The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 2 & 3, 2018
The University of Chicago

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

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Program Schedule

Friday, November 2

1:00 pm – 5:15 pm	**Registration at LaQuinta Inn& Suites Lakeshore** **4900S Lake Shore Dr., Chicago, IL 60615** *(for late arrivals registration will be available outside the Hyde Park room during the program)*	**LaQuinta Inn Lobby**
5:30 pm – 5:40 pm	**WELCOME** John Kennedy and Victoria Prince Symposium Organizers, University of Chicago Michael Seymour, Director – Midstates Consortium for Math and Sciences; Hope College	**Hyde Park Room**
5:40 pm – 6:30 pm	**Keynote Lecture** **Carole Ober Ph.D** **Blum-Riese Distinguished Service Professor** **Chair, Department of Human Genetics** **University of Chicago** *The Hygiene Hypothesis and the Origins of Asthma – Studies in U.S. Mennonite Farming Communities*	**Hyde Park Room**
6:45 pm – 7:45 pm	**Dinner Buffet**	**Hyde Park Room**
8:00 pm – 8:45 pm	**Janet Anderson Lecture** **Dr. Neena Grover** **Professor of Biochemistry** **Colorado College** *My Journey as a RNA Biochemist*	**Hyde Park Room**
Following lecture	**Group Picture**	**Hyde Park Room**

Saturday, November 3

Begins at 6:30 am	**Breakfast**	**LaQuinta Inn Lobby**
Shuttle leaves to campus 7:45 am *(take this to set-up for Poster Session 1, others can take as well)* **8:15 am** *(don't miss this)*	**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 locked room for storage of luggage and posters at the meeting site**	**LaQuinta Inn Lobby**
8:15 am – 8:45 am	**Set-up for poster session 1** Check computer set-up for oral presentations	**GCIS Atrium**
8:45 am – 9:45 am	**Session 1 Poster Presentations** (30)	**GCIS Atrium**
9:45 am – 10:00 am	**Break, remove posters, check set-up for oral presentations in respective rooms**	**GCIS Atrium**
10:00 am -10:45 am	**Session I Oral Presentations of Student Papers** Session I.A: (3) Session I.B: (3) Session I.C: (3) Session I.D: (3)	**Kersten** Room 101 Room 103 Room 105 Room 120
10:55 – 11:50 am	**Presentation and Panel Discussion** *"How to continue your research training: attracting funding and considering whether graduate school is right for you"*	**Room 120**
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** (31)	**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: (4) Session II.F: (3) Session II.G: (3) Session II.H: (4)	**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** (31)	**GCIS Atrium**
4:45 pm – 5:00 pm	**Meeting Concludes** Remove posters Complete evaluations – available online Boxed dinners to go Shuttle pick up and return to the LaQuinta	**GCIS Atrium**

2018 Keynote Lecture

The Hygiene Hypothesis and the Origins of Asthma – Studies in U.S. Mennonite Farming Communities

Carole Ober, PhD
Blum-Riese Distinguished Service Professor
Chair, Department of Human Genetics
University of Chicago

Abstract: The prevalence of asthma and other immune mediated diseases has risen dramatically over the past 50 years in developed countries. A popular theory explaining this rise in prevalence is the Hygiene Hypothesis, which proposes that a “cleaner” lifestyle and less exposure to germs in early life over this time period have led to immune development perturbations that promote immune mediated diseases, such as asthma and allergic diseases. This theory has been supported by observations of very little asthma or allergies in children who grow up on traditional European farms compared to their non-farming neighbors. To further understand these observations, we studied two U.S. Mennonite populations that share overall similar ancestries and lifestyles, but the Amish live as single-family farmers and retain traditional farming practices whereas the Hutterites live on large communal farms that are highly mechanized. As predicted by the Hygiene Hypothesis, rates of asthma and allergic disease are 2.5-fold higher among Hutterite compared to Amish children. These differences are associated with distinct immune cell profiles between these children and strikingly different exposures to microbes in early life. Using mouse models of asthma and inhalation of extracts from dust collected in Amish and Hutterite homes, we implicated the innate immune system as mediating the protective effects of the Amish environment.

About Dr. Ober: Carole Ober's first love as a student was anthropology, and her enduring curiosity about the lives of real people in their cultural settings has helped propel her to the heights of her present field, human genetics and her position as Chairman of the University of Chicago's Dept. of Human Genetics. She obtained her BA in Anthropology at George Washington University and her PhD in Biological Anthropology in 1979 at Northwestern University. Ober drifted into genetics through a series of tangents, corrections and fortuitous connections in graduate school and in subsequent research and teaching positions at Northwestern, including work she did at the university's medical complex in Chicago. In 1988, she moved to the U. of C. as a fully-fledged human geneticist. "I never had a life plan," she said. "I was driven by my love of research." Ober is also heading up one of several research teams nationwide exploring the interplay of genetic and other influences on preterm birth, with a $10 million grant from the March of Dimes. Her particular consortium will bring together researchers from the University of Chicago, Northwestern University Feinberg School of Medicine, and Duke University School of Medicine. Professor Ober is determined to solve some epigenetic mysteries before she retires. Of course, her students are key to this process and she states that "I love to take my students out into the field. It's so important for them to meet the people whose cells and DNA they're studying. It puts a whole different slant on how they think about the research. It makes it so much more personal". "In both preterm birth and asthma studies, I would love to come up with at least one if not multiple great examples of how there is an environmental impact on gene regulation that is modified by your genotype and predictive of disease — something that is translatable into clinical disease or preterm birth," Ober said. "I think we'll get there." *(Information from aaas.org)*

2018 Janet Andersen Lecture
My Journey as a RNA Biochemist

Professor Neena Grover
Professor of Biochemistry and Chair of Faculty Executive Committee
Colorado College

Abstract: My journey to becoming a professor started with wonderful teachers, an early introduction to undergraduate research, and parents who allowed exploration. This led to graduate school and then to the excitement of RNA research. When I was asked to teach an undergraduate class during my post-doctoral years, it changed my focus toward education. My goals as a teacher and research mentor are to allow students to explore, to build on solid foundations, and to develop confidence in their own abilities. Science is fun and I want students to enjoy doing science, along with sharing their scientific knowledge with various communities. I entered the field of RNA when it was getting exciting, after the discovery of catalytic RNA and at the beginning of RNA crystallography. New discoveries regarding RNA's role in the cell have come every few years. My laboratory studies the energetics of small motifs in RNA, especially those that bind to magnesium ions, with a goal to improve RNA structure-function prediction from genomic data. All this may lead to a better understanding of origin of life on earth.

About Professor Grover: The nomination letter for Dr. Grover introduces her as an active and ambitious scholar, an engaged and wise mentor for her research students, and a leader and role-model for the women and women-of-color scientist community within her department and in the Division of Natural Sciences. An example of her innovative learning-centered and student-centered pedagogy is the Community Based Learning approach used in Biochemistry II to understand HIV/AIDS transmission, prevention and treatment. Through Dr. Grover's relationship with the Southern Colorado Aids Project students from the class make community presentations on these topics and use their conceptual learning in interdisciplinary community engagements. Dr. Grover consistently mentors students in collaborative research and regularly publishes results with student co-authors. Her outstanding engagement of students in science outreach and research was recently recognized by a commendation from the Association for Biochemistry and Molecular Biology. Dr. Grover's authentic passion for learning and discovery is seen in comments to a group of faculty: "the joy of science is really in doing it. It's really about having a sense of wonder. I want students to get an idea of why, as well as how one does research, and to see that they can ask and make progress toward answering complex questions."

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.

Janet Anderson Lecture Award Presentations

Year	Biological Sciences and Psychology Recipients	Physical Sciences, Mathematics and Computer Science Recipients
2008	David Hall, Biochemistry Lawrence University	Jeff Wilkerson, Astrophysics Luther College
2009	Ken Yasukawa, Biology Beloit College	Robert Jacobel, Physics St. Olaf College
2010	Sarah Elgin, Molecular Biology Washington University in St. Louis	Graham Peaslee, Nuclear Physics Hope College
2011	William Hammer, Paleo-geology Augustana College	George Lisenksy, Materials Chemistry Beloit College
2012	Eric Cole, Biology St. Olaf College	Tim Pennings, Mathematics Hope College
2013	Daniel Hornbach, Biology & Environmental Studies Macalester College	Bradley Chamberlain, Chemistry Luther College
2014	Phoebe Lostroh, Molecular Biology Colorado College	Kevin Crosby, Physics, Astronomy & Computer Science Carthage College
2015	Laura Listenberger, Biology and Chemistry, St. Olaf College	Julie Bartley, Geology Gustavus Adolphus College
2016	Maria Burnatowska-Hledin, Chemistry and Biology Hope College	Andrew Beveridge, Mathematics Macalester College
2017	Julie Legler, Mathematics, Statistics & Computer Science St. Olaf College	Thomas Varberg, Chemistry Macalester College
2018	Neena Grover, Chemistry and Biochemistry Colorado Collage	Joanne Stewart, Chemistry Hope College

Oral Session I Schedule

SESSION I.A: 10:00 am – 10:45 a.m. Room: Kersten 101			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1 (10:00)	Nivedina Sarma	University of Chicago	Biomedical Device to Target Electrical Disorders in Cardiomyocytes
I.A.2 (10:15)	Olivia Paetz and Tim Renier	St. Olaf College	Lipid droplet protein binding in response to altered phospholipid composition: alcoholic fatty liver disease model
I.A.3 (10:30)	Aleksandra Recupero	University of Chicago	Optimizing BIN1 BioID2 in a mouse neuroblastoma cell line

SESSION I.B: 10:00 – 10:45 a.m. Room: Kersten 103			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1 (10:00)	Christian Porras	University of Chicago	The influence of spatial structure and natural selection on genome-wide association studies
I.B.2 (10:15)	Chelsea Coleman	Beloit College	The Link Between Intrauterine Devices and Pseudotumors
I.B.3 (10:30)	Julia (Gege) Ran	University of Chicago	Intergenerational Health Transmission in Uganda – its Moderators and Persistence

SESSION I.C: 10:00 – 10:45 a.m. Room: Kersten 105			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1 (10:00)	Vijeeth Guggilla	Grinnell College	Treating Aggressive MYC-Driven Cancers through CDK7 Inhibition
I.C.2 (10:15)	Maicy Vossen	Gustavus Adolphus College	Modeling the Consequences of Increased Kinetochore Protein Levels in Cancer using Yeast
I.C.3 (10:30)	Juana Delao	University of Chicago	A model system to study the effects of polymerization on TEL-mediated gene dysregulation

SESSION I.D: 10:00 – 10:45 a.m. Room: Kersten 120			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.D.1 (10:00)	Juliana Olliff	Colorado College	Potential roles for non-coding RNAs in the progression of mating-type switching of Ogataea polymorpha
I.D.2 (10:15)	Karin Cho	Grinnell College	Analysis of ATA-catalyzed Transamination Reactions by Lipase-catalyzed Kinetic Resolution
I.D.3 (10:30)	Abigail Schmid	University of Chicago	The infamous capsular polysaccharide loci of Bacteroides fragilis and their 'conserved hypervariability'

Oral Session II Schedule

SESSION II.E: 2:30 – 3:30 p.m. Room: Kersten 101			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1 (2:30)	Sydney Hart	Washington University in St. Louis	Physiochemical effects of selective serotonin reuptake inhibitors underlie their mechanism of action
II.E.2 (2:45)	Kimberly Breyfogle	Hope College	Parameterizing fluorescent protein chromophores for molecular dynamics simulations
II.E.3 (3:00)	Darren Kahan	University of Chicago	Investigating the pH Sensitivity of Pab1's Phase-Separation
II.E.4 (3:15)	Alicia Bostwick	Hope College	Investigating mechanisms of regulation of mitochondrial DNA transcription

SESSION II.F: 2:30 – 3:30 p.m. Room: Kersten 103			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1 (2:30)	Elizabeth Emanuel	Macalester College	Topical Δ-9-tetrahydrocannabinol reduces mast cell accumulation in a murine model of dinitrofluorobenzene-driven vulvar pain.
II.F.2 (2:45)	Arianna Dart	Macalester College	Hip Synovial Fluid Cell Counts in Children From a Lyme Disease Endemic Area
II.F.3 (3:00)	Aparna Srinivasan	University of Chicago	Investigating recovery from the heat shock response in S. cerevisiae

SESSION II.G: 2:30 – 3:30 p.m. Room: Kersten 105			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.G.1 (2:30)	Esther Rodman	Macalester College	Quantifying the Temporal Dynamics of Huntingtin Protein Aggregation at a Single-Cell Resolution
II.G.2 (2:45)	Harini Shah	University of Chicago	The role of CHOP transcription factor in EAE, a mouse model of multiple sclerosis
II.G.3 (3:00)	Purujit Chatterjee	University of Chicago	Expression of Dprs and DIPs in the Drosophila Neuromuscular System

SESSION II.H: 2:30 -3:30 p.m. Room: Kersten 120			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.H.1 (2:30)	Julia (Gege) Ran	University of Chicago	Improving Genetic Diagnosis for Developmental Delay and its Cost Effectiveness in South Africa
II.H.2 (2:45)	John Havlik	University of Chicago	Rats do not gain empathy for other strains through observational learning
II.H.3 (3:00)	Khanh-Linh Duong	Knox College	The Effects of Race and Friendship Affiliation on Occupational Perceptions
II.H.4 (3:15)	John McMorris	Hope College	Classifying Mass Shootings in the United States

Poster Session P1

8:45 a.m. – 9:45 a.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Luis Almanza and Meiyi Chen	St. Olaf College	How Does the Fly Ormia ochracea Determine Sound Direction in the Vertical Plane?
P1.02	Everett Baxter	Beloit College	Structural analysis of Electromagnetic Perceptive Gene (EPG) protein
P1.03	Kai Bosley	Macalester College	ARE DINOSAURS SPECIAL? Bone Tissue Growth Rates in Late Triassic Vertebrates
P1.04	Anis Buttar-Miller	Colorado College	Morphology of Acinetobacter Baylyi in Different Growth Medias
P1.05	Alexandra Davis	University of Chicago	Digital Proximity Ligation assay for Sensitive Protein Quantification"
P1.06	Katherine DeLong	University of Chicago	Identifying neuronal subtypes expressing Drosophila DIP Ig proteins
P1.07	Emma Dyer	University of Chicago	Genetic determinants of serine containing staphylococcus aureus peptidoglycan cross-bridges
P1.08	Jordan Ellison	Colorado College	Does predation risk by tree squirrels affect nest habitat selection of Flammulated Owls (Psiloscops flammeolus)?
P1.09	Jeremy Fine	Washington University in St. Louis	Prenatal cannabis exposure predicts increased psychosis proneness among children: Results from the ABCD study
P1.10	Belen Herce-Hagiwara	Grinnell College	RNF4 overexpression in MCF7 cells increases DSBs; lack of Sgs1 sumoylation reduces genotoxic drug resistance.
P1.11	Raghuram Inturi	Grinnell College	Selective induction of oxidative stress in cancer cells via targeting of NAD(P)(H) metabolism
P1.12	Jacy Jordahl and Jewel Lee	St. Olaf College	Putative heavy metal transporter expression in Caulobacter crescentus
P1.13	Abdelkarim Khalid Abdelkarim Mahmoud	St. Olaf College	Quantifying the stability of RNA duplexes in aqueous TMAO and Urea solutions
P1.14	Rahul Kukreja	University of Chicago	Rats choose to use helping cues based on social grouping
P1.15	Szu Yu Lu	Washington University in St. Louis	The perception of risk: Differential relations between optimism and risk in 4- to 8-year-old children
P1.16	Katherine Matlin	Colorado College	Range of nonsense-mediated mRNA decay efficiencies detected among homogenous cell cultures

P1.17	Nancy Mora	Beloit College	Analyzing effects of different wavelengths on growth using rapid-cycling Wisconsin Fast Plants (*Brassica rapa*)
P1.18	Hannah Nilsson	St. Olaf College	In vitro selection of acyltransferase DNA enzymes
P1.19	Olivia Ruffins	Beloit College	Effect of nitrates and phosphates on the production of antimicrobial peptides in Xenopus laevis
P1.20	Marietta Saldías Montivero	Macalester College	Accelerated differentiation of hiPSC into midbrain neuronal progenitor cells for the treatment of Parkinson's disease
P1.21	Sayira Silverio	Macalester College	Induction of Mechanical Hyperalgesia and Cytokine Production in a Murine Model of Localized Provoked Vulvodynia
P1.22	Senait Solomon	Washington University in St. Louis	The Effects of Social Media on Self-Esteem and Eating Concern in Adolescent Military Dependents
P1.23	Pietro Tardelli Canedo	Macalester College	Novel findings on the morphology and phylogeography of Neopurcellia salmoni in New Zealand
P1.24	Diane Vargas	St. Olaf College	Investigating Local Adaptation in Common Milkweed
P1.25	Sara Warrington	University of Chicago	TdT labeling of DNA double strand breaks to probe DNA damage signaling and repair
P1.26	Eleanor Wettstein	Macalester College	Contribution of Membrane Proteins and Composition to Microbial Robustness
P1.27	Sophie Wulfing	Colorado College	Effects of sediment characteristics on carbon and methane production in a lake system
P1.28	Mahmoud Yousef	University of Chicago	Quantifying Homogeneity for Pangenomic Gene Clusters
P1.29	Qianchen Zhang	University of Chicago	Prediction of Latrophilin-1/ADGRL1 Biased Signaling Through Statistical Coupling Analysis
P1.30	Victoria Angeles	Beloit College	Investigating Susceptibility of Tadpoles to ranavirus (FV3) with Exposure to Polychlorinated Biphenyl
P1.31	Cristhian Martinez	Gustavus Adolphus College	Assets increasing physical activity and nutritious eating among children of migrant farmworkers in Elysian, Minnesota

