, vegetative, and life-history traits in hybrid recombinant inbred lines derived from *Mimulus guttatus* and *M. laciniatus*, species adapted to meadow and granite outcrop habitats, respectively. Plants ($n = 336$) were grown across four growth-chamber treatments representing current and predicted future conditions. All measured traits differed significantly among treatments ($p < 0.001$), with temperature emerging as the dominant driver of plasticity. Elevated temperature, alone and combined with elevated CO2, accelerated flowering, reduced plant height and leaf area, and increased herkogamy and relative ultraviolet floral patch size. In contrast, elevated CO2 alone primarily increased leaf area, an effect diminished when combined with warming. Several temperature-induced responses shifted phenotypes toward traits characteristic of the granite-adapted *M. laciniatus*, suggesting that warming may induce a coordinated, faster life-history strategy associated with warmer, rapidly drying environments. These results demonstrate that temperature can dominate plant responses to combined climate stressors, with potential consequences for life-history strategies, mating systems, and plant-pollinator interactions.

Presenter(s): Peck, Anna
School: Colorado College
Session: P3.04
Title: Leaf Morphology and Flower Coloration in *Ipomopsis aggregata*
Co-Author(s): M. Shane Heschel
Advisor(s): M. Shane Heschel

Abstract: Anthocyanin pigmentation influences coloration and can mitigate environmental stress in plants. The flowers of *Ipomopsis aggregata* range from dark red to light pink, with higher anthocyanin levels in darker-flowering plants. Anthocyanin absorbs light in the UV spectrum; dark-flowering plants were found to have higher photosystem efficiency than light-flowering plants. To develop a greater understanding of how *I. aggregata* plants cope with different stress

levels due to their flower color and environment, we compared the leaf morphology of individuals with light flowers to individuals with dark flowers at sites with differing light exposure. Leaf samples and environmental data were taken from along Sacramento Creek and along Route 9 in Fairplay, Colorado and in Manitou Experimental Forest in Woodland Park, Colorado. Field measurements included photon flux density, UV, and anthocyanin content. Scanning electron microscopy was used to collect data on leaf hair density, stomatal density, and complex width and pore width of stomata. Light-flowering plants trended toward having higher stomatal density at all sites. This could be a strategy to compensate for their less efficient photosystems due to a lack of protective anthocyanin– more stomata would facilitate increased gas exchange, raising photosynthate levels. Additionally, dark-flowering plants had higher leaf hair density than light-flowering plants at the roadside site in Fairplay, which had the highest UV-A/B levels of the three sites. This could be an additional protective mechanism against UV exposure for dark-flowering plants by reflecting or scattering radiation and may also increase the leaf boundary layer, potentially reducing water loss and thermal load for dark-colored flowers. Dark-flowering plants may have lower stomatal density and therefore less gas exchange, but this drawback could be offset by the benefits of reduced water loss and thermal load due to higher leaf hair density. Leaf morphology in addition to anthocyanin seems to influence population dynamics in I. aggregata at high elevations.

Presenter(s): Peter, Elliott
School: Hope College
Session: P1.14
Title: Effects of Antibiotic Timing and Combination on KP4-Antibiotic Synergy Against *Klebsiella pneumoniae*
Co-Author(s): Christian Kooistra, Amelia Lampi, Yang Yu
Advisor(s): Yang Yu

Abstract: Antibiotic misuse has contributed to antimicrobial resistance (AMR), creating a major threat to global health. Alternative treatments, including bacteriophages combined with antibiotics, have shown potential for suppressing bacterial growth. However, the effect of antibiotic timing on phage-antibiotic synergy remains poorly characterized. Previous work showed that adding tetracycline (Tet) or ciprofloxacin (Cip) 1 hour after KP4 lysis produced greater reduction in *Klebsiella pneumoniae* growth than simultaneous addition. Here, we examined Tet and Cip addition 5 and 1 hours before KP4 lysis, concurrently with KP4, and 1 and 5 hours after lysis. Combining antibiotics with KP4 produced greater inhibition than KP4 alone. Post-lysis antibiotic addition generally produced greater inhibition than pre-lysis or concurrent addition, particularly for KP4+Tet and KP4+Tet+Cip, which maintained OD600 below 0.2 for 24 hours. Tet added 1 hour after lysis produced greater inhibition than addition 5 hours after lysis. KP4+Cip showed less inhibition than KP4+Tet, potentially due to Cip interference with phage replication. Adding amoxicillin (Amx), Cip, or sulfisoxazole (Ssx) to KP4+Tet did not improve inhibition compared with KP4+Tet alone. KP4+Tet+Ssx maintained the most stable inhibition. Overall, antibiotic timing strongly influences KP4-antibiotic synergy, while adding multiple antibiotics does not necessarily enhance bacterial inhibition.

Presenter(s): Pham, Giang
School: Lawrence University
Session: II.E.2
Title: Structured Diagrams, Pretesting, and the Allocation of Visual Attention During Neuroscience Learning

Co-Author(s): Hilary Miller-Goldwater
Advisor(s): Hilary Miller-Goldwater

Abstract: Reading science textbooks can be challenging because learners must integrate text with diagrams and integrate information across separate content areas. The present research examines whether and how the presence of diagrams and pretesting supports students' recall of neuroscience facts and their subsequent self-derivation through memory integration. We also explore whether individual differences in learning performance, specifically measured by verbal comprehension, spatial skills and science knowledge, moderate this relationship. Experiment 1 uses a 2 (diagram: present vs. absent) by 2 (pretest: pretest vs. control) between-subjects design, implemented online via Gorilla with participants recruited through Prolific, measuring both integration across passages and factual recall. Experiment 2 replicates the diagram-present conditions in the laboratory using eye-tracking to examine how attention to task-relevant regions of diagrams predicts learning. We hypothesize that diagrams will improve both integration and factual recall, that learners who attend more to task-relevant regions will perform better, and that pretesting will further direct attention toward those regions and amplify the diagram benefit. We also expect these effects to vary with individual differences in learning performance. To date, 140 participants have completed Experiment 1 and 8 of a planned 60 have completed Experiment 2. Findings will clarify when diagrams support meaningful science learning and inform the design of multimedia instructional materials.

Presenter(s): Reed, Sydney
School: Lawrence University
Session: P3.16
Title: Creation of a CRISPR/Cas9 Teaching Lab That Incorporates Homology-Directed Repair
Co-Author(s): Kim Dickson, Eric Lewellyn
Advisor(s): Eric Lewellyn

Abstract: CRISPR-mediated genome editing is a ubiquitous biotechnology, but many undergraduate students fail to acquire a practical understanding of the technology through cookbook-style labs. Here, we describe a course-based undergraduate research experience (CURE) that guides students through the CRISPR-mediated genome editing workflow as they generate edited Saccharomyces cerevisiae yeast strains. Unlike existing educational CRISPR kits that focus on loss-of-function editing, this teaching lab incorporates homology-directed repair (HDR) to enable targeted sequence replacement. During the course-long module, students identify a gene of interest with measurable loss- or gain-of-function effects, use Benchling software to identify optimal CRISPR target sequences, design oligonucleotide DNAs for guide RNA and repair templates, and assemble the genetic parts via Golden Gate Assembly (GGA). The result is an all-in-one genome editing plasmid encoding Cas9, gRNA, a repair template, and the homing endonuclease I-SceI, which releases the repair template from the plasmid. Students then transform yeast, verify genome editing by PCR, and analyze the effects using student-designed assays. By combining bioinformatics, Golden Gate Assembly, PCR, molecular cloning, and transformation into a cohesive term-long project, this CURE shows benefits for student understanding, proficiency, and confidence.

