The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 4 & 5, 2022
The University of Chicago

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

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Midstates Consortium for Math and Science
Undergraduate Research Symposium for the Biological Sciences and Psychology
At The University of Chicago
November 4 & 5, 2022

Program Schedule

Friday, November 4

1:00 pm – 5:00 pm	Registration at Best Western Hyde Park 4900A Lake Shore Dr., Chicago, IL 60615	Best Western Inn Lobby
4:45 & 5:00 pm	Shuttle to University of Chicago campus	Best Western Inn Lobby
5:30 pm – 5:40 pm	WELCOME Michael Glotzer Professor, Molecular Genetics and Cell Biology University of Chicago Ed Hansen, Director Midstates Consortium for Math and Science Professor Emeritus, Geology & Environmental Science Hope College	Biological Sciences Learning Center (BSLC) 115
5:40 pm – 6:30 pm	Keynote Lecture Elizabeth S. Heckscher Assistant Professor of Molecular Genetics and Cell Biology University of Chicago	BSLC 115
6:45 pm – 7:45 pm	Dinner Buffet	Gordon Center for Integrative Science (GCIS) Atrium
8:00 pm – 8:45 pm	Janet Anderson Lecture Kim Kandl Professor of Biology St. Olaf College	BSLC 115
Following lecture	Group Picture	BSLC 115
9:00pm	Shuttle & vans back to hotel	

Saturday, November 5

Begins at 7:00 am	Breakfast	Best Western Inn Lobby
7:45/8:00 & 8:15 am	Shuttle to campus leaves /all depart for University of Chicago Campus Those with vans or cars will drive to campus. Others will take the shuttle. NOTE: There will be a room for storage of luggage and posters at the meeting site	Best Western Inn Lobby
8:00am – 8:30 am	Set-up for poster session 1 Check computer set-up for oral presentations	Gordon Center for Integrative Science (GCIS) Atrium
8:30 am – 9:30 am	Session 1 Poster Presentations (24)	GCIS Atrium
9:30 am – 9:45am	Break, remove posters, check set-up for oral presentations in respective rooms	GCIS Atrium
9:45am -10:45 am	Session I Oral Presentations of Student Papers Session I.A: (Jean Porterfield) Session I.B: (Elena Tonc) Session I.C: (Shane Heschel) Session I.D: (John Kennedy)	Kersten Room 101 Room 103 Room 105 Room 120
10:55 – 11:50 am	Graduate Student Panel: Life in Graduate School & Faculty Panel for Post Docs & grad students Meredith Course, Colorado College, Kimberly Dickson, Lawrence University, Vince Eckhart, Grinnell College, Edward Hansen, Hope College	Room 120 Room 105
12:00 pm – 1:00 pm	Lunch Buffet	*Baker Dining Hall*
1:00 pm – 1:15 pm	Set-up posters for session 2	GCIS Atrium
1:15 pm – 2:15 pm	Session 2 Poster Presentations (24)	GCIS Atrium
2:15 pm – 2:30 pm	Break, remove posters, check set-up for oral presentations in respective rooms	
2:30 pm – 3:30 pm	Session II Oral Presentations of Student Papers Session II.E: (Steven Henle) Session II.F: (Vicki Isola) Session II.G: (Vince Eckhart) Session II.H: (Kim Kandl)	Kersten Room 101 Room 103 Room 105 Room 120
3:30 pm -3:45 pm	Break, set-up for poster session 3	GCIS Atrium
3:45 pm – 4:45 pm	Session 3 Poster Presentations (24)	GCIS Atrium
4:45 pm – 5:00 pm	Meeting Concludes: Remove posters, boxed dinners to go, shuttle pick up and complete online evaluations	GCIS Atrium

2022 Keynote Lecture

Dr. Elizabeth S. Heckscher

Assistant Professor of Molecular Genetics and Cell Biology
Committee on Development, Regeneration, and Stem Cell Biology and Committee on Genetics, Genomics, and Systems Biology
University of Chicago

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Title: *How circuits develop starting from stem cells*

Abstract: How do neural circuits self-assemble starting from stem cells? In complex brains, a small pool of neural stem cells generates a large diversity of neurons, which ultimately wire together to generate neural circuits. Neural circuits are composed of neurons connected to each other by synapses in stereotyped and specific patterns. Essentially, circuits are networks that process information; their collective activity underlies sensation, cognition, and action. Neural circuits are the fundamental functional units of complex brains. A stem cell is a multi-potent cell that divides asymmetrically to self-renew, maintaining its multi-potency, and to generate a differentiated cell. Neural stem cells divide multiple times to produce a set of neurons that are referred to as a "lineage". Within a lineage, neurons are born in a stereotyped sequence, and they are non-identical. Neurons can be named by their birth order, for example, "first-born", "second-born", and collectively this is referred to as a neuron's "temporal identity". Lineages are fundamental developmental units of complex nervous systems. My lab uses the Drosophila nerve cord as a model to understand how neural stem cell lineages produce functional circuits. The nerve cord is much like the vertebrate spinal cord: It processes somatosensory stimuli (like pain, touch, self-movement), and it generates complex patterns of muscle contractions that underlie movement and behavior; at the gross anatomical level, spinal cords and nerve cords are left-right symmetrical and segmented; at the level of gene expression, many neural genes are conserved. Thus, studies of the Drosophila nerve cord are likely to reveal principles broadly applicable to other neural systems. However, the Drosophila nerve cord is uniquely tractable in that it is the only model in which there are both complete maps of stem cells and circuits at cellular and synaptic resolution. I will discuss how my lab has exploited the experimental power of Drosophila embryos and larvae to characterize relationships between stem cell lineage (i.e., the orderly production of a sequence of neurons with different identities) and mature circuits with well-defined anatomical and functional connectivities.

2022 Janet Andersen Lecture

Broadening our understanding of fat storage in eukaryotic lineages

Professor Kim Kandl
Associate Professor of Biology
St. Olaf College, Northfield, MN

Abstract: Nearly all cells store fat in organelles called lipid droplets. Driven by connections to human metabolic disorders and biofuel production, interest in these organelles has grown significantly over the past 20 years, but most of what we know about lipid droplets comes from studying just a few organisms - mostly yeast and animals. How do evolutionarily divergent organisms cope with the need to store and utilize fat? Three years ago, several faculty in the biology department at St. Olaf College began a collaborative project to study lipid droplet formation and function in Tetrahymena thermophila, a single-celled freshwater ciliate representing an underexplored branch of the evolutionary tree. This project has involved dozens of students pursuing independent research and hundreds of students in the intermediate genetics and cell biology courses. Our research findings so far are exciting and intriguing, and an additional benefit has been the formation of a large, collaborative research community of students and faculty within our department.

About Professor Kandl Dr. Kandl has a vigorous undergraduate research program having worked with 62 research students in the last 4 years alone! According to the writers of her nomination letter "she gets to know her research students' strengths, goals, and career aspirations so that she can tailor her mentoring to best fit their needs", and they particularly noted her efforts on the part of low income, first generation, and BIPOC students. Her dedication to the craft of teaching is evident in her record as an engaged and skilled teacher, in the testimony of her students, and in her service on the Education Committee of the American Society of Cell Biology. Her research and curriculum development are broadly interdisciplinary, and thus is particularly appropriate for an award that honors the spirit and legacy of Janet Andersen.

Information about the Janet Andersen Lecture Award

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

Oral Session I Schedule

SESSION I.A: 9:45 – 10:45 a.m. Room: Kersten 101 Moderator: Jean Porterfield			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1	Lilian A Lopez	Beloit College	Perceptions of Creative Arts Therapists: Reaching Adolescents of Color during the Pandemic
I.A.2	Nhi Hoang	Hope College	Welcome to My House: The Relationship between One's Hospitality and Preference for Houses Exteriors
IA.3	Shawn Lam Thu Nguyen My Le	Knox College	Differential associations between incompleteness and disgust domains
I.A.4	Beck Baird	Knox College	Creation and validation of the observable gender expression scale (OGES)

SESSION I.B: 9:45 – 10:45 a.m. Room: Kersten 103 Moderator: Elena Tonc			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1	Julia Sheehan-Klenk	Grinnell College	Tumor immunologic response activated by β- and α-particle emitting radionuclides is influenced by dose rate
I.B.2	Ben Glazer	Lawrence University	Perturb-seq in A375 human malignant melanoma cells with NK-92 co-culture
I.B.3	Violet Wu	University of Chicago	Tumor Microenvironment Nutrients Constrain Tumor Lipogenesis by Impairing the Activity of SREBP Transcription Factors
1.B.4	Mayher Kaur	University of Chicago	Metabolic rewiring elucidates metastatic behavior in non-small cell lung cancer

SESSION I.C: 9:45 – 10:45 a.m. Room: Kersten 105 Moderator: Shane Heschel			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1	Amelia Wernsing	Gustavus Adolphus College	Changes in the phosphorylation state of p38 MAP kinase accompany RCH induction in Drosophila melanogaster
I.C.2	Emma Stock Kristin Simphoukham	Gustavus Adolphus College	Genome Engineering in Arabidopsis Thaliana to Investigate Environmental Stress Response
I.C.3	Difei Jiang	Lawrence University	Mechanism of PTH Ca2+ sensing on G protein interactions with PTH1

SESSION I.D: 9:45 – 10:45 a.m. Room: Kersten 120 Moderator: John Kennedy			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.D.1	Rachel Trebesch Kristin Martens	Gustavus Adolphus College	Role of mRNA Structure in Gene Regulation by sRNA
I.D.2	Aditya Yelamali	Washington University in St. Louis	Streptavidin-drug conjugates streamline identification of optimal toxic payloads for antibody-based hematopoietic stem cell transplantation conditioning
I.D.3	Jacqueline Gomez-Villa	University of Chicago	Elucidating the effect of chemical chaperones on ATF6 activity in CALRins5 mutant MPN
I.D.4	Anjali Kotamarthi	University of Chicago	Identification of Collateral Lethal Gene Targets in -7/del(7q) Myeloid Neoplasms

Oral Session II Schedule

SESSION II.E: 2:30 – 3:30 p.m. Room: Kersten 101 Moderator: Steven Henle			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1	Emma Rudisel	Hope College	Use of mass spectrometry-based proteomics to study the mitochondrial transcription machinery
II.E.2	Raisa Fatima Perla Viera	Lawrence University	Super-resolution Imaging of Depolymerizing Microtubule Ends
II.E.3	Katherine Miao	University of Chicago	Real-Time Processing of Ultrasound Images to Assess the Outcomes of Ablation Therapies
II.E.4	Emily Shi	University of Chicago	BACH1 modulates the hypoxia response through chromatin organization in Triple Negative Breast Cancer Cells

SESSION II.F: 2:30 – 3:30 p.m. Room: Kersten 103 Moderator: Vicki Isola			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1	Sarah Grimes	Hope College	House sparrow (Passer domesticus) and house finch (Haemorhous mexicanus) active space across an urbanization gradient
II.F.2	Subhiksha Srinivasan	Lawrence University	Exploring the infectious cause underlying dangerous, pain-related behaviors in horses

II.F.3	Bianca Campagnari	University of Chicago	Notch and the Development of Neural Circuits in the Motor System of Drosophila
II.F.4	Linda Nduwimana	Hope College	Can you hear me?: Anthropogenic influence on Auditory Sensitivity of the House Sparrow (Passer domesticus)

SESSION II.G: 2:30 – 3:30 p.m. Room: Kersten 105
Moderator: Vince Eckhart

Session #	Presenter Name	Institution	Title of Presentation
II.G.1	Maya Lines	Lawrence University	Microglial response to autism risk gene perturbation
II.G.2	Neha Damaraju	Washington University in St. Louis	Characterizing the functional roles of bacterial TIR domain proteins
II.G.3	Rhea Shah	University of Chicago	Evaluating the efficacy of stapled peptide inhibitors in dampening regulatory T cell functioning
II.G.4	Isabella Cisneros	University of Chicago	A Comparative Study of Aristaless1 and Aristaless2 Expression During Heliconius Butterfly Development

SESSION II.H: 2:30 -3:30 p.m. Room: Kersten 120
Moderator: Kim Kandl

Session #	Presenter Name	Institution	Title of Presentation
II.H.1	Nidhi Talasani	University of Chicago	Effect of butyrate on tight junction protein and IL-22 expression
II.H.2	Thomas Li	University of Chicago	BACH1 is activated under hypoxia in a proline hydroxylation-dependent manner in Triple Negative Breast Cancer
II.H.3	Emma Montgomery	University of Chicago	Development of transgenic zebrafish model with human insulin
II.H.4	Eliza Wiener	University of Chicago	Understanding the function of neuronal cell surface proteins: Examining human teneurin-2 autoproteolysis

Poster Sessions Schedule

Poster Session P1: 8:30 – 9:30 a.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Avital Fogel	University of Chicago	Novel Biomarkers and Interferon Signature in Progressive Multiple Sclerosis
P1.02	Amira Siddique	Knox College	On the clinical relevance of comparative jaw joint biomechanics across mammals
P1.03	Rebecca Dowe	Carthage College	A Bright Future: Light Sheet Microscopy
P1.04	Arich Fruehling Daniel Bloedow Maya Arakaki	St. Olaf College	Latitudinal variation in key traits of Asclepias syriaca
P1.05	Lily Guo Caitlin Kim Samuel Lee	Colorado College	The Predatory Behavior of Acinetobacter Bacteria Using A Type VI Secretion System
P1.06	Kanon Nakajima	Macalester College	Therapeutic effect of coordinated reset deep brain stimulation on parkinsonian gait
P1.07	Jie Wang	Washington University in St. Louis	Loss of Stathmin-1 Diminishes Hematopoietic Stem Cells' Self-Renewal Capacity in Mice
P1.08	Luca Keon	Colorado College	Investigating Plant-Pollinator Responses to a Warming Climate in the Alaskan Arctic
P1.09	Koffi Amegble	Grinnell College	Chelator Activity of Sirtinol Induces Iron Metabolic Perturbations in NSCLC
P1.10	Ryan Erdmann	Hope College	Effects of POLRMT and MRPL12 Post Translational Modifications on Mitochondrial Protein Synthesis
P1.11	Taeen Jidaan	Lawrence University	Researching Xap5 Expression in C. elegans
P1.12	Marissa Zintel	Lawrence University	Stabilizing Porous Protein-DNA Co-Crystals via Auto-Disulfide Cross Linkages
P1.13	Trinity Pirrone	Macalester College	Overlapping Populations of VIP and CCK Neurons Coexpress the Y1 Receptor in the Inferior Colliculus
P1.14	Audrey Kim	University of Chicago	Racial differences in Quantitative MRI and Histology Reveal Value of DCE MRI for African American
P1.15	Isabella Dobrinski	St. Olaf College	Trinucleotide Bulged-RNA Thermal Stability in Aqueous Glycine-Betaine, Urea, Proline Solutions

Poster Session P1: 8:30 – 9:30 a.m. - Continued			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.16	Hannah Koehlert	Carthage College	Determination of the Factors Predicting Burnout in College Athletes
P1.17	Meghna Bagchi	Colorado College	Alternative splicing variations of Rbfox2 in response to cellular stress
P1.18	Jen Becker	St. Olaf College	Genetically engineering Tetrahymena thermophila DNA to understand the role and function of lipid droplet proteins
P1.19	Jessica Zhong	University of Chicago	Characterizing The Diversity Of Fungal-Algal Associations In Alaskan Lichens
P1.20	Ved Patel	Washington University in St. Louis	The extent and function of SVEP1 glycosylation
P1.21	Morten Lee	University of Chicago	Chemotherapeutic Nanoscale Coordination Polymers (NCPs) for Active Transport to Tumors
P1.22	Franccesca Mamani	Beloit College	Perceptions of Art Therapists and Educators About Art as a Therapeutic Process
P1.23	Kevin Tovar	Macalester College	Characterizing methylisothiazolinone mediated changes in immune activities of murine labial fibroblasts
P1.24	Olivia Dossett	Colorado College	Tamarix Shade Intolerance in Fountain Creek
P1.25	Karina Mak	University of Chicago	Predictive Value Of Auscultatory Crackles For Survival In Patients With Fibrotic Lung Disease
P1.26	Jia Wu	University of Chicago	The Role of Heat Shock Protein 25 (HSP25) on Intestinal Wound Healing

Poster Session P2: 1:15 - 2:15 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Bobby Lerch	Beloit College	Expressing and purifying CbpA for studies into the elucidation of bacterial Hsp70 JDP interaction
P2.02	Julia Owens	Carthage College	Facultative interactions between ants, aphids, and black-eyed pea
P2.03	Ebru Ermis	University of Chicago	Role of the BLT2 receptor in macrophage migration during Type 1 Diabetes pathogenesis
P2.04	Melanie Barksdale	Colorado College	Single-Cell Analysis of RNA Expression following Virus Infection
P2.05	Benjamin Reister	St. Olaf College	Bcd1 localizes to the selected meiotic nucleus in Tetrahymena thermophila conjugation, giving rise to pronuclei.
P2.06	Evan Rao Eve Karowe Leighton Graham	Colorado College	Sex Differences in Morphological Development in Flammulated Owls
P2.07	Avery Cardeiro	Grinnell College	Locating the Neuropeptide NAAG2 in the Mouse Neuromuscular Junction Using a Novel Antibody
P2.08	Isabeau Brathwaite-Burnett	University of Chicago	Examining Racial, Ethnic, and Sex Differences as Predictors of Cannabis Use Disorder Treatment Retention
P2.09	Natalia Quizena	Hope College	Characterization of novel peptide binding in HUVEC cells using fluorescence polarization approach
P2.10	Madeline Taylor	Lawrence University	Exploring the Rhizosphere Microbiome of Hydroponically Grown Leafy Greens
P2.11	Brian Sohn	Washington University in St. Louis	Probing the drivers of Staphylococcus aureus biofilm protein amyloidogenesis and countering biofilms with Hsp104 disaggregases
P2.12	Michelle Vu	Lawrence University	The Honeybee's Thermal Response to Changing Temperature
P2.13	Bedilia Centeno	Macalester College	The effects of e-cigarette vapor on pulmonary function and bone composition in mice
P2.14	Emily Jacobs	University of Chicago	DNA damage-induced immune response in Aspergillus Fumigatus infected human pluripotent stem cell-derived lung model
P2.15	Brandon Fernandez	St. Olaf College	Mapping Microbiome Turnover With Bacteroides

Poster Session P2: 1:15 - 2:15 p.m. - Continued			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.16	Zoe Gonzalez	Grinnell College	Characterization of phenotypic expression of inx-12 and inx-13 mutants during cellular migration and intercalation
P2.17	Margaret Dickey	St. Olaf College	Presumptive Diagnosis of Alcohol as the Etiology of Altered Mental Status in Collegiate EMS
P2.18	Xiu Mei Golden	Macalester College	Investigating central sensitization in a murine model of vulvodynia
P2.19	Lari Rays Wahba	Washington University in St. Louis	Sex-Differences in Seasonal Adaptation of Circadian Behaviours
P2.20	Reese Lavajo	Lawrence University	Influence of algal productivity and predation risk on Daphnia spp. migratory patterns: comparison across lakes
P2.21	Jason Tran	Macalester College	Enhanced peroxidase activity in a directed evolution designed hemin-based enzyme
P2.22	Caitlin Kim	Colorado College	Fluorinated L-Phe dipeptides may inhibit bacterial growth and biofilm formation of P. aeruginosa
P2.23	Leidan Chen	University of Chicago	Characterization of simple structural variation patterns around enhancer regions in cancer genomes
P2.24	Sarah Young Claire Wulf	Carthage College	Tracking regeneration of the zebrafish optic nerve using the optokinetic response
P2.25	Eva McCord	University of Chicago	Designing of an auxin-induced degron (AID) system targeting and depolymerizing nuclear actin in mESCs
P2.26	Courtney Brandt	University of Chicago	Assessment of the Predictive Performance of Five DNA Methylation Clocks Across 9 Tissue Types

Poster Session P3: 3:45 - 4:45 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Jerry Ngo	Beloit College	Is CLIP Fooled by Optical Illusions?
P3.02	Lexi Menendez Abby Groszek	Carthage College	Passive Acoustic Monitoring of Cao-Vit Gibbons (Nomascus nasutus) Utilizing Multilaterations of Vocalizations
P3.03	Sandhini Agarwal	University of Chicago	Evaluating the Transcriptional Activity of Putative FOXF1 Enhancers in the Presence and Absence of FOXF1
P3.04	Ian Johnson	Colorado College	Presence of pathogenic variants in circular RNA of presenilin 1 and 2
P3.05	Gloriah Omwanda Mady Chen	Macalester College	Mast Cell-Fibroblast Co-Cultures to Investigate Cellular Interactions in Mouse Model of Vulvodynia
P3.06	Hayden Bhavsar	Grinnell College	Lectin reactivity effectively Identifies parenchymal and biliary architecture of the Zebrafish (Danio rerio) Liver
P3.07	Katie Lillemon	Gustavus Adolphus College	Inhibition of proteolytic activation of SARS-CoV-2 spike protein in human cardiomyocytes
P3.08	Sarah Grimes	Hope College	An investigation into the effects of forest bathing on the mental health of college students
P3.09	Elizabeth Strandberg	St. Olaf College	Lipid droplet analysis in starved Tetrahymena thermophila: ERG6p expression and localization
P3.10	Aasma Haider	Lawrence University	Role of Estrogen in Genome Regulation in the Developing Human Brain
P3.11	Ani Gribbin	Macalester College	Development of New Visual Discrimination Task in Mice
P3.12	Beth Harshberger	Carthage College	Exploring CO2 Sensitivity at Varying Resolutions in BI and NBI Humans
P3.13	Maya Olcer	University of Chicago	Characterizing SARS-CoV-2 Spike Protein Specific Memory B Cells after Vaccination through Flow Cytometry and ELISpot.
P3.14	Sid Layesa	Macalester College	Role of Rab14 in autophagy
P3.15	Athziri Marcial Rodríguez	St. Olaf College	Understanding the Genetic Architecture of Congenital Hydrocephalus using Whole Genome Sequencing

Poster Session P3: 3:45 - 4:45 p.m. - Continued			
P3.16	Joey Kaczor	University of Chicago	Characterizing the level of a small RNA involved in Vibrio cholerae defense against bacteriophage infection
P3.17	Lecheng (Joshua) Lyu	St. Olaf College	Differential Pathway Analysis of Early vs. Late Recurrences in ER+ Breast Cancer
P3.18	Ken Soe	Washington University in St. Louis	Molecular determinants of Matrin-3 toxicity and misfolding, and suppression of Matrin-3 toxicity by engineered protein disaggregases
P3.19	Courtney Lasserre	Washington University in St. Louis	Zombie Dads: The Effects of Male Guppy Coloration on Posthumous Reproductive Success
P3.20	Ahmed Aldirderi Abdalla Ahmed Alexandra Jabbarpour	Macalester College	Legacies of Redlining: HOLC Grades Influence Past and Present Water Quality
P3.21	Adrianna Hudyma	Lawrence University	Creating a constitutively active version of the enzyme PlpX
P3.22	Sarah Senese	Colorado College	Populus deltoides leaf morphology and developmental age
P3.23	Alejandra Bergquist	University of Chicago	Classifying the Shark MHC Class I-like Molecule UGA through Structural Characterization
P3.24	Ziyu Ren	University of Chicago	Impact of language on promoting blood donation
P3.25	Madeleine Suydman Lee	University of Chicago	Botanicals & Bacterium: An Ethnobotanical Approach to the Modern Antibiotic Resistance Crisis

Abstracts for all Sessions
Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, University of Chicago
November 4-5 2022

All abstracts (poster and oral) are listed alphabetically by presenter last name. Abstracts with multiple presenters appear only once with first listed presenter.