Poster Session P2

1:15 p.m. - 2:15 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Jade Benson	University of Chicago	Loneliness, Social Disconnectedness, and Sleep in Older Adults
P2.02	Nora Bradford	University of Chicago	Piriform Cortex inputs to Granule Cells as Modulators of Excitability leading to Beta Oscillations
P2.03	Emma Carlson	Colorado College	Investigating factors suspected of affecting TFIIIC-dependent boundary function in Schizosaccharomyces pombe
P2.04	Linh Chu	Gustavus Adolphus College	The Impact of Acetyl-CoA Carboxylase 2 mutants on Prolyl Hydroxylase 3 Function
P2.05	Carlee Dawson	Carthage College	Development of fluorescently-labeled uveal melanoma cell lines for tumor transplantation assays in zebrafish
P2.06	Emily Dewald-Wang	Washington University in St. Louis	Do leaf chemical defenses explain changes in density dependence and patterns of local species diversity in temperate forests?
P2.07	Emily Eaton	Hope College	Investigating the role of xCT in neuroregeneration
P2.08	Keenan Ernste	St. Olaf College	Focality and Co-infection of Powassan Virus (Lineage II) within a Population of Ixodes scapularis Ticks in Wells, ME
P2.09	Simone Hall	Colorado College	Thermodynamic examination of magnesium binding in the M-box core 2 4x4 internal loop
P2.10	Sam Hochberger	Macalester College	Neuroligin-3 genetic knock-out's effect on impulsivity and repetitive behavior in mice
P2.11	Jessica Jacobs-Li	University of Chicago	Hedgehog signaling-dependent GLI transcription factor activity maintains the progenitor status of the Second Heart Field.
P2.12	Beminet Kassaye	Macalester College	Impact of BMS chemotherapy and tumor regional immunity on ICBT
P2.13	Yeaseul Kim and Zhiye Lu	Grinnell College	Characterization of Cks2 Localization and Interaction with Cdk1 in Mitotic Cells of Xenopus laevis Embryos
P2.14	John Larson	Hope College	Development of a Rapid Screening Assay to Detect Trafficking-Defective Mutants of System xc
P2.15	Kyung Bae Lee	Washington University in St. Louis	STAT3 signaling mediates FAK inhibitor response and resistance in pancreatic cancer
P2.16	Allen Lu	University of Chicago	On the functional significance of a newly-observed N-terminus segment of the mechanosensitive channel MscS

P2.17	Rebecca Marks	Washington University in St. Louis	A Longitudinal Assessment of Changes in Stress, Depression and Inflammation
P2.18	Kathryn McKinnon and Katie Van Dame	Carthage College	Activity budgets of lowland gorillas (Gorilla gorilla gorilla) at the Memphis Zoo
P2.19	Vishva Nalamalapu	Grinnell College	Candidate hydrologic refuges predict the species distribution of a water limited annual plant
P2.20	Sarah O'Mara	Hope College	Use of CRISPR-Cas9 Approach to Knockout Truncated VACM-1(KLB22) in HUVEC
P2.21	Eleda Plouch	Hope College	Identification and characterization of fungistatic neolignans from the seeds of Phytolacca americana
P2.22	Dulce Saenz	Beloit College	Carbon Cycling in Managed Turf and Restored Ecosystems
P2.23	Monica Smith	Beloit College	Effects of nitrates and phosphates on growth and leukocyte recruitment of Xenopus laevis
P2.24	Jessica Song	Colorado College	Thermodynamics of magnesium ion binding to trinucleotide bulged TAR RNA
P2.25	George Valladares	Beloit College	FINDING THETA OSCILLATIONS USING ECoG & ICA
P2.26	Tiffany Vaughan	University of Chicago	Cellular and Molecular Mechanisms of Neural Tube Closure
P2.27	Meredith Wells	University of Chicago	Limited Changes in Impedance and Current with Constant Voltage in Patients with Bilateral DBS
P2.28	Rebecca Williams	Washington University in St. Louis	Correlations between delay discounting and cognitive functions
P2.29	Ellie Xu	University of Chicago	Protective Factors Fail to Moderate the Association between the Dysregulation Profile and Impairment
P2.30	David Eik	Colorado College	Quantification of mating and mating-type switching with flow cytometry in the methylotrophic yeast Ogataea polymorpha
P2.31	Dahao Feng	Colorado College	Carbon-source dependent regulation of mating in the methylotrophic yeasts Ogataea polymorpha and Komagataella phaffii

Poster Session P3

3:45 p.m. - 4:45 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Markus Barbosa	Knox College	Oxidative stress in age-1 & age-2 mutant strains of Caenorhabditis elegans.
P3.02	Cancelled		
P3.03	Margaret Brown	St. Olaf College	Lipotoxicity: Understanding the Cellular Pathway that Leads from Saturated Fatty Acid to Cell Death
P3.04	Daksh Chauhan	University of Chicago	Hypoxia-Inducible Factor 1-alpha as a therapeutic target for atherosclerosis
P3.05	Anjali Das	University of Chicago	Searching for the Genetic Basis of Alzheimer's Disease in a Founder Population
P3.06	Zoe Dellaert	University of Chicago	Assessing calcification of Astrangia under different temperature and physiological conditions using Scanning Electron Microscopy
P3.07	Cancelled		
P3.08	Carolina Yu	University of Chicago	Functional triplet motifs underlie accurate predictions of single-trial responses in V1 neurons
P3.09	Patricia Zulueta	University of Chicago	Structural Determination of the METTL3-METTL14 Complex by Cryo-Electron Microscopy
P3.10	Anne Havlik	University of Chicago	Modeling Divisive Normalization in Awake Mouse Visual Cortex
P3.11	Sean Hughes	Carthage College	Volatile chemical content in tea (Camellia sinensis) vapor determined by gas chromatography-mass spectrometry
P3.12	Renee' Jalbert and Sarah Schmidt	Carthage College	Using High Performance Liquid Chromatography to quantify chemical compounds in tea (Camellia sinensis)
P3.13	Paul Keene	University of Chicago	Fluctuations in Sustained Attention Predict Working Memory Performance
P3.14	Isadora Kucera	University of Chicago	Dynamic Alternative RNA Splicing Regulation in Cortical Neurogenesis
P3.15	Chase Latour	Washington University in St. Louis	Maternal age at last birth and leukocyte telomere length in nationally representative population of women
P3.16	Owen Lewer and Claire Pfeffer	Carthage College	Space phage: novel environment for undergraduate research
P3.17	Emery Lu	University of Chicago	Defining the early transcriptional role of the cardiogenic transcription factors GATA4, TBX5, and NKX2.5
P3.18	Cancelled		

P3.19	Nikita Mehta	University of Chicago	Wnt Signaling in Schwann Cells Affects Peripheral Nerve Regeneration
P3.20	Nhu Nguyen	Macalester College	Characterization of RNA SHIV+ cells and FoxP3+ cells in lymphoid tissues of rhesus macaques
P3.21	Guadalupe Orbezo-Perez	Beloit College	Differential regulation in defense-related genes by flg22 and elf18 in Arabidopsis thaliana
P3.22	Romy Portieles	University of Chicago	Optimizing Hospitalist Care: A Time in Motion Study
P3.23	Mayu Sakae	Grinnell College	MPC Inhibition Enhances Breast and Lung Cancer Responses to Radio-Chemo-Therapies
P3.24	Sara Siddiqui	University of Chicago	Effects of TPI-1 Inhibitor on Red Blood Cell Differentiation of Erythroleukemic Cells
P3.25	Shreya Sodhi	Washington University in St. Louis	The effects of exposure to diversity on children's racial thinking
P3.26	Skylar Sundquist	Hope College	The Regulation of Cellular Proliferation by VACM-1/CUL5 is Dependent on its Posttranslational Modifications by NEDD8
P3.27	Sunny Vuong	St. Olaf College	Identifying Proteins in Alcoholic Fatty Liver Disease
P3.28	Madeleine Welt	Beloit College	Is petting your plants good for them? Thigmomorphogenesis and transplant shock in peas (*Pisum sativum)*
P3.29	Savannah Wilson	Luther College	Forest communities of Finch Memorial Hardwoods, Winneshiek County, IA
P3.30	Xiaochan Yang	University of Chicago	Effects of Anxiety and Depression on Smoking Cessation Outcomes in a Minority Sample
P3.31	Adam Zabner	University of Chicago	Stimulation Changes the Actin Architecture of the Presynaptic Terminal

Abstracts for all Sessions
Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, University of Chicago
November 2-3, 2018

All abstracts (poster and oral) are listed alphabetically by presenter last name. Abstracts with multiple presenters appear only once with first listed presenter. An alphabetical list of all meeting participants and their respective poster session or oral presentation number follows the abstracts.

Presenter(s): Luis Almanza, Meiyi Chen, St. Olaf College
Session: Poster P1.01
Title: How Does the Fly Ormia ochracea Determine Sound Direction in the Vertical Plane?
Advisor(s): Norman Lee, Biology, St. Olaf College
Co-Author(s): Norman Lee, Meiyi Chen

Abstract: The acoustic parasitoid fly, Ormia ochracea, utilizes a pair of mechanically-coupled eardrums to locate singing host crickets for larval development. Previous studies have shown that O. ochracea can precisely localize sound sources in the horizontal plane. Directional hearing in the horizontal plane is dependent on bilaterally symmetric ears to measure time and intensity differences of sound arriving at each eardrum. These cues vary as a function of sound location in the horizontal plane but do not vary at different angles of elevation for bilaterally symmetric ears. Therefore, it is unknown how O. ochracea can determine sound location while in flight. Here we test the hypothesis that O. ochracea rely on body rotations to generate directional cues inflight. We used a speaker array to present sounds at different angles of elevation to simulate body 'roll' in space. Mechanical response of the eardrums were measured using laser vibrometry. Results indicate that O. ochracea eardrums are broadly sensitive to a range of sound frequencies that include cricket song frequencies. Larger body rotations resulted in larger directional cues at frequencies above cricket song frequencies. Therefore, body rotations alone may not allow flies to determine source location while in flight.

Presenter(s): Victoria Angeles, Beloit College
Session: Poster P1.30
Title: Investigating Susceptibility of Tadpoles to ranavirus (FV3) with Exposure to Polychlorinated Biphenyl
Advisor(s): Tawnya Cary, Department of Biology, Beloit College

Abstract: Amphibian populations have declined dramatically in many areas of the world and has worsened. It has been hypothesized that exposure to agrochemicals and chemical pollutants diminishes components of the innate and adaptive immune systems, which increases the vulnerability to disease. The polychlorinated biphenyl-126 (PCB-126) is a legacy environmental pollutant known to cause immune disruption. We tested whether Lithobates pipiens tadpoles exposed to polychlorinated biphenyl (PCB) would have increased susceptibility to a ranavirus, Frog Virus 3 (FV3). As an indicator of susceptibility, we measured morphometrics of exposed tadpoles. We predicted that the growth of the tadpoles would decrease if exposed to both PCB and FV3. Additionally, we needed to determine whether or not the tadpoles were actually infected with the ranavirus. We extracted DNA from the kidneys

of preserved tadpoles and used polymerase chain reaction (PCR) and gel electrophoresis to identify ranavirus DNA in the kidneys. There were no differences in any growth parameters or organ mass ratios measured between our PCB-treated and PCB + FV3-treated tadpoles. However, we only found FV3 DNA in three of our tested tadpoles. At this time, we are unable to conclude whether or not PCB exposure increased tadpole susceptibility to ranavirus.

Presenter(s): Markus Barbosa, Knox College
Session: Poster P3.01
Title: Oxidative stress in *age-1* & *age-2* mutant strains of *Caenorhabditis elegans*
Advisor(s): Judith M. Thorn, Matthew Jones-Rhoades, Biology, Knox College

Abstract: Oxidative stress is one of the largest contributors to aging. Oxidative stressors form reactive oxygen species that attack cells by damaging important cellular components such as DNA, proteins, and lipids. *Caenorhabditis elegans* has been used as a model of stress resistance due to the homology of stress response pathways in both humans and nematodes, including the insulin signaling pathway. To explore the relationship between stress resistance and the insulin pathway, we studied nematodes with mutations that result in extended lifespans: *age-1*, which encodes a kinase (PI3K) in the insulin signaling pathway, and *age-2*, for which the location of the mutation is unknown. In our study, we found that *age-1* (TJ1052) and *age-2* (HG231) single mutants, as well as *age-1;age-2* double mutants (HG284) confer resistance to arsenite and t-butyl hydroperoxide in survival assays. However, we saw no significant difference between the mutant strains, suggesting that *age-2* may also encode a component of the insulin signaling pathway. In future experiments, we will examine downstream gene regulation to see if there is a significant difference in gene expression between *age-1* and *age-2* mutant strains.

Presenter(s): Everett Baxter, Beloit College
Session: Poster P1.02
Title: Structural analysis of Electromagnetic Perceptive Gene (EPG) protein
Advisor(s): Assaf Gilad, Department of Biomedical Engineering and the Division of synthetic biology and regenerative Medicine, Institute of Quantitative Health Science and Engineering, Michigan State University

Abstract: Electromagnetic perceptive gene (EPG) protein was analyzed for potential application as a neuromodulatory therapeutic to help alleviate neurological diseases such as parkinson's, Amyotrophic Lateral Sclerosis, and Huntington's disease. EPG was newly discovered by Dr. Gilad and Dr. Pelled; originally found in Kryptopterus Bicirrhis. This gene expresses a unique protein that allows the fish to sense and respond to a presence of electromagnetic field. When this gene was cloned into mammalian cells, changes in intracellular calcium concentrations was observed in response to external EMF stimulation. Intracellular calcium levels play an important role for regulating cellular functionality and other body systems that use calcium dependent signaling. Thus, this property of the EPG protein can be useful in developing neuromodulatory therapeutics that can be non-invasively controlled by EMF stimulation. However, the mechanism by which EPG protein converts magnetic signals into biochemical signals remains unknown and is necessary for understanding it's functionality. Therefore, we hypothesize by resolving EPG protein structure we can identify the EMF

perceptive region. Using both DNA and Protein detecting methods, we were able to amplify and target EPG protein. Identifying the EPG perceptive region will aid in designing a more stable and robust EPG protein affected by EMF stimulation.

Presenter(s): Jade Benson, University of Chicago
Session: Poster P2.01
Title: Loneliness, Social Disconnectedness, and Sleep in Older Adults
Advisor(s): Diane Lauderdale, Department of Public Health Sciences, The University of Chicago
Co-Author(s): Diane Lauderdale

Abstract: Objectives: The goals were to analyze whether social connectedness and loneliness are related to sleep, and examine whether these measures varied with subjective and objective measurements of sleep.

Methods: This study used the National Social Life, Health, and Aging Project wave 2 data which is nationally representative of older adults (b. 1920-1947). The sleep study (n = 759) contained both subjective and measurements of sleep. A loneliness score was constructed to measure perceived loneliness. The social disconnectedness score was calculated from eight measurements that describe network size, complexity, and interactions. OLS and ordinal logistic regression was used to explore whether each sleep measurement was associated with loneliness and social isolation, adjusted for potential confounders.

Results: Increased feelings of loneliness are associated with worse sleep measurements. Increased loneliness is strongly associated with increased insomnia symptom score after controlling for age, sex, ethnicity, education and marital status ($p < 0.001$). Increased social isolation is related to worse objective measurements of sleep, but not subjective reports of sleep quality. The more socially isolated an individual is, the more interrupted ($p = 0.042$) and the more fragmented ($p = 0.039$) their sleep.

Discussion: These results suggest that loneliness and social disconnectedness are associated with how people experience sleep.

Presenter(s): Sarah Bonema, Hope College
Session: ~~Poster P3.02~~ CANCELLED
Title: Confirmation and Effects of VACM-1/Cul5 Gene Knockout in T47D Breast Cancer Cells Using CRISPR-Cas9 Approach
Advisor(s): Maria Burnatowska-Hledin, Biochemistry, Hope College
Co-Author(s): Sarah C. Bonema, Maria Burnatowska-Hledin

Abstract: The VACM-1 gene codes for the VACM-1/Cul5 protein, which is a part of the ubiquitin E3 ligase system responsible for ubiquitin-dependent protein degradation. VACM-1/Cul5 dependent E3 ligases are known to decrease cellular proliferation, and lack of regulation in this pathway can lead to cancer. The CRISPR-Cas9 system is a bacterial immune system that functions by targeting specific sequences of DNA. It can be programmed to target genes of interest, enabling specific gene editing in eukaryotic cells. We have used this system to knockout VACM-1/Cul5 in a T47D breast cancer cell line. Confirmation of the knockout was achieved through a T7 Endonuclease 1 mismatch cleavage assay proving a homozygous mutation of both alleles was achieved. AlamarBlue® growth assays support that VACM-1/Cul5

knockouts allows cells to proliferate at an increased rate. The immunostaining results of control and CRISPR-transfected cells indicate knockout of VACM-1. Genomic DNA sequencing is being performed for a final confirmation of VACM-/CUL5 knockout. Together, these results suggest that VACM-1/CUL5 is an important regulator of cellular growth.