Presenter(s): Renwick, Peter
School: Colorado College
Session: P2.12
Title: Analytical Optimization and Comparison of Titratable Acidity, Liquid Chromatography,

and Enzymatic Methods for CAM Acid Quantification
Co-Author(s): Micah Denslow, Quosiah Lawal, Magdalyn Rowley-Lange, Rachel Jabaily, Karolina Heyduk and Eli Fahrenkrug
Advisor(s): Eli Fahrenkrug

Abstract: Crassulean Acid Metabolism (CAM) is central to understanding plant adaptations to arid environments and may provide insight into mitigating anthropogenic climate change. By assimilating carbon dioxide into intermediate compounds at night, a plant can limit its water loss due to the fundamental trade-off of photosynthesis during the day. The product of this process are organic acids, where they are stored and used diurnally for plant growth. Researchers measure organics acids like Malic and Citric acid as proxies for understanding the extent to which a plant is capable of performing CAM. Our study aims to optimize the extraction and quantification methods for measuring these acids while highlighting accessibility, costs and field compatibility concerns. The common extraction solutions that are used include ethanol, water or even liquid nitrogen. For quantification, Titratable acidity (TA) and Ultra Performance Liquid Chromatography (UPLC) are common methods observed in literature, while Enzyme Assays are novel in this line of work. Optimizations of these methods will be performed utilizing a Design of Experiments (DOE) framework, a statistical method that performs multivariate analysis. The Limit of Detection (LoD) and the Limit of Quantification (LoQ) are metrics used to determine a method's sensitivity to the analyte (i.e. Organic acids). These analytical figures of merit will be key in evaluating cross-method comparisons.

Presenter(s): Reynolds, Rebecca
School: Lawrence University
Session: P1.05
Title: Impacts of Human Activity on Parrotfish Wariness and Populations
Co-Author(s): Seth Eaton, Margaret Malone
Advisor(s): Margaret Malone

Abstract: Globally, coral reefs face degradation from multiple threats, including an exponential increase in tourism and recreational diving. However, little is known about the impacts of these human activities on fishes. This study aims to assess impacts of human activity in Bonaire, a Southern Caribbean recreational diving hotspot, on the behavior of an important coral reef herbivore: parrotfish (Family: Scaridae). We hypothesize that there will be a difference in parrotfish populations and wariness behaviors between management zones (open, no-take, and no-entry). Diver activity may reduce parrotfish wariness outside no-entry zones through habituation or a "human shield" effect against perceived predation risk from natural predators. However, if parrotfish perceive human activity as a form of predation risk itself, it may contribute to a "landscape of fear," increasing parrotfish wariness outside no-entry zones. We tested these contrasting predictions within three distinct management zones on Bonaire. Parrotfish wariness and biomass were quantified by Minimum Approach Distance (MAD), fork length, and abundance on 5m x 30m transects (n=66) using diver-operated stereo-videos, which were analyzed using EventMeasure software. These findings will help us understand impacts of human activity on reef fishes, improving managers' ability to identify additional management actions to mitigate impacts from recreational diving.

Presenter(s): Riter, Imogen
School: Beloit College
Session: P1.06

Title: Active Goal Setting for Sleep: The Impact of Implementation Intentions on Sleep Quality & Cognition
Co-Author(s): Ethan Rosenkranz, Allison Nickel
Advisor(s): Allison Nickel

Abstract: Sleep supports many necessary functions such as neuronal development and memory, while a consistent lack of sleep has been linked to the development of serious health issues such as heart disease and cancer. College students are a high-risk group as they experience a variety of factors which contribute to poor sleep. Past endeavors to improve sleep in college students through goal setting have proven largely ineffective. Intentionality on its own is not sufficient to drive change as there are often obstacles which inhibit the path to goal attainment. The current study is aimed at assessing the effectiveness of an active goal setting technique called "implementation intentions" which use "when" "then" statements to keep subjects on track to goal attainment. College students (N≈30, est ages: 18-24) will be randomly assigned to either an active goal condition ("when" "then") or a normal goal condition ("I will ___".) Participants will wear smart watches for data collection. Additional measures will be collected via a set of questionnaires, and cognitive tasks. Results are predicted to show significant improvement for the implementation intentions group only. If predictions hold, findings would suggest that implementation intentions are promising tools for the improvement of sleep quality among college students.

Presenter(s): Rodriguez Poggio, Josefina
School: Colorado College
Session: P2.06
Title: In Situ Carbon Transfer from Fungal Necromass into Soil during Decomposition
Co-Author(s):
Advisor(s): Craig See

Abstract: Soil constitutes the largest pool of terrestrial carbon globally, and understanding the processes contributing to the residence time of this pool is crucial for predicting atmospheric carbon dynamics and global change. Fungal necromass has drawn increasing attention as an important but poorly quantified driver of soil carbon sequestration. Understanding the rate at which carbon moves from necromass into bulk soil carbon pools is a foundational step toward understanding fungal contributions to soil carbon stocks. However, fungal necromass is challenging to measure due to its rapid decomposition and coexistence with living fungi and changing soil conditions. This study quantifies in situ carbon transfer from fungal necromass into surrounding soil using litter bags. Necromass of two common soil fungi, *Mortierella* and *Mucor*, was introduced into soil microcosms alongside a decomposition control with no necromass added. Ten replicate bags per treatment were harvested after 2, 6, and 11 days of decomposition. Carbon transfer due to fungi was quantified as the difference between the total carbon content in the necromass treatment and the necromass-free control. Additional daily sampling of the two fungal treatments was conducted across 10 days. This study provides a baseline understanding of the contribution of fungal necromass to soil carbon pools.

Presenter(s): Rund, Layne
School: Carthage College
Session: P2.23
Title: Match Demands and Workloads in NCAA DIII Women's Soccer
Co-Author(s): Tony Pustina

Advisor(s): Tony Pustina

Abstract: The three main playing positions in soccer require distinct sets of skills and physical demands to perform their roles effectively. The purpose of this study was to compare the demands and workloads of attackers, midfielders, and defenders across the 2024 NCAA Division III Women's soccer season. Wearable GPS tracking devices were employed to measure total distance (m), low-speed running distance (m) (LSR), high-speed running distance (m) (HSR), and top speed (mph). LSR was defined as the total distance covered at a velocity greater than 10km/h (6.2mph). HSR distance was defined as the total distance covered at a velocity greater than 15 km/h (9.3 mph). Means and standard deviations were compared across the three playing positions: defender, midfielder, and attacker. To be included in the analysis, a player had to play more than 45 minutes. A total of 161 match observations were observed across 17 matches (n = 75 defenders, n = 30 forwards, and n = 56 Midfielders). The average minutes played between all groups was 76.1 ± 14.3 minutes. A 2-way mixed ANOVA was used to assess each independent variable: total distance, low- and high-speed running distance, and top speed. We found in the results that there was no difference between the 1st and 2nd halves, but did see a great variety between each position group in all of our datasets.