Presenter(s): Ahmed Aldirderi Abdalla Ahmed, Alexandra Jabbarpour
School: Macalester College
Session: Poster P3.20
Title: Legacies of Redlining: HOLC Grades Influence Past and Present Water Quality
Advisor(s): Anika Bratt, Environmental Studies, Macalester College
Co-Author(s): CJ Denney, Paula Furey and Anika Bratt

Abstract: Redlining is a housing discrimination policy that helped further segregation efforts in residential neighborhoods in the 1930s. Historically redlined neighborhoods have more impervious surfaces and less vegetation, as well as higher air pollution. The effects of historical redlining on water quality and water ecosystems are understudied. These effects were investigated in the Twin Cities Metro Area (TCMA) by intersecting Home Owners' Loan Corporation (HOLC) maps grades with publicly available water monitoring data from the Minnesota Pollution Control Agency (MPCA) and collected data from fieldwork. Intersected data from the MPCA yielded a record ranging from 1978-2021 spanning 53 stations. A one-way ANOVA was applied; it showed that water bodies in D-graded neighborhoods had significantly higher concentrations of nitrogen and phosphorus than in A-graded neighborhoods. Surface water samples were collected from 24 small water bodies across TCMA. Chlorophyll-a (a proxy for algal biomass), total nitrogen, and total phosphorus were analyzed colorimetrically. There was no significant difference in the field samples between average chl-a concentrations across HOLC grades, however, C grade neighborhoods did have less chl-a than A, B, or D grade neighborhoods. D neighborhoods had more duckweed than any other, however, this difference was not significant with a p-value of 0.0818.

Abstract: Presenter(s): Sandhini Agarwal
School: University of Chicago
Session: Poster P3.02
Title: Evaluating the Transcriptional Activity of Putative FOXF1 Enhancers in the Presence and Absence of FOXF1
Advisor(s): Ivan P. Moskowitz, Departments of Pediatrics, Pathology, and Human Genetics**,** University of Chicago
Co-Author(s): Joshua Theisen, Matthew Stocker

Abstract: Congenital heart disease (CHD) is one of the leading causes of neonate mortality. While mutations in specific genes are known to cause some forms of CHD, the mechanistic connection between these genes and dysregulation of cardiac development is poorly understood. Hedgehog signaling in the second heart field has been shown to induce the expression of FOXF1, a forkhead box transcription factor, integral to cell differentiation. However, we do not understand how FOXF1 regulates these genes. In this investigation, we tested the transcriptional activity of putative FOXF1 target enhancers in the presence and

absence of FOXF1. These putative enhancers were identified by ChIP-seq. We selected high-confidence enhancers based on multiple criteria, including binding of the cardiac transcription factors TBX5, NKX2-5, and GATA4, and the presence of the activating histone mark H3K27ac in mature cardiomyocytes. To evaluate the FOXF1-dependent activity of these enhancers, we performed luciferase assays in HL-1 cardiomyocytes. Our preliminary results show that FOXF1 can act as either an activator or repressor of transcription in a context-dependent manner. However, the mechanisms underlying this novel bifunctionality remain a mystery. Further study of these putative FOXF1-dependent enhancers will advance our understanding of how FOXF1 selectively regulates target enhancers to control cardiac development.

Abstract: Presenter(s): Koffi Amegble
School: Grinnell College
Session: Poster P1.09
Title: Chelator Activity of Sirtinol Induces Iron Metabolic Perturbations in NSCLC
Advisor(s): Charvann Bailey, Biology,Grinnell College
Co-Author(s): Michael Petronek, Khaliunna Bayanbold, Ann Tomanek-Chalkley, Bryan Allen, Douglas Spitz

Abstract: A distinctive feature of cancer is the upregulation of sirtuin proteins. Sirtuins are class III NAD+-dependent deacetylases involved in processes such as aging, cell cycle regulation, and oxidative stress. Sirtinol, a sirtuin (SIRT) 1 and 2 specific inhibitor, is a recent anti-cancer agent that sensitizes cancer cells to oxidative stress. SIRTs 1 and 2 are overexpressed in several types of cancers including lung cancer. Preliminary data showed that sirtinol was cytotoxic to two NSCLC cell lines, H1299 and A549. However, the exact mechanism of sirtinol's cytotoxicity remains unknown. Recent studies show that sirtinol may possess iron chelator properties. Cancer cells have greater rates of Fe uptake via transferrin receptor (TfR)-mediated endocytosis resulting in increased Fe content. Cancer cells develop greater iron dependence to enhance cellular proliferation, DNA replication, etc. These observations led to our interest in sirtinol's potential iron chelator properties for treating cancer. This study showed sirtinol depleted labile iron pools prompting the upregulation of TfR protein in A549 cells. These trends were not observed in H1299 cells. The results highlight the fundamental genetic differences that may exist between H1299 and A549 cells and offer a novel mechanism of how sirtinol kills NSCLC cells.

Abstract: Presenter(s): Maya Arakaki, Daniel Bloedow, Arich Fruehling
School: St. Olaf College
Session: Poster P1.04
Title: Latitudinal variation in key traits of Asclepias syriaca
Advisor(s): Emily Mohl, Biology and Education, St. Olaf College
Co-Author(s): Anna Rothfusz

Abstract: Asclepias syriaca, or common milkweed, has been declining for decades. To best support milkweed, conservationists should consider whether the milkweed is locally adapted to its native environment. When non endemic seeds are introduced, the expression of traits like phenology, growth and defense may not be well adapted to the new geographic region. To study this, we conducted a provenance trial with seeds sourced from 20 different

populations across the growing range to identify genetic differences among milkweed populations. Plants from higher latitudes initially grew taller than those from lower latitudes, but growth rate decreased as the season progressed. Higher latitude plants also tended to have more leaves and produce more clones. We infer that plants from northern latitudes could initially grow faster to maximize the shorter growing season. As climate change raises temperatures, understanding how milkweed adapts to novel environments will continue to be increasingly important to study.

Abstract: Presenter(s): Meghna Bagchi
School: Colorado College
Session: Poster P1.17
Title: Alternative splicing variations of Rbfox2 in response to cellular stress
Advisor(s): Lori Sussel, University of Colorado at Anschutz Campus
Co-Author(s): Nicole Moss

Abstract: Pancreatic β cells affected by Type 1 Diabetes become dysfunctional due to autoimmune attack and consequently, the homeostatic regulation of blood glucose is disrupted. Recent studies have shown that there are significant changes in the mRNA regulation of β cells under stress. Specifically, Rbfox2, which codes for the splicing regulator protein RBFOX2, is alternatively spliced itself in β cells under stress conditions. To better understand the expression of Rbfox2 under cellular stress, our goal was to induce and measure cell stress and to analyze splicing patterns of Rbfox2 under stressed conditions using mRNA and protein analysis. To induce cellular stress we used varying concentrations of cytokines as well as variable concentrations of glucose, to mimic diabetes-related stressors. Once we determined the optimal stressed condition, we analyzed the exon expression of Rbfox2. We found that there was variability between exon expression of Rbfox2 in cytokine-treated cells when compared to our control. In glucose-treated cells, there was a greater overall expression of Rbfox2 in the low glucose condition. These findings indicate that there is a difference in Rbfox2 expression under cellular stress, and we can continue research to understand how specific isoform expression of Rbfox2 may relate to Type 1 Diabetes.

Abstract: Presenter(s): Beck Baird
School: Knox College
Session: Oral I.A.4
Title: Creation and validation of the observable gender expression scale (OGES)
Advisor(s): Andrew Hertel, Psychology, Knox College

Abstract: A three-part study was run to create a modern suitable measure for external gender expression. External gender expression is the immediately observable expression of gender. The strongest gender expression measure to date (BSRI; Bem, 1974) includes aspects of gender expression that are not immediately observable and not applicable for life in the 21st century (see Hoffman, 2001 for review). Study one asked transgender participants

to report aspects of observable gender expression which they considered important. Study two asked cisgender participants for confirmation that these aspects of observable gender expression were important in "gendering," or immediately determining the perceived gender of, individuals. Through these two studies, the Observable Gender Expression Scale (OGES) was developed. It aims to capture immediately observable gender expression within masculinity, femininity, and "other" score categories through participants' endorsements of the frequency with which their physical appearance includes stereotypically masculine or feminine attributes (e.g. carrying a purse, muscularity). Study three used exploratory factor analysis and correlational analysis to create the final OGES and its scoring methods. We validated the OGES against an adapted version of the Gender Identity Scale (Ho & Mussap, 2019), which captured participants' perceptions of how others view their gender expression.

Abstract: Presenter(s): Melanie Barksdale
School: Colorado College
Session: Poster P2.04
Title: Single-Cell Analysis of RNA Expression following Virus Infection
Advisor(s): Linda van Dyk, Immunology & Microbiology, University of Colorado Anschutz School of Medicine
Co-Author(s): Kyra Noell, Ashley Tseng, Linda van Dyk, Eric Clambey

Abstract: The gammaherpesviruses cause lifelong infections and can result in inflammatory disease and tumorigenesis. Gammaherpesvirus infection of macrophages is poorly understood, regarding potential for lytic replication, latency, or a combination. MHV68 (small animal gammaherpesvirus model) infection of macrophage and fibroblast cell lines show equivalent viral entry, however, only the macrophage cells show a defect in viral replication and viral gene expression. These findings are consistent with little gene expression in all cells, or with gene expression limited to only a few cells (heterogeneity). To analyze viral gene expression, we applied single-cell analysis of RNA using fluorescent probes detected by flow cytometry. Probes were specific to 1) abundant viral non-coding RNAs that are expressed through all phases of infection and to 2) a viral late RNA only expressed in late lytic infection. Viral gene expression in macrophage cells was low relative to control fibroblast cells, with a greater decrease in the late viral mRNA. This experiment demonstrated how single cell analysis can be used to investigate heterogeneous responses within cell populations.

Abstract: Presenter(s): Jen Becker
School: St. Olaf College
Session: Poster P1.18
Title: Genetically engineering Tetrahymena thermophila DNA to understand the role and function of lipid droplet proteins
Advisor(s): Jean Porterfield, Biology, St. Olaf College
Co-Author(s): Samantha Dodoo, Thomas Quello

Abstract: Lipid droplets (LDs) are found across all eukaryotic organisms and some bacteria. Most of the knowledge about LDs is derived from research on animals, plants, and fungi; however, these groups represent a relatively small slice of biodiversity. We study LDs in Tetrahymena thermophila (Tet), a ciliate, to provide a stronger context for understanding how

specific LD-associated proteins impact lipid storage and metabolism. Putative LD-associated proteins were discovered in a previous proteomic screen, and we use molecular cloning techniques to engineer plasmid DNA molecules that contain modified versions of these protein-coding genes. These engineered molecules are ultimately incorporated into the genomes of Tet cells, where they will either knock out or endogenously fluorescently tag expression their protein. This allows us to assess how the Tet cell behaves without the protein, or use fluorescence microscopy to observe where the protein functions normally. Several proteins, including some that are characterized in other organisms like yeast and some that are hypothetical genes in the Tet genome, are currently at various stages of this research workflow. More broadly, this research contributes to the comparative knowledge about lipid droplets, which can be used to better understand the mechanisms of fat-associated disease in humans.

Abstract: Presenter(s): Alejandra Bergquist
School: University of Chicago
Session: Poster P3.23
Title: Classifying the Shark MHC Class I-like Molecule UGA through Structural Characterization
Advisor(s): Erin Adams, Biochemistry and Molecular Biology, University of Chicago

Abstract: The adaptive immune system present in mammals began evolving about 500 million years ago in jawed vertebrates, specifically in cartilaginous fish where MHC-I molecules, which play a vital role in the body's immune response as they allow T-cells to detect infected cells, seemed to have first appeared evolutionarily. Curiously, some nonclassical MHC class I-like molecules have been found to be absent in bony fish and amphibians but present in shark ancestors. However, not all shark nonclassical MHC class-I like molecules have been identified. Through comparative immunology and biochemical research, we have found that a specific shark MHC molecule known as UGA, which is unknown in its structure and function, clusters with other types of classical and nonclassical MHC molecules as well as MR1, a mammalian MHC that presents small molecules. Identifying whether UGA presents lipids, small molecules, or peptides could further our understanding of its function and classification as possibly another nonclassical MHC class I-like molecule. Through protein purification and crystallography, we have successfully purified and crystallized UGA. Future laser processing and imaging of UGA crystals will further allow us to identify its structure and the type of molecule it presents.

Abstract: Presenter(s): Hayden Bhavsar
School: Grinnell College
Session: Poster P3.06
Title: Lectin reactivity effectively Identifies parenchymal and biliary architecture of the Zebrafish (Danio rerio) Liver
Advisor(s): Pascal Lafontant, Biology, Grinnell College
Co-Author(s): Zoe Robinson, Matthew Benson, Pascal J. Lafontant

Abstract: Lectins are carbohydrate-binding proteins that display both broad and specific binding to glycoconjugates expressed on cell membranes of various tissue, including the liver. Lectins have proved of substantial utility as histochemical, biochemical, and clinical

diagnostic tools in human and mouse models of liver health and diseases. However, little is known about their applicability in zebrafish liver. We have investigated the binding patterns of twelve commonly used lectins in zebrafish liver to ascertain their potential usefulness. We found that four of these lectins, Tomato lectin (TL), wheat germ agglutinin (WGA), concanavalin A (Con A), and Jacalin show strong reactivity to various cells, including hepatocytes, to sinusoidal, to parenchymal and biliary structure of the zebrafish liver. Another five lectins display moderate reactivity, while three others, including Ulex europaeus (UAE), Bandeirarea simplicifolia (BS lectin), Dolichis biflorus (DBA) lectins displayed no to low reactivity to liver parenchymal components. Moreover, several of these binding patterns could also be observed in the closely related species Devario malabaricus. Importantly, we found that TL reacted specifically to glycoconjugates at every level of the adult zebrafish biliary network and as early as the first week post-fertilization. Altogether, these studies provide evidence that lectins can serve as important tools in studies of structural and functional characteristics of the developing and adult zebrafish liver.

Abstract: Presenter(s): Courtney Brandt
School: University of Chicago
Session: Poster P2.26
Title: Assessment of the Predictive Performance of Five DNA Methylation Clocks Across 9 Tissue Types
Advisor(s): Brandon Pierce, Department of Public Health and Department of Genetics, University of Chicago
Co-Author(s): Mark Richardson, Kathryn Demanelis, Muhammad Kibriya, Farzana Jasmine

Abstract: As lifespan has increased, age related diseases are increasingly prevalent, causing strain on individuals and healthcare systems. Biologically, aging is associated with the deterioration of tissue function and with the increased variability of cellular regulation pathways. Aging-related changes in DNA methylation have been shown to be associated with susceptibility to ageing associated disorders and mortality.DNA methylation data have recently been used to develop DNA methylation (DNAm) clock algorithms. These “epigenetic clock” algorithms use methylation data to estimate age and various indicators of health and lifespan. Most of the DNAm clocks developed to date were trained (and subsequently test/applied) using DNAm obtained from blood cells. Thus, it is unknown how these clocks perform across diverse tissue types. To assess differences across tissues with respect to biological age predictions, we used DNAm data from the GTEx (Genotype-Tissue Expression) Project to obtain epigenetic age estimates for five popular DNAm clocks (Horvath, Hannum, GrimAge, PhenoAge, and EpiTOC) across 9 different tissue types. We characterize DNAm aging estimates across tissues in terms of the (1) distribution of DNAm clock estimates, (2) strength of each clock’s association with age, (3) correlation of clock estimates between tissue types, and (4) associations of participant characteristics with clock estimates.

Abstract: Presenter(s): Isabeau Brathwaite-Burnett
School: University of Chicago
Session: Poster P2.08
Title: Examining Racial, Ethnic, and Sex Differences as Predictors of Cannabis Use Disorder Treatment Retention

Advisor(s): Erin A. McClure, Addiction Sciences (Psychiatry), Medical University of South Carolina
Co-Author(s): Nathaniel L. Baker, Rachel L. Tomko, Aimee L. McRae-Clark, Kevin M. Gray

Abstract: Treatment trials for cannabis use disorder (CUD) lack racial, ethnic, and sex representation. This limits the generalizability of study results and reduces access to effective therapies for underrepresented groups. No literature to date has explored if underrepresented groups are being retained in research at the same rates as their non-minority counterparts. This secondary analysis identifies racial, ethnic, and sex differences in CUD treatment trial retention using a combined data set of seven pharmacotherapy treatment trials for CUD conducted at MUSC (N=948). The final dataset is 30% female; 27% African American; 11% Hispanic/Latinx. Mixed effects logistic regression models were utilized to assess differences in study completion across minority groups. In adjusted models, Non-Hispanic White participants were more likely to complete treatment than all others combined (66% vs. 59%; OR=1.4 (1.0, 1.9); p=0.04). There were no overall differences between males and females (62% vs. 66%; OR=0.8 (0.6, 1.1); p=0.17). Results suggest that sex differences do not independently contribute to study retention, but racial and ethnic minorities have lower retention rates- showing that one of the barriers to diversity in research is retention, not just recruitment.

Abstract: Presenter(s): Bianca Campagnari
School: University of Chicago
Session: Oral II.F.3
Title: Notch and the Development of Neural Circuits in the Motor System of Drosophila
Advisor(s): Elizabeth Heckscher, Department of Molecular Genetics & Cell Biology, University of Chicago

Abstract: Many questions remain in developmental neurobiology on how neural circuits develop. The transcription factor Notch regulates cell fate in many Drosophila neural stem cell lineages. We will test if Notch activity is necessary and sufficient to alter neural circuit membership for motor neurons descended from two lineages called NB3-1 and NB7-1. In these lineages, the neuroblast divides to produce a new neuroblast and an intermediate, which divides into two neurons that both inherit Notch. Only one neuron inherits Notch's inhibitor. The neuron with the inhibitor becomes Notch OFF. The other becomes Notch ON. This repeats for multiple neuroblast divisions to produce Notch ON and Notch OFF hemilineages. The hemilineages differ in gene expression, morphology, and circuit membership. In NB7-1, only Notch ON cells become motor neurons. In NB3-1, only Notch OFF cells become motor neurons. Experiments suggest that misexpressing inhibition-resistant Notch in NB7-1 doubles the number of NB7-1 descended motor neurons. We will test if these extra motor neurons functionally contribute to neural circuits. After expressing inhibition-resistant Notch in NB3-1, we expected to lose neuromuscular synapses. Sometimes we did, but sometimes we found unexpected synapses that we hypothesize are due to compensating innervation from neighboring neurons. Our future experiments will test this hypothesis.

Abstract: Presenter(s): Avery Cardeiro
School: Grinnell College
Session: Poster P2.07

Title: Locating the Neuropeptide NAAG2 in the Mouse Neuromuscular Junction Using a Novel Antibody
Advisor(s): Clark Lindgren, Biology, Grinnell College

Abstract: N-acetyl-aspartyl-glutamate (NAAG) is the most abundant neuropeptide in the mammalian nervous system and has been implicated in the treatment of schizophrenia and neuropathic pain. However, not much is known about the NAAG-family peptide N-acetyl-aspartyl-glutamyl-glutamate (NAAG2). The possibility for NAAG2 to be similarly abundant and important makes it an intriguing polypeptide to study. By using protein immobilization affinity purification, this study was able to purify a novel anti-NAAG2 serum for use in immunofluorescence. Confocal microscopy using this serum was able to uncover initial evidence of NAAG2 in the mouse neuromuscular junction. The resulting images were difficult to quantify due to nonspecific binding by secondary antibodies. This research presents a case for future studies which can build upon these procedures to further investigate NAAG2 in the mouse neuromuscular junction.