Presenter(s): Kai Bosley, Macalester College
Session: Poster P1.03
Title: ARE DINOSAURS SPECIAL? Bone Tissue Growth Rates in Late Triassic Vertebrates
Advisor(s): Kristi Curry-Rogers, Biology & Geology, Macalester College
Co-Author(s): Abby Dillon, Lily Neuleib-Madden, Robert Anigbogu and Pietro Canedo Tardelli

Abstract: What comes to mind when thinking of the primitive dinosaurs to come from the late-Triassic? The late-Triassic (~230 Ma), itself, might conjure up images of large-scale predators having razor-sharp teeth and claws that were utilized in anything from combating rivals to decimating prey. In reality, the most basal dinosaurs to emerge from this period might have seemed unremarkable to our standards given their actual sizes and similar-looking reptilian counterparts. What is remarkable is that they were able to rule terrestrial ecosystems for the next 130 million years even after a series of late-Triassic extinctions. What made the earliest dinosaurs to walk the land, special? This answer warranted a deep, and a little intrusive, analysis of both their bone growth and latent blood vessels. Bone histological examinations were conducted for both basal dinosaurs and their non-dinosaurian relatives from the Ischigualasto Formation of San Juan Province, Argentina during the Late Triassic period.

Presenter(s): Alicia Bostwick, Hope College
Session: Oral II.E.4 (3:15)
Title: Investigating mechanisms of regulation of mitochondrial DNA transcription
Advisor(s): Kristin Dittenhafer-Reed, Chemistry and Biochemistry, Hope College
Co-Author(s): Mackenna Senti, Kristin Dittenhafer-Reed

Abstract: Mitochondrial DNA (mtDNA) encodes for 13 protein components required for cellular energy production. While the critical roles of mitochondria in metabolism and cellular function are well established, mechanisms regulating expression of mtDNA-encoded genes are poorly understood. mtDNA is complexed to proteins in structures known as nucleoids. Our objective is to determine whether reversible post-translational modifications (PTMs) of nucleoid proteins, including acetylation of lysine and phosphorylation of threonine, serine, and tyrosine, regulate mtDNA transcription. Our hypothesis is that PTMs affect the function of these proteins, providing a means of regulating mtDNA transcription. We highlight work on the characterization of nucleoid protein PTMs, focusing on bacterial expression, purification, and analysis of four nucleoid proteins essential for mtDNA transcription. These include the ribosomal protein MRPL12, the mitochondrial RNA polymerase (POLRMT), and two mitochondrial transcription factors (TFB2M and TFAM). Site-directed mutagenesis was used to replace amino acids known to be post-translationally modified with amino acids mimicking the modified or unmodified state. Purified mutants will be used in transcription assays and mtDNA binding assays to determine the effects of these PTMs on protein function and mtDNA transcription. Increased knowledge of fundamental mechanisms regulating mitochondria will lay the groundwork for understanding mitochondrial impairment in human diseases.

Presenter(s): Nora Bradford, University of Chicago
Session: Poster P2.02
Title: Piriform Cortex inputs to Granule Cells as Modulators of Excitability leading to Beta Oscillations
Advisor(s): Leslie Kay, Mind and Biology, University of Chicago
Co-Author(s): Vivian Nguyen, Wenxi Xiao, Boleslaw Osinski, Emily Tao

Abstract: Excitability of granule cells in the mammalian olfactory bulb regulates the power of both gamma (40-100 Hz) and beta (15-30 Hz) oscillations in local field potential (LFP). Gamma oscillations have been associated with odor discrimination while beta oscillations occur in response to sensitization to strong odors and odor learning. Both may arise from the dendrodendritic microcircuit between excitatory mitral cells (MCs) and inhibitory granule cells (GCs). Modeling suggests heightened GC excitability leads to sufficient MC inhibition which causes a switch from gamma to beta oscillations. A previous study from the lab showed that inhibition of heightened GC excitability state leads to increased gamma power and decreased beta power, supporting modeling results. This project investigates a possible top-down modulator of GC excitability, strong projections from pyramidal cells in the piriform cortex. We use dopamine agonist (D1-D2) and antagonist cocktails to modulate excitation of pyramidal cells in the piriform cortex. We present high and low volatility odors and expect to see a change in beta oscillations after administration of the agonist or antagonist cocktail at different concentrations. Preliminary data shows a trend towards increased beta power for low volatility odors in response to the agonist cocktail at both concentrations.

Presenter(s): Kimberly Breyfogle, Hope College
Session: Oral II.E.2 (2:45)
Title: Parameterizing fluorescent protein chromophores for molecular dynamics simulations
Advisor(s): Brent P. Krueger, Chemistry, Hope College
Co-Author(s): Dalton L. Blood, Andreana M. Rosnik

Abstract: Fluorescent proteins (FPs) are important to many studies of protein function, and we plan to examine them in the future using molecular dynamics (MD) simulations. Before running MD, fluorescent protein chromophore parameters must be determined that are consistent with the latest version of the Cornell et al. force field (1995, J. Am. Chem. Soc.), ff14SB (Maier et al.,2015, J. Comp. Theo. Chem.) along with the generalized AMBER force field (Wang et al., 2004, J. Comput Chem.). Parameterization was carried out using quantum mechanical calculations to determine the optimized geometry and electrostatic potential of each chromophore. The restrained electrostatic potential (RESP) charge fitting procedure was used to derive atomic charges. All other parameters (Lennard-Jones, Bond length, Bond Angle, Dihedral Angles) were assigned by analogy to pre-existing force field parameters. Complete MD parameters are presented for the chromophores of six common FPs: EGFP, mCherry, DsRed, EBFP, EYFP, and ECFP.

Presenter(s): Margaret Brown, St. Olaf College
Session: Poster P3.03
Title: Lipotoxicity: Understanding the Cellular Pathway that Leads from Saturated Fatty Acid to Cell Death
Advisor(s): Laura Listenberger, Biology/Chemistry, St. Olaf College
Co-Author(s): Hannah Nilsson

Abstract: An excess of saturated fatty acids causes cell dysfunction and death, which has been linked to obesity-related health problems like heart disease and type II diabetes. In this study, we aimed to determine if the incorporation of saturated phospholipids into the endoplasmic reticulum (ER) membrane would trigger ER stress, leading to cell death. To understand the mechanisms of this pathway, cells were treated with the saturated fat palmitate under conditions that decreased phospholipid synthesis. The effects of palmitate treatment were measured with cell viability assays and fluorescence microscopy. Our experiments show that reducing choline, the main component of the prevalent membrane phospholipid phosphotidylcholine, does not rescue cells from lipotoxic effects. Limiting choline caused no significant decrease in lipotoxicity when cells were treated with 400μM palmitate, as quantified by measurements of mitochondrial function and reactive oxygen species levels. Future studies will aim to determine what factors contribute to oxidative stress in the lipotoxic pathway.

Presenter(s): Anis Buttar-Miller, Colorado College
Session: Poster P1.04
Title: Morphology of Acinetobacter Baylyi in Different Growth Medias
Advisor(s): Kristine Lang, Physics; Phoebe Lostroh, Molecular Biology, Colorado College

Abstract: Acinetobacter Baylyi are bacteria that are closely related to Acinetobacter Baumannii which are a major cause of nosocomial infections, infections picked up in hospitals. We looked at the morphology of A. baylyi grown in nutrient conditions made with different sources of carbon. This research sheds light on the morphology of A. baumannii, which can inform the treatment of nosocomial infections. Images were taken using an Atomic Force Microscope (AFM), capable of imaging cells within micrometers, of the A. baylyi cells grown in different nutrients. The cells were then measured for length and width. We found that the longer the doubling time of the cells, the shorter and skinnier they were, but the higher the surface area to volume ratio was. A. baylyi cells grown in standard media are rod shaped, whereas cells grown in medias with different carbon sources were often spherical or very long and thin. This data is part of a larger project on the overall morphology of A. baylyi, which will help determine methods for treating nosocomial infections caused by A. baumannii.

Presenter(s): Emma Carlson, Colorado College
Session: Poster P2.03
Title: Investigating factors suspected of affecting TFIIIC-dependent boundary function in Schizosaccharomyces pombe
Advisor(s): Jennifer Garcia, Molecular Biology, Colorado College
Co-Author(s): Alex Barone-Camp

Abstract: Gene expression, which is essential for cell function, can be controlled by DNA organization. In eukaryotic cells, DNA is wrapped around histone proteins to form chromatin. There are two main types of chromatin: euchromatin, which is accessible and gene-rich, and heterochromatin, which is packaged tightly and inaccessible for transcription. Heterochromatin

is differentiated by a specific modification to histone proteins, generally called repressive histone methylation. Although repressive histone methylation is essential for proper cell function, if uncontained it will spread, silencing other regions of the genome, thus interfering with gene expression. In Schizosaccharomyces pombe, the spread of silencing can be prevented by specific DNA elements called boundary elements, which require the RNA polymerase III transcription factor TFIIIC. Other factors critical for TFIIIC-dependent boundary element function remain unknown. Previous research identified ten mutants that may interfere with this pathway. We confirmed the presence of four mutations. We aim to introduce these mutations into wild type cells via CRISPR/Cas9 to observe their effect on boundary function. Chromatin Immunoprecipitation can then be performed to test for the spread of methylation. This analysis will identify factors that contribute to boundary function and give insight to mechanisms by which boundary elements limit the spread of repressive histone methylation.

Presenter(s): Purujit Chatterjee, University of Chicago
Session: Oral II.G.3 (3:00)
Title: Expression of Dprs and DIPs in the Drosophila Neuromuscular System
Advisor(s): Robert Carrillo, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s): Veera Anand

Abstract: Highly specific recognition between synaptic partners is crucial to the development of a functional nervous system. Thus, elucidating the poorly understood molecular and developmental programs that drive synaptic specificity is essential to our understanding of basic nervous system function. Previous studies, using Drosophila melanogaster as a model system, identified biochemical interactions between two subfamilies of the immunoglobulin superfamily: the 21 defective proboscis extension response (Dpr) proteins and 9 Dpr-interacting proteins (DIPs) (Ozkan et al., 2013). Follow-up studies demonstrated that Dpr-DIP interactions regulate the development and plasticity of the Drosophila larval neuromuscular junction (Carrillo et al., 2015). The functions of most Dprs and DIPs are largely unknown, and as a first step, we characterized their expression profiles in the neuromuscular system during the larval stage by employing microdissections, immunohistochemistry, and microscopy. We found that the Dprs and DIPs are expressed in varying subsets of motor neurons, suggesting that axon-axon interactions may be important for neural circuit wiring. These data contribute to a comprehensive map of Dpr- and DIP-expressing cells in the neuromuscular system and a more complete picture of neural development to guide future studies.

Presenter(s): Daksh Chauhan, University of Chicago
Session: Poster P3.04
Title: Hypoxia-Inducible Factor 1-alpha as a therapeutic target for atherosclerosis
Advisor(s): Yun Fang, Section of Pulmonary/Critical Care, University of Chicago
Co-Author(s): Daksh Chauhan1, Myung-Jin Oh, Tzu-Pin Shentu, Ru-Ting Huang, Yun Fang

Abstract: Atherosclerosis involves formation of lesions containing macrophages and lipids on the endothelial cell layer of arteries. These lesions preferentially localize at branches and curvatures, which are characterized by disturbed blood flow (DF)— a turbulent flow pattern. DF triggers atheroprogressive cell-signaling pathways, including ones triggering hypoxia-inducible factor 1-alpha (HIF-1a). Previously, HIF-1a was implicated in progressing atherosclerosis via

greater accumulation of lipids and macrophages. We hypothesize that inhibiting HIF-1a will slow atheroprogression and lesion formation. DF induced changes in endothelial cells also result in inflammation, which increases vascular adhesion molecule-1 (VCAM-1) expression. Theoretically, nanoparticles targeting VCAM-1 can specifically deliver HIF-1a inhibitors at DF sites. We will assess the efficacy of VCAM-1 targeting micelles in delivering HIF-1a inhibitors. We will use western blot and qPCR, two techniques used to measure protein and mRNA expression. We studied expression of HIF-1a under DF by exposing human aortic endothelial cells (HAECs) to different flow patterns- unidirectional flow and DF- and carried out western blot analyses. Western blot analyses revealed that under DF, HIF-1a protein expression was 1.6 times greater than that under UF. In future, we will assess the efficacy of VCAM-1 targeting micelles in delivering HIF-1a inhibitors in vitro by subjecting HAECs to different treatments.

Presenter(s): Karin Cho, Grinnell College
Session: Oral I.D.2 (10:15)
Title: Analysis of ATA-catalyzed Transamination Reactions by Lipase-catalyzed Kinetic Resolution
Advisor(s): Hanna M. Key, Chemistry, Grinnell College
Co-Author(s): Hanna M. Key

Abstract: Chiral amines are an important functional group in many biologically active compounds. Synthesis of such compounds can be done using biocatalysts, such as transaminases (ATAs); however, assessing the enantioselectivity of enzymes can be a tedious process if the products exhibit poor separation on chiral columns. To overcome this, a lipase catalyzed kinetic resolution (KR) was developed for assessing the enantioselectivity of an ATA catalyzed reaction. For this study, ATA JS17 from Vibrio fluvialis and lipase B from Candida Antarctica (CalB) were used. Acetophenone was the amine acceptor and o-xylylenediamine was the amine donor for the ATA-catalyzed reaction, yielding methylbenzylamine (1). In the CalB-catalyzed reaction, 1 was acetylated in EtOAc to yield N-(1-phenylethyl)acetamide. By using lipases to selectively favor the acetylation of R-1 over S-1, it was demonstrated that this KR approach is a potential alternative to conventional analytical methods.

Presenter(s): Linh Chu, Gustavus Adolphus College
Session: Poster P2.04
Title: The Impact of Acetyl-CoA Carboxylase 2 mutants on Prolyl Hydroxylase 3 Function
Advisor(s): Haejin Yoon, Department of Cell Biology, Harvard Medical School

Abstract: In low nutrient condition or cellular stress, AMP-activated protein kinase (AMPK) phosphorylates acetyl-CoA carboxylase (ACC) at residue S212, which activates mitochondrial fatty acid oxidation (FAO) to boost ATP levels. In high nutrient condition, stress sensing enzymes prolyl hydroxylase 3 (PHD3) hydroxylates ACC2. ACC2 then activates the conversion of acetyl-CoA to malonyl-CoA, which inhibits the fatty acid transport protein CPT1 and thus represses FAO. Since ACC2 hydroxylation site (P450) is essential for PHD3-mediated FAO, we hypothesized that human ACC2 P450A or mouse ACC2 P440A mutant will inhibit the hydroxylation of ACC2 by PHD3 and thus activates FAO. In contrast, human ACC2 S222A or mouse ACC2 S212A mutant promotes the hydroxylation of ACC2 by PHD3 and represses FAO as a result. The goal of the study is to generate ACC2 S212A and P440A mutant in C2C12 cell

line (mouse mesenchymal stem cell) by utilizing CRISPR/Cas9 system. We cut our target sites using 6 different single guide RNAs (sgRNAs) and established knock in mutant with single strand ODN (ssODN). sgRNA and ssODN were transfected using FuGENE 6 and colonies were selected to get one site mutated CRISPR cell lines. Genomic DNA was sequenced to confirm CRISPR mutants and the cell proliferation will be measured. The ultimate goal is to examine the regulation of fat oxidation by PHD3 and the role of P440 and S12 residue in ACC2 in mouse cell system for the first time, and can help identify new pathways in lipid metabolism.

Presenter(s): Chelsea Coleman, Beloit College
Session: Oral I.B.2 (10:15)
Title: The Link Between Intrauterine Devices and Pseudotumors
Advisor(s): Dr. James Schulte, Biology, Beloit College

Abstract: Speculation about the causes of pseudotumor cerebri triggered by intrauterine devices (IUDs) led me to begin a study focusing on addressing questions centered around the topic. Previous studies strongly suggest correlation between the condition and the device through surveys taken by intrauterine device users. In the study detailed below I have made connections to support the claim of causation. I worked towards identifying the medical mechanisms of pseudotumor cerebri and hormonal IUD use to develop these connections. These connections were made through survey distribution and content analysis and set up a future study that delves deeper into the idea that the use of intrauterine devices cause pseudotumor cerebri development. It was determined that side effects from the use of hormonal IUDs, such as changes in fat metabolism, could be the factor that leads to the development of the condition.

Presenter(s): Arianna Dart, Macalester College
Session: Oral II.F.2 (2:45)
Title: Hip Synovial Fluid Cell Counts in Children From a Lyme Disease Endemic Area
Advisor(s): Lise Nigrovic, Emergency Department, Boston Children's Hospital, Harvard Medical School

Abstract: Children with septic hip arthritis require surgical drainage but can be difficult to distinguish from children with Lyme arthritis. We assembled a retrospective cohort of patients under 21 years of age with hip monoarticular arthritis who presented to emergency departments located in Lyme disease endemic areas. Septic arthritis was defined as a positive synovial fluid culture or synovial fluid pleocytosis (WBC > 50,000 cells/microliter) with a positive blood culture. Lyme arthritis was defined as a positive two-tiered Lyme disease serology and negative synovial fluid bacterial cultures. All other children were classified with other arthritis. Of the 238 eligible children, 26 (11%) had septic arthritis, 32 (13%) had Lyme arthritis and 180 (76%) had other arthritis. Children with septic arthritis had a higher median synovial fluid WBC [126,130 cells/microliter interquartile range (IQR) 83,303-209,332 cells/microliter] than children with Lyme arthritis (53,955 cells/microliter, IQR 33,789-73,375 cells/microliter). 18 children (56%) with Lyme arthritis had synovial fluid WBC > 50,000 cells/microliter. Of the 94 children who underwent surgical drainage, 13 were later diagnosed with Lyme arthritis. In Lyme disease endemic areas, synovial fluid WBC count cannot always differentiate septic from Lyme arthritis.