Presenter(s): Samnang, Raska
School: Hope College
Session: P2.05
Title: Experimental Analysis Of *Escherichia coli* on Carbon Sources
Co-Author(s): Matthew B. Love, Jacquelin D. D'Lamater, Frederick T. Melges
Advisor(s): Clayton G. Piehl, Lauren M. Cribbs, Natalie L. H. Huisman, Brent P. Krueger, Aaron A. Best, Michael J. Pikaart

Abstract: *Escherichia coli* strains play an important role in a variety of habitats, including open aquatic environments. Using samples from the local Macatawa Watershed, we isolated 10,000 and sequenced over 500 water-derived *E. coli* strains, generating a genome-scale metabolic model predicting whether individual strains could metabolize specific substrates. To evaluate the prediction, previous lab members utilized Biolog metabolic phenotype plates to analyze metabolic activity of 32 watershed strains and one reference strain (*E. coli* MG1655) across 190 carbon-based substrates. Experimental results were compared with metabolic model prediction, to assess the model's predictive performance and identify its limitations. Two primary limitations emerged. First, an operon-level issue resulted in a major discrepancy between model predictions and experimental results. As demonstrated by substrate D-serine, the model focused on the presence of the deaminase gene and summed it as sufficient for metabolism, while experiential and genomic analyses demonstrated the importance of the complete operon, including permease, deaminase, and an activator. Second, a limitation beyond the operon composition was identified through a frameshift in the N-terminus of the Sdar gene, which is responsible for activating the operon involved in galactaric acid metabolism. These findings demonstrate limitations in predicting metabolic capabilities based solely on gene presence.

Presenter(s): Schroeder, Paul
School: Carthage College
Session: II.F.1
Title: Fighting Gram-Negative and Gram-Positive Bacteria: The Antibacterial Properties of an L-leucine-Based Surfactant

Co-Author(s): Ryan Del Alcazar, Iman Deanparvar, Jessica Schultz, David Brownholland, and Deborah Tobiason
Advisor(s): Deborah Tobiason

Abstract: Bacterial pathogens and humans have battled since long before we were ever aware of their existence. The ever-evolving nature of bacteria necessitates an ever-evolving arsenal of treatments to defeat them. In pursuit of a new way to counteract pathogenic bacteria, this study examines a bio-based L-leucine surfactant. Surfactants have been widely used as antibacterial topical antiseptics, disinfectants, and general antibacterial cleaners; however, bio-based surfactants account for a much smaller share of the worldwide volume of surfactants used than petroleum-based surfactants. We have determined that a leucine-based surfactant inhibits bacterial growth in *Escherichia coli* (gram-negative), *Staphylococcus aureus* (gram-positive), *Acinetobacter baylyi* (gram-negative), and *Enterococcus faecalis* (gram-negative). Bacterial inhibition was determined through minimum inhibitory concentration (MIC), the minimum concentration of the surfactant required to inhibit bacterial growth. All tests are conducted using a standard serial dilution protocol in triplicate, with non-pathogenic representatives of common antibiotic-resistant bacteria. The behavior of the surfactant in solution was also analyzed to determine the possible mechanism of bacterial inhibition and the surfactant's viability when solubilized in different solvents. Further analysis of the possible mechanism of bacterial inhibition is being investigated.

Presenter(s): Seidl, Marina
School: Colorado College
Session: P2.15
Title: SUP-26 and cytoskeletal mRNA regulation in *C. elegans* neuron morphology
Co-Author(s): Estefanía Izarnotegui Cerda, Mica Hart, and Darrell Killian
Advisor(s): Darrell Killian

Abstract: Dendrites are complex neuronal structures critical for receiving signals, and defects in dendrite branching are linked to neurological disorders. The PVD neuron in *C. elegans* is an excellent model for a genetic investigation of dendrite branching—PVD neurons have a complex morphology and *C. elegans* is amenable to genetic manipulation and live imaging. Previous work identified the RNA-binding protein, SUP-26, as important for PVD dendrite morphology (Antonacci et al., 2015; Schachtner et al., 2015; Olesnicky et al., 2018). Biochemical analyses revealed that SUP-26 binds primarily to the 3’ UTR of mRNAs and interacts with the Poly(A)-binding protein, suggesting a potential role in translational regulation (McJunkin and Ambros et al., 2017; Olesnicky et al., 2018). Our previous research found that ~20 of the SUP-26 target mRNAs encode cytoskeletal proteins, the regulation of which could impact dendrite morphology. Six of these genes (erm-1, frm-4, spc-1, F53E2.2, unc-70, and unc-115) were selected to study. We sought to determine if SUP-26 regulates the translation of these target genes. Using transgenes that express a fluorescent protein (GFP) with a 3’ UTR of each target gene, we tested the change in expression with and without sup-26 using RNA interference. By evaluating 20 individuals for each genetic reporter for each condition, no statistically significant results in SUP-26 expression were found. Further research is needed to further understand the translation regulation of this gene on dendrite morphology.

Presenter(s): Simon, Kiran
School: University of Chicago
Session: I.A.2

Title: Exploring Myeloid/T cell crosstalk in the Skin
Co-Author(s): Tianhao Wei, Molly Tully, Martina Damo
Advisor(s): Martina Damo

Abstract: Checkpoint blockade (CPI) is a widely used cancer treatment strategy that enhances T cell-mediated anti-tumor activity by inhibiting checkpoint receptors on the surface of T cells. Although effective, most CPI-treated patients develop autoimmune flare-ups in unrelated tissues. This suggests that checkpoint receptors have a significant role in regulating T cells in healthy tissue. To investigate the role of checkpoint receptors in healthy tissue, we used Rosa26-NINJA-creERT2;CAG-rtTA3 Tg(NCR) mice. The NCR mouse contains an inducible skin-specific protein antigen which recruits T cells into the skin that do not cause tissue damage unless CPIs are administered. Upon antigen induction, we found that a population of CD11b+ CD11c+ myeloid cells accumulates within the skin. CD11b+ CD11c+ myeloid cells colocalized with T cells and expressed checkpoint receptor ligands. Additionally, when T cells are depleted from the skin, CD11b+ CD11c+ myeloid cell accumulation is abrogated, suggesting that it is T cell dependent. Ultimately, we demonstrate that there is some degree of myeloid/T cell crosstalk within the skin which may play a role in maintaining skin homeostasis. Ongoing studies in our lab are investigating whether myeloid/T cell interactions are mediated through checkpoint receptors and if they are required to regulate T cells in the skin.