Abstract: Presenter(s): Bedilia Centeno
School: Macalester College
Session: Poster P2.13
Title: The effects of e-cigarette vapor on pulmonary function and bone composition in mice
Advisor(s): Todd Vanderah, Pharmacology, University of Arizona
Co-Author(s): Kelly Karlage, Joseph Trejo

Abstract: In recent years, electronic cigarettes (e-cigs) have become increasingly popular, especially among adolescents, due to their promotion as a “healthier” alternative to cigarettes. Although previous studies have shown that e-cigs have harmful effects on multiple body functions in humans and animals, there is still limited research addressing the impacts e-cigs have on lung and bone health. Our study used a mice model to determine the effects of e-cig vapor on bone composition by examining fat percentage (Fat%) and bone mineral density (BMD), and on pulmonary function, by assessing breaths per minute (BPM), minute volume (MVb), and tidal volume (TVb). We exposed the vehicle group to e-cig vapor containing 95% propylene glycol and 5% glycerin (PG/G) for 12 weeks and the acute and chronic groups to PG/G + nicotine for 1 and 12 weeks, respectively. BPM, MVb, and TVb were immediately taken after exposure through plethysmography. Fat% and BMD were obtained from DXA scans. The results showed that acute and chronic exposure to PG/G + nicotine reduced fat percentage but had little effect on BPM, MVb, TVb, or BMD.

Abstract: Presenter(s): Mady Chen, Gloriah Omwanda
School: Macalester College
Session: Poster P3.05
Title: Mast Cell-Fibroblast Co-Cultures to Investigate Cellular Interactions in Mouse Model of Vulvodynia
Advisor(s): Elena Tonc, Biology, Macalester College

Abstract: Mast cells are tissue-resident immune orchestrators of local inflammatory responses by immune and tissue cells. They are also the main mediators of maladaptive immune responses such as allergies and are involved in several pain conditions. Vulvodynia

is one such condition with an increase in local mast cell density. It affects ~10% of women-identifying individuals and is characterized by chronic, debilitating pain in the vulvar region, but its etiology is unknown. Increased risk of developing vulvodynia has been associated with allergies, such as exposure to the chemical methylisothiazolinone (MI). We established a murine model of vulvodynia, demonstrating that repeated MI exposure leads to prolonged mast cell-dependent genital hypersensitivity. In addition to mast cells, fibroblasts play both an inflammatory and homeostatic role in the tissues. Fibroblasts from vulvodynia patients have an elevated inflammatory cytokine profile. Thus, in the present study, we examined mast cell and fibroblast interactions to elucidate how the interplay between the two cell types might lead to the establishment of chronic pain by measuring the production of inflammatory mediators TNF-α, IL-1β, and IL-6. We also examined the impact of therapeutic approaches such as Gleevec and THC on mast cell and fibroblast viability.

Abstract: Presenter(s): Leidan Chen
School: University of Chicago
Session: Poster P2.20
Title: Characterization of simple structural variation patterns around enhancer regions in cancer genomes
Advisor(s): Lixing Yang, Ben May Department for Cancer Research, The University of Chicago

Abstract: Structural variations (SV), also known as genomic rearrangements, are a significant source of genomic instability and genetic diversity. However, their roles in gene regulation and disease susceptibility are largely unknown, as well as the molecular mechanisms for SV generation. We hypothesize that the accessible and active nature of gene regulatory elements makes them prone to generate SVs, which may subsequently alter target gene expression. This computational project aims to characterize the patterns of simple SVs mapped to enhancer regions and hypothesizes related molecular mechanisms. SV data are acquired and processed from cancer genome sequencing projects, including PCAWG, ICGC, Hartwig, and POG, and enhancer data are downloaded from ENCODE and NCBI GEO. Pancancer analysis validated the enrichment of SV breakpoints around enhancer regions. Subsequent tumortype analysis revealed heterogeneity across tumortypes, and SV-type analysis highlighted the enrichment of duplications in most tumor types. SV mutational signature analysis demonstrated that middle-sized duplications are significantly enriched around enhancer regions in all datasets. Future work will investigate the specific enhancer activity that drives the generation of middle-sized duplications.

Abstract: Presenter(s): Isabella Cisneros
School: University of Chicago
Session: Oral II.G.4
Title: A Comparative Study of Aristaless1 and Aristaless2 Expression During Heliconius Butterfly Development
Advisor(s): Marcus Kronforst, Department of Ecology & Evolution, University of Chicago
Co-Author(s): Erick Bayala, Darli Massardo, Nicholas VanKuren

Abstract: The gene aristaless is a homeodomain transcription factor associated with appendage patterning and extension during insect embryonic development. In Lepidoptera, a gene duplication event gave rise to two versions of the gene: aristaless1 (al1) and aristaless2

(al2). Our recent work showed al1 is still related to this ancestral appendage formation role, but also controls the switch between white and yellow pigmentation in Heliconius butterfly wings. However, whether al2 is also functional with respect to the ancestral appendage role and if it has any relevance to pigmentation remains unclear. Characterizing al2 and comparing it to what we know from al1 will inform our understanding of functional divergence between these gene copies following their gene duplication event. Our work shows that al2 is also associated with appendages. Furthermore, our work highlights that al1 and al2 have evolved temporally distinct expression domains, with al1 shifted earlier and al2 shifted to later time points of embryonic development. Finally, we also describe differences in the cellular localization between al1 and al2, both of which exhibit clear differences with respect to nuclear colocalization. These results suggest that al1 and al2 may have functionally diverged through the evolution of shifted temporal expression patterns and subcellular locations.

Abstract: Presenter(s): Neha Damaraju
School: Washington University in St. Louis
Session: Oral II.G.2
Title: Characterizing the functional roles of bacterial TIR domain proteins
Advisor(s): Aaron DiAntonio, Developmental Biology, Washington University in St. Louis

Abstract: The ancient family of Toll/interleukin-1 receptor (TIR) domain proteins are hydrolases of the essential metabolic cofactor nicotinamide adenine dinucleotide (NAD+). The role of animal and plant TIR domains within various cell death pathways has been well studied in recent work. However, though a handful of enzymatically active bacterial TIR domains have been identified, the functional significance of their activity has not been well characterized. In this study, we examined the representation and expressed NADase activities of TIR domains across 7,000 bacterial proteomes. Enzymatic activity was observed for TIR domains with diverse amino acid sequences and taxonomic origins. In-vitro assays of TIR domain activity showed that active TIR domains cleave NAD+ to produce the previously identified catabolites adenine diphosphate ribose (ADPR), cyclic adenine diphosphate ribose (cADPR), and variant cADPR (v-cADPR-x). Our assay discovered that TIR domains also produce a novel variant cADPR catabolite (v-cADPR-y). The first report of v-cADPR-y production was made in HopAM1, a TIR domain from the phytobacterial pathogen Pseudomonas syringae. We determined that HopAM1 exploits TIR domain activity to sabotage NAD+ metabolism and promote virulence in plants. Our in-vitro assays also identified a number of v-cADPR-x producing TIR domains within the human gut microbiome. We discovered that the abundance of v-cADPR-x producing TIR domains was significantly higher in the microbiomes of healthy infants as compared to those of undernourished infants, as were the levels of v-cADPR-x in fecal samples. These results indicate that v-cADPR-x may be an informative biomarker of healthy gut microbiome development.

Abstract: Presenter(s): Margaret Dickey
School: St. Olaf College
Session: Poster P2.17
Title: Presumptive Diagnosis of Alcohol as the Etiology of Altered Mental Status in Collegiate EMS
Advisor(s): Kevin Crisp, Biology, St. Olaf College

Abstract: Altered mental status (AMS) is a common emergency call on college campuses, and for Collegiate-Based Emergency Medical Service (CBEMS) providers, this chief complaint is frequently found secondary to alcohol intoxication. Although it is important to consider alcohol when determining the etiology of AMS patients, a presumptive diagnosis of intoxication without a thorough differential diagnosis can delay or prevent vital treatments of life threats. The purpose of this study is to determine if CBEMS providers make premature diagnoses of alcohol intoxication as the etiology of AMS due to underutilization of key AMS assessments. This study was conducted as a retrospective analysis of de-identified Patient Care Reports (PCRs) submitted between 2015-2022 from one service. Each PCR was compared to predetermined criteria for AMS and examined for evidence of alcohol consumption and key assessments for AMS differential diagnosis (blood glucose, pupils, SpO2, head trauma assessment, temperature, stroke assessment). Differential diagnoses were underutilized on all AMS calls with respect to key assessments; furthermore, there was a 15% decrease in assessments completed when alcohol consumption was reported compared to when it was not ($p < 0.05$). These results may suggest an underestimation by CBEMS providers of the seriousness of AMS and intoxication as medical emergencies.

Abstract: Presenter(s): Isabella Dobrinski
School: St. Olaf College
Session: Poster P1.15
Title: Trinucleotide Bulged-RNA Thermal Stability in Aqueous Glycine-Betaine, Urea, Proline Solutions
Advisor(s): Jeffery Schwinefus, Chemistry, St. Olaf
Co-Author(s): Stephanie Amann Otessa Olsen

Abstract: This study investigated the thermal stability of four trinucleotide bulged motifs of the HIV-TAR 1 RNA core helix in aqueous cosolute solutions using thermal denaturation monitored by ultraviolet-absorbance spectroscopy at 280 nm. The RNA unfolding equilibrium constant dependence on the molality of the cosolutes glycine betaine, proline, and urea was used to quantify cosolute stabilization or destabilization of the RNAs. Relative to the core helix, all four different trinucleotide bulged RNAs were less thermally stable. The cosolutes destabilized the core helix and trinucleotide bulged RNAs to different extents. This result suggests the different surface areas exposed during bulged trinucleotide RNA unfolding can be distinguished by these three cosolutes, promoting their use as probes of biopolymer surface area changes. Our data showed that glycine betaine and proline were the most effective probes in differentiating between trinucleotide bulged RNAs during an unfolding event.

Abstract: Presenter(s): Olivia Dossett
School: Colorado College
Session: Poster P1.24
Title: Tamarix Shade Intolerance in Fountain Creek
Advisor(s): Shane Heschel, Organismal Biology and Ecology, Colorado College

Abstract: The invasive species, Tamarix ramosissima, has been rapidly colonizing riparian ecosystems throughout the southwestern US, including areas along Fountain Creek in Colorado. Many of these areas are riparian forests dominated by native cottonwoods (Populus deltoides) and willows (Salix exigua). In recent years, however, there have been

high levels of cottonwood mortality, most likely due to drought stress and climate change, which has reduced the canopy coverage in these forests. The purpose of this study was to examine how tamarisk functional traits and morphology respond to varying light exposure to further understand tamarisk physiology and advance conservation management efforts. We measured photosystem efficiency, chlorophyll content, and stomatal conductance as well as number of flowering branches, number of stems, and stem diameter in two sites of differing light exposure along Fountain Creek. The study is based on the following research questions: How do changes in light exposure from canopy mortality impact the functional traits of tamarisks? How does light exposure impact allocation to stem and reproductive biomass in tamarisks?

Abstract: Presenter(s): Becca Dowe
School: Carthage College
Session: Poster P1.03
Title: A Bright Future: Light Sheet Microscopy
Advisor(s): Steven Henle, Neuroscience, Carthage College

Abstract: Within the last decade, light sheet fluorescence microscopy has gained traction as a method of imaging biological specimens. The microscope's laser light is formed into a thin sheet, in which only a single plane of the specimen is illuminated at a time and together form a full 3D image. This method is gaining traction primarily because of its low phototoxicity, due to single-plane illumination, which is significantly less harmful for the specimen compared to other imaging methods. After comparing a few options for software to run the microscope, I opted for Micro-Manager because of its simplicity, and began configuring the hardware. The software and hardware also need to be coordinated through a triggerscope, which optimizes the speed of the imaging sequences. This is a process that is ongoing, where eventually the microscope will be used to study visual system development in zebrafish.

Abstract: Presenter(s): Ryan Erdmann
School: Hope College
Session: Poster P1.10
Title: Effects of POLRMT and MRPL12 Post Translational Modifications on Mitochondrial Protein Synthesis
Advisor(s): Kristin Dittenhafer-Reed, Chemistry and Biochemistry, Hope College
Co-Author(s): Alexis Erickson, Hope Markley, Matthew Gross, Katelynn Paluch

Abstract: Mitochondria contain their own genome that encodes 13 subunits required for oxidative phosphorylation (OXPHOS). The nuclear genome encodes other OXPHOS subunits along with machinery needed for transcription and translation. The regulation of transcription in the mitochondria is not well understood. We hypothesize that post-translational modifications (PTMs) of proteins required for mitochondrial transcription may alter their function and serve to regulate gene expression. PTMs alter the function of proteins required for mtDNA transcription. We characterized post-translationally modified amino acids identified by mass spectrometry on the mitochondrial RNA polymerase (POLRMT) and ribosomal protein L12 (MRPL12) using in vitro and cellular studies. Site-directed mutagenesis was performed to create MRPL12 and POLRMT mutants mimicking these PTMs. Proteins were purified and mtDNA binding affinity was assessed using fluorescence polarization. POLRMT and MRPL12 mimics were also overexpressed in human cell lines. DNA, RNA, and

protein were isolated to determine mtDNA content, transcript level, and OXPHOS subunit abundance, respectively. Cell viability was also measured. mtDNA content is largely unchanged across POLRMT mutants, while transcript levels are variable. Western blot analysis showed POLRMT is successfully overexpressed, and CYTB protein levels decreased in HeLa cells transfected with POLRMT mutants.

Abstract: Presenter(s): Ebru Ermis
School: University of Chicago
Session: Poster P2.03
Title: Role of the BLT2 receptor in macrophage migration during Type 1 Diabetes pathogenesis
Advisor(s): Raghu G. Mirmira, Biological Sciences Division, The University of Chicago
Co-Author(s): Isabel Casimiro, Raghu G. Mirmira, Ryan M. Anderson

Abstract: Type 1 Diabetes (T1D) is an autoimmune disease, associated with β cell destruction. Catalytic production of 12-HETE by 12-LOX promotes macrophage migration to pancreatic islets, which contributes to T1D pathogenesis. BLT2 has been identified as a low-affinity receptor for 12-HETE, suggesting a proinflammatory role in the islet. Here, we have used zebrafish models to examine the roles of BLT2 in macrophage migration during tissue injury. The 12-LOX pathway is conserved in zebrafish with two BLT2 orthologues: blt2a, blt2b. First, to investigate whether BLT2 mediates macrophage migration, we used morpholinos (MO) to knockdown BLT2 expression and then performed tailfin injury assays. We found significantly fewer macrophages at the injury site following blt2a, but not blt2b MO injection. We rescued the blt2a MO phenotype with blt2a mRNA co-injection, and observed a similar diminished macrophage migration phenotype upon using a small molecule inhibitor of BLT2, affirming that the observed effects were indeed due to knockdown of blt2a. Lastly, we performed islet injury assays to determine if BLT2a mediates macrophage migration to injured islets. We observed fewer macrophages at the islet following blt2a knockdown. Taken together, our results suggest that BLT2a, but not BLT2b, is an important contributor to macrophage migration during tissue injury.

Abstract: Presenter(s): Raisa Fatima, Perla Viera
School: Lawrence University
Session: Oral II.E.2
Title: Super-resolution Imaging of Depolymerizing Microtubule Ends
Advisor(s): Douglas S. Martin, Physics Department, Lawrence University

Abstract: The cytoskeleton is composed of protein filaments that play major roles throughout the cell's life cycle. One type of these filaments consists of microscopic tubular (25 nm diameter) structures called microtubules. Microtubules are able to generate force during cell division, anaphase, to pull apart chromosomes. The force-generating structure of microtubules attached to kinetochores remains unclear, and hence multiple models for the mechanism of force-generation by microtubules during anaphase exist. We use optical super-resolution microscopy (stochastic optical reconstruction microscopy, STORM) to image the ends of bare microtubules to explore the structure of depolymerizing microtubules. In this talk, we present images and analysis of these microtubule ends.

Abstract: Presenter(s): Brandon Fernandez
School: St. Olaf College
Session: Poster P2.15
Title: Mapping Microbiome Turnover With Bacteroides
Advisor(s): Seth Walk, Microbiology, Montana State University
Co-Author(s): Zea Cain, Paul van Erp, Seth Walk

Abstract: Members of the human gut microbiome can be classified as transient (short-lived) or resident (long-lived). The goal of this project is to obtain a better understanding of the variability of bacterial turnover in order to further detail relationships with and between bacterial populations in the digestive system. Through this work, more potent and efficient antibiotics can be developed to target bacterial infections or to more efficiently establish beneficial gut microbiome members. By utilizing selective and differential growth media, PCR, and 16S rRNA encoding gene sequencing we are attempting to isolate Bacteroides, the most abundant bacterial genus in humans, from donated fecal samples. We expect to develop a repeatable protocol to successfully isolate and genetically identify resident and transient strains with the overall goal of quantifying strain turnover within human subjects**.**

Abstract: Presenter(s): Avital Fogel
School: University of Chicago
Session: Poster P1.01
Title: Novel Biomarkers and Interferon Signature in Progressive Multiple Sclerosis
Advisor(s): Anthony Reder, Neurology, University of Chicago Medicine
Co-Author(s): Xuan Feng

Abstract: Multiple sclerosis is an inflammatory neurodegenerative disease with decreased immune control and subnormal type I interferon (IFN) signaling responses. IFN-B therapy reduces attacks, delays disease progression, and corrects abnormal IFN-B signaling in relapsing-remitting MS (RRMS). However, most RRMS patients develop secondary progressive MS (SPMS), where attacks wane, progression is relentless, and the benefits of IFN-B treatment diminish for unclear reasons.

RNA and serum were obtained from 59 patients' immune cells. We investigated differential gene expression and compared serum protein levels.

Gene and protein data suggest that SPMS patients have less aberrant gene expression than RRMS patients, despite being more progressive. This was demonstrated in both global gene expression patterns and specific pathways, such as wnt/B-catenin that regulates immune cell infiltration across the blood-brain barrier. In addition, massive dysregulation of a family of chemosensory genes provides another mode of distinction and evidence of heightened immune reactivity in RRMS.

The reduction of aberrant gene signaling in the transition from RRMS to SPMS may coincide with loss of regulatory and repair mechanisms and help explain progressive resistance to immunomodulatory therapies. These findings suggest new biomarkers for SPMS as well as target pathways for developing future MS therapies**.**

Abstract: Presenter(s): Ben Glazer

School: Lawrence University
Session: Oral I.B.2
Title: Perturb-seq in A375 human malignant melanoma cells with NK-92 co-culture
Advisor(s): Livnat Jerby, Genetics, Stanford University

Abstract: Perturb-seq is the combination of pooled CRISPR-based screens with single-cell RNA-seq to identify the transcriptional profiles of cells across a range of genetic perturbations. This method is a powerful tool for elucidating the pathways contributing to phenotypic differences associated with specific cells, and in cancer cells it could reveal pathways for novel therapeutic treatments. In this project, 12 genes of interest were chosen by comparing previous gene-specific studies in human melanoma models with novel spatial transcriptomic data. The selected genes are expected to significantly promote or inhibit malignant cell survival under NK cell selection. I generated a lentivirus stock containing 42 sgRNA plasmids and used this to create a 12-gene knockout pool in A375 human malignant melanoma cells. This A375 knockout pool was then incubated in NK-92 cell co-culture or in monoculture, and surviving A375 cells were prepared for scRNA-seq. The resulting scRNA-seq data will be analyzed for knockouts associated with survival under NK cell selection and related transcriptomic changes. Future work should investigate the mechanisms of the most significant genes from these data.

Abstract: Presenter(s): Xiu Mei Golden
School: Macalester College
Session: Poster P2.18
Title: Investigating central sensitization in a murine model of vulvodynia
Advisor(s): Elena Tonc, Biology, Macalester College
Co-Author(s): Mady Chen, Gloriah Omwanda, Devavani Chatterjea

Abstract: A history of allergies is linked to the development of the chronic pain condition, vulvodynia. Our lab has established an allergen-driven mouse model of vulvodynia using a standard chemical preservative, methylisothiazolinone (MI). Female mice were sensitized with MI on the flank and subsequently challenged with MI or vehicle for 10 consecutive days on the labial skin. Repeated challenges induced transient production of inflammatory mediators and long-term sensitivity, in the absence of active inflammation, in the genital region of mice. As inflammation has been linked with chronic pain development, we have examined the expression of inflammatory mediators that can lead to central sensitization in the spinal cords of challenged mice at various time points after 10 challenges. MI-treated mice showed an upregulation of IL-6 mRNA expression when compared to the vehicle control as well as a downregulation of IL-1β mRNA. We are currently examining the expression of additional markers such as TLR-4, CGRP, and NK-1 also implicated in central sensitization by quantitative PCR and immunofluorescence. We are also exploring how multiple routes of MI-exposure may impact hyperalgesia in the genital region of mice to better model various environmental exposures in humans.

Abstract: Presenter(s): Jacqueline Gomez-Villa
School: University of Chicago
Session: Oral I.D.3
Title: Elucidating the effect of chemical chaperones on ATF6 activity in CALRins5 mutant MPN

Advisor(s): Shannon E. Elf, Ben May Department of Cancer Research, University of Chicago
Co-Author(s): Nicole S. Arellano, Harrison S. Greenbaum, Michele Ciboddo, Deborah Rodriguez, Amy Chen, Lulu Allie, Jonathan Dowgielewicz, Alex Rosencrance

Abstract: Myeloproliferative neoplasms (MPNs) are clonal hematopoietic disorders that result in the overproduction of mature myeloid cells. MPNs include polycythemia vera, essential thrombocythemia (ET), and primary myelofibrosis (PMF). About 40% of patients with ET and PMF have heterozygous mutations in the gene calreticulin (CALR), which is a gene that encodes a calcium (Ca2+)-binding protein in the endoplasmic reticulum (ER). CALR has two primary functions: calcium binding ability and chaperone function. The chaperone function of CALR means that it is a critical effector of the unfolded protein response (UPR), a stress response pathway that is activated when there is a detection of an abundance of misfolded/unfolded proteins. The 5-bp insertion mutations in exon 9 of CALR exhibit a loss of chaperone function in patients with myeloproliferative neoplasms. The loss of chaperone function has been hypothesized to be attributed to structural interferences of calreticulin's C-terminal end. However, CALRin5 may also lose its chaperone function due to its dominant negative function since FLAG-CALRins5 has been confirmed to bind to wild-type CALR. The two primary aims of this study is to determine which hypothesis is accurate and to investigate further if tauroursodeoxycholic acid (TUDCA) can restore ER chaperone ability and induce apoptosis in CALRins5 cells.