Presenter(s): Anjali Das, University of Chicago
Session: Poster P3.05
Title: Searching for the Genetic Basis of Alzheimer's Disease in a Founder Population
Advisor(s): Carole Ober, Human Genetics, University of Chicago

Abstract: Alzheimer's disease (AD) is a progressive neurodegenerative disorder that results in loss of cognitive processes, affecting approximately 5.5 million individuals in the nation. To date, the genetic basis of late-onset AD is not well understood, with the APOE-e4 allele being the only established genetic risk factor. There are likely other genetic factors that contribute to the disease. Founder populations facilitate mapping of complex phenotypes such as AD because they descend from few ancestors and therefore have decreased genetic variation. In this study, we investigate the genetic basis of AD in the Hutterites in 5 cases and 26 controls. Fourteen variants within and close to the MGMT gene in chromosome 10q26.3 region were present in all cases and absent in all controls and thus significantly associated with AD (p-value = 7.49×10^{-16}). While 10q26.3 has been highlighted in association with AD, none of the significant variants pinpointed in this study have been previously identified. The combination of variants on chromosome 10 and APOE-e4 were then shown to be associated with olfactory dysfunction (p-value = 0.0164), a known preclinical marker of dementia. These results suggest that variants in the chr10q26.3 region, possibly in combination with APOE-e4, contribute to decline in olfactory function and the development of AD in the Hutterites, which also has implications for the development of AD in the general population.

Presenter(s): Alexandra Davis, University of Chicago
Session: Poster P1.05
Title: Digital Proximity Ligation assay for Sensitive Protein Quantification
Advisor(s): Savas Tay, Institute for Molecular Engineering, University of Chicago
Co-Author(s): Luke Vistain

Abstract: Conventional proteomic assays, while useful, are not highly sensitive. They often rely on qPCR, which at best only detects fold changes for protein quantification. Additionally, these methods are also typically limited to bulk cell population measurements. However, biology shows that single cell heterogeneity cannot be ignored – gene expression, although not typically prone to error, can vary between cells in seemingly identical populations. By averaging protein levels within a population, a representation that does not match the profile of any single cell may emerge. It is therefore important to develop an easy approach for absolute protein quantification that can also be translated to single cell studies.

Digital proximity ligation assay (digital PLA) combines the highly specific protein detection of proximity ligation assay and the precision of droplet digital PCR (ddPCR) to quantify proteins (Albayrak et al). When oligonucleotide-conjugated antibodies mere nanometers apart bind to their epitopes, an additional connector oligonucleotide forms double-stranded DNA (dsDNA) during ligation -- an indirect measurement of target protein. PLA samples are emulsified into thousands of droplets containing zero or one dsDNA molecules and amplified by ddPCR. DNA counts can be converted to protein numbers. In this study, digital PLA is applied to cystatin B (CSTB) quantification in human lung cancer (H1299) cells. The assay's results demonstrate its functionality's breadth as well as sensitivity, which is crucial for quantitative cell signaling studies and clinical diagnostics.

Presenter(s): Carlee Dawson, Carthage College
Session: Poster P2.05
Title: Development of fluorescently-labeled uveal melanoma cell lines for tumor transplantation assays in zebrafish
Advisor(s): Andrea Henle, Biology, Carthage College
Co-Author(s): Stefanie Huttelmaier and Andrea Henle

Abstract: Uveal Melanoma (UM) is a cancer originating from melanocytes in the uvea. Primary eye tumors are typically treated successfully with radiation. However, UM often returns 10-15 years later in the liver in a more metastatic and aggressive state. There is strong need to better understand how the cancer develops from its primary stage to the more aggressive stage. The goal of our research was to develop fluorescently-labeled UM cell lines that can be used to understand how the disease develops and spreads within the zebrafish model organism. Uveal melanoma cell lines from a primary tumor, Mel290, and from a metastatic tumor, OMM2.5, were transfected with two different plasmids containing either a red fluorescent protein (RFP) or a green fluorescent protein (GFP). A dosage curve was completed to determine the appropriate concentration of the antibiotic, geneticin, to allow for selection of the cells that were transfected with the plasmids. Through this approach, we achieved cell lines that were ~20% positive for either RFP or GFP. We plan to use fluorescence activated cell sorting to further purify and enrich our fluorescent cells. The cells will then be injected into zebrafish to better visualize and track the behavior of cancer within an organism.

Presenter(s): Juana Delao, University of Chicago
Session: Oral I.C.3 (10:30)
Title: A model system to study the effects of polymerization on TEL-mediated gene dysregulation
Advisor(s): Ilaria Rebay, Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Matt Hope, Ilaria Rebay

Abstract: Many human cancers are driven by mutations in transcription factors (TFs), yet how such mutations dysregulate gene expression is not well understood. TEL/ETV6 is an evolutionarily conserved repressive TF with the distinct ability to homotypically polymerize through a N-terminal Sterile Alpha Motif (SAM). TEL regulates blood development in humans and is the target of chromosomal translocations that fuse its SAM to the DNA binding domain of another TF, leading to leukemia. However, the relationships between polymerization to target gene regulation are not well understood in either the normal or oncogenic context. To answer these questions, I have engineered a set of biochemically characterized TEL SAMs with a range of affinities for use in Drosophila melanogaster. Using the developing eye as a model system, the consequences of their overexpression with respect to gene expression, cell fate specification, and overall tissue patterning can be assessed. The contribution of polymer length and protein-protein affinity to TEL-mediated dysregulation can be uncoupled by restricting TEL to dimers and then independently modulating SAM-SAM affinity. Here we show a positive correlation between the SAM-SAM interaction strength and the severity of disruption in the normally well-organized eye. Further, even at wild-type affinity, dimers are insufficient to recapitulate full-length TEL activity.

Presenter(s): Zoe Dellaert, University of Chicago
Session: Poster P3.06
Title: Assessing calcification of Astrangia under different temperature and physiological conditions using Scanning Electron Microscopy
Advisor(s): Loretta Roberson, Marine Biological Laboratory

Abstract: Symbiotic and aposymbiotic colonies of the temperate coral Astrangia poculata were reared for four weeks in seawater at 10ºC, 20ºC, or 27ºC. Buoyant weight measurements were used to investigate the effects of temperature and symbiont state on growth rate. Scanning electron microscopy (SEM) was used to describe how these physiological and environmental conditions are reflected in the crystal structure of the coral skeletons. Symbiont state and temperature both significantly affect growth rates. SEM of corals kept at 27ºC revealed that symbiont absence appears to result in a lower density of calcium carbonate at growing septa tips. Furthermore, the crystal structure of growing septa tips appears to be affected by temperature. This is one of the first studies examining the skeleton of Astrangia using SEM, so these results unlock new insights into the skeletons of temperate corals. In today's changing climate, tropical corals face higher frequencies of warmer ocean temperatures, ocean acidification, and coral bleaching events. This study could inform further research regarding the effects of symbiont state and temperature on the calcification of these integral at-risk corals. This study can also provide insight into historical coral health based on the crystal structures of coral skeletons from the past.

Presenter(s): Katherine DeLong, University of Chicago
Session: Poster P1.06
Title: Identifying neuronal subtypes expressing Drosophila DIP Ig proteins
Advisor(s): Robert Carrillo, Molecular Genetics and Cell Biology, The University of Chicago
Co-Author(s): Meike Lobb-Rabe

Abstract: Single neurons form specific circuits within the brain, and the precise molecules and mechanisms underlying axonal development has unclear. DIPs (Dpr interacting proteins) are cell-surface proteins required in neuromuscular development, but little is known of their roles in the Drosophila visual circuits. DIP-α significantly influences motor axon targeting and is co-expressed with DIP-η and ζ in several motor neurons. This co-expression suggests that these DIPs may play redundant roles in nervous system development. Thus, we wanted to identify neuronal subtypes in the fly visual system which co-express these DIPs. We utilized a stochastic multi-colored FLP-out (MCFO) technique to determine expression of DIP-α, η, and ζ. The technique allows us to identify distinct neuronal morphologies to simplify their identification. We compared the morphologies of the labeled neurons to a study by Fischbach and Dittrich 1989 that performed Golgi labeling of most neurons within the optic lobe. This comparison allowed for the clear identification of labeled neurons. DIP-α, η, and ζ expression was found in laminal, trans-medulla, medulla, and trans-lobula cells. Of the neurons which co-expressed DIPs, most functioned in motion processing, suggesting that these proteins may function in a subset of neurons within the motion detection circuit.

Presenter(s): Emily Dewald-Wang, Washington University in St. Louis
Session: Poster P2.06
Title: Do leaf chemical defenses explain changes in density dependence and patterns of local species diversity in temperate forests?
Advisor(s): Jonathan Myers, Department of Biology, Washington University in St. Louis
Co-Author(s): Joseph LaManna, Brian Sedio, Jonathan Myers

Abstract: Explaining the mechanisms responsible for the maintenance of biodiversity is a fundamental goal of ecology. Within the temperate zone, previous research reveals a correlation between species diversity and the strength of negative density dependence experienced by same-species individuals (conspecifics). The mechanisms that drive conspecific negative density dependence (CNDD), and that ultimately maintain local species diversity, are unknown but thought to be either intraspecific competition or antagonistic interactions with species-specific natural enemies. This study attempts to elucidate the role of specialized enemies in determining CNDD and local diversity in a temperate oak-hickory forest using defensive chemical profiles. Leaves were collected from 282 saplings across 46 tree species in a large, stem-mapped forest dynamics plot. Chemical extractions were analyzed with nuclear magnetic resonance (NMR) and compared to estimate the "uniqueness" of chemical profiles across species – a signature of the specialization of natural enemies. We then compared the uniqueness of species chemical profiles to the strength of CNDD and neighborhood diversity across species to test the hypotheses that specialized enemies drive 1) changes in CNDD and 2) observed patterns of local diversity in temperate forests. This study provides novel chemical data and addresses the driving mechanisms of biodiversity.

Presenter(s): Sarah Dible, Hope College
Session: ~~Poster P3.07~~ CANCELLED
Title: The Role of OPI1 In The Regulation of OLE1 Expression
Advisor(s): Virginia McDonough, Biology, Hope College

Abstract: Opi1p is a negative transcriptional regulator of a variety of phospholipid metabolism genes, that have a consensus sequence, termed UASINO, found in their promoter. Opi1p works through binding the positive transcriptional interactor Ino2p and thereby preventing its interaction with its partner Ino4p and subsequent activation of target gene expression. Inspection of the OLE1 promoter revealed several sequences that are close matches to UASINO, and work was undertaken to determine if Opi1p played a role in regulation of OLE1 expression. Reporter gene analysis showed that when uracil prototrophy was placed under control of the OLE1 promoter, OLE1 did not express well in an opi1 mutant. When lacZ was placed under control of the OLE1 promoter, reporter assays confirmed that expression was poor in the opi1 mutant. Fatty acid analysis revealed that normal regulation of OLE1 occurred in response to unsaturated fatty acid (UFA) supplement. Finally, the 2 hybrid assay was used to examine potential interactions between Opi1p and Ole1p, Ino2p, Ino4p and known OLE1 regulators Mga2p and Spt23p in response to UFA. This preliminary work indicates that Opi1p plays a role in regulating OLE1 expression.

Presenter(s): Khanh-Linh Duong, Knox College
Session: Oral II.H.3 (3:00)
Title: The Effects of Race and Friendship Affiliation on Occupational Perceptions
Advisor(s): Francis T. McAndrew, Psychology, Knox College
Co-Author(s): Francis T. McAndrew

Abstract: Two online experiments were conducted to examine the effects of friendship affiliation on the relationship between race and social status. In Experiment 1, participants were found to associate more high-status occupations with White targets than with Black targets and with females than with males. In Experiment 2, the same finding was replicated. A trending interaction between the target race and friendship affiliation was also found. White targets were associated with fewer high-status occupations when they were affiliated to be friends with Blacks, and Black targets were associated with more high-status occupations when they were thought to be friends with Whites. These findings suggest that participants associate high social status with Whites than with Blacks and there was a trending increase/decrease in the targets' perceived social status when associated with White/Black friends.

Presenter(s): Emma Dyer, University of Chicago
Session: Poster P1.07
Title: Genetic determinants of serine containing staphylococcus aureus peptidoglycan cross-bridges
Advisor(s): Dominique Missiakas, Olaf Schneewind, Stephanie Willing, Microbiology, University of Chicago
Co-Author(s): Stephanie Willing

Abstract: Staphylococcus aureus, a Gram-positive human pathogen, demonstrates resistance to many antibiotics. Cell wall peptides and associated anchor proteins are known S. aureus virulence factors. We investigated mutations in cell wall anchor proteins conferring antibiotic resistance to better understand the cell wall structures of therapeutic interest. Wall peptidoglycan is linked together by pentaglycine crossbridges assembled by the FemAB machinery. It is known that fem (factors essential for methicillin resistance) homologs fmhA and fmhC insert seryl moieties rather than glycyl moieties into pentaglycine crossbridges, impairing crossbridge cleavage by bacteriocins such as lysostaphin. Through biochemical approaches and MALDI-MS, we show that the loss of two genes, fmhA and fmhC, eliminates serine insertions in the pentaglycine crossbridge of a femAB mutant strain. The identification and characterization of fmhA and fmhC provides a better understanding of the genetic determinants of peptidoglycan, a protein crucial for S. aureus virulence, and reveals new considerations for the development of therapeutics targeting peptidoglycan and the cell wall.

Presenter(s): Emily Eaton, Hope College
Session: Poster P2.07
Title: Investigating the role of xCT in neuroregeneration
Advisor(s): Brent P. Krueger, Chemistry, Hope College
Co-Author(s): Kevin C. Franz, Marissa A. Solorzano, Mallory L. Luke, Nicole A. Ladd, Christopher O. DaSilva, Shannon M. Degnan, Meredith M. Olesh, Leah A. Chase, Aaron P. Putzke

Abstract: xCT, found in neuroprotective cells like astrocytes and microglia, is an important protein in the regulation of oxidative stress within neurons (Jackman, Glia. 2010, 15, 1806). xCT controls production of glutathione, a critical reducing agent (McBean, Trends Pharmacol Sci. 2002, 7, 299). We hypothesize that because the neuroregenerative process is metabolically taxing and results in formation of reactive oxygen species, there is a vital need for antioxidants and, therefore, xCT. The study currently focuses on creation of genetic constructs incorporating a fluorescent protein, mCherry, and an xCT-EGFP fusion protein. These proteins will be inserted into zebrafish expression vectors operating under the hb9 and GFAP promoters using subcloning. This will allow us to visualize trafficking of xCT during the neuroregenerative process, which will be initiated using laser ablation. Initial images from a home-built confocal fluorescence microscope are presented, demonstrating the imaging ability of the instrument.

Presenter(s): David Eik, Colorado College
Session: Poster P2.30
Title: Quantification of mating and mating-type switching with flow cytometry in the methylotrophic yeast Ogataea polymorpha
Advisor(s): Sara Hanson, Molecular Biology, Colorado College
Co-Author(s): Sara Hanson, Olivia Hatton

Abstract: Reproductive mechanisms play a vital role in a species' ability to evolve. Ogataea polymorpha, like many yeast species, exhibits asexual and sexual reproductive capabilities and can undergo mating-type switching before mating. However, unlike other species, O. polymorpha exists primarily as haploid and only mates under stress. The molecular mechanisms and environmental conditions required for mating and mating-type switching in methylotrophic yeast remain unclear and current testing protocols are time consuming and inefficient. Here, we attempt to create a high throughput assay to test mating and mating-type switching efficiencies with flow cytometry. We apply three methods including (1) nuclear DNA staining and cell cycle arrest to establish variations in ploidy indicative of mating, (2) bilateral mating using a fluorescent marker to track mating frequencies, and (3) fluorescent tagging at the MAT locus with GFP and RFP to observe mating-type switching frequencies. Initial results reveal indistinguishable cell cycle histogram plots in O. polymorpha. Bilateral mating and MAT locus tagging assays are in progress and have yet to be tested on the flow cytometer. Completion of these assays will streamline the study of genetic and environmental conditions in which yeast reproduce and will assist with biotechnological manipulation techniques of various yeast species.

Presenter(s): Jordan Ellison, Colorado College
Session: Poster P1.08
Title: Does predation risk by tree squirrels affect nest habitat selection of Flammulated Owls (Psiloscops flammeolus)?
Advisor(s): Brian Linkhart, Organismal Biology and Ecology, Colorado College

Abstract: Nest predation is known to influence the evolution of life-history traits and habitat selection across avian taxa. In cavity nesting species, the increased structural protection of trees affords greater concealment of nests from predators, resulting in lower rates of predation. The Flammulated Owl (Psiloscops flammeolus) is a small, cavity-nesting raptor that breeds in montane forests of western North America. Throughout Colorado, the primary nest predator of Flammulated Owls is the North American Red Squirrel (Tamiasciurus hudsonicus). To determine how predation risk by Red Squirrels may affect owl nest habitat selection, several characteristics of the nest site were quantified at owl nests from 2010-2018 and compared to available but unused sites. I found a higher mean cavity height in owl nests (6.7 ± 0.2m) compared to available cavities (6.1 ± 0.2m; $t=2.0$, $p<0.01$). The selection of higher cavities may be an adaptive response to predation risk by squirrels, as lower cavities experience higher rates of predation. The mechanisms leading to this response are uncertain, but higher cavities may increase vulnerability of squirrels to predation by forest hawks (Accipiter spp, or increased vigilance by female owls, given our observation that females are more likely to flush from lower nests when disturbed.