Presenter(s): Soltwedel, Blaine
School: Carthage College
Session: P1.07
Title: Religions Mediation Effect on Disgust Sensitivity and Attitudes Toward Gay Men and Lesbian Women
Co-Author(s): Sara O'Brien
Advisor(s): Sara O'Brien

Abstract: This research examines whether moral foundations mediate the relationship between disgust sensitivity and attitudes toward gay men and lesbian women. The current study is a replication of prior research, which found that sanctity/purity would mediate the relationship between disgust sensitivity and attitudes toward gay men and lesbian women. Participants will be 100 students recruited from Carthage College undergraduate psychology courses; they will complete 3 surveys: the Moral Foundation Questionnaire, Attitudes Toward Gay Men and Lesbian Women scale, and Disgust Scale-Revised. It is hypothesized that our results will yield a positive correlation between disgust sensitivity and negative attitudes toward gay men and lesbian women. It is also hypothesized that sanctity/purity will mediate the relationship between disgust sensitivity and attitudes toward gay men as well as attitudes toward lesbian women. Unlike the previous study, which examined a more religious Chinese population, this study examines students from a small American college. If consistent, the role of moral foundations theory in these attitudes may warrant further cross-cultural research.

Presenter(s): Song, Jianfei
School: Washington University in St. Louis
Session: P1.09
Title: Characterization of 2A Peptide-mediated Dual scFv Production in *S. boulardii* against Inflammatory Bowel Disease
Co-Author(s): Ana Romani, Ayse Ece Gulen, Ta-Chiang Liu, Gautam Dantas
Advisor(s): Gautam Dantas

Abstract: 2A peptides are a group of 18-22-amino-acid-long polypeptide sequences that mediate a co-translational peptide-bond-skipping event of the prokaryotic ribosome. While widely used in protein expression systems across a variety of species, the effectiveness of 2A peptides has not been characterized in *Saccharomyces boulardii* (Sb), a prominent probiotic yeast. In this study, we designed a 2A peptide-mediated dual protein expression system for Sb and provided the first demonstration of 2A peptide functionality in this strain. To probe the therapeutic potential of our system, we engineered Sb to secrete a two-scFv cocktail therapy targeting a key pro-inflammatory mediator in inflammatory bowel disease (IBD). By refining genetic sequence contexts, modulating payload architecture, and evaluating multiple 2A sequences, we increased the peptide-bond-skipping efficiency of the system to 100%. Our findings reveal that while activity is context-dependent, 2A peptides can achieve high skipping efficiency in Sb, establishing a robust tool for probiotic synthetic biology and polycistronic biotherapeutic delivery.

Presenter(s): Srinivasan, Vishnu
School: Washington University in St. Louis
Session: P1.20
Title: Identification of ERO1α-Selective Inhibitor Derivatives of M6766 as an Antithrombotic Strategy
Co-Author(s):
Advisor(s): Jaehyung Cho

Abstract: Heart attacks and strokes from arterial blood clots are leading causes of death in the U.S., occurring when platelets clump at injury sites. Current antiplatelet drugs block platelet function body-wide, raising bleeding risk and creating a need for a drug that stops harmful clotting without impairing normal clotting. My lab previously used platelet-specific ERO1α knockout mice to identify ERO1α as a distinct drug target, then screened nearly 40,000 compounds and identified M6766, a selective ERO1α inhibitor that prevents arterial clotting and stroke damage in mice without prolonging bleeding time. However, M6766 has poor water solubility, limiting its drug potential. My project tested 13 new versions of M6766 redesigned to be more soluble while maintaining ERO1α inhibition. I used a fluorescence-based assay measuring ERO1α-driven hydrogen peroxide production, confirmed by a counter-assay to rule out nonspecific reactivity. Seven of the 13 compounds were then tested via flow cytometry, measuring platelet activation after thrombin and collagen-related peptide stimulation. Four compounds — WU-4913, WU-5975, WU-2784, and WU-4668 — stood out, dropping ERO1α activity to 21–37% of normal, matching or beating M6766. Next steps include counter-screening against MAO-A and aggregation assays, a first step toward a safer, more soluble ERO1α inhibitor.

Presenter(s): Swanlund, Jenna
School: Lawrence University
Session: P3.10
Title: Engineering Oxidative Resistance in Human Ribonuclease Inhibitor 1 (RNH1)
Co-Author(s):
Advisor(s): Kimberly Dickson

Abstract: The human ribonuclease inhibitor (RNH1) protein is involved in many important cellular processes, acting as a regulator, a protector, and an indicator of cell stress. RNH1 is highly sensitive to oxidation and loses all function in a cell under oxidative stress, potentially initiating several mechanisms and pathways in its absence. RNH1 variants with different degrees

of oxidation resistance have been designed and modeled in AlphaFold with various combinations of purification tags and rigid protein linkers—the construct containing a Strep Tag® II purification tag and an (EAAAK)3 linker was identified as the most promising and built with Gibson Assembly. An encouraging level of expression of the wild-type RNH1(wtRNH1) purification construct has been achieved in CHO-K1 cells. Current work is aimed at scaling up expression for purification of wtRNH1. Once purified, the stability and ribonuclease-binding activity of wtRNH1 will be measured; the oxidation-resistant variants will be similarly characterized. This data will then be used to inform experiments on the role of RNH1 in cells under oxidative stress in which oxidation-resistant RNH1 variants are introduced to KO RNH1 cells to study what happens in an oxidized cell with functional RNH1 present.

Presenter(s): Syed, Zainab
School: Gustavus Adolphus College
Session: P3.21
Title: Influence of caloric restriction and estrous state on sucrose-seeking behaviors
Co-Author(s): Shayma Said, Arwen Baer
Advisor(s): Kelle Nett

Abstract: Circulating gonadal hormones interact with neural pathways to influence learning and motivated behaviors. Sex differences have also been identified in addiction-related behaviors, including craving and relapse. In humans, fluctuating levels of ovarian hormones across phases of the menstrual cycle have been associated with changes in cognition and reward processing. In rodents, a similar hormonal fluctuation occurs across the four phase estrous cycle, providing a compelling model for investigating how reproductive state and dietary conditions influence reward-seeking behavior. The present study investigates factors contributing to sucrose craving in Sprague Dawley rats, focusing on estrous and chronic caloric restriction. To examine these factors, female (n=10) and male (n=6) rats were trained to press a lever to gain a sucrose pellet reward. Then, cued sucrose-seeking tests were administered across three different periods (Days 0, 30, and 60). Rats were food restricted following the first seeking test. Estrous stage was determined using vaginal lavage and cell suspension prior to daily sessions. Together, these experiments explore conditions contributing to persistent sucrose-seeking behavior, allowing us to better characterize underlying biological mechanisms of reward-seeking behaviors, improve the generalizability of preclinical models, inform understanding of addiction, and apprise strategies on optimizing learning across hormonal states.