Abstract: Presenter(s): Zoe Gonzalez
School: Grinnell College
Session: Poster P2.16
Title: Characterization of phenotypic expression of inx-12 and inx-13 mutants during cellular migration and intercalation
Advisor(s): Vida Praitis, Biology, Grinnell College

Abstract: During C. elegans development, the highly coordinated cell rearrangement process called cell intercalation is important for tissue development. While some aspects of intercalation are known, less is known about its developmental control and regulation in vivo. Prior work in the Praitis lab identified a set of genes as potential candidates for roles in migration. I sought to examine phenotypes of migrating cells in strains carrying mutations of identified candidate genes noah-2, inx-12, and inx-13. Utilizing a series of genetic crosses, we introduced the AJM-1::GFP marker to visualize cell position during intercalation and later stages in strains carrying mutations in the candidate genes. Confirmation utilized phenotype analysis of embryonic viability and PCR testing. Initial microscopy imaging analysis indicated no significant differences in cell positioning due to inx-12 and inx-13 loss-of-function alleles. Slight variance in cell size appeared during intercalation stages, potentially indicative of a specific role for inx-12 and inx-13 in these cells, though further quantitative imaging analysis is necessary. Further analysis of cell positioning in inx-12 and inx-13 loss-of-function strains should be conducted in order to better understand causes for observed embryonic and larval lethality and to gain greater understanding of the role these genes play in cellular migration.

Abstract: Presenter(s): Leighton Graham, Evan Ra, Eve Karowe
School: Colorado College
Session: Poster P2.06

Title: Sex differences in Morphological development in Flammulated Owls
Advisor(s): Brian Linkhart, Organismal Biology and Ecology, Colorado College

Abstract: Flammulated Owls (Psiloscops flammeolus) are insectivorous migratory owls that typically breed in Ponderosa Pine ecosystems in North America. Like many other raptors, Flammulated Owls exhibit reverse sexual size dimorphism, wherein female birds are larger than their male counterparts. Prior research has not identified the developmental stage at which female owls' growth outpaces that of the males due to the need for a long-term comprehensive dataset. We seek to address this lack of research by analyzing owlet growth rates and blood sex data in order to reveal sex-based growth trends in owlets. Over the span of about 40 years, data has been collected on various broods of owlets, measuring their weight and feather growth over the duration of their nestling period. In the past 20 years, blood samples have also been collected from the owlets and analyzed in a lab to determine the sex of the owlets. By combining the blood sex data and growth data we are able to reveal trends in owlet growth based on their sex.

Abstract: Presenter(s): Ani Gribbin
School: Macalester College
Session: Poster P3.11
Title: Development of New Visual Discrimination Task in Mice
Advisor(s): Timothy Buschman, Neuroscience, Princeton University
Co-Author(s): Caroline Jahn

Abstract: Visual discrimination is a key function for behavior. It allows us to discern the differences between visual stimuli and select the correct behavior for a stimulus. This ultimately contributes to our wider understanding of our environment. Learning to discriminate between different stimuli is thought to involve the visual cortex as well as other cortical areas, but how learning emerges from the coordination of different brain regions is mostly unknown. Here, we create a new paradigm to look at the emergence of visual discrimination in mice, showing the various stages of learning and training. The experimental set up pairs a motor task (running on a wheel) with visual input, such that mice run along a virtual corridor with visual stimuli appearing and disappearing from the screen at the speed at which they run. In this visual corridor, mice must discriminate between different visual stimuli to obtain a reward. We show that mice learned the task through different stages of training, and we quantified learning throughout the training at the individual and group level. Future work will examine the emergence of visual discrimination throughout the dorsal cortex using wide-field calcium imaging and contribute to a larger study into the neural basis of executive control.

Abstract: Presenter(s): Sarah Grimes
School: Hope College
Session: Oral II.F.1
Title: House sparrow (Passer domesticus) and house finch (Haemorhous mexicanus) active space across an urbanization gradient
Advisor(s): Kelly Ronald, Biology, Hope College
Co-Author(s): Eliza Lewis, Linda Nduwimana, Kelly Ronald

Abstract: Urbanization and the accompanying auditory pollution can affect avian communication and song propagation. This study investigates how anthropogenic

disturbances alter the ability of birds to communicate. Specifically, this study examined differences in active space, or the maximum distance a receiver can detect a signal, across an urbanization gradient. This study utilized the house sparrow (Passer domesticus) and the house finch (Haemorhous mexicanus), as both species can inhabit urban areas and rely on vocal cues from conspecifics. Recorded songs were played back with a speaker at urban, rural, and suburban locations in Holland, MI, and recorded at distances up to 100 meters. This set-up mimicked bird communication, with the speaker acting as the sender, the song as the signal, and the recorder as the receiver. We expected songs in rural areas to have a larger active space compared to urban environments due to lower noise pollution. Preliminary results suggest a two way interaction between species and urbanization level ($F=3.13$, $df=2,207$, $p = 0.044$). This suggests that the communication of certain species birds may be inhibited depending on the level of urbanization in their habitat.

Abstract: Presenter(s): Sarah Grimes
School: Hope College
Session: Poster P3.08
Title: An investigation into the effects of forest bathing on the mental health of college students
Advisor(s): Alyssa Cheadle, Benjamin R. Meagher, Psychology, Hope College

Abstract: Mental health issues are a growing problem for college students. Attention Restoration Theory (Kaplan & Kaplan, 1989) has been applied to examine how nature exposure restores mental health. Previous studies have found affective benefits following forest bathing, or spending time in nature. However, few studies have investigated forest bathing in relation to positive psychosocial variables or potential moderators of this relationship. This quasi-experimental study will examine differences in mental health (anxiety, depression, stress), positive psychosocial factors (flourishing, resilience, satisfaction with life), and potential moderators in a sample of Hope College students exercising in an urban setting versus a nature setting. Participants will take two, 90-minute walks each week for two weeks. They will walk in an urban area or a forest during week 1 and in the other setting the following week. At the end of each walking session and each week, participants will provide information on their mental health and positive psychosocial resources. We expect improvements in mental health and positive psychosocial factors following forest bathing. We will examine moderators including participants' historical and current connection to nature, and socioeconomic status. The results of this study will provide valuable information regarding the benefits of green space access for college students.

Abstract: Presenter(s): Abby Groszek, Alexis Menendez
School: Carthage College
Session: Poster P3.02
Title: Passive Acoustic Monitoring of Cao-Vit Gibbons (Nomascus nasutus) Utilizing Multilaterations of Vocalizations
Advisor(s): Angela Dassow, Biology, Carthage College

Abstract: Since their rediscovery in 2002, the cao-vit gibbon population has remained critically endangered and thus, a limited amount of information regarding their vocalization and general behaviors has been discovered. The use of Passive Acoustic Monitoring has been utilized as a non-invasive method to monitor individuals and wildlife populations alike.

In this study, twenty GPS-synced audio recording units were deployed in a limestone karst rainforest in Northern Vietnam. The goal of the deployment was to determine the feasibility of finding precise locations of these individuals. Approximately 3,000 hours of audio data was collected and manually marked to locate times in which male or female calls were received at the units. The results of the multilateration analysis successfully generated a map showing the locations that different groups of cao-vit gibbons were calling. Future goals that have arisen from this research include gathering data for long-term research on gibbon communication, intraspecific behavioral interactions, as well as the potential development of technologically based solutions for applied conservation.

Abstract: Presenter(s): Lily Guo, Caitlin Kim, Sam Lee
School: Colorado College
Session: Poster P1.05
Title: The Predatory Behavior of Acinetobacter Bacteria Using A Type VI Secretion System
Advisor(s): Phoebe Lostroh, Molecular Biology, Colorado College

Abstract: Acinetobacter baumannii is a harmful pathogenic bacteria commonly implicated in widespread hospital infections due to its resistance to antibiotic treatments and high propensity for natural transformation1. Previously, it was confirmed that Acinetobacter baylyi (BD4), a related but harmless soil-dwelling bacteria is able to kill Escherichia coli (E. coli) through a similar Type VI secretion system (T6SS)2. To better understand the mechanics of T6SS and importance of twitching motility for predation in Acinetobacter, this study investigates BD4 predation of thirteen lab-cultivated streptomycin-resistant soil isolates (StrR). In comparisons of pairwise encounters between BD4 and StrR, two potential prey were identified: #2302 (Salmonella bongori) and #2308 (unknown soil isolate). Competent BD4 bacteria were transformed with DNA extracted from ADP1 strain to obtain antibiotic resistance as well as genetic mutations involving either their twitching motility (comB-F) or Type VI secretion system functioning (evpG). Antibiotic-treated LB-succinate agar plates were used to quantitatively compare predation across conditions. Of the tested StrR, BD4 was found to be an effective predator of #2308, with manipulations in twitching motility and T6SS functioning reducing predation ability. In contrast, BD4 is not an effective predator of #2302 and genetic manipulations of either system increased predation rates.

Abstract: Presenter(s): Aasma Haider
School: Lawrence University
Session: Poster P3.10
Title: Role of Estrogen in Genome Regulation in the Developing Human Brain
Advisor(s): Donna Werling, Genetics, UW Madison

Abstract: Autism spectrum disorder (ASD) has a higher prevalence in males than females (4:1). Hormone exposure during pubertal maturation can allow steroid hormones to create sex differences in the brain during a critical period. The regulation of gene expression through sex steroid hormones, such as estrogen and ERα binding to DNA, are principal factors for sex differential biology in the brain. However, it is unclear if estradiol plays a mechanistic role in ASD. To address this, we examined genomic regions associated with ERα binding and open chromatin regions in response to estrogen exposure in mouse neurons from subcortical brain regions. We evaluated the proximity of estradiol-responsive open chromatin regions in human mid-gestation brain to ASD risk genes (protein-truncating mutations identified by

exome sequencing) and modules of co-expressed genes elevated or reduced in autistic brains. Gene set enrichment analysis demonstrated an overlap of nine ASD-associated gene sets of interest, including 10 genes from ASD risk genes, and a significant overlap from the M9 module. This study suggests that estrogen may produce an indirect pathway to autism phenotypes through its effects on the M9 module, which is shown to have an enrichment of astrocytes in autistic brains.

Abstract: Presenter(s): Beth Harshberger
School: Carthage College
Session: Poster P3.12
Title: Exploring CO2 Sensitivity at Varying Resolutions in BI and NBI Humans
Advisor(s): Paul F. Martino, Biology, Carthage College
Co-Author(s): Olivia Wolf, Dan P. Miller, Justin R. Miller**,**

Abstract: Behavioral inhibition (BI) is believed to be a genetically determined trait that affects roughly 33% of the human population. These individuals tend to respond to stressful situations differently than non-behaviorally inhibited (NBI) individuals. In order to better understand behavioral inhibition in humans, our laboratory set out to explore varying responses of BI individuals to stressful stimuli of breathing enhanced CO2 (carbon dioxide). We measured blood pressure, breathing, heart rate, heart rate variability, cortisol, and amylase. The first experiment exposed college-aged students to 7% CO2. The findings suggest that BI individuals display significant differences compared to NBI individuals in heart rate variability. The second experiment uncovered differences in cortisol and amylase production between BI and NBI individuals. The third experiment exposed college-aged students to 3%, 5%, and 7% CO2, respectively. From this experiment, a CO2 sensitivity slope (inspired minute ventilation ((L/min) / end-tidal CO2 (The percent of CO2 recorded at the end of a breath)) was produced. It was found that BI individuals had increased, exaggerated responses to the respiratory stressors of the three levels of enhanced CO2 as denoted by a steeper slope.

Abstract: Presenter(s): Nhi Hoang
School: Hope College
Session: Oral I.A.2
Title: Welcome to My House: The Relationship between One's Hospitality and Preference for Houses Exteriors
Advisor(s): Benjamin R. Meagher, Department of Psychology, Hope College

Abstract: The U.S. real estate market is a trillion-dollar industry, yet little empirical research has explored how psychological variables affect housing preferences. The present study investigates the relationship between hospitality, a personality trait entailing one's level of welcomingness, responsibility, and lack of imposition when hosting others, and preferences for certain physical environments. Hospitality is predicted to be a moderator of people's preference for houses based on three exterior features: the presence of a front porch, the absence of a fence, and the closeness to the sidewalk. Participants (N = 256) completed an online survey answering measures on hospitality, the Big Five Inventory, and Home Attachment and evaluated a series of pictures of house exteriors. Only the closeness to the sidewalk, or walkability feature, produced a statistically significant interaction with hospitality. Further analysis of each factor in the hospitality scale revealed that participants who scored

high on responsibility for guests, low on welcomingness, and feel less imposition from guests preferred houses more distant from the sidewalk. This study contributes to the general understanding of people's sense of hospitality and its manifestation in preferences for physical spaces. Future research may look at the relationship between hospitality and housing interiors.

Abstract: Presenter(s): Adrianna Hudyma
School: Lawrence University
Session: Poster P3.21
Title: Creating a constitutively active version of the enzyme PlpX
Advisor(s): Alanna Schepartz, Department of Chemistry, University of California, Berkeley
Co-Author(s): Carly Schissel, Alanna Schepartz

Abstract: Ribosomally-synthesized and post-translationally modified peptides (RiPPs) contain interesting chemistry and structures introduced by RiPP enzymes. One recently discovered example is PlpX, which, when combined with its maturase PlpY, is the only known enzyme that creates an α-keto-β-amide in its substrate's core sequence. This chemical moiety is uniquely reactive allowing for biorthogonal chemistry to introduce pharmacologically relevant functionality. However, a core recognition sequence is required for the enzyme to function. Our aim was to increase the utility of PlpX by creating a constitutively active version of the enzyme, which may be able to recognize and modify a truncated motif due to its increase activity. I tackled this by creating a fusion enzyme by linking the substrate's recognition sequence to PlpX. I confirmed with LC-MS analysis that my fusion enzyme modified substrate at the same or better percent conversion than the native enzyme. The end goal is to be able to insert a small sequence into many proteins without disrupting their structure or function but allowing for the site-specific installation of a α-keto-β amide. This enzyme will provide a new site-specific way to label proteins over traditional cysteine labeling and provide site specific reactivity for the creation of bioconjugations**.**

Abstract: Presenter(s): Emily Jacobs
School: University of Chicago
Session: Poster P2.14
Title: DNA damage-induced immune response in Aspergillus Fumigatus infected human pluripotent stem cell-derived lung model
Advisor(s): Huanhuan Joyce Chen, Molecular Engineering and Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Clara Kim, Jingwen Xu**,**

Abstract: Although aspergillus fumigatus is a mild pathogen that can normally be eliminated by human immunity, its abundance makes it life-threatening to the immunocompromised population. It can lead to bronchopulmonary aspergillosis, aspergilloma, and invasive aspergillosis in these patients—infections presently treated by organ transplantation and stem cell therapy. Evidence has shown DNA damage was induced in aspergillus-infected cells, however the molecular mechanism behind it and how the host cells or human immune system respond to this event are poorly understood. The research progress has been hindered due to the shortage of human lung cells or models available for functional studies. Here, we exploit a novel human pluripotent stem cell-derived semi-3D lung organoid (iLung) system, that was developed in our lab, which contains lung progenitor and the major types of

epithelial cells. Using the iLung system, we found extensive DNA damage, in which significant point mutation motifs were identified by whole exosome sequencing. These results have the potential to link fungal genotoxicity to other diseases. Furthermore, we discovered the activation of DNA damage response immune pathways including STING and IL-33 pathways. These data provide deep insight to fungal infection in human lungs and will lead to potential therapeutic targets.

Abstract: Presenter(s): Difei Jiang
School: Lawrence University
Session: Oral I.C.3
Title: Mechanism of PTH Ca2+ sensing on G protein interactions with PTH1
Advisor(s): Dr. Kelly Culhane, Chemistry, Lawrence University

Abstract: Parathyroid hormone 1 receptor (PTH1R) is a family B GPCR that plays a crucial role in bone remodeling. Previous studies show extracellular Ca2+ is a positive allosteric modulator for one PTH1R ligand, parathyroid hormone (PTH), which is approved by US FDA to treat severe osteoporosis. Moreover, PTH residues E19 & E22 have shown to involved in Ca2+ sensing. However, the effects of PTH Ca2+ sensing on intracellular G protein binding are unknown. Here, we use FRET based SPASM sensors to study the interaction between PTH1R and different Ga peptides. SPASM sensors contain PTH1R followed by the acceptor fluorophore, a flexible linker, the donor fluorophore and a peptide from a Ga subunit that mimics the interaction of the full G protein heterotrimer. In the current study, a membrane preparation protocol was optimized to isolate PTH1R in native HEK293T membranes. FRET experiments quantified activation different Ga isoforms by PTH and PTHE19AE22A. Differential activation of specific Ga isoforms by PTH and PTHE19AE22A will delineate mechanistic details of PTH1R activation and its role in bone diseases. Further, understanding the extracellular Ca2+ modulation of PTH signaling will provide insight for developing treatments for chronic hypocalcemia associated with hypoparathyroidism, while uncovering novel regulation of bone remodeling**.**

Abstract: Presenter(s): Taeen Jidaan
School: Lawrence University
Session: Oral P1.11
Title: Researching Xap5 Expression in C. elegans
Advisor(s): Elizabeth Ann De Stasio, Biology,Lawrence University

Abstract: Homologous genes in different phyla may have similar functions and thus be considered true orthologs, or their functions may diverge in different phyla. Caenorhabditis elegans are commonly used as model organism for molecular and neurological studies. We are investigating the function and expression of X-CHROMOSOME ACTIVATED PROTEIN 5, or XAP5. The xap5 gene function was first elucidated in the alga, Chlamydomonas, and acts as a transcription factor to activate some cilia genes. Research by Yu-Ri Lee suggests that mutations of FAM50A, a gene in Homo sapiens, lead to aberrant splicing of other gene products. Another article suggests that XAP5 CIRCADIAN TIMEKEEPER, or XCT, functions as a timer for photomorphogenesis in Arabidopsis. We are investigating the role of xap5 in C. elegans. We seek first to determine which tissues expresses XAP5 protein and the cellular location of it by producing a translational fusion of the gene and its putative control region with Green Fluorescent Protein (GFP). Using the sequence information available at

wormbase.org, we designed primers to PCR-amplify the C47E8.4 (xap5 homolog) gene including 622 base pairs from the upstream region. I've then determined the plasmid vector that would correctly place the Green-Fluorescent Protein (gfp) in-frame with the xap5 gene to produce a chimeric protein of both XAP5 and GFP. We used genomic DNA from N2 worms as a template for PCR of the xap5 gene. We then purified the PCR product and the vector was digested with SphI and BamHI enzymes, dephosphorylated with CIP and then purified. we ligated the insert and vector and transformed E. coli with ampicillin selection. Finally, we grew single colonies so that we could grow a pure culture of cells and mini-prep DNA from the transformants. we are confirming whether the cloning worked properly through restriction digest and sequencing. Microinjection of purified plasmids will allow us to create transgenic strains of worms expressing the fluorescently tagged XAP5 protein for further analysis.

Abstract: Presenter(s): Ian Johnson
School: Colorado College
Session: Poster P3.04
Title: Presence of pathogenic variants in circular RNA of presenilin 1 and **2**
Advisor(s): Meredith Course, Molecular Biology, Colorado College

Abstract: Alzheimer's Disease (AD) is the most common form of neurodegenerative disease, currently affecting over 6 million Americans. Previous research suggests that circular RNA is heavily implicated in neuronal gene regulation; however, the precise role of circular RNA in AD pathogenesis has yet to be established. In this study, we aim to identify pathogenic variants in circular RNA of two AD-causing genes, presenilin 1 and 2 (PSEN1 and PSEN2). Brain tissue from individuals with familial AD were obtained within 12 hours post-mortem, RNA purified, and converted to cDNA using both an oligo(dT) and random hexamer approach, to amplify mRNA and all forms of RNA respectively. cDNA containing five pathogenic variants of interest were PCR amplified to target backspliced regions specific to circular RNA. Successful amplification of pathogenic areas of interest were visualized via gel electrophoresis, purified, and Sanger sequenced. Four variants, three in PSEN1 and one in PSEN2, were identified in circular RNA. The presence of pathogenic variation in circular RNA provides the groundwork for future investigation concerning their potential role in AD pathogenesis. Additionally, this research is the first of its kind to identify pathogenic variations in circular RNA.

Abstract: Presenter(s): Joey Kaczor
School: University of Chicago
Session: Poster P3.16
Title: Characterizing the level of a small RNA involved in Vibrio cholerae defense against bacteriophage infection
Advisor(s): Kimberley D. Seed, Plant & Microbial Biology, University of California, Berkeley
Co-Author(s): Drew T. Dunham, Reid T. Oshiro

Abstract: Vibrio cholerae, the bacterial perpetrator of the disease cholera, is in a dynamic evolutionary arms race with the lytic bacteriophage ICP1. To resist ICP1 predation, V. cholerae evolved a mobile genetic element, the phage-inducible chromosomal island-like element (PLE). PLE is activated upon ICP1 infection and stops the production of new ICP1 progeny. PLE encodes a small RNA, SviR, which alters PLE and ICP1 transcript levels. We embark to further characterize SviR expression during phage infection. While PLE is known

to inhibit productive ICP1 infection, PLE gene expression has only been profiled in a subset of the 11 known PLEs, each encoding its own SviR homolog. To compare SviR expression between the phylogenetically distinct PLEs, V. cholerae isolates containing each different PLE were infected with ICP1, and SviR expression was evaluated using Northern blot analysis. Also, it was hypothesized that the inverted repeat sequences flanking SviR are involved in its expression. To directly assess the inverted repeats' role, we compared SviR expression with and without the left inverted repeat present through Northern blot analysis. Studying the genetic factors needed for SviR expression during ICP1 infection aids in deciphering strategies that V. cholerae uses in bacteriophage defense, broadly informing host-virus co-evolutionary dynamics.