Presenter(s): Elizabeth Emanuel, Macalester College
Session: Oral II.F.1 (2:30)
Title: Topical Δ-9-tetrahydrocannabinol reduces mast cell accumulation in a murine model of dinitrofluorobenzene-driven vulvar pain.
Advisor(s): Devavani Chatterjea, Biology, Macalester College
Co-Author(s): Beebie Boo, Marietta Saldias Montivero, Devavani Chatterjea

Abstract: Vulvodynia is a chronic vulvar pain condition with a complex etiology, affecting 10-28% of women of reproductive age. Vulvar tissues from vulvodynia patients are characterized by increased mast cell infiltration, key effector cells of the allergic immune response, indicating that chronic vulvar pain may be initiated by a local inflammatory immune response. We have developed a murine model of allergen-induced vulvar pain using the hapten dinitrofluorobenzene (DNFB). Ten daily topical applications of DNFB in the vaginal canal of sensitized ND4 mice led to increased mechanical sensitivity and mast cell accumulation in the local tissues, consistent with clinical diagnoses of vulvodynia. Recent studies have also identified Δ-9-tetrahydrocannabinol (THC), the main psychoactive phytocannabinoid of cannabis, as a compound of therapeutic potential with antinociceptive and anti-inflammatory abilities. With our model of DNFB-induced vulvar pain, we investigated whether topical THC application could reduce sensitivity or mast cell infiltration in the vaginal canal. We found that THC lowered both sensitivity and mast cell levels compared to the no treatment controls. Considering that little is known about effective vulvodynia treatments, these results have important implications for potential therapies. More research should be conducted in the future on the antihyperalgesic mechanisms of THC in the vaginal canal.

Presenter(s): Keenan Ernste, St. Olaf College
Session: Poster P2.08
Title: Focality and Co-infection of Powassan Virus (Lineage II) within a Population of Ixodes scapularis Ticks in Wells, ME
Advisor(s): Rebecca Robich, Vector-borne disease laboratory, Maine Medical Center Research Institute
Co-Author(s): Kyle Timmer, Rebecca Robich, Susan Elias, Charles Lubelczyk, Elizabeth Henderson, Danielle Cosenza, Margaret Welch, Robert Smith

Abstract: Powassan virus (Flaviviridae: Flavivirus) is a vector-borne disease transmitted by Ixodes scapularis ticks (deer ticks) that causes deadly encephalitis for humans in about 10% of infections. Two lineages exist in North America: lineage I (POWV) and lineage II (DTV). Within the past two decades there has been a more than threefold increase in human infections across North America, which has been attributed to increasing populations of deer ticks. Studies have indicated that POWV may exhibit nidality, meaning it is transmitted and maintained in small microenvironments called foci, or nidi. We collected deer ticks from five different habitat-types: shrub (little-to-no tree cover), forest with invasive shrub species in the understory, field (grassland), edge (forest-field intersection), and forest with sparse, native shrub species in the understory. Ticks were tested for POWV/DTV by PCR and genomic sequencing to determine if certain habitat types are more or less likely to support the virus and which environmental characteristics contribute to natural pathobiocenoses. Of the 373 ticks flagged and tested, ten were sequence-positive for DTV. Using the Hotspot Analysis tool in ArcGIS, hotspots were found within the forested area with invasive shrub species in the understory. 70% of DTV-positives were also Lyme disease positives.

Presenter(s): Dahao Feng, Colorado College
Session: Poster P2.31
Title: Carbon-source dependent regulation of mating in the methylotrophic yeasts Ogataea polymorpha and Komagataella phaffii
Advisor(s): Sara Hanson, Molecular Biology, Colorado College

Abstract: The conditions for mating in the species Saccharomyces cerevisiae are nutrient-rich environments, where haploid yeasts can readily mate with one another to form diploids. Then, sporulation can only take place if there is a lack of nitrogen and the absence of a fermentable carbon source, ultimately leading to the rapid restoration of the haplophase. In contrast, methylotrophic yeast species such as Ogataea polymorpha and Komagataella phaffii do not readily mate in nutrient-rich conditions, but need a nitrogen starved environment. The carbon requirements for mating in these yeast species are not completely known. The results of this study suggest that mating-type switching and mating in these species take place not only in a non-fermentable carbon source, but any carbon source. Specifically, glucose and maltose were most suitable for O. polymorpha to undergo mating, however, the process was less efficient on ethanol and methanol containing media. For K. phaffii, glucose and ethanol were suitable for mating. Future studies will include additional replicates of O. polymorpha and K. phaffii assays, as well as an assay investigating the role of rapamycin in mating-type switching for methylotrophic species.

Presenter(s): Jeremy Fine, Washington University in St. Louis
Session: Poster P1.09
Title: Prenatal cannabis exposure predicts increased psychosis proneness among children: Results from the ABCD study
Advisor(s): Ryan Bogdan, Psychological and Brain Sciences, Washington University in St. Louis
Co-Author(s): Allison Moreau, Ryan Bogdan

Abstract: We used data from the ongoing Adolescent Brain Cognitive Development (ABCD) study to test whether maternal report of cannabis use during pregnancy (both before and after knowledge of pregnancy) is associated with psychosis proneness among 4,361 8.9-11.0 year-old children born between 2005-2008 to 3,774 mothers through 3,926 pregnancies. As the sample contains twin and non-twin siblings, as well as 20 research sites, linear mixed effect models were used to nest data on these parameters. Analyses were conducted with and without potentially confounding covariates (i.e., child, mother, and pregnancy-related variables; e.g., maternal alcohol and tobacco use during pregnancy, maternal education, socioeconomic status, familial history of psychosis, unplanned pregnancy, birth weight, child substance exposure using the lme4 R package. Persisting marijuana use following knowledge of pregnancy (n=63, 1.44%) predicted significantly increased psychosis proneness (without fixed effect covariates β=0.053, 95% CI: 0.023, 0.082, $p<0.0005$; with all covariates: β=0.045, 95% CI: 0.0083, 0.083, $p<0.017$). As associations between offspring psychosis proneness and marijuana use post-pregnancy knowledge were robust to the inclusion of other potential confounding factors and, importantly, preceded the initiation of offspring marijuana use, these data increase the plausibility that prenatal cannabis exposure may increase offspring psychosis risk.

Presenter(s): Vijeeth Guggilla, Grinnell College
Session: Oral I.C.1 (10:00)
Title: Treating Aggressive MYC-Driven Cancers through CDK7 Inhibition
Advisor(s): Mohan Kaadige, Translational Genomics Research Institute
Co-Author(s): Trason Thode, Alexis Weston, Mohan Kaadige, Sunil Sharma

Abstract: The Sharma Lab's drug discovery research team identifies druggable targets to develop novel cancer treatments. The process begins with in silico structural modeling screens to identify novel candidate small molecules. Top hits are further optimized and tested in both in vitro and in vivo models. This study explores CDK7 as a novel therapeutic target.

Deregulated expression of the MYC oncogene drives many aggressive cancer types due to the MYC protein's role in global transcription. Inhibiting CDK7, an upstream regulator of MYC transcription, can suppress MYC activity and cause tumor regression. Previously developed CDK7 inhibitors are disadvantageous due to their non-reversibility and low efficacy. We developed a novel reversible CDK7 inhibitor, designated "TGN-1044", and tested its effect as a cancer therapeutic in vitro through enzymatic and cell-based assays.

Our enzymatic results showed that TGN-1044 is a potent CDK7 inhibitor, with an IC50 of 78 nM. Cell viability assays in different pancreatic cancer lines of varying MYC expression showed TGN-1044 can kill pancreatic cancer cells with IC50's ranging from 61 to 508 nM. TGN-1044 satisfies many requirements the Sharma Lab seeks from an ideal CDK7 inhibitor. The continued development of this project will further the goal of treating high MYC expression cancers.

Presenter(s): Simone Hall, Colorado College
Session: Poster P2.09
Title: Thermodynamic examination of magnesium binding in the M-box core 2 4x4 internal loop
Advisor(s): Neena Grover, Biochemistry, Colorado College
Co-Author(s): Ellie Gilbertson

Abstract: Riboswitches are RNA structures that regulate protein synthesis by changing the m-RNA structures in the presence of cognate ligands. The Salmonella typhimurium M-box riboswitch binds to magnesium ions, regulating their intracellular levels by increasing translation of the magnesium transporting protein CorA. Crystal structure of the M-box riboswitch RNA shows eight magnesium binding sites clustered in three cores. The core 2 of the M-box riboswitch is made up of a 4x4 adenine-rich internal loop that binds magnesium ions at residues A63 and A80. RNA constructs were designed to mimic the wild type core 2 and modified at A63 and A80. Energetics of the constructs were determined using UV-visible thermal denaturation and isothermal calorimetry (ITC) experiments in buffers containing 1 M KCl or 10 mM MgCl2; two different pH were also tested. The wild type gains 3.4 kcal/mole stability in magnesium ions as compared to potassium ions; when magnesium binding sites are modified the RNA loses 0.7-3.2 kcal/mol, in magnesium buffer. ITC shows two distinct type of binding sites. Thermodynamic properties of the wild type and modified constructs will be presented in the absence and presence of magnesium ions.

Presenter(s): Sydney Hart, Washington University in St. Louis
Session: Oral II.E.1 (2:30)
Title: Physiochemical effects of selective serotonin reuptake inhibitors underlie their mechanism of action
Advisor(s): Timothy R. Peterson, Internal Medicine-Bone & Mineral Diseases, Washington University in St. Louis

Abstract: Selective serotonin reuptake inhibitors (SSRIs) like Prozac and Zoloft are believed to inhibit the serotonin transporter, SLC6A4, preventing the reuptake of serotonin by the presynaptic cell. However, there are issues with this hypothesis as SSRIs inhibit SLC6A4 within minutes, but their therapeutic effects can take days or weeks to become apparent. Recently, there have been several explanations for how SSRIs work including limiting inflammation, improving mitochondrial function, preventing ceramide accumulation, and facilitating lipid raft formation. Here we provide a unifying molecular mechanism that explains these seemingly disparate effects. We perform unbiased genetic screening and show that SSRIs selectively influence several gene networks that control acidic organelle physiology. SSRIs are strongly lysosomotropic agents, and as such they impact the late endosomal/lysosomal system and the Golgi. In these acidic organelles, SSRIs become protonated and then trapped, causing organelle swelling, which must be compensated for by increases in fluid volume as well as phospholipid and cholesterol content. The genes we identified affect lysosome-related organelles such as melanosomes, suggesting that SSRIs target monoamine pathways even in the absence of SLC6A4. Collectively, this work suggests that physiochemical effects of SSRIs rather than target inhibition may underlie their mechanism.

Presenter(s): Anne Havlik, University of Chicago
Session: Poster P3.10
Title: Modeling Divisive Normalization in Awake Mouse Visual Cortex
Advisor(s): Jason MacLean, Department of Neurobiology, University of Chicago
Co-Author(s): Zaina Zayyad, Subhodh Kotekal

Abstract: Divisive normalization is a brain computation in which the activity of a neuron is divided by the activity of its neighbors, resulting in a weighted average of activity. By following the divisive normalization model of a visual stimulus evoked response of a neuron in V1, computations can be applied accounting for the linear response of the neuron and the pooled neuronal surrounding neurons' response. Divisive normalization has been described in many species and brain modalities, indicating that it may be a canonical computation. Here we evaluate whether the divisive normalization model explains neuronal responses in awake mouse V1 in response to plaid gratings. Neuronal response data was collected using two-photon calcium imaging of a population of L2/3 pyramidal V1 neurons in awake, ambulating mice during presentation of gratings and plaids. We then fit the recorded fluorescence values to a divisive normalization model. Furthermore, data gathered were evaluated based on mathematical computations of explained variance to test how well the newly proposed model fit the data. We used our model and experimental measures to evaluate the validity of the canonical computation of the proposed divisive normalization model. The divisive normalization model accurately represented the neuronal responses in visual cortex.

Presenter(s): John Havlik, University of Chicago
Session: Oral II.H.2 (2:45)
Title: Rats do not gain empathy for other strains through observational learning
Advisor(s): Peggy Mason, Neurobiology, University of Chicago

Abstract: Rats have been shown to display helping behaviors towards others; these displays of empathy make the small mammals valuable models of human behavior (Bartal et Al., 2011). Rats have previously been shown to learn empathy for a foreign strain through extended exposure during co-housing (Bartal et Al., 2014). Rats have exhibited observational learning in previous work (Havlik and Clement, unpublished findings). Using an arena-restrainer paradigm, we examined the necessity of co-housing relative to observational learning of empathy from a rat of the same strain. This observational learning opportunity was created using an arena-restrainer paradigm, by placing a trapped rat in a restrainer which could only be opened from the outside to create an effective distress scenario (Bartal et Al., 2011). We observed no significant increase in helping behaviors with rats exposed to the observational learning opportunity compared to controls. Moreover, we noted a significant decrease in helping behaviors for a foreign strain relative to a familiar strain when rats were placed in groups. The lack of empathy towards a foreign strain exhibited by these rats strengthens the notion that extensive exposure to a foreign strain is the only way to develop empathy for that strain.

Presenter(s): Belen Herce-Hagiwara, Grinnell College
Session: Poster P1.10
Title: RNF4 overexpression in MCF7 cells increases DSBs; lack of Sgs1 sumoylation reduces genotoxic drug resistance.
Advisor(s): Yee Mon Thu, Biology, Allegheny College

Abstract: Doubles stranded breaks (DSBs) are a common indication of genomic instability and many proteins are involved in their formation and repair. The SUMO-targeted E3 ubiquitin ligase, RNF4, is critical in the repair of DNA damage, specifically double stranded DNA breaks. Although RNF4 has been found to be overexpressed in cancer tissues, it is not clear if this phenomenon contributes to genome stability. We demonstrated here that in MCF7 cells RNF4 overexpression increased DSBs. With a mutation in RNF4's ARM domain, DSB frequency did not change indicating no critical involvement in DSB repair functions of RNF4. Another protein important in DSB repair is Sgs1, which is also among the many proteins found to become sumoylated in response to DNA damage. We generated SUMO tagged Sgs1 mutants to observe sumoylation's role in S. cerevisiae's sensitivity to genotoxic drugs. In strains where Sgs1 lacked sumoylation sensitivity to the genotoxic drugs hydroxyurea (HU) and methyl methanesulfonate (MMS) increased. Our findings suggest that accumulation of RNF4 may disrupt its normal interactions with other DSB repair proteins, possibly including Sgs1, which depends on sumoylation to regulate some of its DNA damage repairing functions.

Presenter(s): Sam Hochberger, Macalester College
Session: Poster P2.10
Title: Neuroligin-3 genetic knock-out's effect on impulsivity and repetitive behavior in mice
Advisor(s): Marc Pisansky, Translational Neuroscience, University of Minnesota

Abstract: Autism Spectrum Disorders (ASD) are commonly-characterized by impulsive and repetitive behaviors. One genetic cause of ASD involves neuroligin-3 (Nlgn3), a synaptic molecule that influences the balance of D1 and D2 medium spiny neurons in the striatum. Mutations of Nlgn3 are associated with ASD in humans as well as synaptic dysfunction and behavioral changes in mouse models. Previous work has shown increased rotarod learning in Nlgn3 KO mice. Still, little is known about how genes affect the brain circuitry and behavior behind ASD. Our study showed no repetitive behaviors found in either the wild type or Nlgn3 KO mice, however, wild type mice were found to have more premature responses throughout the study than the Nlgn3 KO mice. These contradictory results to previous studies shows a lack in understanding or the behavioral phenotypes of Nlgn3 KO. Our results question what behaviors Nlgn3 KO mice show during the intertrial interval (ITI). Behavioral differences between Nlgn3 KO and wild-type mice may be attributable to differences in medium spiny neuron activity in the striatum. Future studies will utilize fiber photometry to monitor the real-time activity of D1 and D2 medium spiny neuronal activity in the striatum during the behavioral tasks.

Presenter(s): Sean Hughes, Carthage College
Session: Poster P3.11
Title: Volatile chemical content in tea (Camellia sinensis) vapor determined by gas chromatography-mass spectrometry
Advisor(s): Dan Choffnes, Biology, Carthage College
Co-Author(s): Renee' Jalbert

Abstract: Every different type of tea has its own unique flavor. This flavor is the result of interactions between chemicals in the tea leaves that, when released, appeal to the sensations of smell and taste. The taste component of tea and the chemicals responsible have been studied extensively in past research. Many of these compounds observed have been found to have antioxidant properties and other implications for use in human medicine. However, volatiles--the chemicals responsible for tea aroma--have been less deeply examined. In this study, I sought to create a working method for identifying and quantifying volatiles, and to compare the difference in volatile chemical content between multiple cultivars of oolong teas. Currently there is no standardized method for analyzing volatiles in tea. Using solid-phase microextraction, I have created a protocol for gathering volatile compounds from freshly brewed samples of oolong tea. I used ethyl decanoate as an internal standard to allow for a known point of reference during analysis of the tea. Samples were analyzed via gas chromatography--mass spectrometry. Preliminary results will be presented.

Presenter(s): Raghuram Inturi, Grinnell College
Session: Poster P1.11
Title: Selective induction of oxidative stress in cancer cells via targeting of NAD(P)(H) metabolism
Advisor(s): Douglas Spitz, Free Radical and Radiation Biology, University of Iowa
Co-Author(s): Collin D. Heer, Sebastian J. Sciegienka, David B. Riffe, Kranti A. Mapuskar, and Douglas R. Spitz

Abstract: Due to differences in metabolism between cancer cells and normal cells, cancer cells heavily rely on certain metabolites such as nicotinamide adenine dinucleotide (NAD(H)) to support vital cellular functions such as anti-oxidant capacity. NAD+ is the only known precursor to NADP+ and NADPH, both of which are necessary for the elimination of harmful reactive oxygen species (ROS). In order to synthesize a significant amount of NAD+, tumor cells upregulate the NAD+ salvage pathway (recycling degraded NAD+) instead of the de novo pathway (using the amino acid tryptophan as a starting building block). Moreover, normal cells typically rely on de novo synthesis for maintaining their NAD+ supply. The salvage pathway is driven by the rate-limiting enzyme nicotinamide phosphoribosyltransferase (NAMPT). We hypothesize that inhibitors of NAMPT (FK866 & GMX-1778) will cause a selective induction of oxidative stress in cancer cells as a result of a depletion in cellular NAD(P)(H) and glutathione supply. In addition, we hypothesize that NAMPT inhibition will exhibit synergistic cell death when coupled with other agents that elevate oxidative stress.