Presenter(s): Tripathi, Vinisha
School: Washington University in St. Louis
Session: II.F.3
Title: The Impact of Molecular Xenomonitoring on Assessing the Efficacy of Moxidectin in Controlling Lymphatic Filariasis
Co-Author(s): Fidele Assamoi; Kerstin Fischer; Lucia Di Maggio; Sarah Greene; Philip Budge; Benjamin Koudou; Peter Fischer
Advisor(s): Anthony Smith

Abstract: Lymphatic filariasis (LF) is a vector-borne, parasitic disease that affects 51 million people globally. Spread primarily by Anopheles mosquitoes, LF results from infection with Wuchereria bancrofti and causes lymphedema or hydrocele. Community-wide distribution of anti-filarial medications successfully reduces LF prevalence, but tracking residual transmission remains a critical challenge. One approach is identifying parasites within vectors, called

xenomonitoring. In Côte d'Ivoire, Moxidectin combination therapies were administered to three endemic communities with ongoing W. bancrofti transmission in the Akoupé district in 2023. We tested for W. bancrofti DNA in Anopheles gambiae mosquitoes collected from 75 sites at baseline (2023) and post-treatment (2024). 5,180 mosquitos were sorted into pools of up to 20 mosquitos based on species and capture characteristics. DNA extractions and qPCRs were performed on 283 mosquito pools. At baseline, 5 of 75 (6.67%) pools tested positive for W. bancrofti DNA. One-year post-treatment, 9 of 208 (4.32%) pools tested positive for W. bancrofti. Further statistical analysis using the xenomonitoring software PoolScreen will be performed to test the significance of changes in filarial DNA prevalence. However, this study demonstrates a reduction in W. bancrofti within A. gambiae mosquitos after preventative treatment and shows that xenomonitoring is an effective transmission surveillance technique.

Presenter(s): Tung, Man Sin Michelle
School: Macalester College
Session: P2.21
Title: Alzheimer's Disease and Sleep Deprivation: Neuroendocrine and Behavioral Assessment in APOE4 Female Mice
Co-Author(s):
Advisor(s): Meagan McManus, Jerry Edward Carr

Abstract: The three major risk factors of Alzheimer's Disease (AD) include aging, apolipoprotein E4 (APOE4) genotype and the female sex, which converged mechanistically through mitochondrial dysfunction. Our lab previously demonstrated that bioenergetic deficits emerge in perimenopausal females. Using the apolipoprotein 4 (APOE4) AD mouse model, we investigated whether sleep deprivation (SD), as a physiological stressor, exacerbates AD-prodromal neurobehavioral changes and endocrinological aging in APOE4 carriers compared to APOE3 controls. Endocrine aging was assessed by vaginal cytology, body composition by EchoMRI, and neurobehavioral function by open-field and novel object recognition assays. Our results showed accelerated endocrine aging in APOE4 mice at baseline and enhanced irregularity in estrous cycling across both genotypes after SD. APOE4 mice also exhibited reduced fat mass post-SD, consistent with increased energetic demands, alongside impaired locomotion and memory following SD. Collectively, these findings demonstrate that APOE4 accelerates baseline endocrine aging and amplifies neurological vulnerability, establishing SD as a physiological stress model for future investigation of mitochondrial pathways. Pre and post-SD blood samples were collected via submandibular sampling for future cytokine analysis of mitochondrial damage-associated molecular patterns (mtDAMPs), which could provide insight on the role of mitochondria in stress-related endocrine and cognitive dysfunction in neurodegeneration.

Presenter(s): Turetzky, Marisen
School: Gustavus Adolphus College
Session: P1.18
Title: Elucidation of RyhB target prioritization in *E. coli*
Co-Author(s):
Advisor(s): Janie Frandsen

Abstract: Bacterial small RNAs (sRNAs) are non-coding RNAs that regulate gene expression by binding to mRNAs to repress or activate protein expression. sRNAs have a targetome of multiple mRNAs that they regulate. We hypothesized that these mRNA targets vary in priority; higher-priority targets are regulated when sRNA levels are low, while lower-priority targets are affected

as sRNA levels increase. We aim to elucidate the hierarchy of the *Escherichia coli* RyhB targetome to better understand what dictates target prioritization. To investigate the regulatory hierarchy of the RyhB targetome, we are using two complementary assays. To assess the hierarchy of the binding interactions between RyhB and its mRNA targets, we have developed a pull-down assay by modifying the MS2 affinity purification coupled with RNA sequencing (MAPS) technique. Instead of using RNA sequencing at one time point, we use RT-qPCR to quantify the amounts of the RyhB mRNA targets pulled down over a time course after MS2-RyhB induction. To assess the hierarchy of the change in protein expression from mRNA targets, we are using a two-plasmid assay similar to one used previously to study SgrS. In this assay, RyhB and a target mRNA fused to GFP are expressed using independently controlled inducible promoters; in the presence of different combinations of inducers, we use a plate reader to monitor GFP fluorescence and bacterial growth over time. When comparing different mRNA targets, differences in GFP expression over the inducer range and time course suggest differences in the regulatory hierarchy. We inserted each RyhB mRNA target into the GFP fusion plasmid and began analyzing each target independently. After elucidating the hierarchy, we plan to assess mRNA target features, such as binding-site accessibility, to better understand the features that dictate prioritization and promote the dismantling of bacterial protein regulation in the fight against antibiotic resistance.

Presenter(s): Turuspekov, Almazbek
School: Knox College
Session: P2.08
Title: Tracking Intracellular Digestion and Waste Release in *Stentor coeruleus*
Co-Author(s):
Advisor(s): Mark Slabodnick

Abstract: *Stentor coeruleus* is a large freshwater ciliate that allows intracellular digestion and waste release to be observed within a single living cell. Fluorescent dextran was used to label food vacuoles, and their lifetime was tracked over time under different feeding conditions. Food vacuoles remained visible for about 13 hours with dextran alone, but algae feeding shortened this time to approximately 9–10 hours and made waste release easier to predict. Sequential imaging directly captured a fluorescent food vacuole being released from the cell. Together, these experiments provide a practical way to study how Stentor coordinates feeding, digestion, and waste removal.

Presenter(s): Urosevic, Jovanna
School: University of Chicago
Session: P2.14
Title: Metabolic regulation of transcriptional plasticity in medullary thymic epithelial cells
Co-Author(s):
Advisor(s): Andrew Koh

Abstract: Central immune tolerance depends on the ability of medullary thymic epithelial cells (mTECs) to negatively select autoreactive T cells before they reach the peripheral immune system. To differentiate between “self” and “non-self,” mTECs promiscuously express tissue-restricted genes otherwise limited to specialized organ systems. However, the mechanisms of mTEC transcriptional plasticity are not well understood. Canonically, metabolism is associated with sustaining the cell, however, research has made the metabolic-epigenetic interplay increasingly clear. Since metabolites like acetyl-CoA directly influence chromatin accessibility,

metabolism may be an important determinant of the epigenetic landscape. During mTEC maturation, at the stage of development where tissue-restricted genes are expressed, a decline in mitochondrial oxidative phosphorylation is observed. Simultaneously, the cells significantly upregulate gene programs responsible for peroxisomal fatty acid-beta-oxidation. Preliminary data suggests that acyl-CoA oxidase 1(Acox1)-mediated peroxisomal beta-oxidation of fatty acids supports plasticity in mTECs with deficient mitochondrial oxidative phosphorylation. The hypothesis is explored using an Acox1 conditional knockout mouse model, bulk RNA sequencing, and single-cell transcriptomic analysis.