Abstract: Presenter(s): Mayher Kaur
School: University of Chicago
Session: Oral I.B.4
Title: Metabolic rewiring elucidates metastatic behavior in non-small cell lung cancer
Advisor(s): Brandon Faubert, Hematology/Oncology, University of Chicago

Abstract: During metastasis, cancer cells must detach from the primary tumor and survive in circulation. Detachment from the extracellular matrix and the introduction to hostile, oxidative environments like the blood eliminate most cells that escape the primary tumor. How the remaining cells adapt to survive this stress is largely unknown, but a key hypothesis is that circulating tumor cells (CTCs) rewire metabolic programs to adapt to these stresses. In this work, we investigate the metabolic differences between anchorage-dependent and anchorage-independent growth in non-small cell lung cancer (NSCLC). Importantly, standard cell culture conditions do not accurately recapitulate the in vivo environment. To better model the CTC environment, we cultured NSCLC cells in normal media conditions, tumor interstitial fluid media (TIFm), and human plasma like media. To elucidate differences in nutrient use and metabolic adaptations between these conditions, we performed stable isotope labelling with multiple fuel sources (glucose, lactate, glutamine, etc.). Preliminary results indicate key metabolic and proliferative differences between these conditions. Specifically, cells cultured in TIFm are not using glucose and glutamine to derive most of the TCA metabolites, and nonadherent cells are primarily using glutamine to fuel TCA intermediates. We anticipate that these assays will be a starting point for more sophisticated, in vivo models of circulating tumor cells, and that this metabolic reprogramming may lead to context-specific therapeutic vulnerabilities.

Abstract: Presenter(s): Luca Keon
School: Colorado College
Session: Poster P1.08
Title: Investigating Plant-Pollinator Responses to a Warming Climate in the Alaskan Arctic
Advisor(s): Roxaneh Khorsand, Organismal Biology and Ecology, Colorado College

Abstract: The Arctic is the fastest warming region on earth. Warming can shift timing of flowering and pollinator activity, potentially introducing a plant-pollinator asynchrony. The short flowering season and low insect diversity make the plant-pollinator network of this region especially vulnerable. More is known about effects of experimental warming on plant phenology and growth than plant-pollinator interactions. This study asks: How does climate change affect plant-pollinator interactions and plant reproductive success in the Low Arctic?

We specifically quantify effects of experimental warming on flower phenology and timing of insect visitation, floral rewards, and plant reproductive success. Since 2019, we have used open-top chambers, the standard passive warming system of the International Tundra Experiment (ITEX) on the North Slope of Alaska. Our 2019-2020 data suggest heterogeneous responses to warming among species and growth forms. For example, flowering lasted longer in warmed forbs and floral density was higher in warmed evergreen shrubs. Dipterans (i.e. flies and mosquitoes) were the most common floral visitors, but Hymenopterans (primarily bumblebees) carried more pollen. Experimental warming increased nectar quantity but had no effect on quality. Future research will focus on obtaining higher taxonomic resolution of insect visitors and conducting a network analysis of this plant-pollinator community.

Abstract: Presenter(s): Audrey Kim
School: University of Chicago
Session: Poster P1.14
Title: Racial differences in Quantitative MRI and Histology Reveal Value of DCE MRI for African American
Advisor(s):
Co-Author(s) : Gregory Asare, Aritirck Chatterjee, Xiaobing Fan, Ambereen Yousuf, Tatjana Antic, Scott Eggener, Gregory Karczmar, Aytekin Oto

Abstract: This study investigates whether quantitative MRI and quantitative histology analysis of the prostate reveal differences between African Americans (AA) and Caucasian Americans (CA) that may affect prostate cancer diagnosis. This IRB approved study involved retrospective analysis of data from patients (47 CA, 15 AA) that underwent prostate mpMRI before radical prostatectomy. Quantitative mpMRI metrics: ADC, T2, and DCE-MRI signal enhancement rate or uptake rate (;) from empirical mathematical models was calculated for regions of interest (ROIs) on sites of prostatectomy-verified PCa and benign tissue. Quantitative histology measured prostate tissue composition (stroma, epithelium, and lumen) on digitized H&E stained pathology sections corresponding to ROIs on MRI. There are no significant differences between AA and CA based on ADC values for both benign (AA:1.67±0.42 μm2 /ms vs CA:1.62±0.37 μm2 /ms, p=.98) and cancerous tissue (AA:1.17±0.35 μm2 /ms vs CA: 1.06±0.34μm2 /ms, p=.24). Similar results were found for T2 values as well; for benign (AA: 162.3±80.9 ms vs CA: 159.1±73.5 ms, p=.89) and cancerous tissue (AA:109.4±21.4 ms vs CA: 99.7±27.7 ms, p=.25). No significant difference (p=.28) was also found in DCE α; for benign tissue between AA (7.3±5.4 s-1) and CA (5.3±3.8 s-1) However, DCE α; was significantly higher (p=0.02) in cancer for AA (11.4±4.7s-1) compared to CA (6.1±4.7s-1). This resulted in improved diagnostic accuracy (area under the ROC curve) in cancer detection (p=0.002) using DCE in AA (0.73) vs CA (0.57). Histology analysis for tissue composition showed similar breakdown of tissue components between AA (epithelium 28.7±9.02%, lumen 28.8±13.3%) and CA (epithelium 29.6±9.2%, lumen 27.4±11.1%) for benign tissue. However, in cancerous tissue, there were greater proportions of epithelium and lower lumen (p<.05) in CA (epithelium 50.9±12.3%, lumen 10.5±6.9%) compared to AA (epithelium 44.7±12.8%, lumen 16.2±6.8%). Our results reveal differences between cancers in AA and CA based on quantitative histology and MRI, specifically, DCE MRI. Quantitative DCE-MRI can improve PCa diagnosis in AA's.

Abstract: Presenter(s): Caitlin Kim
School: Colorado College
Session: Poster P2.22
Title: Fluorinated L-Phe dipeptides may inhibit bacterial growth and biofilm formation of P. aeruginosa
Advisor(s): Olivia Hatton, Molecular Biology, Colorado College

Abstract: Biofilm formation allows for pathogenic bacterial infections that can be resistant to treatment and deleterious to collateral tissues in hosts. Pseudomonas aeruginosa is an opportunistic pathogenic bacteria which causes harmful biofilm-mediated infections such as those fatal to cystic fibrosis patients. Previously, D-amino acids have been found to trigger disassembly of biofilms, such as those formed by P. aeruginosa. Similar findings from the Distributive Drug Discovery (D3) Project suggest that fluorinated L-amino acids may also allow for biofilm disassembly. In collaboration with the D3 project, this study investigates the biological activity of various prodrug formulations of fluorinated L-Phenylalanine dipeptides. The ultimate goal is to find a compound with selective toxicity against P. aeruginosa and its associated biofilms. The PA14 strain of P. aeruginosa was cultured in the presence of D3 compounds or controls. Bacterial growth and biofilm formation were analyzed by optical density at 600 nm (OD600) and crystal violet staining, respectively. Of the compounds tested, compound #42 reduced bacterial growth, although not significantly, and did not inhibit biofilm formation. Interestingly, compounds #2, #3, and #5 increased biofilm formation. Future studies may replicate these results and investigate the exact concentration necessary, mechanisms of the prodrug, and toxicity in human cell line.

Abstract: Presenter(s): Hannah Koehlert
School: Carthage College
Session: Poster P1.16
Title: Determination of the Factors Predicting Burnout in College Athletes
Advisor(s): Cynthia Allen , Exercise and Sport Science, Carthage College

Abstract: Athlete burnout can be defined by two domains; physical and psychological exhaustion and cynicism and disengagement. Questions remain concerning risk and protective factors in burnout among student athletes. This study assessed factors hypothesized to increase the risk of burnout including years playing the sport, perceived sport climate (based on the Social Cognitive Theory), satisfaction with playing time, and hours spent dedicated to the sport each week. Data was collected on 112 athletes at a DIII college. Results from the multiple regression suggest that the most significant risk factors for athlete burnout are the perceived sport climate and the athlete's satisfaction with playing time. Student athletes' perceptions of the climate created by their head coach predicted nearly 25% of burnout symptoms while satisfaction with the amount of time competing in game/match play predicted 5% of burnout symptoms. Coaches and their athletes will benefit from focused attention to providing some level of autonomy with regards to training and practice routines and methods. Athletes will also likely benefit from honest conversations about playing time being facilitated by their coach. This coaching practice may create a level of trust and understanding between the two as well as setting adequate player expectations.

Abstract: Presenter(s): Anjali Kotamarthi,
School: University of Chicago

Session: Oral I.D.4
Title: Identification of Collateral Lethal Gene Targets in -7/del(7q) Myeloid Neoplasms
Advisor(s): Megan McNerney, Department of Pathology and pediatric hematology/oncology, University of Chicago
Co-Author(s): Madhavi Senagolage

Abstract: -7/del(7q) Acute Myeloid Leukemia (AML) is a high-risk leukemia that accounts for about 8% of all AML patients, resulting in a poorer prognosis as many generalized therapy methods such as chemotherapy are rendered ineffective. In order to provide more effective and less cytotoxic treatment, a need for targeted therapies which prove lethal to a select group of cells remains a high unsolved priority. To investigate whether any genetic vulnerabilities exist in this subset of patients, previously published genome-wide CRISPR-CAS9 knockout screens conducted in AML cell lines were used to identify genes on chromosome 7 essential for AML cell proliferation. Out of all genes on chromosome 7, we identified 239 essential genes in AML cell lines and further narrowed this list to 44 genes which can be targeted by a commercially available drug. From these potential genes, cyclin dependent kinase 6 (CDK6), important for transition from the G1 phase and an already established therapeutic target in breast cancer, significantly inhibited cell proliferation in AML cell lines conferring its status as an essential gene in AML through CRISPR knockout of CDK6. CDK6 also demonstrated potential for -7/del(7q) specificity given -7/del(7q) AML cell lines were more sensitive to pharmacological inhibition with a potent inhibitor of CDK6. These findings encourage further investigation into avenues for more effective therapeutics for high-risk AMLs.

Abstract: Presenter(s): Shawn Lam, Thu Nguyen, Myrissa Le
School: Knox College
Session: Oral I.A.3
Title: Differential associations between incompleteness and disgust domains
Advisor(s): Sara O'Brien, Psychology, Carthage College
Co-Author(s): Antonio Ramirez, Sara O'Brien

Abstract: OCD symptoms are driven by distinct motivations, including incompleteness (INC), harm avoidance (HA), and disgust. While INC is broadly associated with OCD symptoms, disgust is associated with a narrow set of OCD symptoms. In this study, we examined the relationship between INC and disgust domains in comparison with the relationship between HA and disgust.
205 US-based adults with an average age of 33 were recruited on Prolific. Self-reported assessments completed on Qualtrics included the DPSS-R (Fergus & Valentiner, 2009), DS-R (Olatunji et al., 2007), OCCDQ-Trait (Summerfeldt et al., 2014), and PANAS (Watson et al., 1988). Multiple regressions were performed with HA and INC as dependent variables and each of the DPSS-R and DS-R subscales as independent variables.
Results revealed that only Animal-Reminder, Disgust Sensitivity, and Disgust Propensity were significantly and positively correlated with HA and INC. Compared to INC, HA showed stronger correlations with both Animal-Reminder ($\beta = .28$, $p < 0.01$) and Disgust Sensitivity ($\beta = .27$, $p < 0.01$) while INC showed a stronger correlation with Disgust Propensity ($\beta = .21$, $p < 0.01$) compared to that of HA. Results suggested INC is uniquely related to Animal-Reminder disgust and that INC and disgust proneness may relate to OCD via different mechanisms.

Abstract: Presenter(s): Courtney Lasserre
School: Washington University in St. Louis
Session: Poster P3.19
Title: Zombie Dads: The Effects of Male Guppy Coloration on Posthumous Reproductive Success
Advisor(s): Swanne P Gordon, Ecology and Evolution, Cornell University
Co-Author(s): Lauren Renna, Yusan Yang, Lauren E Johnson

Abstract: Exaggerated sexual ornaments like coloration affect mate choice in many animals, and can even have a strong effect post-copulation via cryptic mate choice. In Trinidadian guppies (Poecilia reticulata), it is known that males with more conspicuous carotenoid coloration have higher reproductive success. Additionally, female guppies can store sperm from males with whom they have mated, allowing some males to reproduce posthumously in the wild. However, it is unclear whether the reproductive advantage of conspicuous male coloration extends to the post-death state. In this study, we test the hypothesis that males with more conspicuous carotenoid coloration sire a greater proportion of a litter via stored sperm. We allow a virgin female guppy to freely interact with both a colorful and dull male until two litters are born, then randomly remove one male from the tank. Two more litters are collected, after which point the female is left alone for two final litters of offspring. Pedigree and sperm count analyses allow us to assess the role of male coloration in reproductive success via pre- versus post-copulatory female choice. Results of this study will help us understand how male coloration affects posthumous reproduction in wild animal populations with the ability to store sperm.

Abstract: Presenter(s): Reese Lavajo
School: Lawrence University
Session: Poster P2.20
Title: Influence of algal productivity and predation risk on Daphnia spp. migratory patterns: comparison across lakes
Advisor(s): Bart De Stasio, Biology, Lawrence University
Co-Author(s): Eleanor Meng, Gretchen Gerrish

Abstract: Small aquatic crustaceans like the waterflea Daphnia exhibit migratory patterns in response to various selective pressures. They're known to perform diel vertical migration (DVM) in which they move towards deeper depths during daytime to evade visual predators like planktivorous fish and move towards the surface at night to feed on algae. We examined how differences in algal productivity and predator abundance impact these behaviors across multiple lakes. Daytime and nighttime replicate Schindler trap samples were taken at even depth intervals in three lakes in Wisconsin with varying algal availability and predator assemblages. Daphnia spp. were preserved, counted at each depth, and measured for body length. In each lake we observed typical DVM behaviors, but amplitudes of migration differed across lakes. DVM distances scaled in relation with lake productivity with Daphnia in highly productive Grenlie Lake moving 1.7m, mid productivity Big Musky Lake moving 1.4m, and low productivity Sparkling Lake moving 0.8m. Daphnia size differences and fish abundances also indicate differences in predation intensity in these lakes. We observed that Daphnia tracked depths of high food abundance, especially at night in lower productivity lakes.

Studying zooplankton migration provides insights into how lakes respond to human impacts like eutrophication and fisheries management.

Abstract: Presenter(s): Sid Layesa
School: Macalester College
Session: Poster P3.14
Title: Role of Rab14 in autophagy
Advisor(s): Jean M. Wilson, Department of Cellular and Molecular Medicine, University of Arizona - Tucson, AZ
Co-Author(s): Samina Momtaz

Abstract: Autophagy plays an important role in the degradation and recycling processes in cells. It is a highly conserved pathway that helps cells eliminate unnecessary or damaged proteins and organelles through autophagosome-mediated lysosomal degradation.

Rab14 has been known to play a role in intracellular membrane trafficking, but its role in Autophagy has not been investigated. Using HeLa cells, our preliminary data shows that knockdown of Rab14 results in an increase in the number and size of LC3B puncta. In addition, our data shows decrease in LC3B and LAMP1 colocalization in HeLa Rab14 knockdowns. Western blot analysis also shows blockade of autophagic flux in Rab14 knockdown HeLa cells.

Overall, our results suggest that Rab14 plays an important role in either autophagosome and lysosome fusion or induction of autophagosome formation.

Abstract: Presenter(s): Madeline Suydman Lee
School: University Chicago
Session: Poster P3.25
Title: Botanicals & Bacterium: An Ethnobotanical Approach to the Modern Antibiotic Resistance Crisis
Advisor(s): Cassandra Quave, Phytochemistry, Emory University

Abstract: As fungi and bacteria have increased their ability to defeat the drugs designed to kill them over the past decades, plant-based medicine has emerged as a viable solution to this crisis. Investigation of botanical folk remedies for infection and wounds has led researchers to study S. terebinthifolia (Brazilian Peppertree) – an evergreen shrub native to South and Central American – as a potential source of virulence inhibition. Indeed, the peppertree has demonstrated great experimental potential as a virulence inhibitor against bacterial strains like MRSA and CRAB. Combining flavone extraction methods with bioassay-guided fractionation, researchers have isolated the fraction 430D-F5 as the compound responsible for inhibiting the complex system of bacterial communication known as quorum-sensing. From this finding, researchers further isolated the compounds directly responsible for this activity, including three triterpenoid acids and pentagalloyl glucose (PGG). The purpose of my research with the Quave Research Group was to refine my technical phytochemical skills by scaling up the extraction of S. terebinthifolia and additionally isolating other fractions of the compound that have not been previously chemically explored.

Abstract: Presenter(s): Morten Lee

School: University of Chicago
Session: Poster P1.21
Title: Chemotherapeutic Nanoscale Coordination Polymers (NCPs) for Active Transport to Tumors
Advisor(s): Wenbin Lin, Chemistry, University of Chicago
Co-Author(s): Xiaomin Jiang, Wenbo Han, Jianqiao Liu, Jianming Mao, Megan Rodriguez, Youyou Li, Taokun Luo, Ziwan Xu, Kaiting Yang, Marc Bissonnette, Ralph R. Weichselbaum

Abstract: Cancer drug treatment has been limited by lack of target specificity and subsequent systemic toxicity. Nanoscale coordination polymer (NCPs) nanoparticle delivery systems are a useful approach in chemotherapy because of their ability to stabilize, circulate, and deliver anticancer molecules to tumors. Nonetheless, efficacious accumulation of current NCPs in tumors is severely inhibited by nonspecific binding to in-vivo off-target components and clearance by the mononuclear phagocytic system. Here, NCPs carrying cytotoxic oxaliplatin and SN38 prodrugs demonstrated an active transport strategy via targeting of the low-density lipoprotein receptor (LDLR). Low-density lipoproteins play a dominant role in the delivery of cholesterol to peripheral cells by LDLR-mediated endocytosis. In tumor cells, LDLR is overexpressed and highly active. By loading cholesterol into the NCP shell in the form of a cholesterol-conjugated SN38 prodrug, these NCPs exhibited preferential adsorption by low-density lipoproteins and enriched in tumors via LDLR endocytosis. This effect was observed in-vitro with immunofluorescence and binding assays and in-vivo with LDLR knockout studies. Tumor deposition of NCP-loaded OxPt and SN38 increased by 4.9 and 6.0 times, respectively, compared to free drugs, achieving 92-98% tumor growth inhibition without serious systemic toxicity. The paradigm of low-density lipoprotein mediated transport and delivery offers a promising method for targeted nanoparticle therapy.

Abstract: Presenter(s): Bobby Lerch
School: Beloit College
Session: Poster P2.01
Title: Expressing and purifying CbpA for studies into the elucidation of bacterial Hsp70 JDP interaction
Advisor(s): Taylor Arhar, Chemistry, Beloit College

Abstract: OCD symptoms are driven by distinct motivations, including incompleteness (INC), harm avoidance (HA), and disgust. While INC is broadly associated with OCD symptoms, disgust is associated with a narrow set of OCD symptoms. In this study, we examined the relationship between INC and disgust domains in comparison with the relationship between HA and disgust.
205 US-based adults with an average age of 33 were recruited on Prolific. Self-reported assessments completed on Qualtrics included the DPSS-R (Fergus & Valentiner, 2009), DS-R (Olatunji et al., 2007), OCCDQ-Trait (Summerfeldt et al., 2014), and PANAS (Watson et al., 1988). Multiple regressions were performed with HA and INC as dependent variables and each of the DPSS-R and DS-R subscales as independent variables.
Results revealed that only Animal-Reminder, Disgust Sensitivity, and Disgust Propensity were significantly and positively correlated with HA and INC. Compared to INC, HA showed stronger correlations with both Animal-Reminder ($\beta = .28$, $p < 0.01$) and Disgust Sensitivity ($\beta = .27$, $p < 0.01$) while INC showed a stronger correlation with Disgust Propensity ($\beta = .21$, $p <$

0.01) compared to that of HA. Results suggested INC is uniquely related to Animal-Reminder disgust and that INC and disgust proneness may relate to OCD via different mechanisms.

Abstract: Presenter(s): Thomas Li
School: University of Chicago
Session: Oral II.H.2
Title: BACH1 is activated under hypoxia in a proline hydroxylation-dependent manner in Triple Negative Breast Cancer
Advisor(s): Marsha Rosner, Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Long Nguyen,

Abstract: Metastasis is a major cause of lethality in cancer. Hypoxia is an important hallmark of metastatic solid tumors. The Rosner Lab recently identified that the BTB and CNC homolog 1 transcription factor (BACH1), which is known to promote metastasis in various cancer types, is prolyl-hydroxylated by Prolyl Hydroxylase 1 (PHD1) in an oxygen-dependent manner. In addition, the Rosner Lab has demonstrated that BACH1 is stabilized and exhibits greater DNA binding under hypoxia (unpublished). However, it remains unclear how proline hydroxylation modifications contribute to the regulation of BACH1 transcriptional activity or its regulation of metastasis. Using a triple negative breast cancer (TNBC) cell line containing a doxycycline-inducible GFP:BACH1 genetic circuit, I confirmed that nuclear BACH1 signals were greater in hypoxia compared to normoxia, which is consistent with greater BACH1 DNA binding under hypoxia. Furthermore, I showed that BACH1 mutated at two hydroxylated proline sites demonstrated higher DNA binding levels to the canonical HMOX1-enhancer binding site and further repression of HMOX1 gene expression. These findings support the hypothesis that the proline hydroxylation modifications of BACH1 directly regulate BACH1's activity as a transcription factor, which potentially enables hypoxic activation of BACH1, hypoxia-induced pro-metastatic signaling, and therapeutic resistance in TNBC.