Presenter(s): Jessica Jacobs-Li, University of Chicago
Session: Poster P2.11
Title: Hedgehog signaling-dependent GLI transcription factor activity maintains the progenitor status of the Second Heart Field.
Advisor(s): Ivan P. Moskowitz, Departments of Pediatrics, Pathology, and Human Genetics, University of Chicago
Co-Author(s): Megan Rowton, Andrew D. Hoffmann, Jeffrey Steimle, Sonja Lazarevic, Emery Lu

Abstract: Congenital Heart Disease (CHD), or disrupted heart formation during embryonic development, affects ~1% of human births every year. Our previous research has demonstrated that Hedgehog (Hh) signaling is active exclusively in cardiac progenitors, not in the heart itself, and is required for formation of critical cardiac structures like the atrial septum. GLI transcription factors (TFs) mediate Hh signaling in the nucleus, activating or repressing genes in the Hh-dependent gene regulatory network. In order to define the mechanism of GLI activity during cardiac differentiation, we identified a putative regulatory element upstream of the Hh-dependent gene Foxf1. We hypothesized that GLI activity at this regulatory element was important for switching Foxf1 expression on in cardiac progenitors, and off in differentiated cardiomyocytes. We found that activating GLI TFs increased transcription from this enhancer and repressive GLI TFs decreased transcription, and that GLI binding was required to maintain the progenitor-specific activity of this enhancer. Using CRISPR-Cas9 mediated mutagenesis, we are now investigating the requirement of this enhancer for Foxf1 expression levels and atrial septum formation in vivo. We now aim to determine the generalizability of the GLI TF “switch” mechanism during cardiac differentiation, thus linking Hh-regulated differentiation timing to the etiology of CHD.

Presenter(s): Renee' Jalbert, Sarah Schmidt, Carthage College
Session: Poster P3.12
Title: Using High Performance Liquid Chromatography to quantify chemical compounds in tea (Camellia sinensis)
Advisor(s): Dan Choffnes, Biology, Carthage College
Co-Author(s): Sarah Schmidt, Renee' Jalbert, Sean Hughes

Abstract: The popularity of tea (Camellia sinensis) is in part attributed to the wide variety of flavors, aromas, and potential health benefits, which are caused by naturally occurring chemicals within tea leaves. These chemicals are oxidized during the multiple fermentation processes used to prepare different types of tea from fresh leaves. The most common types of tea produced are white, black, green, oolong, and pu-erh. Each of these teas are expected to have different concentrations of chemical compounds within them due to the different fermentation processes used during preparation. In this study we sought to characterize these teas based on their chemical content using High Performance Liquid Chromatography (HPLC). Using a standardized brewing procedure, we measured the concentrations of catechin, epicatechin, epigallocatechin, epicatechin gallate, epigallocatechin gallate, and theaflavin in multiple samples of tea with HPLC. The less fermented teas, such as green tea and white tea, are expected to have greater concentrations of polyphenolic catechins compared to the more fermented teas, such as black tea and oolong tea. In contrast, concentrations of theobromine, theophylline, and caffeine are expected to stay relatively consistent despite varying levels of tea leaf fermentation.

Presenter(s): Jacy Jordahl, Jewel Lee, St. Olaf College
Session: Poster P1.12
Title: Putative heavy metal transporter expression in Caulobacter crescentus
Advisor(s): Lisa Bowers, Biology, St. Olaf College
Co-Author(s): Jacy Jordahl, Jewel Lee, Thomas Lerdall, and Lisa Bowers

Abstract: Caulobacter crescentus is a bacterium that lives in water everywhere. These cells thrive in nutrient-limited environments because they have a large set of cell surface proteins called TonB dependent receptors that actively transport sugars, vitamins, and essential metals into the cell. Little is known about these receptors in Caulobacter. We sought to identify TBDRs that transport essential metals. In particular, we looked at three TBDR genes from an mRNA sequencing experiment that showed a decrease in expression in metal excess compared to metal limited conditions. We first validated those results with a new technique, RT-qPCR. As expected, we found that the expression of these three genes decreased in the metal excess compared to metal limited conditions. We further explored which specific metal caused this difference in gene expression.

Presenter(s): Darren Kahan, University of Chicago
Session: Oral II.E.3 (3:00)
Title: Investigating the pH Sensitivity of Pab1's Phase-Separation
Advisor(s): Tobin Sosnick, Department of Biochemistry and Molecular Biophysics, University of Chicago
Co-Author(s): Joshua Riback, Chris Katanski, Isabelle Gagnon, Tobin Sosnick

Abstract: Poly-A-Binding Protein (Pab1, Budding Yeast) phase-separates into a hydrogel in vitro when exposed to cellular stresses, including low pH or elevated temperatures. Solutions below physiological pH (i.e. pH 5.6) shift Pab1's demixing temperature (TDemix) to below physiological temperatures. We hypothesize that histidine residues in Pab1's RNA Recognition Motifs (RRMs) are responsible for Pab1's pH sensitivity, since TDemix is sensitive to pH changes near histidine's pKa (6.0). Although the location of His residues in Pab1's RRMs vary across yeast species, the total number of His residues (8) is conserved, further suggesting their importance.

To investigate the role of histidines in the pH sensitivity of Pab1's TDemix, mutants were constructed missing some or all histidine residues in the RRMs. The mutants missing some histidines all exhibit a slightly elevated TDemix, suggesting histidines in each RRM participate in demixing. Importantly, the mutant missing all RRM histidines displayed a moderately elevated TDemix near physiological pH, but a highly increased TDemix at lower pHs. This trend corresponds to Pab1's charge; although Wild Type Pab1's charge becomes positive below pH 5.8 as histidine residues titrate, this mutant only becomes positively charged below pH 5.2 once acidic resides begin to titrate, justifying its insensitivity to higher pH. These results suggest that charge is a regulator of Pab1's TDemix, with histidines responsible for tuning the charge near physiological pH.

Presenter(s): Beminet Kassaye, Macalester College
Session: Poster P2.12
Title: Impact of BMS chemotherapy and tumor regional immunity on ICBT
Advisor(s): Subree Subramanian, Department of Surgery, University of Minnesota
Co-Author(s): Xianda Zhao, Dechen Wangmo, Subree Subramanian

Abstract: Approximately all patients with cancer are heavily treated with chemotherapy and removal of the tumor along with the sentinel and regional lymph node. Immune checkpoint blockade therapy is an adjuvant treatment and not a first-line of treatment for patients. For immune checkpoint blockade therapy to effectively work it requires a functional immune system and that has been degraded due to the first-line of treatment. The experiment was conducted using two laboratory-bred strain. We mapped and identified the sentinel, regional and naive tumor draining lymph node. We took a step further and compared the sentinel, regional, naive lymph node, spleen with tumor, and naive spleen in terms of immune signature to understand the difference in immune cells. As chemotherapy being the standardized treatment, we tested the effect of antiCD3 monoclonal antibody and 5Fluorouracil drug in the depletion of proliferating haematopoietic stem cells. Tcell depletion results in the change of the immune response such as the inhibition of the specific function of that Tcell subtype. We are demonstrating the real conditions of patients to understand these conditions affect ICBT treatment.

Presenter(s): Paul Keene, University of Chicago
Session: Poster P3.13
Title: Fluctuations in Sustained Attention Predict Working Memory Performance
Advisor(s): Ed Awh, Department of Psychology, University of Chicago
Co-Author(s): Megan DeBettencourt

Abstract: Our attentional state fluctuates between highly attentive moments, severely disengaged moments, and everything in between. To characterize the role that attentional fluctuations play in working memory, we developed a novel hybrid attention/memory experiment that consists of a repetitive clicking task interleaved with a surprise memory test. In Experiment 1, we establish a link between attention and memory based on how quickly participants were responding. We replicate previous work that faster response times precede and predict attentional lapses, and present new evidence that memory performance is reduced following lapses in attention. In Experiment 2, we monitor fluctuations of attentional state in real time, so as to directly target moments when attention is high or low. Once we identify such a moment of extreme attentional state, we then trigger a memory test. We find that a subject's attentional state when we trigger a memory test influences their performance on that test. In Experiment 3, we use pupil size to predict subjects' memory performance. We find pupil size is lower for tests where the subject had high memory accuracy, giving us a neural indication of attentional state that predicts memory performance. With these experiments, we show that the current attentional state influences memory performance.

Presenter(s): Abdelkarim Khalid Abdelkarim Mahmoud, St. Olaf College
Session: Poster P1.13
Title: Quantifying the stability of RNA duplexes in aqueous TMAO and Urea solutions
Advisor(s): Jeff Schwinefus, Chemistry, St. Olaf College
Co-Author(s): Kathryn Stein

Abstract: Solutes in the cellular milieu can modulate the stability of folded biopolymers, such as proteins and nucleic acids. For instance, urea is a well-characterized destabilizer of protein three-dimensional structure while trimethylamine N-oxide (TMAO) is a known protein stabilizer. However, the influence of both urea and TMAO on the stability of nucleic acids has received scant attention. In this work, the attenuation or enhancement of the unfolding equilibrium constant of twelve base-pair RNA duplexes was quantified in aqueous urea and TMAO solutions using thermal denaturation monitored by absorbance spectroscopy. Urea destabilized 25% and 50% guanine-cytosine (GC) content RNA duplexes in a salt-dependent manner. TMAO stabilized the 25% GC duplex to a greater extent than the 50% GC duplex also in a salt dependent manner. Urea destabilization of RNA duplexes is dependent on TMAO concentration and vice versa. Our results support a universal mechanism of TMAO and urea interactions with biopolymers and will facilitate using these solutes as probes of solvent accessible surface area changes during biochemical reactions.

Presenter(s): Yeaseul Kim, Zhiye Lu, Grinnell College
Session: Poster P2.13
Title: Characterization of Cks2 Localization and Interaction with Cdk1 in Mitotic Cells of Xenopus laevis Embryos
Advisor(s): Joshua Sandquist, Biology, Grinnell College

Abstract: Although extensively studied, some aspects of mitotic regulation are not fully understood. In yeast it has been shown that the protein Cks2 serves as a targeting subunit for the mitotic kinase Cdk1. Specifically, Cks2 may direct Cdk1 activity towards the APC and help control mitotic exit. We attempt to explore Cks2 in a vertebrate system, Xenopus laevis. We visualized Cks2 in fixed epithelial tissues of frog embryos through confocal microscopy, and overexpressed Cks2 protein in the embryos. Our early data show that Cks2 localization overlaps that of a phosphorylated version of Cdk1(pY15) at cell junctions, and overexpression of GFP-tagged Cks2 protein results in increased phosphorylation of Cdk1 at Y15. These data are a first step toward a greater characterization of Cks2's role in regulating mitotic progression in vertebrate organisms.

Presenter(s): Isadora Kucera, University of Chicago
Session: Poster P3.14
Title: Dynamic Splicing of KDM5B in Cortical Neurogenesis
Advisor(s): Xiaochang Zhang, Department of Human Genetics, University of Chicago
Co-Author(s): Cai Qi, Irena Feng

Abstract: Dynamic gene expression is of utmost importance to generate diverse neuronal cell types in the human neocortex. Histone 3 lysine 4 (H3K4) methylation is associated with gene activation, but how is it regulated during neuron fate specification remains unknown. KDM5B removes methyl groups specifically from H3K4 me3/me2, and KDM5B mutations have been

associated with Autism Spectrum Disorders and agenesis of corpus callosum. KDM5B has been reported to prevent mouse embryonic stem cells from differentiation, but its role in cortical neurogenesis and neuronal type specification remains unknown. Our RNAseq analyses of developing mouse cortices uncovered a retained intron in KDM5B, and the intron retention is predicted to remove a critical protein domain required for substrate binding. Here we show that KDM5B intron retention level increases during brain development, suggesting a role of dynamic alternative RNA splicing in regulating H3K4 methylation and global gene expression during neuronal differentiation.

Presenter(s): Rahul Kukreja, University of Chicago
Session: Poster P1.14
Title: Rats choose to use helping cues based on social grouping
Advisor(s): Peggy Mason, Department of Neurobiology, University of Chicago
Co-Author(s): Rahul Kukreja, John Havlik, Peggy Mason

Abstract: Rats decide to help another rat in distress based on social grouping. Sprague-Dawley (SD) rats that have only lived with rats of their own strain will help any SD rat, but will not help a rat of another strain. However, SD rats that have lived with rats of another strain, such as black Long Evans (LE) rats, appear to consider LE rats as part of their in-group and help LE rats that are in distress (Bartal et al., 2014). In addition, the Mason Lab has used an arena-restrainer paradigm to explore the Bystander Effect. Rats have reduced helping when among “confederate” non-helping bystanders compared to when by themselves. Since rats will not help other rats that they consider to be out-group members and rats are less likely to help when in the company of confederates, we hypothesized that SD rats will not even integrate information from LE confederates if they have never lived with an LE rat, and therefore they will have reduced helping with the presence of LE confederates in an arena-restrainer paradigm. Our hypothesis was correct and our results showed that the SD rats that had lived with LE rats had fewer and less consistent openings and higher opening latency times compared to the SD rats that had never seen LE rats. The reduced helping behavior likely occurred due to SD rats considering the LE rats as out-group members because they had never lived with them before.

Presenter(s): John Larson, Hope College
Session: Poster P2.14
Title: Development of a Rapid Screening Assay to Detect Trafficking-Defective Mutants of System xc
Advisor(s): Leah Chase, Biochemsitry/Neuroscience, Hope College

Abstract: System xc- is a membrane transporter that exchanges extracellular cysteine for intracellular glutamate. The transporter is a heterodimer of two subunits, a transport-specific protein, xCT, and a heavily glycosylated associated protein, 4F2HC. Recent studies in the Chase lab have shown that the cell surface expression of this transporter may be regulated by trafficking motifs localized to the C-terminus of the xCT protein. The goal of this project is to develop a fluorescence-based assay that will allow for rapid screening of potential trafficking-defective mutants of the transporter. A similar assay has been successfully employed to study trafficking behavior of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)

(Holleran, J.P., et al., 2012). This assay requires the construction of a fusion protein in which an extracellular fluorogen-activating protein (FAP) is attached to the N-terminus of xCT. Once the fusion protein is created and expressed recombinantly in a mammalian cell line, the xCT on the cell surface can be labeled in real time by adding a membrane-impermeable fluorogen which only will fluoresce when bound to FAP. The relative fluorescence of the sample can then be measured (or imaged using a confocal microscope). Finally, a membrane-permeable fluorogen can be added to label the total pool of expressed xCT protein, and the relative fluorescence can be measured again, thus allowing one to calculate the percent cell surface expression of xCT. This assay can be adapted to 96 well plates to allow for rapid screening of putative-trafficking defective mutants.

Presenter(s): Chase Latour, Washington University in St. Louis
Session: Poster P3.15
Title: Maternal age at last birth and leukocyte telomere length in nationally representative population of women
Advisor(s): Mengmeng Du, Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center

Abstract: Maternal age at last birth and telomere length have been associated with risk of chronic health conditions. However, the association between the two has only been explored in one small study of older white women, and it is unknown if the association varies by sociodemographic and biological factors. Using nationally representative, cross-sectional data from the National Health and Nutrition Examination Survey (NHANES), we evaluated the association between maternal age at last birth and telomere length among 1,232 women peri- and postmenopausal women over age 40 years, surveyed between 1999 and 2002. After adjusting for confounders, we observed no association between maternal age at last birth and telomere length in the overall population (p-trend = 0.17). However, exploratory subgroup analyses suggested longer telomere length associated with late maternal age for women who were highly educated (p-trend = 0.03), under 70 years (p-trend= 0.03), and with history of 1 or 2 live births (p-trend = 0.02), although not all interactions were statistically significant. These results provide exploratory evidence that the association between age at last birth and telomere length may be modified by education, age at blood collection, and parity.

Presenter(s): Kyung Bae Lee, Washington University in St. Louis
Session: Poster P2.15
Title: STAT3 signaling mediates FAK inhibitor response and resistance in pancreatic cancer
Advisor(s): David G. DeNardo, Department of Pathology and Immunology, Washington University in St. Louis School of Medicine
Co-Author(s): Hong Jiang, Brett L. Knolhoff, Samarth Hedge, Audrey Bearden, David G. DeNardo

Abstract: Pancreatic cancer is not responsive to targeted therapy. This may be due to the presence of a uniquely fibrotic and immunosuppressive tumor microenvironment present in pancreatic ductal adenocarcinoma (PDAC). Critical obstacles to targeted therapy in PDAC tumors include the dense desmoplastic stroma that acts as a physical barrier to drug delivery and the high numbers of tumor-associated immunosuppressive cells. In our previous study, we

identified hyperactivated focal adhesion kinase (FAK) activity in neoplastic PDAC cells as a significant regulator of the fibrotic and immunosuppressive tumor microenvironment (TME). FAK inhibition (VS-4718) significantly limited tumor progression, and prolonged mice survival. Herein, we observed that STAT3 signaling was constantly activated in non-responsive and rebounded tumors, suggesting STAT3 signaling pathway regulates FAK inhibitor (FAKi) response and resistance.

We proposed that overcoming STAT3 reactivation upon FAK inhibition would enhance pancreatic cancer sensitive to FAK inhibitor. Together, our data indicate that STAT3 inhibition sensitizes PADC to FAKi and overcomes FAKi resistance.