Presenter(s): Vohra, Urja
School: University of Chicago
Session: P1.19
Title: SynCom15 Suppresses Excessive CKD Gut Tryptophan-to-Indole Flux, Limiting Indoxyl Sulfate Formation and Preserving AVF Patency
Co-Author(s): Sara Gaines, Sadhana Samant
Advisor(s): Sara Amelia Gaines

Abstract: CKD is associated with AVF failure within a year in roughly half of patients, largely driven by neointimal hyperplasia caused by the uremic toxin indoxyl sulfate, a gut-derived metabolite of indole produced when bacteria like E. coli ferment dietary tryptophan. This study tested whether CKD is linked to elevated baseline indole production, and whether SynCom15 -a defined 15-strain synthetic bacterial community engineered to outcompete indole producers for tryptophan - can suppress indole through genuine substrate competition. Indole was measured colorimetrically across three experiments: baseline stool from CKD vs. non-CKD individuals; SynCom15 co-cultured with high- and low-indole-producing E. coli strains at 4, 6, and 8 h; and SynCom15 co-cultured with complex CKD stool at 12 and 24 h. CKD stool showed ~48% higher baseline indole than non-CKD stool (~79 vs. ~53 μM), confirming excess indole-producing capacity in CKD microbiota. SynCom15 significantly reduced indole from the high-producer strain at all timepoints (e.g., ~140→100 μM at 4 h; $p<0.01$–0.05), while leaving low-producer output (~35–45 μM) unchanged—indicating specific substrate diversion rather than nonspecific antibacterial killing. This suppression held in complex CKD stool, lowering indole from ~110–130 to ~65–100 μM at 12 h and ~75–110 to ~40–65 μM at 24 h ($p<0.0001$).

Presenter(s): Wang, Huilun
School: Washington University in St. Louis
Session: I.C.1
Title: Impact of a Rare Neurodevelopmental Disorder on PKA Dynamics Across Sleep-Wake Cycle
Co-Author(s): Yao Chen, Kane Goggans, Elizabeth Tilden, Walter Saide, Stefan Strack
Advisor(s): Yao Chen

Abstract: Sleep is essential for brain and body functions, yet the molecular mechanisms that regulate sleep remain unclear. Protein kinase A (PKA) is a cAMP-dependent signaling enzyme whose downstream substrate phosphorylation (PKA-SP) exhibits state-dependent dynamics across the sleep–wake cycle, decreasing progressively during sleep and increasing upon arousal. Pathogenic variants in PRKAR1B, which encodes the RIβ regulatory subunit of PKA, cause Marbach–Schaaf neurodevelopmental syndrome (MASNS), a rare disorder associated with sleep disturbances. However, whether and how mutant PKA regulation alters state-dependent PKA-SP dynamics and sleep structure remains unknown. Here, we measured state-dependent PKA-SP in

freely behaving PRKAR1B R335W mice and littermate controls using fluorescence lifetime photometry while quantifying sleep architecture across behavioral states. Compared with littermate controls, mutant mice exhibited blunted PKA-SP dynamics during sleep–wake state transitions, characterized by smaller decreases during sleep onset and smaller increases following arousal. These molecular changes were accompanied by increased sleep time, prolonged sleep bouts, and shorter wake bouts. Together, these findings strengthen the link between PKA signaling and sleep regulation and provide insight into the molecular basis of sleep disturbances in MASNS.

Presenter(s): Wiley, Olivia
School: Hope College
Session: II.G.3
Title: Inflammatory Responses Following Brain Trauma Regulate Neurogenesis in the Olfactory Epithelium of Zebrafish
Co-Author(s): Becca Post, Aidan Shattuck, Lexus Putt, Erika Calvo-Ochoa
Advisor(s): Erika Calvo-Ochoa

Abstract: Zebrafish (*Danio rerio*) can repair their brain in response to damage, displaying comprehensive neuroplasticity throughout their lifetime. The olfactory system, including the olfactory bulb (OB) and epithelium (OE) mediates important roles like processing odors. Injuries to the OB cause neurodegeneration, as well as an immune response, demonstrated by microglial activation. Furthermore, in the zebrafish brain, neuroinflammation supports recovery through neural stem cell (NSC) proliferation, which contributes to neurogenesis. Little is known about how inflammation impacts regeneration in the OE. We use a model of retrograde degeneration of the OE through excitotoxic lesions in the OB using quinolinic acid (QA) in adult zebrafish. To further investigate inflammation, we used the anti-inflammatory drug pranlukast, a selective antagonist of the cysteinyl leukotriene receptor 1. Immunohistochemistry was utilized to study various markers of inflammation and regeneration, including Lcp1 (leukocyte marker), BrdU (proliferation marker), and HuC/D (mature neuron marker). We found that OB lesions induce transient OE inflammation, with increased leukocyte activity between 1 hour-post-lesion (hpl) 72 hpl. Pranlukast inhibited this response at all times. Furthermore, OB lesions induce OE cell proliferation (BrdU+) and neurogenesis as soon as 6 hpl. Pranlukast ablates proliferation, indicating that inflammation is necessary in the neurogenesis process.

Presenter(s): Williamson, Ryan
School: Washington University in St. Louis
Session: P3.14
Title: Profiling the Differential Effects of Peptide MHCII CAR T Cells on the Blood-Brain Barrier
Co-Author(s): Kevin Harris, Greg Wu, Angela Archambault, Matthew Cain
Advisor(s): Greg Wu

Abstract: Chimeric antigen receptor (CAR) T cell therapy is an immunological treatment often used in B Cell malignancies with emerging utilization in autoimmune disorders such as multiple sclerosis (MS). Traditionally, antigen recognition for CAR T cells has been achieved using single chain variable fragments (scFvs). A common complication of scFv-based CAR treatment is immune effector cell associated neurotoxicity syndrome (ICANS) due to disruptions in the blood-brain barrier (BBB). Our lab has engineered peptide MHCII (pMHCII) CARs to deplete CD4+ T cells in an antigen specific manner. To profile their safety, we investigated whether

pMHCII-CARs cause similar disruptions to the BBB in experimental autoimmune encephalomyelitis (EAE), a murine model of MS. We observed that pMHCII-CAR T cells induce BBB disruption upon engagement with their cognate T cell receptors in mice without underlying disease. Modulation of the intracellular signaling domains within these CAR constructs differentially impacted the extent of BBB disruption. However, this dysfunction is absent in EAE: BBB integrity is restored to baseline levels within six days of CAR T cell administration without meaningful increases during disease resolution. We attribute this divergence to cytokine saturation within the inflammatory milieu and a concurrent polarization toward an Arg1+ macrophage phenotype in mice with EAE.

Presenter(s): Wu, Yifan
School: Macalester College
Session: II.F.3
Title: Investigating the Role of GelE during *Enterococcus faecalis* Recovery from Inhibition by *Streptococcus mutans*
Co-Author(s):
Advisor(s):

Abstract: Interactions between bacterial species influence competition within the oral microbiome. *Enterococcus faecalis* encounters other bacteria in the mouth, including *Streptococcus mutans*. Previous work showed that *S. mutans* inhibits *E. faecalis* during co-culture, but *E. faecalis* growth recovers from inhibition by 24 h. *E. faecalis* encodes GelE, a secreted metalloprotease that is regulated by the Fsr regulatory system and is required to promote recovery from inhibition. This study examined whether GelE expression during co-culture is consistent with the Fsr-activated model or whether alternative regulatory mechanisms contribute under competitive conditions. A PgelE-gfp reporter was used so that GFP fluorescence reflected gelE promoter activity. *E. faecalis* was grown in monoculture or co-culture with *S. mutans*, and GFP fluorescence and CFU were measured at 2, 4, 6, 8, and 24 h. E. faecalis growth increased in monoculture, while co-culture showed early inhibition followed by recovery at 24 h. Reporter activity increased over time in monoculture but remained relatively stable during co-culture. The absence of a later increase in normalized gelE reporter activity during co-culture suggests that additional factors may influence gelE regulation or that further reporter validation is needed.