Abstract: Presenter(s): Katie Lillemon
School: Gustavus Adolphus College
Session: Poster P3.07
Title: Inhibition of proteolytic activation of SARS-CoV-2 spike protein in human cardiomyocytes
Advisor(s): Chanakha Navaratnarajah Virology and Gene Therapy, Mayo Clinic Graduate School for Biomedical Sciences
Co-Author(s): Biruhalem Taye, Wei Zhou, Michael Ackerman, Roberto Cattaneo

Abstract: SARS-CoV-2 spike protein undergoes two major activation steps before becoming fully primed for cellular membrane fusion and cell-cell syncytia formation; an S1/S2 activation in which a furin-like protease cleaves between the S1 and S2 subunits and an S2' cleavage where the fusion peptide is released for viral entry and cell fusion. In lung epithelia, the virus utilizes the TMPRSS2 protease for this S2' cleavage, but TMPRSS family proteases are not expressed in cardiomyocytes. Therefore, we seek the protease that activates the spike protein by cleaving it at the S2' site, leading to cell-cell fusion. Using quantitative and qualitative cell fusion assays to determine the level of spike protein processing, we can eliminate furin and cathepsins as proteases involved in this spike protein activation. Based on

preliminary data, it is believed that ADAM family proteases are most likely involved in S2' activation in some way.

Abstract: Presenter(s): Maya Lines
School: Lawrence University
Session: Oral II.G.1
Title: Microglial response to autism risk gene perturbations
Advisor(s): Helen Rankin Willsey, Psychiatry, UCSF Weill Institute for Neurosciences
Co-Author(s): Micaela Lasser, Vivian Norris

Abstract: Over 100 high-confidence, large-effect risk genes for Autism Spectrum Disorders (ASDs) have been identified. These genes are largely co-expressed in developing excitatory neurons of the prefrontal cortex during brain development; however, post-mortem ASD brain samples show an enrichment in microglia-associated transcriptional signatures. We have previously shown that perturbation of a top ASD risk gene DYRK1A causes neuronal cell death during brain development; therefore, we hypothesize that ASD risk gene mutations cause neuronal cell death, which in turn activates and recruits microglia. To test this hypothesis, we deploy the high-throughput in vivo genetic model, Xenopus tropicalis, diploid frogs. By modeling loss of function of two top ASD risk genes, DYRK1A and CHD8, we show that ASD risk gene perturbations can cause alterations in microglia number and morphology in vivo. Future work will focus on determining the contribution of ASD risk gene perturbations within microglia versus within neurons to these phenotypes. In this way, this work may help illuminate the reason for the discrepancy between ASD risk gene developmental expression patterns and post-mortem transcriptional signals. If microglia play key roles in responding to neuronal cell death in this context, it could potentially point to areas of therapeutic intervention.

Abstract: Presenter(s): Lilian A Lopez
School: Beloit College
Session: Oral I.A.1
Title: Perceptions of Creative Arts Therapists: Reaching Adolescents of Color during the Pandemic
Advisor(s): Suzanne Cox, Psychology, Beloit College

Abstract: Rates of mental health challenges such as depression and anxiety among adolescents and emerging adults have increased during the COVID-19 pandemic, especially due to early recommendations for social distancing, and especially for adolescents of color. The current research focuses on creative arts therapy as a rising unconventional mechanism for addressing mental health. Using an exploratory, qualitative approach, the research aims to answer: what are performing art therapists' perceptions of their treatment approaches, particularly as related to the ongoing pandemic and for adolescents of color? Participants included performing art therapists who were interviewed about their perspective and their approaches to the field. The interview data were analyzed for thematic content. The interviews revealed three major themes: a) the history of psychotherapy, b) the impact of the pandemic on their lives and their self-awareness of their role in therapy, and c) the influence of socio-historical roots of therapy on people of color seeking therapy. Future research that

explores the role of performing arts therapy as related to the well-being of adolescents of color is needed.

Abstract: Presenter(s): Lecheng (Joshua) Lyu
School: St. Olaf College
Session: Poster P3.11
Title: Differential Pathway Analysis of Early vs. Late Recurrences in ER+ Breast Cancer
Advisor(s): Robert Clarke, Biochemistry, Molecular Biology and Biophysics, The Hormel Institute, University of Minnesota, Austin, MN
Co-Author(s): Lu Jin, Surojeet Sengupta

Abstract: As breast cancer and its recurrence remain a major global health problem, we sought to identify the biological pathways by investigating enriched gene sets in the microarray of pre-treatment patient samples that led to either early (<3 yrs) or late (>5 yrs) recurrences. We hypothesized that the pathways were enriched differentially between early and late recurrences. Our results unveiled several common and unique pathways as well as genes that may contribute to early versus late breast cancer recurrence. These patterns among pathways and genes could serve as biomarkers to guide particular breast cancer therapy. In the future, our project aims to elucidate networks among pathways to build predictive models that would open new venues for personalized medicine.

Abstract: Presenter(s): Eva McCord
School: University of Chicago
Session: Poster P2.25
Title: Designing of an auxin-induced degron (AID) system targeting and depolymerizing nuclear actin in mESCs
Advisor(s): Eugene Chang, Cadence Cham, University of Chicago Department of Medicine, University of Chicago

Abstract: Mucosal healing is an essential physiological response to inflammatory and injurious diseases of the intestinal tract, including inflammatory bowel diseases (IBD). Complete mucosal healing is closely associated with favorable clinical outcomes, more prolonged remission, and lower risks of complications. Yet, critical gaps remain in the "players" involved and their mechanisms of action. In this regard, we found that a member of the heat shock protein family, Hsp25/27 (Hsp27 is the human homolog), is essential for the initiation and maintenance of mucosal healing following injury to the intestinal tract. Using in vitro scratch assays of intestinal epithelial cells from HSP25 WT, HSP25 KO, and HSP25+IEC mice, we will thus provide much-needed mechanistic insight into the role of HSP25 on a molecular and cellular level. Our studies can ultimately lead to the development and treatment of restoring intestinal homeostasis in patients with inflammatory diseases of the intestinal tract.

Abstract: Presenter(s): Karina Mak
School: University of Chicago
Session: Poster P1.25
Title: Predictive Value Of Auscultatory Crackles For Survival In Patients With Fibrotic Lung Disease
Advisor(s): Ayodeji Adegunsoye, Pulmonary Medicine, The University of Chicago

Co-Author(s): Spring A. Maleckar; Rachel Strykowski; Cathryn T. Lee; Kavitha Selvan; Renea Jablonski; Rekha Vij; Mary E. Strek

Abstract: Auscultatory crackles are assessed during clinical physical examinations, and may suggest scarring within the lungs of patients with fibrotic lung disease (FLD), which is associated with substantially reduced life expectancy. Few studies have assessed whether crackles can be used as a diagnostic tool for the early identification of FLD. We conducted a retrospective analysis of patients enrolled in the University of Chicago ILD Registry (2006-2021). We investigated the prevalence of crackles at baseline and evaluated their relationship with mortality. 1176 subjects with FLD were included in this analysis. Most patients had auscultatory crackles (n=922, 78.40%). Crackles were prevalent across all subtypes, with idiopathic pulmonary fibrosis (n=344, 37%) being the leading diagnostic subtype. Most patients who died had crackles (n=349, 88%), and this majority was consistent across all subtypes. Overall, patients with crackles were associated with higher rates of mortality (n=308, 33.4%) than patients without crackles (n=41, 16.1%; P<0.0001). Patients with crackles had a shorter mean time to death (n=308, 1073.95 days) than patients without crackles (1477.2 days, n=41, P=0.021). Auscultatory crackles are associated with increased mortality in fibrotic lung disease, suggesting the importance of early identification for interventions to improve outcomes. Future studies could differentiate further within types of crackles.

Abstract: Presenter(s): Franccesca Mamani
School: Beloit College
Session: Poster P1.22
Title: Perceptions of Art Therapists and Educators About Art as a Therapeutic Process
Advisor(s): Suzanne Cox, Psychology, Beloit College
Co-Author(s):

Abstract: Latinx youth experience increased rates of mental health challenges, such as depression and anxiety, compared to other cultural groups. Art and art therapy can provide ways for youth to express their difficulties. The current study explores the experiences of art therapists and educators to better understand the use of art as a therapeutic process for Latinx youth. Implementing qualitative research methods, three participants – two art therapists and one art teacher – were interviewed in order to identify areas of concern among professionals working with Latinx youth. In addition, the approaches professionals use with clients and students when using art as a therapeutic process were also also explored. The interviews were coded for thematic content. Three themes emerged from the interviews: (1) stress rooted in immigration issues, (2) pandemic impacts, and (3) approaches to using art with children. The role of stress related to both immigration concerns and the ongoing pandemic are particularly relevant for the mental health of today's Latinx youth. The application and incorporation of an intersectional lens are critical next steps for future research addressing and fulfilling the mental health needs of Latinx youth.

Abstract: Presenter(s): Athziri Marcial Rodríguez
School: St. Olaf College
Session: Poster P3.15
Title: Understanding the Genetic Architecture of Congenital Hydrocephalus using Whole Genome Sequencing

Advisor(s): Sheng Chih (Peter) Jin, Genetics and Pediatrics, Washington University School of Medicine

Abstract: Congenital hydrocephalus (CH) describes the drainage failure of cerebrospinal fluid (CSF) and subsequent abnormal accumulation of CSF in the brain of newborns. As a result of CH, cerebral ventricles are enlarged, causing increased cerebral pressure. With approximately 69,000 reported cases of CH in the United States each year, this condition makes up one-third of all congenital malformations in the nervous system (Bondurat et al. Pediatric neurosurgery 1995). Research suggests that nearly 40% of familial CH cases result from uncertain genetic etiologies. (Haverkamp et al. European Journal of Pediatrics 1999). Given the severity of CH, in addition to the inefficiency of its treatment, a pressing need exists to understand the genetic underpinnings of CH to improve therapeutic approaches. Whole-genome sequencing (WGS) has allowed for the uncovering of both coding and non-coding variants associated with CH. We identified de novo coding and non-coding variants in three parent-offspring trios using an extensive bioinformatics pipeline.

Abstract: Presenter(s): Kristin Martens, Rachel Trebesch
School: Gustavus Adolphus College
Session: Oral I.D.1
Title: Role of RNA structure in gene regulation by sRNA
Advisor(s): Janie Frandsen, Biology and Molecular Biology, Gustavus Adolphus College

Abstract: Antibiotic resistance is a major public health issue worldwide. As researchers work to develop new antibiotics against these infections, targeting bacterial non-coding RNAs such as small RNAs (sRNAs) will be crucial. These RNAs regulate gene expression during bacterial stress responses. It is known that sRNAs bind to multiple mRNAs; however, it is not understood what features of this interaction dictate mRNA binding order. This research seeks to understand the structure-function relationship of the sRNA-mRNA interaction in Escherichia coli by studying sRNA binding site accessibility within mRNAs. Computational data mining of existing structure probing data of the E. coli genome provides insight into mRNA structures and the accessibility of the sRNA binding sites. Based on what is known about the mechanism of regulation by sRNAs, we hypothesize that repressed genes will have a higher sRNA binding site accessibility, and activated genes will have a lower sRNA binding site accessibility. Analysis of numerous mRNA targets has helped determine trends in binding site accessibility for four sRNA targetomes. Overall most targets follow the hypothesis, though outliers exist and warrant further study. Ultimately, applying the knowledge gained from this work will be useful in developing antibiotics that hinder regulation by sRNAs.

Abstract: Presenter(s): Katherine Miao
School: University of Chicago
Session: Oral II.E.3
Title: Real-Time Processing of Ultrasound Images to Assess the Outcomes of Ablation Therapies
Advisor(s): Kenneth Bader, Department of Radiology, University of Chicago

Abstract: Histotripsy is a focused ultrasound therapy that can ablate tissue noninvasively using highly intense ultrasound pulses, which generate bubbles spontaneously within the tissue that destroy cells through their mechanical activity. Histotripsy is guided by ultrasound, which can track the bubbles. However, changes in the tissue due to ablation are not as apparent with ultrasound imaging, and physicians must use additional imaging modalities to determine the ablation extent, which increases the time, complexity, expense, and possibly degree of radiation exposure. Improving the ability to identify ablation zones through the integration of real-time feedback through a machine learning model is thus crucial for increasing the efficacy of histotripsy treatment. The mechanism of creating real-time feedback involved retraining the ResNet-18 convolutional neural network through transfer learning on B-mode ultrasound imaging data. Frame-by-frame segmentation was performed on images acquired by the Verasonics research ultrasound system obtained from tissue-mimicking red blood cell phantoms during histotripsy treatment, resulting in classifications of viable and ablated tissue and displaying a labeled overlay of the network output on the original images in real time. Statistical assessments of segmented images reveal the need for the network to be retrained on unmodified, rather than high-contrast, data to more accurately perform segmentation.

Abstract: Presenter(s): Emma Montgomery
School: University of Chicago
Session: Oral II.H.3
Title: Development of transgenic zebrafish model with human insulin
Advisor(s): Ryan Anderson, Department of Medicine,University of Chicago
Co-Author(s): Raghavendra Mirmira and Ryan Anderson

Abstract: Certain coding mutations in the insulin gene underlie Mutant Insulin-gene-induced Diabetes of Youth (MIDY), a genetic form of Diabetes Mellitus. These drive hyperglycemia by disrupting insulin folding, secretion, and signaling, yet many mutations remain sparsely characterized. Zebrafish, given their experimental attributes as well as their conserved digestive anatomy and insulin signaling pathway, are effectively used to model human metabolic diseases. Here, we describe a 'humanized' zebrafish designed to investigate cellular and physiological consequences of MIDY. A human preproinsulin sequence with C-peptide embedded EGFP (ICE) was cloned into a transgenesis vector containing zebrafish insulin promoter to generate ins:ICE, which drives ICE expression specifically in zebrafish beta cells. When transgenic zygotes bearing ins:ICE were injected with an anti-preproinsulin morpholino (insaMO), insulin was undetectable by immunofluorescence in insaMO-injected control embryos; however, both EGFP and human insulin were detected in injected ins:ICE embryos. Moreover, EGFP was expressed in a punctate manner, indicating human C-peptide-GFP is trafficked with insulin to secretory granules. insaMO-injected embryos showed elevated blood glucose that was abated by the presence of ins:ICE, demonstrating that human insulin can compensate for the diminution of piscine insulin. This model is tailor-made to investigate various MIDY mutations and probe the molecular pathogenesis of MIDY.

Abstract: Presenter(s): Kanon Nakajima
School: Macalester College
Session: Poster P1.06
Title: Therapeutic effect of coordinated reset deep brain stimulation on parkinsonian gait
Advisor(s): Jing Wang, Neurology, University of Minnesota - Twin Cities

Co-Author(s): Kai Bosley, Ziling Luo, Wyatt Doepke

Abstract: Traditional deep brain stimulation (tDBS) is effective in treating motor deficits in Parkinsonian patients, however, spread of current into unintended brain regions has been associated with undesired side effects. Coordinated Reset DBS (CR DBS) has shown therapeutic effects that can sustain for days or weeks after stimulation cessation by delivering electric pulse trains at a significantly reduced current level through multiple, randomized DBS lead contacts and thus alleviating undesired current spread. This study examined effects of CR DBS on parkinsonian gait in a non-human primate. An adult rhesus macaque was rendered parkinsonian via MPTP injections and implanted with a DBS lead in the subthalamic nucleus. CR DBS was delivered for 4 hours per day over 5 days. Changes in rigidity, akinesia and bradykinesia were assessed using a clinical rating scale (mUPDRS) before, during, and after CR DBS and gait was assessed before and after CR DBS. Mixed results were seen in the animal's gait (Matlab) although significant improvements were observed in other motor symptoms. In addition, Specifically, the animal's stride length and swing speed were decreased at a few limbs, however, the variance in these parameters was reduced, suggesting that the gait pattern became more consistent after CR DBS.

Abstract: Presenter(s): Linda Nduwimana
School: Hope College
Session: Oral II.F.4
Title: Can you hear me?: Anthropogenic influence on Auditory Sensitivity of the House Sparrow (Passer domesticus)
Advisor(s): Kelly Ronald Biology, Department, Hope College
Co-Author(s): Suihnem Mawi

Abstract: Animal communication involves a sender producing a signal (e.g., a vocalization) that travels through the environment before being detected by a receiver. Increased urbanization can complicate receiver sensory processing as anthropogenic activities (e.g., noise pollution) affect the way birds communicate. This study examined the influence of urbanization on the auditory processing system of house sparrows (Passer domesticus), known for inhabiting urban areas and relying on vocal cues from conspecifics. Birds (N = 48) were collected across an urbanization gradient in Holland, Michigan. Auditory brainstem response (ABR) tests were performed to examine auditory sensitivity, specifically ABR amplitude (magnitude of the response) and threshold (the lowest intensity level at which there is still an ABR). We predicted decreased auditory sensitivity in urban birds because they are exposed to consistent anthropogenic noise. Moving from rural to urban, we expected decreases in amplitude and increases in threshold. Our results showed a significant three-way interaction between frequency, sex, and urbanization level on threshold. ABR amplitude was affected by a three-way interaction between date of ABR test, frequency, and urbanization level. Results of this study will provide insight to understanding the impacts on bird communication, especially in regards to mate choice and reproductive success.

Abstract: Presenter(s): Jerry Ngo
School: Beloit College
Session: Poster P3.01
Title: Is CLIP Fooled by Optical Illusions?
Advisor(s): Mehmet Dik, Department of Mathematics, Beloit College

Co-Author(s): Swami Sankaranarayanan, Phillip Isola

Abstract: Recent large machine learning models have achieved impressive performance on perception tasks such as classification or object detection, especially on unseen data. While it is unclear if they model the human cognitive process, they provide a compelling framework for case study and analysis. In this work, we test one such hypothesis: To what extent do large vision language models mimic the human cognitive system? We attempt to answer this question by focusing our attention on the ability of such models to perceive optical illusions. We analyze the CLIP model as a visual system, presenting stimuli in the form of image and text prompts and observing how the model's classification score changes under different illusory strengths. Our results show that CLIP is fooled by different types of illusions relating to lightness and geometry.

Abstract: Presenter(s): Maya Olcer
School: University of Chicago
Session: Poster P3.13
Title: Characterizing SARS-CoV-2 Spike Protein Specific Memory B Cells after Vaccination through Flow Cytometry and ELISpot**.**
Advisor(s): Angeline Rouers, Infectious Diseases Labs - Laboratory of Pathogen Immunobiology, Agency for Science, Technology and Research (A*STAR**)**

Abstract: Over 11 billion Covid-19 vaccines have been administered around the world, reducing the severity and morbidity of Covid-19 disease. The production of long-lasting memory B cells (MBCs) specific for SARS-CoV-2 following vaccination is essential for protection against new emerging variants. This project focused on the characterization of MBCs specific for the spike Receptor Binding Domain (RBD) of SARS-CoV-2 in vaccinated individuals at different timepoints and those receiving different booster types. An RBD-DyLight probe was validated and implemented in flow cytometry to reveal RBD-MBCs. In parallel, we developed a B-cell ELISpot assay to detect antibody-secreting RBD-MBCs. In line with previous studies, a sharp increase in RBD-MBCs post-vaccination was noted alongside a more effective response in individuals who received two doses of BNT162b2 followed by mRNA-1273 compared to a triple BNT162b2 regime. We identified subpopulations of MBCs based on CD21 and CD27 expression where RBD-MBCs mostly displayed activated memory (CD21-CD27+) and resting memory (CD21+CD27+) profiles. While flow cytometry and B-cell ELISpot highlight different aspects of the RBD-MBC response, we found a positive correlation between the two methods. We finally proposed to integrate ELISpot and flow cytometry to obtain a more comprehensive platform to characterize RBD-MBCs for the purpose of vaccine monitoring.

Abstract: Presenter(s): Julia Owens
School: Carthage College
Session: Poster P2.02
Title: Facultative interactions between ants, aphids, and black-eyed pea
Advisor(s): Mary McKenna, Biology, Howard University

Abstract: Black-eyed pea (Vigna unguiculata) produces nectar in extrafloral nectaries (EFNs), on stems and leaves. EFNs attract ants that consume EFN nectar and protect plants from herbivores. This ant-plant mutualism can be disrupted when aphids are present. Aphids are

herbivores that provide sugar to ants by excreting “honeydew”. Aphids can parasitize the ant-plant mutualism by stealing the plant’s sugar and protection from ant “bodyguards”. The previously low population of aphids increased rapidly after ants established themselves on plants in the field plot, and we observed aphid-tending behavior by ants. Ant presence negatively affected shoot and fruit weight, which is likely related to the high costs of ant-tended aphids removing sugar from plants. The lowest plant growth and reproduction was seen in plants with ants and sealed EFNs. Aggressive aphid tending behavior is likely on these plants since ants received no EFN-nectar. A trend for less severe negative effects of ants was found on shoot and fruit weight when nectar was available. Vigna unguiculata is a critical source of global food security in the face of climate change threats. This study may provide ecological insights for ways to employ agroecological approaches to increase yields of black-eyed pea in the future.

Abstract: Presenter(s): Ved Patel
School: Washington University in St. Louis
Session: Poster P1.20
Title: The extent and function of SVEP1 glycosylation
Advisor(s): Nathan O. Stitziel, Cardiovascular Genetics, Washington University in St. Louis
Co-Author(s): Paul Lee, Ryan Wagoner, Jared S. Elenbaas, Arturo Alisio,

Abstract: SVEP1 is an extracellular matrix protein that promotes coronary artery disease in humans and mice, although its biochemical characteristics remain largely unstudied. Leveraging results of a recent genome-wide association study of plasma SVEP1 levels, we identified proteins that may influence the production or modification of SVEP1.