Presenter(s): Owen Lewer, Claire Pfeffer, Carthage College
Session: Poster P3.16
Title: Space phage: novel environment for undergraduate research
Advisor(s): Deborah Tobiason, Biology, Carthage College
Co-Author(s): Owen Lewer, Claire Pfeffer, Deborah Tobiason, Andrea Henle

Abstract: Currently, undergraduates across the country are able to get first-hand research experience through the Phage Hunters program which is a part of the Howard Hughes Medical Institute Science Education Alliance. Through this course, students isolate a novel bacteriophage, and characterize it through a multitude of techniques. The purpose of this study is to pilot an extension of this program in which students would be introduced to Space Biology by testing the stability of bacteriophages in the space environment on the International Space Station (ISS). Different phages have shown to have various levels of stability under various temperatures, but the reason for varying stability is unknown. Preliminary results have shown that both Mycobacteriophages Cerasum and GreaseLightnin show high stability at both 4°C and 30°C making either phage a good candidate to send to the ISS.

Presenter(s): Szu Yu Lu, Washington University in St. Louis
Session: Poster P1.15
Title: The perception of risk: Differential relations between optimism and risk in 4- to 8-year-old children
Advisor(s): Lori Markson, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Laura Hennefield, Lori Markson

Abstract: Optimism is the tendency for people to underestimate negative outcomes and overestimate positive outcomes. Whereas optimism is linked to health, social, and motivational benefits, research suggests that optimism can lead children to take more risks when negative outcomes are significantly overlooked. Studies further indicate a discrepancy between how risky children perceive certain activities and their intentions to participate in those activities. To explore whether more optimistic children perceive activities as less dangerous and take more risk than less optimistic children, we presented 12 novel outdoor activities varying in three risk levels to 4- to 8-year-olds. Children indicated how dangerous they thought the activities were and whether they would try the activities. Then, children played a guessing game measuring optimism. We found that older children rated high-risk activities as more dangerous and demonstrated lower risk-taking than younger children. Boys demonstrated greater risk-taking than girls, though there were no gender differences in risk perception. As hypothesized, more

optimistic children rated activities as less dangerous than less optimistic children but only for high-risk activities. However, optimism did not predict risk-taking. Our findings suggest that the processes underlying risk perception and risk-taking differ and that both constructs should be considered in promoting children's safety.

Presenter(s): Allen Lu, University of Chicago
Session: Poster P2.16
Title: On the functional significance of a newly-observed N-terminus segment of the mechanosensitive channel MscS
Advisor(s): Eduardo Perozo, Biochemistry and Molecular Biology, University of Chicago

Abstract: MscS is a membrane protein linked to E. Coli's hypo-osmotic shock response. Recent electron-microscopy data reveals an MscS region unresolved from the x-ray crystal-structures, including an extension of TM-helices and a novel N-terminus fold. From this, I hypothesize that the N-terminus and TM-helices are located "higher" in the bilayer than previously modeled, and that this newly-observed region may be part of a novel gating mechanism.

Individual downshock assays were performed on MJF465 (osmoregulating-channel-deficient E. Coli) transformed with different alanine point-mutations of the newly-resolved region, including another mutant "Cryst" in which the region is cleaved. Mutants with significantly lower survival rates than cells with wild-type-MscS were deemed functionally important and examined further in liposomes using patch clamp electrophysiology to determine their pressure-dependent open probability.

These tests revealed many significant residues, including "Cryst", suggesting the newly-resolved region is indeed functionally important for gating. In particular, residues involved in intersubunit interactions seemed most relevant to relieving osmotic pressure. Because MscS is a force-from-lipid channel, the importance of the newly-resolved region suggests the N-terminus and TM-helices are docked "higher-up" in the bilayer rather than, as previously thought, along the helices. Therefore, previous models utilizing the incomplete crystal-structure or incorrect docking location must be reinterpreted.

Presenter(s): Emery Lu, University of Chicago
Session: Poster P3.17
Title: Defining the early transcriptional role of the cardiogenic transcription factors GATA4, TBX5, and NKX2.5
Advisor(s): Ivan Moskowitz, Departments of Pediatrics, Pathology, and Human Genetics, University of Chicago
Co-Author(s): Megan Rowton and Ivan P. Moskowitz

Abstract: Congenital heart disease (CHD) is one of the most prevalent birth defects, occurring in 1-3% of live births. While the genetic basis of some CHD has been characterized, the molecular mechanisms underlying the etiology of CHD are not fully understood. Cardiogenic transcription factors (TFs), such as TBX5, NKX2.5, and GATA4 are essential for heart development, and mutations in these TFs have been implicated in the development of CHD. However, the diverse mechanisms by which these TFs control gene expression throughout the

process of cardiac differentiation have not yet been elucidated. Using a mouse embryonic stem cell (mESC) model of cardiomyocyte differentiation, we show that GATA4 expression begins at the early mesoderm stage, TBX5 is expressed at the cardiac progenitor stage, and NKX2-5 expression begins during terminal differentiation. These results suggest that these TFs may activate different gene regulatory networks to drive differentiation. GATA4 is known to initiate the transcriptional cascade in liver development, and its early expression in cardiac differentiation suggests that it may play a similar “pioneer factor” role in heart progenitors. In these studies, we aim to define the early transcriptional roles of GATA4, TBX5, and NKX2-5 and link their activity during differentiation to the onset of CHD.

Presenter(s): Rebecca Marks, Washington University in St. Louis
Session: Poster P2.17
Title: A Longitudinal Assessment of Changes in Stress, Depression and Inflammation
Advisor(s): Ryan Bogdan, Psychological and Brain Sciences, Washington University in St. Louis
Co-Author(s): Michaela Voss, Michael Boudreaux, Tom F. Oltmanns, Ryan Bogdan

Abstract: Stress commonly precipitates depression and both are associated with elevated levels of inflammation. However, longitudinal changes in stress, inflammation, and depression have not been rigorously assessed. Using data collected in the ongoing longitudinal St. Louis Personality and Aging Network (SPAN) study, we examined whether changes in recent stressful life events (List of Threatening Experiences), depression (Beck Depression Inventory), and interleukin-6 (IL-6; morning fasting serum) over a 2.5-year period are correlated among 463 older adults and 163 older adults, respectively. Data for the second time point are still being collected; we anticipate a total N of 750 across all variables. Increased stress over the 2.5-year period was correlated with increases in inflammation and depression over the same time. Further, increased inflammation was associated with increased depressive symptoms. While these within subject correlations increase the plausibility that stress, inflammation, and depression may causally affect one another, the directionality of these relationships remains unclear. Drawing from other literature it is possible that stress prospectively increases both inflammation and depression which both reciprocally influence one another. We will explore cross-lagged mediational models to test these plausible directions of association.

Presenter(s): Cristhian Martinez, Gustavus Adolphus College
Session: Poster P1.31
Title: Assets increasing physical activity and nutritious eating among children of migrant farmworkers in Elysian, Minnesota
Advisor(s): Iris Borowsky, Department of Pediatrics, University of Minnesota
Co-Author(s): Calla Brown; Iris Borowsky

Abstract: Migrant farmworkers are people that migrate from their permanent home in order to find temporary work in the agricultural sector. The children of migrant and seasonal farmworkers have a high prevalence of overweight and obesity, with reports ranging from 31% to 73%. The purpose of this study was to identify and describe assets that could promote healthy eating and increase physical activity of migrant children in the Elysian community. In

person and phone call interviews were conducted with staff members from different business in the community. Responses were analyzed to create a community asset map and the strengths and barriers for the assets and recommendations they had for the community were noted. Two city parks, a state trail, a migrant Head Start, a library, and a bakery & deli were identified as assets. The biggest recommendation for the Elysian community was the building of a grocery store. Throughout the interviews, the information on the availability of other assets was strong. However, there was a lack of knowledge between the different assets on what resources or options they offered that could help children of migrant farmworkers live healthier lives.

Presenter(s): Katherine Matlin, Colorado College
Session: Poster P1.16
Title: Range of nonsense-mediated mRNA decay efficiencies detected among homogenous cell cultures
Advisor(s): Sara Hanson, Molecular Biology, Colorado College

Abstract: Nonsense-mediated mRNA decay (NMD) is a well-categorized eukaryotic quality control mechanism for the dynamic regulation of gene expression. NMD degrades transcripts containing a premature termination codon (PTC) about 55 nucleotides upstream from the final exon junction complex. While most transcripts containing a PTC are degraded via NMD, transcripts containing a PTC can also produce truncated or full-length proteins. NMD efficiency may vary based on gene sequence, intracellular location, tissue, or on an individual level; however, the scope of NMD efficiency and specificity remains unclear. This study aimed to aid the understanding of NMD as an endogenous control for gene expression. We determined the in vivo inconsistency of NMD efficiency among cells of the same mammalian tissue culture using fluorescent reporters, flow cytometry, and single-cell sorting. Western blotting for NMD factors revealed their correlation with NMD efficiency. Preliminary analysis of NMD efficiency and cell cycle via western blotting did not show a correlation. To examine how RNA expression and protein production correlate with detected NMD levels, qPCR was used to determine fold change in NMD factor gene expression. Future directions include repeating expression analysis, including performing RNA-seq, and further investigation into NMD efficiency as it correlates with cell cycle.

Presenter(s): Kathryn McKinnon, Katie Van Dame, Carthage College
Session: Poster P2.18
Title: Activity budgets of lowland gorillas (Gorilla gorilla gorilla) at the Memphis Zoo
Advisor(s): Angela Dassow, Biology, Carthage College

Abstract: The western lowland gorilla (Gorilla gorilla gorilla) is the largest and most widespread gorilla subspecies, however due to poaching, disease and habitat loss their populations have declined. Captive breeding programs strive to preserve rare and important genes; however little is known about captive gorilla behavior. The Memphis Zoo houses four western lowland gorillas, who have yet to successfully breed in captivity. Understanding captive gorilla behavior can help conservationists improve reproductive activity in captive populations. On September 30th, 2017, four gorillas were video recorded for approximately four hours, and thirty behavioral activities were coded using a 1/0 ethogram to observe the presence/absence of each behavior

at one-minute increments. From this, time budgets were individually tallied and compared across all four gorillas. Sitting was the most common activity and ranged from 25.96-39.52% of the total time budgets. The second and third most common activities varied for each gorilla, but included visual side glancing, eating, lying, walking quadrupedally, and squatting. These activities represent 57.22-70.65% of the behaviors observed. Initial time budgets have been valuable in understanding the gorilla's general behavior. Additional observations will be necessary to fully understand the annual activity budgets of each gorilla.

Presenter(s): John McMorris, Hope College
Session: Oral II.H.4 (3:15)
Title: Classifying Mass Shootings in the United States
Advisor(s): Yew Meng Koh, Mathematics (Psychology), Hope College
Co-Author(s): Yew Meng Koh, Tyler Gast

Abstract: Mass shootings in the US appear to be random and unpredictible events. However, a closer examination of these events reveals certain trends and commonalities between them. In this study, we classify mass shootings using various statistical clustering algorithms. The implementation of these methods, their relative merits, and conclusions regarding similarities and distinct features between mass shooting incidents which arise from the different clusters of incidents are discussed.

Presenter(s): Nikita Mehta, University of Chicago
Session: Poster P3.19
Title: Wnt Signaling in Schwann Cells Affects Peripheral Nerve Regeneration
Advisor(s): Brian Popko, Neurology department, The University of Chicago
Co-Author(s): Nikita Mehta, Benayahu Elbaz, Ani Solanki, Betty Soliven, and Brian Popko

Abstract: The peripheral nervous system (PNS) is unique in its ability to recover from nerve injury. In a process termed Wallerian degeneration, the axons and myelin distal to the site of injury degenerate and are cleared by Schwann cells and macrophages. Subsequently, Schwann cells dedifferentiate, proliferate, guide axons to their germane targets, redifferentiate, and myelinate the axons. Nevertheless, the molecular mechanisms controlling PNS regeneration are not fully understood. We have demonstrated a role of the canonical Wnt/β-catenin signaling pathway in developmental myelination of the PNS. The ablation of *APC,* a critical inhibitor of Wnt signaling, from Schwann cells activates this pathway, leading to impaired developmental PNS myelination. These results suggest that Wnt signaling may also play crucial role in PNS regeneration. We used reporter mice to study Wnt pathway activation following sciatic nerve crush injury. Wnt signaling was strongly activated in Schwann cells as early as three days, and at least up to seven days post-crush injury. We have preliminary electrophysiology and electron microscopy data that suggests that the conditional ablation of APC in adult Schwann cells activates the Wnt pathway and delays recovery from peripheral nerve injury. Our data suggests that the activation of Wnt signaling in Schwann cells impedes PNS regeneration. We will next examine the potential of pharmacological mechanisms to inhibit Wnt signaling following PNS injury and to improve regeneration.

Presenter(s): Nancy Mora, Beloit College
Session: Poster P1.17
Title: Analyzing effects of different wavelengths on growth using rapid-cycling Wisconsin Fast Plants (*Brassica rapa*)
Advisor(s): Yaffa Grossman, Biology, Beloit College

Abstract: Phototropism is defined as the orientation in growth of the plant when the direction of the light source is the determining factor, as the plant is turning or bending in response to the light. Growth towards the light source is referred to as positive phototropism, while growth away from light is called negative phototropism. Phototropism works due to elongation on the dark side of the stem, caused by the influence of auxin in cells on the shaded sides of the tip. The purpose for this experiment was to construct an in-class lab activity that could be used in an introductory botany course to teach and introduce first year students about plant growth and further their understanding of phototropism. Five Wisconsin Fast Plants (*Brassica rapa*) were placed into boxes containing either blue, red, and white LEDs located on the exterior side of the box. Data were collected for length and angle of growth at the beginning of experiment as well as 12 and 24 hours later. No statistically significant differences were detected for the first experiment, but a follow up experiment will be conducted to eliminate potential errors.

Presenter(s): Vishva Nalamalapu, Grinnell College
Session: Poster P2.19
Title: Candidate hydrologic refuges predict the species distribution of a water limited annual plant
Advisor(s): Vince Eckhart, Biology, Grinnell College

Abstract: Organisms in seasonally arid regions are often water-limited. In a changing climate characterized by years of drought areas of high-water status within regions of low water status, allow these organisms to persist. These areas may be a result of, and therefore may be identifiable by, topographic variables. They may also be identifiable by areas of more vegetation within regions of less vegetation. My objective was to study whether topographic and vegetation variables predict the distribution of the annual plant Clarkia xantiana ssp. xantiana in a seasonally arid region at two spatial scales. I conducted binary logistic regression to determine whether rock outcrops, predicted C. xantiana. I used the standard deviation of elevation to construct topographic heterogeneity. I used NDVI (vegetation index) images to construct consistency of seasonal vegetation dynamics and consistency of vegetation. I combined these variables to create four Maxent models and conducted binary logistic regressions to analyze the relationships between model values and presences and absences. Rock outcrops, consistency of seasonal vegetation dynamics, and consistency of vegetation all predicted C. xantiana distribution. This study improves predictions of C. xantiana's current and future distribution, as well as designs a method for predicting distributions of other water-limited species.

Presenter(s): Nhu Nguyen, Macalester College
Session: Poster P3.20
Title: Characterization of RNA SHIV+ cells and FoxP3+ cells in lymphoid tissues of rhesus macaques
Advisor(s): Elizabeth Connick, Infectious Disease, University of Arizona

Abstract: HIV-1 replication has found to be concentrated in T follicular helper (TFH) cells within B cell follicles of lymphoid tissues. Recent studies have found a subpopulation of regulatory T cells, referred to as follicular regulatory T (TFR) cells. They derive from extrafollicular Treg cell precursors and localize to the follicle and GC. They have been shown to directly suppress TFH cell function in mice (3), nonhuman primates (2), and humans (2). TFR cells are a subset of CD4+ T cells in the lymphoid follicles. Although TFR cells are highly permissive to HIV-1, the rate of infection of TFR cells to SHIV-1 is unknown. TFR cells express FoxP3, along with other transcription factors, and are CD4+ T cells. One model our lab focuses is SHIV-infected Rhesus Macaques. SHIV is a virus that has been constructed by replacing the envelope gene region of the SIV pathogenic clone with the counterpart from HIV-1 subtype B. Based on our understanding of HIV pathogenesis, we hypothesize that there will be more SHIV+ cells within the follicle in both chronic-untreated and chronic-treated samples. Additionally, we explored the Treg phenotype both in chronic-untreated and chronic-treated samples.

Presenter(s): Hannah Nilsson, St. Olaf College
Session: Poster P1.18
Title: In vitro selection of acyltransferase DNA enzymes
Advisor(s): Laura Listenberger, Biology and Chemistry, St. Olaf College

Co-Author(s): Tianjiong Yao and Scott K. Silverman
Abstract: Amino acid acylation is an important type of post-translational modification that influences a variety of different biological functions including gene expression; however, few proteins capable of acyl group transfer to an amine have been characterized in nature. In this study, we aimed to identify DNA molecules that exhibited acyltransferase activity. To identify deoxyribozymes, in vitro selection was performed on a random DNA pool. Acyl donor substrates were synthesized and reaction conditions were optimized before selection rounds were initiated. Results indicate that acyl donors of moderate reactivity and stability are likely required substrates for selection of acyltransferase DNA enzymes. Selection is currently underway. Future studies will aim to find and characterize DNA enzymes capable of amine acylation.