Presenter(s): Xiang, Chenxin
School: Colorado College
Session: P1.17
Title: Thermodynamic Analysis of Ion Binding to miR-184 RNA and DNA Constructs
Co-Author(s): Torah Delaney
Advisor(s): Neena Grover

Abstract: MicroRNAs (miRNAs) are non-coding sequences of RNA that regulate genes. MicroRNA, like miRNA-184, is linked to cancer suppression and regulation. Calcium ions are hypothesized to impact the induction of miR-184 in skin cancers. Mutations in the miR-184 gene are also connected to epithelial dysregulation in the eye. The purpose of this project is to investigate the thermodynamic properties and structural stability of miR-184 RNA and DNA constructs under different pH and ionic conditions. Comparisons between the full-length wild-type DNA and RNA constructs, and smaller fragments derived from it, were used to determine the impact of sequence on structural stability under different ionic conditions. Impact of changes in sequence are also being examined. Thermal denaturation (melting) and isothermal

titration calorimetry (ITC) experiments were performed. Thermodynamic data from these experiments will be presented.

Presenter(s): Xu, Sophia
School: University of Chicago
Session: I.C.3
Title: NEDD4 and Degradation of Connexin 46
Co-Author(s): Peter Minogue, Viviana M. Berthoud, Eric C. Beyer
Advisor(s): Eric C. Beyer

Abstract: The connexin proteins form gap junction channels that support intercellular communication that is critical for the survival of many tissues. In the eye lens, degradation of Connexin 46 (Cx46) disrupts internal circulation of water, ions, and nutrients that is essential for an avascular system, leading to the development of cataracts. In the lenses of mice that develop cataracts, levels of the ubiquitin-protein ligase NEDD4 increased. Since NEDD4 tags membrane proteins for degradation, we studied the impact of NEDD4 expression on Cx46. We transfected HeLa-Cx46 cells with wild-type or mutant (non-functional) NEDD4. NEDD4 and Cx46 were detected by immunofluorescence microscopy. Photomicrographs were captured and analyzed. While 82.5% of cell-cell interfaces contained Cx46 in cells expressing non-functional NEDD4 (compared to untransfected cells), the frequency of interfaces containing Cx46 plaques was 3.33% in cells expressing wild-type NEDD4. This massive– and significant– reduction indicates that NEDD4 promoted the loss of gap junctions, likely by tagging Cx46 for degradation by proteasomes. Our next step will be to determine the interactions between a putative PY motif in Cx46 with NEDD4 to elucidate the role of Cx46 degradation in cataract development.

Presenter(s): Yang, Ruiyan
School: Macalester College
Session: P1.15
Title: Identifying Genes Required for *Enterococcus faecalis* Susceptibility to Inhibition by *Streptococcus mutans*
Co-Author(s):
Advisor(s): Ruth Isenberg

Abstract: *Enterococcus faecalis* is an opportunistic pathogen associated with persistent endodontic infections and is able to survive competition with other microorganisms in polymicrobial environments. *Streptococcus mutans* strongly inhibits *E. faecalis* during co-culture through the production of mutanobactin, a non-ribosomal cyclic lipopeptide that increases *E. faecalis* membrane permeability. However, the *E. faecalis* genes influencing susceptibility to *S. mutans*-mediated inhibition remain largely unknown. To identify these genes, an *E. faecalis* OG1RF 10K transposon library was repeatedly co-cultured with S. mutans for 4 hours. Surviving *E. faecalis* populations were recovered and passaged to enrich for inhibition-resistant mutants. Following repeated selection, the enriched library showed increased survival during *S. mutans* co-culture compared with parental OG1RF. Individual mutants were isolated from the enriched population and screened for inhibition resistance during 4-hour co-culture with *S. mutans*. Several isolates exhibited increased survival relative to parental OG1RF and were selected as candidate inhibition-resistant mutants for further genetic characterization. Together, these results demonstrate that repeated exposure to *S. mutans* enriched the OG1RF transposon library for mutants with increased survival and provide candidate mutants for identifying genetic determinants of susceptibility to *S. mutans*-mediated inhibition.

Presenter(s): Yonzon, Anuva
School: Grinnell College
Session: P3.20
Title: Conformational Stability of the MTHFR Phe184Leu Variant Under Urea-Induced Denaturation Investigated via HDX-MS
Co-Author(s):
Advisor(s): Elaine Marzluff

Abstract: Methylenetetrahydrofolate reductase (MTHFR) is a key enzyme in folate metabolism that catalyzes the production of 5-methyltetrahydrofolate, which supports the remethylation of homocysteine to methionine. Genetic variants of MTHFR may alter protein conformation and dynamics, potentially affecting enzymatic function. This study investigates the structural consequences of the Phe184Leu substitution by comparing the conformational dynamics of wild-type (WT) and Phe184Leu MTHFR. Although phenylalanine and leucine are both hydrophobic amino acids, replacement of the aromatic phenylalanine side chain may alter local interactions and influence protein structure or stability. We hypothesize that Phe184Leu produces detectable changes in MTHFR conformational dynamics relative to WT. Recombinant WT and Phe184Leu MTHFR are being characterized using hydrogen-deuterium exchange mass spectrometry (HDX-MS), which measures differences in backbone amide hydrogen exchange as a probe of protein dynamics and solvent accessibility. Differential deuterium uptake between WT and Phe184Leu will be mapped across the protein to identify regions affected by the substitution. These ongoing studies will provide molecular-level insight into how the Phe184Leu substitution influences MTHFR structure and dynamics and contribute to understanding the effects of genetic variation on MTHFR.

Presenter(s): Yu, Sarah
School: Washington University in St. Louis
Session: P2.11
Title: Small Molecule Inhibition of SERPINB3 as an Anticancer Strategy in Cervical Cancer
Co-Author(s): Liyun Chen, Eric Liu, Ethan Memming, Cliff Luke, Gary Silverman, Stephanie Markovina
Advisor(s): Stephanie Markovina

Abstract: SERPINB3, also known as squamous cell carcinoma antigen (SCCA), is a cysteine protease inhibitor and prognostic marker associated with poor outcomes in cervical cancer. SERPINB3 blocks lysosomal-mediated cell death by inhibiting lysosomal cysteine proteases such as Cathepsin L and S (CatL, CatS) promoting radioresistance, metastasis, and recurrence. Thus, SERPINB3 is a promising target for translational treatment. We hypothesize that SERPINB3-binding small molecules will sensitize tumor cells to radiation therapy (RT) by disrupting its protease inhibitor activity. Cervical cancer cell lines CaSki vector control (CTRL) and SERPINB3-overexpressing (B3OE) cells were treated with SERPINB3-targeting small molecules for four hours, followed by increasing doses of RT. Cell death and viability were measured using LDH and CCK8 assays at 48 and 72 hours post-RT, respectively, and significance assessed with ANOVA analyses. Protease activity assays were performed using fluorogenic CatS substrate conversion following preincubation of recombinant SERPINB3 with candidate small molecules at a 3:1 inhibitor to protease ratio. SERPINB3-OE cells displayed even more radiosensitization by this compound compared to CTRL cells. Additionally, no cytotoxic effects were observed in non-malignant END1 cervical epithelial cells. Collectively, these results suggest

that small molecule approaches may represent promising therapeutic avenues for targeting SERPINB3 to overcome radioresistance in cervical cancer.