Variation in the ST3GAL4 and ASGR1 loci, which encode proteins related to glycosylation, associated with altered SVEP1 protein concentrations at genome-wide significance, leading us to hypothesize that SVEP1 is glycosylated. Enzymatic deglycosylation of recombinant SVEP1 resulted in a ~30 kDa mass shift, confirming that SVEP1 is a glycoprotein, and mass spectrometry identified 11 high-confidence N-linked glycosylation sites. Using biolayer interferometry (BLI), we found that deglycosylated SVEP1 had a fivefold-lower binding affinity to PEAR1 relative to native SVEP1. SVEP1 deglycosylation did not result in a difference in canonical PEAR1 signaling in VSMCs or cell adhesion in HUVECs compared to native SVEP1. siRNA-mediated inhibition of ST3GAL4, a sialyltransferase suspected to be involved in SVEP1 glycosylation, did not affect SVEP1 abundance or secretion in transfected HEK293T cells.

SVEP1 glycosylation alters binding affinity with PEAR1, but the physiological impact of decreased binding remains unclear. Future studies investigating the role of glycosylation on SVEP1 oligomerization and stability are planned.

Abstract: Presenter(s): Trinity Pirrone
School: Macalester College
Session: Poster P1.13
Title: Overlapping Populations of VIP and CCK Neurons Coexpress the Y1 Receptor in the Inferior Colliculus
Advisor(s): Michael Roberts, Otolaryngology, University of Michigan
Co-Author(s): Audrey Drotos

Abstract: The inferior colliculus (IC) is an auditory midbrain region. It is an essential site for the processing of complex vocalizations, among other auditory functions. Recently, we discovered the first molecularly identifiable markers of distinct neuron classes in the IC: vasoactive intestinal peptide (VIP) and neuropeptide-Y (NPY) neurons. Current research suggests that NPY neurons input to neurons that express the Y1 receptor (Y_1R). Additionally, other research has suggested CCK as a potential distinct neuron class. Based on this previous research, our study aims to answer two questions: (1) Do CCK and VIP neurons express the Y_1R receptor, suggesting input from NPY neurons? (2) Does VIP and CCK expression represent distinct neuron populations? To explore these questions, we performed an RNAscope assay in mouse IC slices and specified probes for three biomarkers: CCK, VIP and Y_1R. The slices were imaged using a confocal microscope. Quantification of images was approached using a customized MATLAB code for colocalization and counting using Neurolucida. Our results indicate that most CCK and VIP neurons coexpress Y_1R, suggesting that CCK and VIP neurons receive input from NPY neurons. The results also indicate that CCK and VIP are coexpressed by a subset of inferior colliculus neurons.

Abstract: Presenter(s): Natalia Quizena
School: Hope College
Session: Poster P2.09
Title: Characterization of novel peptide binding in HUVEC cells using fluorescence polarization approach
Advisor(s): Maria Burnatowska-Hledin, Biology, Hope College
Co-Author(s):

Abstract: Previous studies in our lab identified a novel peptide Ligand Barno (LB) that regulates cellular signaling in endothelial cells (HUVEC) and inhibits cell proliferation. The aim of this study was to determine if this effect is dependent on the presence of VACM-1/cul5 gene known to regulate cell growth. Fluorescently labeled ligand was used to determine its binding characteristics in control HUVEC and in cells where VACM-1/cul5 was knocked out using the CRISPR approach. Our preliminary results suggest that there is no difference in LB in the two cell lines. Further studies are needed to identify the protein LB binds to.

Abstract: Presenter(s): Rays Wahba
School: Washington University in St. Louis
Session: Poster P2.19
Title: Sex-Differences in Seasonal Adaptation of Circadian Behaviours
Advisor(s): Erik Herzog, Biology, Washington University in St Louis
Co-Author(s): KL Nikhil

Abstract:
The avian group of raptors exhibits a trait known as Reverse Sexual Size Dimorphism. Females in the raptor group are larger than males, while in most other birds males are the larger sex. Despite its prevalence among raptorial species, when sex differences in morphology manifest during development is little understood, particularly in owls. We sought to address this gap by studying morphological development in Flammulated Owls (Psiloscops flammeolus), an insectivorous owl that breeds in Ponderosa Pine ecosystems in western North America, and winters in Mexico and Central America. Specifically, we analyzed growth

rates and blood sex data in nestling owls in order to reveal sex-based patterns of development. Over the span of about 40 years, data has been collected on various broods of owlets, measuring their weight and growth of flight feathers over the duration of their nestling period. In the past 20 years, blood samples have also been collected from the owlets and analyzed in a lab to determine the sex of the owlets, since sex of owls cannot be determined by plumage characteristics or external morphology. By combining the blood sex data and growth data, we were able to reveal trends in owlet growth based on their sex.

Abstract: Presenter(s): Benjamin Reister
School: St. Olaf College
Session: Poster P2.05
Title: Bcd1 localizes to the selected meiotic nucleus in Tetrahymena thermophila conjugation, giving rise to pronuclei
Advisor(s):
Co-Author(s): Eric Cole, Biology, St. Olaf College

Abstract: The BCD1 gene has been shown to be involved in conjugation through analysis of the conjugal-block phenotypes of defective mutant alleles (bcd1.1 and bcd1.2). Until now, no research has been done to localize the BCD1 gene product during conjugation. Using a wild type cell line that is expressing a BCD1:GFP fusion-gene from the endogenous BCD1 promoter, three matings were performed: a diploid x diploid mating, a diploid x aneuploid mating, and a diploid x bcd1.2 mutant. Samples of each mating were taken at various times during conjugation, fixed, dried onto coverslips, and the labeling was enhanced using anti-GFP antiserum. Microscopy of the resulting samples revealed consistent Bcd1:GFP decoration of the 'selected' micronucleus for each mating, the specific nucleus that subsequently gives rise to gametic pronuclei through a 3rd, gametogenic mitosis. In aneuploid matings, Bcd1:GFP labeling of gamete pronuclei persisted long after it was cleared from the nuclei of diploid matings. We discuss implications of Bcd1 localization on our understanding of the bcd1 conjugal phenotype.

Abstract: Presenter(s): Ziyu Ren
School: University of Chicago
Session: Poster P3.24
Title: Impact of language on promoting blood donation
Advisor(s): Boaz Keysar, Department of Psychology, University of Chicago
Co-Author(s): Leigh H. Grant

Abstract: Blood donation is an essential component of a functioning healthcare system. However, globally there are critical blood shortages. Therefore, it is important to find techniques to increase blood donation, such as utilizing more effective messaging. Previous studies show that self-oriented, benevolent messaging is more effective in driving blood donation intentions and behaviors than other-oriented, altruistic messaging. However, these studies were conducted in more individualistic, Western countries where people value independence and self-interest. Here, we tested whether benevolence messaging still outperforms altruistic messaging in China, or if in a collectivistic context, altruistic messaging may outperform self-oriented benevolence messaging. We recruited 105 native Chinese speakers who speak English as a second language, and randomly assigned them to read either an altruistic-focused message or a benevolence-focused message. Then, we assessed

their blood donation intentions, attitudes around blood donation, and finally whether they clicked a link to find a donation center. We found that following the altruism-focused message, Chinese participants were more likely to follow the link to look up a donation center than after reading the benevolence-focused message. These findings are both theoretically and practically important, as effective blood donation messaging may need to be culturally tailored to best appeal to a target audience.

Abstract: Presenter(s): Emma Rudisel
School: Hope College
Session: Oral II.E.1
Title: Use of mass spectrometry-based proteomics to study the mitochondrial transcription machinery
Advisor(s): Kristin Dittenhafer-Reed, Chemistry, Hope College

Abstract: Mitochondria are unique sub-cellular compartments that contain their own genome that carries the genetic code for 13 protein subunits required for the synthesis of ATP. Currently, the regulation of mitochondrial gene transcription in response to changing energetic needs is not well understood. We hypothesize that protein post-translational modifications (PTMs) play a role in nutrient sensing and the control of mitochondrial transcription, similar to some mechanisms that control nuclear gene expression. We used liquid chromatography tandem mass spectrometry (LC-MS/MS) to identify PTMs on the mitochondrial protein expression machinery, including the mitochondrial RNA polymerase protein (POLRMT) and the ribosomal protein L12 (MRPL12). POLRMT and MRPL12 were overexpressed in mammalian cells and immunoprecipitated. Immunoprecipitated proteins were subject to trypsin digestion and the resulting peptides were analyzed by LC-MS/MS. Spectral library searching was then used to identify peptides and PTMs. We obtained 41% sequence coverage for MRPL12 and 20% for POLRMT. We identified three distinct PTM sites on MRPL12 and nine on POLRMT, including acetylation and phosphorylation sites. These PTM sites are being further characterized in the Dittenhafer-Reed lab in order to develop a better understanding of the roles of PTMs in mitochondrial transcription and translation regulation.

Abstract: Presenter(s): Sarah Senese
School: Colorado College
Session: Poster P3.22
Title: Populus deltoides leaf morphology and developmental age
Advisor(s): Shane Heschel, Organismal Biology & Ecology, Colorado College

Abstract: Native cottonwoods are keystone species in riparian ecosystems across the Southwest. Populus deltoides grows from the eastern to southwestern United States and thrives in riparian habitats. Across the genus, poplars have been shown to exhibit either a conservative strategy where they restrict water use under stress conditions, or a riskier strategy in which they continue to function under increasing water stress despite the low soil moisture and/or high vapor pressure deficit. Facing varied physical and biotic conditions throughout Populus deltoides large species range, population variation—especially in leaf economic traits and morphology—is common and pronounced (Dunlap and Stettler 2001). Leaf morphological traits like stomatal density and aperture and their regulation are of main interest in the study of drought adaptation and plasticity in semi-arid and heat-stressed

climate conditions. Interestingly, past work has indicated that cottonwood leaf traits and water relations can vary with development, such that the importance of leaf traits to viability might change with age. Population transition matrices might depend on a combination of leaf morphology/physiology and cottonwood age in the riparian systems of the Southwest. We asked the following: How do leaf/stomatal morphology traits with age? Do stomatal traits and photosystem efficiency have any significant relationship?

Abstract: Presenter(s): Rhea Shah
School: University of Chicago
Session: Oral II.G.3
Title: Evaluating the efficacy of stapled peptide inhibitors in dampening regulatory T cell functioning
Advisor(s): James LaBelle, Section of Pediatric Hematology-Oncology, Department of Pediatrics, University of Chicago
Co-Author(s):

Abstract: Immune homeostasis is maintained largely through regulatory T cells (Tregs), which suppress effector T cell function to prevent autoimmunity. However, in the context of cancer, excess Tregs diminish the tumor-battling ability of effector T cells. By targeting the protein-protein interactions (PPIs) of the master transcription factor Forkhead Box P3 (FOXP3), we aim to limit suppressive programs in Tregs while allowing for effector T cell expression programs, thus amplifying the anti-tumor immune response. LaBelle laboratory members have previously synthesized and tested several stapled alpha-helical peptides (SAHs) targeting the FOXP3 homodimer PPI, supporting the hypothesis that the FOXP3 SAHs have a deleterious impact on Treg function. My project investigates the second iteration of FOXP3 SAHs, optimized to have increased membrane permeability and a shortened length with the aim of dampening Treg functioning more effectively. I aim to evaluate the specificity of the SAHs in binding FOXP3 through binding assays, as well as the effectiveness of the SAHs by analyzing genetic changes in regulatory T cell functioning upon peptide treatment. Preliminary studies demonstrate promise of their being effective anti-cancer therapeutic agents.

Abstract: Presenter(s): Julia Sheehan-Klenk
School: Grinnell College
Session: Oral I.B.1
Title: Tumor immunologic response activated by β- and α-particle emitting radionuclides is influenced by dose rate
Advisor(s): Zachary Morris, Department of Human Oncology, University of Wisconsin School of Medicine and Public Health
Co-Author(s): Caroline P. Kerr, David Adam, Joseph J. Grudzinski, Thanh Phuong T. Nguyen, Maria Powers, Paul A. Clark, Carolina A. Ferreira, Reinier Hernandez, Bryan Bednarz, Jamey P. Weichert

Abstract: Targeted radionuclide therapy (TRT) can deliver systemic, immunomodulatory radiation to all tumor sites. The distinct physical properties of radionuclides (e.g., emission type, linear energy transfer (LET)) could confer timing, magnitude, and duration differences in tumor microenvironment immunologic responses. Three radionuclides – Y-90, Lu-177 (beta-particle emitters), Ac-225 (alpha-particle emitter) – were compared in vitro to measure the

type I interferon (IFN1) response using MOC2 head and neck squamous cell carcinoma / B78 melanoma murine tumor models. Radionuclides free-floating in culture media above the cell monolayer delivered continuous radiation: 12 Gy (MOC2) and 4 Gy (B78) (Medical Internal Radiation Dose method). RT-qPCR was performed on cDNA isolated from cells 1, 3, and 7 days after irradiation. Cells were fixed and stained with DAPI/γ-H2AX antibody for immunofluorescence microscopy at the same timepoints. Given its greater LET, Ac-225 induced more double stranded DNA breaks than Y-90 or Lu-177. Y-90 and Ac-225 upregulated IFN1-response associated genes: Ifnb1, Mx1. γ-H2AX foci counts/cell increased significantly, accumulating over time following Ac-225, but not Y-90 nor Lu-177. For radionuclides with varying LET and pathlengths, dose rate influences in vitro tumor immunologic response timing. Understanding radionuclide-induced immunologic effects on cancer cells could further integrate TRT and immunotherapies clinically, enhancing patient anti-tumor immunity.

Abstract: Presenter(s): Emily Shi
School: University of Chicago
Session: Oral II.E.4
Title: BACH1 modulates the hypoxia response through chromatin organization in Triple Negative Breast Cancer Cells
Advisor(s): Marsha Rosner, Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Long Nguyen, Peter Yang

Abstract: Hypoxia is a hallmark of aggressive solid tumors. Pro-metastatic transcription factor BTB and Domain CNC Homolog I (BACH1) is shown by the Rosner Lab to be stabilized and activated under hypoxia. However, the role of BACH1 in hypoxic stress to promote tumorigenesis is largely uncharacterized. Through ATAC-sequencing analysis, we first showed that BACH1 promotes maintaining chromatin accessibility under chronic hypoxia. Moreover, genome motifs of chromatin epigenetically affected by chronic hypoxic stress were similar to known BACH1 motifs, which suggests BACH1 potentially acts as a direct remodeler of chromatin under hypoxia. We discovered that BACH1 binds directly to the promoter region of and promotes the expression of lysine methyltransferase 2A (KMT2A), an enzyme responsible for H3K4me3. Consistently, knocking out BACH1 reduced global histone 3 lysine 4 trimethylation (H3K4me3), which is a canonical chromatin opening marker. Combining RNA-seq and ATAC-seq data showed 761 genes, with a top function of chromatin organization, had both decreased expression and more chromatin closure under hypoxia in BACH1 knockout. Genes involved in chromatin organization are also highly correlated to BACH1 expression and poorer survival in breast cancer patients. This observation proposed a novel BACH1-dependent chromatin remodeling of tumor cell adaptation under hypoxia to promote metastasis.

Abstract: Presenter(s): Amira Siddique
School: Knox College
Session: Poster P1.02
Title: On the clinical relevance of comparative jaw joint biomechanics across mammals
Advisor(s): Nicholas J Gidmark , Biology, Knox College
Co-Author(s): L Odette Herrand, Alyssa Stringer, Emily D McParland, Courtney Orsbon, Peishu Li

Abstract: Mammalian masticatory musculoskeletal anatomy is diverse and correlated with functional demands – e.g. processing various food types. One implication for such interspecific anatomical variation is that pathologies in the jaw-closing system could present differently across taxa. Disorders of the human jaw joint (termed temporomandibular disorders or TMD) afflict millions worldwide. Experimental studies of TMD utilize a wide range of model organisms (mice, rats, rabbits, sheep, pigs, and monkeys) with astounding variation in musculoskeletal form. Here we compare a wide variety of biomechanically-relevant musculoskeletal attributes across these model organisms. Specifically, we explore which of these attributes are similar and different to humans to determine which model organisms' jaw-closing system musculoskeletal anatomy most closely resemble humans'. Preliminary multivariate analyses show that TMJ skeletal anatomy of humans (e.g., fossa depth, eminence height, condylar angle, etc.) is most similar to sheep, pigs, and monkeys. Rabbit TMJ morphology deviates from that of humans via steeper and deeper articular eminences. Human jaw adductor anatomy most closely resembles monkeys and rats, with similar length and torque moments of all four main masticatory muscles. We hope these results provide clinical researchers a framework for selecting the most appropriate model organism when studying TMD.

Abstract: Presenter(s): Kristin Simphoukham, Emma Stock
School: Gustavus Adolphus College
Session: Oral I.C.2
Title: Genome engineering in Arabidopsis thaliana to investigate environmental stress response
Advisor(s): Katie Leehy, Biology, Gustavus Adolphus College

Abstract: Climate change is an ever-evolving issue, impacting food supplies and crops. As climate change becomes more pressing, the need for specialty crops that can withstand changes increases. Arabidopsis thaliana is an important model organism in research as it has an easily manipulated genome, and is closely related to important plants. A recent stress screen identified hundreds of long intergenic noncoding RNAs (lincRNAs) in Arabidopsis that may relate to tissue-specific responses. Some noncoding genes have not yet been characterized in-vivo, and can be studied using CRISPR/Cas9. CRISPR constructs were developed to target twenty lincRNA genes to determine functionality. The long term goal is to further characterize these stress responses by knocking out the responsible genes, and to deepen the understanding of the role of lincRNAs under stress. To accomplish this, plasmids containing the Cas9 gene and synthetic guide RNAs were constructed. At this point, five gene-targeting Cas9 constructs have been transformed into Arabidopsis. These plants have produced seeds, which are being screened for modifications of the targeted genes. Once confirmed, we will use high-throughput phenotyping to evaluate the consequence of the loss of each of these lincRNAs on the growth of the plants in response to abiotic stress.

Abstract: Presenter(s): Ken Soe
School: Washington University in St. Louis
Session: Poster P3.18
Title: Molecular determinants of Matrin-3 toxicity and misfolding, and suppression of Matrin-3 toxicity by engineered protein disaggregases
Advisor(s): Meredith Jackrel, Department of Chemistry, Washington University in St. Louis

Abstract: Matrin-3 (MATR3) is an RNA- and DNA- binding protein with a wide range of physiological functions, including gene transcription, DNA damage response, and RNA splicing and degradation. Its dysfunction has been implicated in numerous neurodegenerative disorders, such as amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), and distal myopathy. Here, we report the development of a yeast model of MATR3 proteotoxicity and aggregation. Through protein overexpression, we recapitulate MATR3 misfolding in neurodegenerative diseases. By creating a series of domain deletions and mutations, we have elucidated the contribution of each binding domain of MATR3 in regulating its toxicity. Additionally, we study these constructs alongside a disaggregase in yeast, Hsp104, that has been previously shown to disaggregate and rescue toxicity of TDP-43 and FUS aggregates. We observe that MATR3 toxicity is largely driven by its RNA recognition motifs (RRM). Further, deletion of one or both RRMs drives protein coalescence into phase-separated condensates as seen in other RNA binding proteins (RBP) like TDP-43. Finally, by co-expressing the disease-associated variants with engineered Hsp104 variants, we demonstrate that we can reverse the misfolding of aggregates and rescue their toxicity. We suggest that these Hsp104 variants might be employed against a range of ALS/ FTD-associated aggregation-prone proteins.

Abstract: Presenter(s): Brian Sohn
School: Washington University in St. Louis
Session: Poster P2.11
Title: Probing the drivers of Staphylococcus aureus biofilm protein amyloidogenesis and countering biofilms with Hsp104 disaggregases
Advisor(s): Meredith E. Jackrel, Chemistry, Washington University in St. Louis
Co-Author(s): Matthew K. Howard, Karlie R. Miller, Jeremy J. Ryan, Andy Xu, Meredith E. Jackrel

Abstract: Bacteria primarily live in either the “free-floating” planktonic state or the “multicellular” sessile state. Once the “free-floating” bacterial cells transition to a surface-attached lifestyle, they transform from the planktonic state to the sessile state by forming complex three-dimensional polymer networks termed biofilms. Biofilms confer bacteria various advantages, such as antibiotics and antimicrobial resistance. Previous studies have shown that Phenol-Soluble Modulins alpha peptides (PSMα) heavily contribute to formation of these biofilms. Because we have limited understanding of the PSMα contribution of PSMαs to biofilm formation, we developed a genetically tractable yeast model system to study the properties of the PSMα peptides. We demonstrate that the PSMα peptides are toxic and insoluble in yeast. We find that the PSMα peptides form hollow, spherical vesicle-like structures. We also show that the glycine and threonine residues at position 6 may be key drivers of PSMα toxicity and aggregation. Beyond understanding biofilms, it is also important that new approaches be developed to counter them. We show that Hsp104, a hexameric AAA+ ATPase disaggregase, can counter toxicity, aggregation, and vesicle-formation of PSMα peptides. These findings are significant because our work not only improves molecular understanding of PSMα peptides, but also proposes Hsp104 disaggregases as a novel approach for countering potential therapeutic against biofilms.

Abstract: Presenter(s): Subhiksha Srinivasan
School: Lawrence University

Session: Oral II.F.2
Title: Exploring the infectious cause underlying dangerous, pain-related behaviors in horses
Advisor(s): LaTasha Crawford, Department of Pathobiological Sciences, University of Wisconsin - Madison

Abstract: Horses in pain will sometimes display behaviors that are misinterpreted as “bad” or dangerous, leading to punitive treatment or, in many cases, euthanasia due to safety concerns for the owners and quality of life concerns for the horse. Our collaborative veterinary research team found that horses displaying dangerous behaviors often showed signs of neck pain. Specialized post-mortem evaluation of these horses demonstrated inflammation affecting sensory neurons of the dorsal root ganglia, termed ganglionitis. Histology and immunohistochemistry studies showed neuronal injury and necrosis, suggesting the horses were experiencing neuropathic pain. Our goal was to determine the cause of this ganglionitis. In a retrospective study using FFPE blocks, we first had to optimize RNA/DNA extraction protocols to get the best yield. Next, we developed quality control PCR assays using the housekeeping gene, GAPDH, to test the DNA quality. We then investigated PCR and RT-PCR probes and parameters that can detect pathogens known to affect the nervous system in horses. Ongoing studies will build upon these data to determine if an infectious agent is associated with ganglionitis in these horses. Finding the cause of these pain-related behaviors will help us develop treatments and ultimately extend the lives of horses with ganglionitis pain syndrome.

Abstract: Presenter(s): Elizabeth Strandberg
School: St. Olaf College
Session: Poster P3.09
Title: Lipid droplet analysis in starved Tetrahymena thermophila: ERG6p expression and localization
Advisor(s): Kim Kandl, Biology, St. Olaf College
Co-Author(s): Sean Rogers, Evan Shoemaker

Abstract: Lipid droplets (LD) are organelles involved in cellular energy storage and lipid metabolism. Under starvation conditions, eukaryotic organisms respond by accumulating lipid droplets. However, the effect of starvation on lipid droplets and their associated proteins in the model organism Tetrahymena thermophila, a single-celled freshwater ciliate, is poorly understood. This research seeks to determine the precise timing of starvation in Tetrahymena and the effect of starvation on LD composition and associated proteins. Using fluorescent microscopy, we qualitatively observed a distinct visual difference between lipid droplets in cells starved for 0 to 3 hours and cells starved 6 to 24 hours in 10 mM Tris buffer (pH 7.4). One lipid droplet-associated protein of interest is ERG6p, an enzyme involved in the biosynthesis of ergosterol, a cholesterol-like membrane component. Using Tetrahymena genetically modified to express ERG6p-YFP, a modified ERG6p that fluoresces when induced with cadmium, we previously showed that ERG6p binds to lipid droplets. A change in ERG6p-YFP expression or localization between non-starved and starved cells may suggest that lipid droplets in nutritionally stressed cells undergo a change in chemical composition.

Abstract: Presenter(s): Nidhi Talasani
School: University of Chicago
Session: Oral II.H.1

Title: Effect of butyrate on tight junction protein and IL-22 expression
Advisor(s): Cathryn Nagler, Department of Pathology, University of Chicago

Abstract: The Nagler laboratory investigates mechanisms by which the gut microbiome can protect against the development of food allergies. More specifically, short-chain fatty acids such as butyrate have a variety of downstream effects to strengthen the epithelial lining and diminish an allergic response. Earlier work from the Nagler lab showed that butyrate-producing Clostridia induce a barrier protective response mediated by IL-22 that is important for maintaining immune homeostasis in the gut. Through this project, I hope to investigate the effects of butyrate and better understand the molecule's effects on strengthening the epithelial barrier. More specifically, I wish to investigate the expression of IL-22 by the lamina propria in butyrate-receiving mice. It has also been shown that tight junction proteins are necessary to barrier integrity and therefore I wish to measure the expression of different families of tight junction proteins by intestinal epithelial cells in butyrate-receiving mice. Through these experiments, I hope to determine if butyrate is essential to IL-22 and tight junction protein expression.

Abstract: Presenter(s): Madeline Taylor
School: Lawrence University
Session: Poster P2.10
Title: Exploring the Rhizosphere Microbiome of Hydroponically Grown Leafy Greens
Advisor(s): Relena Ribbons, Geosciences, Lawrence University
Co-Author(s): Amber Newma

Abstract: Microgreens are immature leafy vegetables that are popular superfoods for their short growing times and versatile growing conditions. Classifying the microbial communities for different microgreens can help us understand possible pathways to prevent crop diseases and promote plant growth; however, little information is available on the rhizosphere microbiome of leafy greens. We aimed to: 1) optimize hydroponic manifold assembly to support the growth of microgreen monocultures 2) design and optimize the process for harvesting rhizosphere film for DNA analysis and 3) determine the rhizosphere microbiome composition of four microgreens – Swiss chard, lettuce, kale, and basil. We used 16S rRNA and ITS genetic markers to quantify bacterial and fungal abundance for our four microgreens growing in hydroponic manifold set-ups. We engineered a single-level manifold holding 36 seedlings with its own growth light and water reservoir is an ideal set-up for monocultures. We developed, refined, and optimized a root scraping procedure to maximize the amount of rhizosphere film obtained from plant roots to consistently extract viable DNA. Future work should focus on further classifying and understanding the mechanistic role of rhizosphere microbiome in promoting plant growth in hydroponics settings.

Abstract: Presenter(s): Kevin Tovar
School: Macalester College
Session: Poster P1.23
Title: Characterizing methylisothiazolinone mediated changes in immune activities of murine labial fibroblasts
Advisor(s): Elena Tonc, Biology, Macalester College
Co-Author(s): Gloriah Omwanda, Mady Chen, Devavani Chatterjea

Abstract: Vulvodynia is a chronic vulvar pain condition, affecting ~10% of women identifying individuals. A history of allergies and recurrent vulvovaginal yeast infections are associated with an increased risk of vulvodynia. Exposure to solvents, paints, and household cleaners has also been connected to elevated vulvodynia risk, but no single agent has been linked to adverse outcomes. A significant portion of people have allergies and exacerbated inflammatory responses to methylisothiazolinone (MI), a widely used chemical preservative. We have previously shown dermal application of MI causes long-lasting genital sensitivity in mice. This suggests that MI is a candidate allergen that could provoke chronic pain in humans through increased and prolonged tissue inflammation. Furthermore, vulvar fibroblasts from patients with vulvodynia exhibit heightened inflammatory cytokine production upon ex-vivo activation. We are investigating the mechanism behind these inflammatory changes in our murine model of allergy-driven vulvodynia by characterizing fibroblast function following MI and bacterial activation. Specifically, given that tissue fibroblasts are capable of producing inflammatory cytokine IL-6 after repeated MI exposure, we are exploring if there is a difference in production of other cytokines, including IL-1β and TNF-α. Additionally, preliminary data show increased fibroblast death following ex-vivo treatment with MI that we are further investigating.

Abstract: Presenter(s): Jason Tran
School: Macalester College
Session: Poster P2.21
Title: Enhanced peroxidase activity in a directed evolution designed hemin-based enzyme
Advisor(s): Kathryn Splan, Chemistry, Macalester College

Abstract: Protein engineering is an emerging field that aims to enhance naturally occurring protein function by selective modification of structural motifs to gain functional changes. The field shows promise for improving efficiency in a variety of synthetic reactions. LmrR is a dimeric protein derived from Lactobacillus aureus bacteria, and has several traits making it an ideal platform for protein engineering projects. Its clear dimeric structure, distinct binding pocket and relatively small size make it easy to manipulate, and prior work with the Roelfes Group at the University of Groningen demonstrated catalytic potential. Directed evolution techniques were used to find several mutations of catalytic interest. In this work peroxidase-like activity was engineered into LmrR, with key mutations at sites A11H and A92H. Self assembly was used to integrate a hemin binding site, and binding site saturation was assessed using fluorescent assaying. Peroxidase activity was observed with UV-Vis Spectroscopy, with notable differences in peroxidase activity between mutants. The highest activity was observed in A11H A92H, reaching levels where concerns about spectroscopic limitations were noted. Overall, this work shows the potential of LmrR as a flexible, versatile catalytic platform for a wide range of possible functions.

Abstract: Presenter(s): Michelle Vu
School: Lawrence University
Session: Poster P2.12
Title: The Honeybee's Thermal Response to Changing Temperature
Advisor(s): Israel Del Toro, Biology, Lawrence University

Abstract: The European honeybee (Apis mellifera) is critically important for agricultural pollination ecosystem services. Even though Apis mellifera is a species known for its great

adaptive potential, populations have shown alarming declines in recent years. Climate change, along with parasites, pathogens, and pesticides, has been identified as one of the main reasons for the honeybee's decline. Still, we have limited knowledge of its effect on honeybees' thermal responses. In this study, upper and lower thermal tolerance was used to investigate the honeybee's response to changing ambient environmental temperatures. In the preliminary data, 394 honeybees in 18 colonies were tested. The Critical Thermal Maximum (CT max) was calculated to be 45.19 ± 4.93°C and the Critical Thermal Minimum (CT min) was 17.24 ± 2.63°C. There appears to be a weak positive relationship between the CT max of the honeybee and the monthly ambient temperature. On the other hand, the CT min is negatively correlated to the daily temperature of the environment. Results suggest that heat and cold tolerance is a unique additional Criterion for successful and sustainable beekeeping.

Abstract: Presenter(s): Jie Wang
School: Washington University in St. Loui**s**
Session: Poster P1.07
Title: Loss of Stathmin-1 Diminishes Hematopoietic Stem Cells' Self-Renewal Capacity in Mice
Advisor(s):
Co-Author(s): Laura Schuettpelz, Pediatrics, Washington University in St. Louis

Abstract: Stathmin-1 (Stmn-1) encodes a microtubule destabilizer phosphoprotein critical in cell-cycle progression. Stmn-1 has been correlated with poor prognosis in several cancers and is overexpressed in leukemia cells. Additionally, Stmn-1 is highly expressed in normal hematopoietic stem cells (HSCs), yet its role in them is not well-studied. We hypothesized that Stmn-1 may regulate key HSC properties including differentiation, self-renewal, and cycling. To assess these properties, in vitro colony-forming assays were conducted using HSCs from Stmn-1 wild-type (WT) and knockout (KO) mice. HSC cycling was analyzed using flow cytometry both at baseline and following 24 hours of cytokine stress. Preliminary studies show that loss of Stmn-1 results in reduced colony replating capacity as well as increased quiescence, with more WT than KO HSCs actively cycling (S/G2/M phase) both at baseline and after G-CSF stimulation. These data support our hypothesis that Stmn-1 regulates HSC differentiation, self-renewal, and cycling. In the lab, correlative in vivo studies are being performed and ongoing experiments are exploring the mechanisms of these effects, including the role of Stmn-1 on HSC microtubule dynamics. Given the relationship between HSC cycling and proliferation with leukemia, our data implicate Stmn-1 as a potential target for future therapies.

Abstract: Presenter(s): Amelia Wernsing
School: Gustavus Adolphus College
Session: Oral I.C.1
Title: Changes in the phosphorylation state of p38 MAP kinase accompany RCH induction in Drosophila melanogaster
Advisor(s): Yuta Kawarasaki, Biology, Gustavus Adolphus College

Abstract: Rapid cold-hardening (RCH) is a type of phenotypic plasticity that has been most extensively studied in insects. With its swift induction that occurs within minutes to hours, this response is recognized as one of the fastest acclimatory responses to cold in nature. Previous studies suggested the induction of RCH might be mediated by the function of the

p38 MAP kinase. In this project, we examined the changes in phosphorylation of the p38 MAPK by RCH induction in the fruit fly Drosophila melanogaster. In D. melanogaster, exposure to 5°C for 2 h was highly effective in inducing RCH, significantly improving survival of adult males to -4.5°C from 37% to 100%. Accordingly, we compared levels of phosphorylated p38 MAPK between untreated control and flies exposed to 5°C for 2 h using Western blot. In untreated control, relatively high abundance of phospho p38 was present. However, following 2 h at 5°C, intensity of the band corresponding to phospho p38 substantially diminished. Our initial results suggest that changes in the phosphorylation state of the p38 MAPK are associated with RCH induction in D. melanogaster. Future studies will investigate the rate at which levels of phospho p38 MAPK change during the induction of RCH.

Abstract: Presenter(s): Eliza Wiener
School: University of Chicago
Session: Oral II.H.4
Title: Understanding the function of neuronal cell surface proteins: Examining human teneurin-2 autoproteolysis
Advisor(s): Demet Araç, Biochemistry and Molecular Biology, University of Chicago
Co-Author(s): Jorge Alvarado

Abstract: Teneurin-2 (hTEN2) is a highly conserved transmembrane protein, with structural homologs found in organisms from C. elegans to humans. In humans, teneurin is essential for synapse formation and axon guidance, and its malfunction has been associated with neurodevelopmental and neurodegenerative diseases like Alzheimer's, Attention Deficit Hyperactivity Disorder, and Autism Spectrum Disorder. However, the mechanism of teneurin function remains unknown. Interestingly, hTEN2 is structurally similar to bacterial Tc toxins, proteins which self-cleave their C-terminal toxic domain to infect cells. Thus, self-cleavage, or autoproteolysis, of hTEN2's C-terminal toxin-like domain may be involved in its function. While autoproteolysis of the toxin-like domain was not previously observed in full length hTEN2, it was seen in an hTEN2 expression without the Ig-like domain. To test the role of the Ig-like domain in toxin-like domain release, this project examines the effect of targeted mutagenesis on several conserved residues in the interface between the Ig-like domain and toxin-like domain. Western blot showed evidence of a possible C-terminal cleavage product at 55 kDa, suggesting that the Ig-like domain contact site may contribute towards regulation of autoproteolysis. Thus, the Ig-like domain could be an avenue for further investigation into hTEN2 autoproteolysis.

Abstract: Presenter(s): Jia Wu
School: University of Chicago
Session: Poster P1.26
Title: The Role of Heat Shock Protein 25 (HSP25) on Intestinal Wound Healing
Advisor(s): Eugene Chang, Cadence Cham, University of Chicago Department of Medicine, University of Chicago

Abstract: Mucosal healing is an essential physiological response to inflammatory and injurious diseases of the intestinal tract, including inflammatory bowel diseases (IBD). Complete mucosal healing is closely associated with favorable clinical outcomes, more prolonged remission, and lower risks of complications. Yet, critical gaps remain in the

“players” involved and their mechanisms of action. In this regard, we found that a member of the heat shock protein family, Hsp25/27 (Hsp27 is the human homolog), is essential for the initiation and maintenance of mucosal healing following injury to the intestinal tract. Using in vitro scratch assays of intestinal epithelial cells from HSP25 WT, HSP25 KO, and HSP25+IEC mice, we will thus provide much-needed mechanistic insight into the role of HSP25 on a molecular and cellular level. Our studies can ultimately lead to the development and treatment of restoring intestinal homeostasis in patients with inflammatory diseases of the intestinal tract.

Abstract: Presenter(s): Violet Wu
School: University of Chicago
Session: Oral I.B.3
Title: Tumor Microenvironment Nutrients Constrain Tumor Lipogenesis by Impairing the Activity of SREBP Transcription Factors
Advisor(s): Alexander Muir, Ben May Department of Cancer Research, University of Chicago
Co-Author(s): Juan Apiz Saab, Patrick Jonker

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest cancers, with a 5-year survival rate of 11%. PDAC is characterized by a poorly perfused tumor microenvironment (TME), which leads to limited nutrient availability. To adapt to this nutrient-limited environment, cancer cells must adapt their metabolism. Identifying such PDAC adaptations to nutrient stress would help discover novel targets for the treatment of PDAC. With this in mind, we profiled metabolite concentrations in the interstitial fluid (IF), the perfusate of solid tissues and tumors, in a murine model of PDAC. We have used this information to develop a novel ex vivo cell culture model we called Tumor Interstitial Fluid Medium (TIFM) where PDAC cells can be grown in TME nutrient levels. We hypothesized that characterizing the metabolism of PDAC cells growing in TME nutrient constraints would reveal targetable metabolic liabilities. Transcriptomic analysis of PDAC cells growing in TIFM shows a substantial downregulation of target genes of the transcription factor SREBP. SREBPs are transcription factors that activate lipid biosynthesis in cells. We hypothesize that one or more nutrient(s) in the TME of PDAC tumors constrain lipogenesis by impairing the activity of SREBP transcription factors. We are now seeking to identify the exact nutrients that constrain SREBP activity and lipogenesis. To accomplish this, we are leveraging the tractable nature of TIFM to systematically identify the metabolite(s) responsible for this phenotype. Furthermore, we are also studying whether genetic or pharmacological inhibition of lipid uptake and transport effectively reduce cancer cell growth. Altogether, our work to understand how the nutrient microenvironment of PDAC tumors regulates lipid metabolism and cell growth suggests that the TME plays a crucial role in regulating SREBP regulation of lipid biosynthesis and could lead to the development of novel targeted therapies against PDAC.

Abstract: Presenter(s): Claire Wulf, Sarah Young
School: Carthage College
Session: Poster P2.24
Title: Tracking Regeneration of the Zebrafish Optic Nerve using the Optokinetic Response
Advisor(s): Steven Henle, Neuroscience, Carthage College

Abstract: Zebrafish have eyes similar to humans making them a useful model organism for studying vision. However, zebrafish are different in that they are able to regenerate their optic nerve after injury, which most other animals cannot. Measuring vision in people who have communicative ability is achieved using eye charts. Because fish cannot use an eye chart, we utilize the optokinetic response (OKR) that is present in virtually all vertebrates to determine if a zebrafish has eyesight. The OKR is observed by monitoring eye movement in response to visual stimuli. By injuring the optic nerve on a zebrafish we can track its regeneration by measuring the return of its OKR. Recorded videos of the OKR are then analyzed through a deep learning software called DeepLabCut. The analysis could be done manually, but computational methods save significant amounts of time. The software is trained through input of videos to recognize and track eye movement. It then produces a graph comparing the OKR of each eye. This provides insight to the functional process of regeneration, whereas previous work has focused on the anatomical process. Understanding the functional regeneration in zebrafish will aid in developing treatment for humans with optic nerve injuries.

Abstract: Presenter(s): Aditya Yelamali
School: Washington University in St. Louis
Session: Oral I.D.2
Title: Streptavidin-drug conjugates streamline identification of optimal toxic payloads for antibody-based hematopoietic stem cell transplantation conditioning
Advisor(s): John F. DiPersio, Department of Medicine, Division of Oncology Washington University in St. Louis (School of Medicine)
Co-Author(s): Stephen P. Persaud

Abstract: Although allogeneic hematopoietic stem cell transplantation (allo-HSCT) provides the best chance for cure of acute myeloid leukemia (AML), it requires that patients first undergo toxic, bone marrow-ablative conditioning with chemotherapy and/or irradiation. Antibody-drug conjugates (ADCs) provide a promising alternative, potentially enabling allo-HSCT conditioning with fewer toxicities. To facilitate the identification of optimal ADC payloads for allo-HSCT, we developed novel streptavidin(SAv)-drug conjugates which can be joined with any biotinylated antibody to rapidly produce ADCs. Using Click chemistry, we conjugated SAv to three toxic payloads: monomethyl auristatin E (MMAE), Duocarmycin SA (Duo), and PNU-159682 (PNU). We mixed each conjugate 1:1 with biotinylated murine anti-CD45.2 antibodies to produce CD45-ADCs, which we tested in vitro for cytotoxicity against the YAC-1 cell line, primary hematopoietic stem cells, and primary leukemia cells. We found that while CD45-Duo and CD45-PNU were effective against all tested cell types, CD45-MMAE was largely ineffective, suggesting that MMAE is an ineffective payload for ADC conditioning in mice. In conclusion, our novel system enabled rapid production of ADCs with various toxic payloads and screening of their efficacy as allo-HSCT conditioning agents. Future studies will evaluate human ADCs in vitro and in vivo for their ability to target human HSCs and AML cells.

Abstract: Presenter(s): Jessica Zhong
School: University of Chicago
Session: Poster P1.19
Title: Characterizing The Diversity Of Fungal-Algal Associations In Alaskan Lichens

Advisor(s): Matthew P. Nelson Negaunee Integrative Research Center, The Field Museum/The University of Chicago
Co-Author(s):
Abstract: Lichens, a stable and obligate association between fungi and algae, present one of the most striking models of symbiosis known to biology. However, the mechanisms that drive these partnerships are poorly understood due to both a relative lack of active research and their slow-growing and sensitive nature. Each symbiont varies in its partner selectivity and promiscuity and many even share partners. This ongoing project aims to shed light on how evolutionary history and ecological traits generate novel lichen structures by using DNA barcoding techniques to highlight variation in fungal-algal associations in the setting of the Alaskan tundra. The algal DNA from 338 samples across over 15 Alaskan lichen species was extracted and sequenced using FDG primers. This poster reports primarily on algae from Masonhalea richardsonii, a vagrant lichen, and Flavocetraria cucullata, a substrate-attached lichen, within the family Parmeliaceae. These closely related species share habitat ranges and compete for light and resources, so the degree to which they share algal communities is of interest. The highest quality sequences were used to generate a nucleotide alignment tree showing broad clustering of related Trebouxia algae lineages across the lichen species, revealing a significant degree of similarity between the photobionts present in these species across the central Alaskan range.

Abstract: Presenter(s): Marissa Zintel
School: Lawrence University
Session: Poster P1.12
Title: Stabilizing Porous Protein-DNA Co-Crystals via Auto-Disulfide Cross Linkages
Advisor(s): Christopher Snow, Chemical and Biological Engineering, Colorado State University

Abstract: Protein structure determination is a critical area of biochemical research, as a protein's 3-D structure can refine our understanding of its molecular mechanisms, suggest additional functions, and/or identify functional domains shared by other similar proteins. However, protein structure determination often depends on X-ray diffraction of protein crystals, which are time- and resource-consuming to produce. To address this, the Snow Lab has designed and validated a novel porous protein-DNA co-crystal scaffold where the DNA sequence acts as a customizable binding site for proteins of unknown structure. Unfortunately, these co-crystals are fragile in solutions other than their growth conditions. Thus, this project strategically engineered disulfide bonds at the crystal's protein-protein interfaces, thereby strengthening the crystal for guest addition. To create these disulfide bonds we targeted specific amino acids which, by mutating to cysteine, can form auto-disulfide linkages with neighbor proteins. The cysteine mutants were generated via site-directed mutagenesis, then expressed, purified, and tested with a thiol-reactive chemical to confirm the presence of the newly engineered free thiol. Future work will involve crystallization of the protein-DNA co-crystals, producing a strengthened crystal connected by strong covalent bonds. This stable molecular scaffold can then be used for efficient guest protein structure determination.

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Biological Sciences and Psychology
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