Presenter(s): Zeng, Andrew
School: Carleton College
Session: P3.01
Title: An Information-Theoretic Analysis of Gene Expression Dynamics During Mus-musculus Prenatal Development
Co-Author(s):
Advisor(s): Arjendu Pattanayak

Abstract: We use an information-theoretic approach relying on ideas from non-equilibrium thermodynamics to examine the seemingly stochastic gene expression dynamics that give rise to high levels of biological organization and complexity during development. We hypothesize that development should be understood as an irreversible thermodynamic transition between non-equilibrium states; we further use 'Permutation Entropy of Indexed Ensembles' (PI entropy) as an information-theoretic proxy for this transition measuring micro-level information complexity to be compared against macro-level phenotypic developmental stages. Making use of a publicly available mouse transcriptome profiled by single-cell RNA sequencing over the course of prenatal development (from gastrulation to birth), our preliminary results reveal signatures of irreversibility as well as correspondence to macro developmental stages. These results are also visible when we apply PI entropy on PCA-indexed data where genes with similar trajectories are clustered together, revealing consistency across metric spaces. Further work will focus on mapping PI to developmental stages and understanding information complexity in UMAP space.

Presenter(s): Zhang, Alex
School: University of Chicago
Session: I.B.2
Title: The Genetic Basis of Fin Expansion in a Walking Fish
Co-Author(s): Amy Herbert
Advisor(s): Amy Herbert

Abstract: The genetic mechanisms underlying trait gain remain less understood than those underlying trait loss. To study this, we use sea robins — saltwater fish with evolutionary innovations including wing-like pectoral fins and leg-like structures used for walking and tasting. We crossed two species to produce hybrids and explore the genetic basis of species-specific differences, including significant pectoral fin size variation. Allele-specific expression analysis showed that aldh1a2, a retinoic acid synthesis gene, is upregulated in the larger-finned species and is regulated in cis-. Notably, aldh1a2 promotes increased forelimb size in flying fishes while reduced expression correlates with smaller wings in emus. When we disrupted aldh1a2 in sea robins using CRISPR-Cas9 editing, larvae developed without pectoral fins. We identified a candidate cis-regulatory element: an 89bp monomer repeated 400 times immediately downstream of aldh1a2, absent from the smaller-finned species. This monomer is unique to sea robins and forms large arrays genome-wide, suggesting a broad regulatory role. To test its function, we will clone this array upstream of a minimal promoter driving GFP and assay reporter expression. We will also use CRISPR-Cas9 perturbations to assess its in vivo contribution to fin development. Together, these studies illuminate how variation in noncoding elements drive morphological innovation.

Presenter(s): Zhang, Zhiming
School: Grinnell College
Session: P3.02
Title: The Role of Vimentin in the Injury Response of the Zebrafish Heart
Co-Author(s): Kai-Li Updegrove, Delaney Nguyen
Advisor(s): Pascal J Lafontant

Abstract: Vimentin is a type III intermediate filament, highly expressed in neuronal progenitor cells, mesenchymal cells, including endothelial cells and cardiac fibroblasts. Vimentin has been shown to contribute to tissue remodeling in wound repair after injury. We hypothesized that vimentin plays a role in tissue remodeling and regeneration of the zebrafish heart. To determine the spatiotemporal pattern of vimentin expression in zebrafish, we developed a mutant line using CRISPR-generated vimentin-RFP fusion protein. We found that vimentin was highly expressed in the spinal cord and peripheral nerves in developing and adult fish. In the adult zebrafish heart, vimentin is highly expressed in the atrium, along nerve plexi, and in mixed vimentin-nerves filaments in the compact heart's outer layer. However, following heart injury in a model of myocardial infarction, vimentin expression was not expressed within the wound during the remodeling phase of cardiac repair. Our findings suggest that unlike mammalian wound repair, vimentin does not play a direct role in repair and regeneration of the zebrafish heart. Our results suggest possible compensatory mechanisms by a number of vimentin-related genes in zebrafish.

All Students Presenting at
MCMS Undergraduate Research Symposium
Biological and Psychological Sciences
University of Chicago
November 13-14, 2026

Beloit College: Imogen Riter

Carleton College: Ocean Fan, Alice Lin, Dylan MacLehose, Andrew Zeng

Carthage College: Karishma V. Bhatara, Cameron Gruenberg, Edie Hamilton, Lily Kaestner, Layne Rund, Paul Schroeder

Colorado College: Dillon Beaudette, Marisa Brashar, Faith Frazier, Owen Johnson Graves, Sabrina Ng, Anna Peck, Peter Renwick, Josefina Rodriguez Poggio, Marina Seidl, Chenxin Xiang

Grinnell College: Pallavi Baliyara, Adella Catanzaro, Dominic D'Ascenzo, Anh Le, Mariah Mendez, August Ngo, Delaney Nguyen, Chloe Pearl, Anuva Yonzon, Jimmy Zhang

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Hope College: Eleanor Burke, Jacob Caballero, Amelia Lampi, Elliott Peter, Raksa Samnang, Olivia Wiley

Knox College: Jay Kronbach, Monique Micallef, Nga Nguyen, Nhi Nguyen, Almaz Turuspekov

Lawrence University: Tomás Avilés Tamariz, Giang Pham, Sydney Reed, Rebecca Reynolds, Jenna Swanlund

Macalester College: Nour Khayou, Michelle Tung, Ivana Wu, Amy Yang

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Washington University in St. Louis: Yukai Gu, Tierney Johnson, Ruby Koo, Will Li, Yixuan Liu, George Naismith, Jay Patel, Jason Song, Vishnu Srinivasan, Vinisha Tripathi, Serena Wang, Ryan Williamson, Sarah Yu

Participating Faculty at
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Kristina Blanke, Assistant Professor, Department of Biology, Carthage College

Laura Burrack, Professor and Chair, Department of Biology, Gustavus Adolphus College

Tom Clayton, Professor, Knox College, Department of Chemistry

Kimberly Dickson, Associate Professor and Chair, Department of Biology, Lawrence University

Jill Dietz, Professor, Department of Mathematics, Statistics and Computer Science, St. Olaf College

Vince Eckhart, Professor, Department of Biology, Grinnell College

Dustin Haskell, Assistant Professor, Department of Biology, Lawrence University

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

Ruth Isenberg, Assistant Professor, Department of Biology, Macalester College

Allison Nickel, Assistant Professor, Department of Psychology, Beloit College

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

Angel Solis, Assistant Professor, Department of Biology, Carleton College

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