Presenter(s): Sarah O'Mara, Hope College
Session: Poster P2.20
Title: Use of CRISPR-Cas9 Approach to Knockout Truncated VACM-1(KLB22) in HUVEC
Advisor(s): Maria Burnatowska-Hledin, Biochemistry, Hope College
Co-Author(s): Emma Wabel, Schuylar Brunink, Philip Versluis, and Maria Burnatowska-Hledin

Abstract: VACM-1/CUL5 a scaffold protein in E3 ligase and is important in the protease-protein degradation pathway and impacts cellular proliferation. An alternative start codon in the VACM-1 sequence can lead to the production of a 59 kDa protein and is considered a truncated form of VACM-1/Cul-5. The expression of the truncated VACM-1(KLB22) protein, as determined by

western blot, is tissue-specific and can be detected in the kidney and in the heart atrium. Previous results suggest that KLB22 increases cell proliferation through a MAPK pathway. Our study aimed to explore the success of a KLB22 gene knockout using CRISPR-Cas9. The CRISPR-Cas9 system is a bacterial immune system that functions by targeting specific sequences of DNA. It can be programmed to target genes of interest through the use of short guide DNA sequences, thus enabling specific gene editing in eukaryotic cells. Our results showed a knockout KLB22 in a human umbilical vein endothelial cell line (HUVEC).

Presenter(s): Juliana Olliff, Colorado College
Session: Oral I.D.1 (10:00)
Title: Potential roles for non-coding RNAs in the progression of mating-type switching of Ogataea polymorpha
Advisor(s): Sara J. Hanson, Molecular Biology, Colorado College

Abstract: Sexual reproduction is a complex and evolutionarily illogical process, as only half of an organism's genome is inherited. In many yeast species, a unique aspect of the sexual cycle known as mating-type switching (MTS) exists; by studying the mechanisms behind the process of MTS, we can hypothesize about the evolutionary function of sexual reproduction in a variety of eukaryotic species. Ogataea polymorpha is methylotrophic yeast species distantly related to the more studied baker's yeast. In this work, we look for the long non-coding RNAs that are primary actors in the progression of MTS in O. polymorpha. We hypothesize that an overabundance of the transcription factor STE12, which is produced during MTS, results in the upregulation and production of non-coding RNAs. We used a transgene that promoted overexpression STE12 in the presence of methanol. We confirmed MTS after overexpression of STE12 using PCR, and performed RNA-seq to identify targets of STE12. We plan to identify non-coding RNAs produced during MTS using total *de novo* RNA sequencing.

Presenter(s): Guadalupe Orbezo-Perez, Beloit College
Session: Poster P3.21
Title: Differential regulation in defense-related genes by flg22 and elf18 in Arabidopsis thaliana
Advisor(s): Amy G. Briggs, Biology, Beloit College
Co-Author(s): Jenna M. Nordin, Amy G. Briggs

Abstract: Plants protect themselves from pathogenic infection with a form of innate immunity called pattern triggered immunity (PTI), which is activated when microbe-associated molecular patterns (MAMPs) bind to pattern recognition receptors (PRRs) on the plants' cell membranes. MAMPs are proteins that are highly-expressed by pathogenic bacteria, and they are used in the lab to induce and study plant immunity without the direct use of pathogens. Flg22 and elf18 are two common MAMPs that are used interchangeably in the lab given the similar defense responses they trigger in plants, but due to previous research, we hypothesized that flg22 and elf18 affect transcriptional regulation differently for defense-related genes in plants. In the present study, we treat Arabidopsis thaliana seedlings with flg22 and elf18 to analyze the expression levels of certain defense-related genes with real-time quantitative PCR. We obtained no statistically significant results; however, we saw distinct patterns of transcription regulation worth of further research.

Presenter(s): Olivia Paetz, Tim Renier, St. Olaf College
Session: Oral I.A.2 (10:15)
Title: Lipid droplet protein binding in response to altered phospholipid composition: alcoholic fatty liver disease model
Advisor(s): Laura Listenberger, Biology and Chemistry, St. Olaf College

Abstract: Alcoholic Fatty Liver Disease (AFLD) involves the alcohol-induced accumulation of excess lipids in hepatocyte lipid droplets. Lipid droplets are encased in phospholipid monolayers predominantly composed of phosphatidylcholine (PC) and phosphatidyl-ethanolamine (PE). Protein binding to lipid droplets affects droplet size and activity. Previous experiments with a rat model of AFLD show lipid droplet surfaces have a decreased ratio of PC:PE. We aimed to determine if the altered phospholipid surface in AFLD leads to differential binding of several proteins of interest, selected for their monolayer binding motifs and roles in lipid droplet regulations. By culturing AML12 cells in choline-deficient media with oleate, an unsaturated fatty acid, we simulated the altered phospholipid composition of AFLD. With this model, we used western blotting to compare binding of rab18, lanosterol synthase (LSS), and αCCT1 in choline sufficient and deficient conditions. No significant difference in binding existed between choline sufficient and deficient conditions for either rab18 or LSS. αCCT1 exhibited increased binding in choline deficient conditions. By evaluating how altered phospholipid monolayer composition affects the binding of these interest proteins, we seek to further elucidate the biochemical pathways that contribute to AFLD.

Presenter(s): Eleda Plouch, Hope College
Session: Poster P2.21
Title: Identification and characterization of fungistatic neolignans from the seeds of Phytolacca americana
Advisor(s): Elizabeth M. Sanford, K. Greg Murray, Chemistry, Biology, Hope College
Co-Author(s): Jordan Dischinger-Smedes, Elizabeth M. Sanford, K. Greg Murray

Abstract: Phytolacca americana, know commonly as pokeweed, is a pioneer species native to the northeastern United States. After a period of dormancy, pioneer species like P. americana grow rapidly during high light conditions, such as during canopy gaps caused by tree falls. Due to their longevity in the seed bank, numerous chemical defenses of pioneer species have been studied. This research seeks to identify and characterize the compounds in P. americana that may protect the seeds of this pioneer species from fungal attack while dormant in the soil. To isolate possible anti-fungal components of P. americana, methanol extracts of the crushed seeds were prepared, and the components separated using a cyclograph, preparative TLC, and HPLC. These compounds were identified via NMR and MS. Their anti-fungal properties were characterized by poisoned-medium bioassays with pathogenic fungi on the separated and identified fractions.

Presenter(s): Christian Porras, University of Chicago
Session: Oral I.B.1 (10:00)
Title: The influence of spatial structure and natural selection on genome-wide association studies
Advisor(s): John Novembre, Human Genetics, University of Chicago
Co-Author(s): Daniel Rice

Abstract: Genome-wide association studies (GWAS) have shown that much of the variation in disease risk is due to rare deleterious alleles. When considering the geographic distribution of a population, we expect these alleles to be removed by selection before they can spread beyond their original location. However, the spatial distributions of these alleles have not been characterized in detail. We aim to understand how natural selection, spatial structure, and geographic sampling bias interact to determine the inferred local and global genetic architecture of a trait.

Here we develop theoretical models for the geographic spread of rare deleterious alleles. The essential output of our population genetics analysis is the expected allele frequency spectrum as a function of: the sampling scheme, the selection coefficient for an allele, and the spatial structure. Our theoretical results highlight the dependence of the inferred genetic architecture of a trait on the geographic sampling scheme and the evolutionary process, with implications for the interpretation of geographically localized GWAS cohorts.

Presenter(s): Romy Portieles, University of Chicago
Session: Poster P3.22
Title: Optimizing Hospitalist Care: A Time in Motion Study
Advisor(s): Andrew Schram, Section of Hospital Medicine, University of Chicago
Co-Author(s): Anna Feldkamp

Abstract: Doctors and patients are increasingly dissatisfied with the amount of time physicians spend with patients; this study sought to generate quantitative data on how much of physicians' time is spent doing non-physician-critical activities and how that affects the amount of time spent with patients. To better understand how physician's time is spent, two research assistants directly observed 5 different Hospitalist doctors at the University of Chicago Hospitals for one week. During this time, physicians' activities were recorded every minute of the day into a pre-prepared spreadsheet of possible tasks. Upon analyzing the data, physicians' activities were broken down into physician-critical, non-critical, administrative activities, and time spent walking, as well as into time spent in direct patient care vs. indirect patient care. We found that on average, less than 20% of physicians' time is spent directly caring for patients and that doctors spend ~30 minutes per day on average doing non-critical work. Hospitalist physicians spend a significant portion of their days performing non-critical activities, thereby limiting the amount of time spent in direct patient care. As a result, hospitalist physicians spend very little time in face-to-face interactions with their patients. Interventions aimed at reducing the time spent in such activities could potentially improve quality of care, and the doctor-patient relationship.

Presenter(s): Julia (Gege) Ran, University of Chicago
Session: Oral II.H.1 (2:30)
Title: Improving Genetic Diagnosis for Developmental Delay and its Cost Effectiveness in South Africa
Advisor(s): Zané Lombard, Amanda Krausea, Department of Human Genetics, University of Witwatersrand, Johannesberg, South Africa
Co-Author(s): Lydia Wu, Emma Wiener, Zané Lombard, Amanda Krausea

Abstract: Developmental delay (DD) refers to a failure in attaining age-appropriate motor, behavioral, and other developmental milestones. Accurate molecular diagnosis of DD is the first step in providing timely care. In South Africa, the National Health Laboratory Services (NHLS) currently employs various traditional genetic tests to diagnose patients with DD, but the efficacy of existing techniques has never been evaluated. While exome sequencing has made accurate diagnosis possible in rich countries, it has traditionally been dismissed as financially unviable for South Africa's healthcare system, although such claim has never been proved statistically.

In a retrospective chart review of 213 patients seen at the nation's largest genetic clinic in 2017, we compared the diagnostic outcome and cost for DD patients to that of two control groups: patients with known chromosomal disorders, and patients without DD. We found that not only is the majority (53%) of DD patients undiagnosed, the average cost of genetic investigations for DD patients is also significantly greater than for other groups of patients ($p<0.05$). For currently undiagnosed DD patients with more than 3 genetic investigations, exome sequencing would have been a cheaper alternative. The present study is the first attempt to evaluate genetic investigations in South Africa.

Presenter(s): Julia (Gege) Ran, University of Chicago
Session: Oral I.B.3 (10:30)
Title: Intergenerational Health Transmission in Uganda – its Moderators and Persistence
Advisor(s): Jenny Trinitapoli, Department of Sociology, University of Chicago
Co-Author(s):

Abstract: Children born to malnourished mothers are more likely to suffer from growth impairment – such is the phenomenon of intergenerational health transmission. Stunting affects more than 33% children under five in Uganda, yet the connection between a child's nutritional status and maternal health is seldom studied in sub-Saharan Africa in general. Using maternal height as a proxy for long-term maternal nutritional status, this study explores the intertwined influence of health endowment from the previous generation and socioeconomic environment on childhood stunting. Logistic regressions and marginal analysis are performed on anthropometric measurements from 9190 mother-child pairs recorded in Uganda Demographic and Health Surveys between 2001 and 2010, to examine the effect of maternal height, location of residence and maternal education attainment on child's age-standardized height. The study found stunting to be almost twice as prevalent for children of the shortest fifth of mothers than for the tallest fifth. While urban residence and maternal secondary education magnifies the protective effect of maternal height against childhood stunting for non-stunted mothers, the high risk of stunting for child born to a stunted mother (<145cm) is unmoderated by socioeconomic improvement. A life-course approach to improving long-term maternal health is critical in tackling the global stunting epidemic.

Presenter(s): Aleksandra Recupero, University of Chicago
Session: Oral I.A.3 (10:30)
Title: Optimizing BIN1 BioID2 in a mouse neuroblastoma cell line
Advisor(s): Gopal Thinakaran, Department of Neurobiology, University of Chicago
Co-Author(s): Robert Andrew, Gopal Thinakaran

Abstract: The Bin1 gene has been identified through genome-wide association studies as the second most prevalent genetic susceptibility locus for late-onset Alzheimer's disease. The function of BIN1 in the brain and its contribution to Alzheimer's disease (AD) pathogenesis remain largely unknown. Therefore, to better understand the function of BIN1 and its isoform specific differences in AD, we sought to identify proteins that interact with BIN1 through BioID2. BIN1 BioID2, or biotin identification, utilizes a promiscuous biotin ligase-BIN1 fusion that biotinylates proteins proximal to BIN1. We cloned Bin1 isoform 1 and isoform 9 into BioID2 vector backbones. These constructs were then transfected into N2a cells to generate stable cell lines. Immunofluorescence staining of the stable cell lines revealed biotin labelling in the cells expressing BIN1:BioID2 fusions. Next, primary cultures of neurons and oligodendrocytes will be transfected with the Bin1:BioID2 constructs. The biotinylated proteins will be recovered by streptavidin-conjugated beads, separated by SDS-PAGE, and identified through mass spectrometry. The identified proteins will provide a large dataset of proteins that either interact with or are present within the cellular environment of BIN1. The discovery of novel proteins that may interact with BIN1 will help elucidate the role of BIN1 as an AD risk gene.

Presenter(s): Esther Rodman, Macalester College
Session: Oral II.G.1 (2:30)
Title: Quantifying the Temporal Dynamics of Huntingtin Protein Aggregation at a Single-Cell Resolution
Advisor(s): Amir Mitchell, Systems Biology, UMass Medical School
Co-Author(s): Payam Khoshkenar, Ophir Shalam, Amir Mitchell

Abstract: Protein aggregation is caused by the disruption of proteostasis, which can be triggered by extracellular stressors, and aggravated by mutations in the aggregating protein or the cellular machinery maintaining proteostasis. Accumulation of protein aggregates is associated with numerous neurodegenerative disorders, including Huntington's disease. A known mutation in the Huntingtin protein (HTT) leads to an expansion of an existing CAG repeat, causing aggregation of HTT. We use time-lapse microscopy to quantify the temporal dynamics of HTT aggregation in an immortalized human cell-line. Aggregation is monitored under unperturbed growth conditions and after transient heat shock and oxidative stress. We identified three types of aggregation states dependent upon extracellular conditions: single aggregate, two types of aggregates, and multiple aggregates. In unstressed cells, about 15-20% of the population developed aggregates. This fraction increases under stress, to about 90% after heat-shock and to about 30% under oxidative stress. Excitingly, our observations lay the ground for a sensitive single-cell assay that can be used to screen chemical and genetic libraries, and to identify druggable gene targets. This screen may reveal novel aggregation modulators that remain undetectable by current bulk population approaches. Identification of such novel modulators will uncover new targets for therapeutic intervention in neurological disorders.

Presenter(s): Olivia Ruffins, Beloit College
Session: Poster P1.19
Title: Effect of nitrates and phosphates on the production of antimicrobial peptides in Xenopus laevis
Advisor(s): Tawnya Cary, Biology Department, Beloit College
Co-Author(s): Monica Smith, Tawnya Cary

Abstract: Amphibian populations are declining rapidly, with at least 32.5% of amphibians currently listed as endangered. One possible cause of the declines may be pollutants. Being in southern Wisconsin, there is a lot of agriculture in the area, which caused us to consider whether agricultural run-off, specifically nitrates and phosphate, is impacting local amphibian populations. We tested whether exposure to nitrates and phosphates have an impact on the innate immune system in amphibians, specifically looking at the production of antimicrobial peptides. Antimicrobial peptides (AMPs) are skin peptides that inhibit the growth of bacteria, fungus and viruses on the surface of the skin of amphibians. We exposed 64 juvenile Xenopus laevis to an 18 day exposure of nitrates, phosphates and a combination of both nitrates and phosphates. In our analysis, we did not find evidence that the combination of nitrates and phosphates impacted concentrations of AMPs differently than just the exposure to nitrates or phosphates.

Presenter(s): Dulce Saenz, Beloit College
Session: Poster P2.22
Title: Carbon Cycling in Managed Turf and Restored Ecosystems
Advisor(s): Chantal Koechli, Biology, Beloit College
Co-Author(s): Luke Zimmerman

Abstract: Microbial communities play an essential role in the soil carbon cycle. In the process of decomposing of organic matter, microbes produce CO_2, a greenhouse gas, as a by-product. Soil microbial community function may impact whether soils are sinks or sources of CO_2, potentially impacting the magnitude of climate change. I studied carbon cycling and microbial community composition in turf and native soil ecosystems along the Rock River in Beloit, WI, where restoration of native plants was recently done to prevent erosion. I hypothesized that the native soil would have greater CO_2 respiration than the grass soil. Replicate soil cores in the grass and native sites were taken and geochemical analyses, including soil moisture, water holding capacity, soil organic matter content, and pH, were done. I also measured soil CO_2 respiration over the course of five days. Geochemical properties of soil were not significantly different between the two treatments, but respiration did differ significantly. The turf soil respired more CO_2 than the native soil, which may indicate that carbon is more accessible to microbial communities in the turf soil than in the native soil. To further explore my results, I am planning to conduct extended periods of CO_2 measurement and characterize the microbial community in both sites through PCR and DNA sequencing.

Presenter(s): Mayu Sakae, Grinnell College
Session: Poster P3.23
Title: MPC Inhibition Enhances Breast and Lung Cancer Responses to Radio-Chemo-Therapies
Advisor(s): Douglas Spitz, Free Radicals and Radiation Biology, University of Iowa
Co-Author(s): Shane R. Solst, Samuel N. Rodman, Sean C. Tompkins, Melissa A. Fath, Eric B. Taylor, Douglas R. Spitz

Abstract: Breast and lung cancers are two deadly cancer types that appear to exist under conditions of metabolic oxidative stress characterized by increased production of mitochondrial superoxide and hydrogen peroxide. Radiation and chemotherapy produce free radicals and oxidative stress in cancer cells. It has been previously observed that many cancer cells have increased rates of glycolysis that produces pyruvate. Pyruvate transport into mitochondria through the mitochondrial pyruvate carrier (MPC) provides substrates (isocitrate, glutamate, malate, etc.) capable of regenerating NADPH from $NADP^+$ that could contribute to detoxifying H_2O_2 through glutathione and thioredoxin dependent hydroperoxide metabolic pathways. This study was conducted to determine if inhibition of pyruvate import into mitochondria, by inhibiting the MPC, increases oxidative stress and improves cancer therapy responses in lung (H292, H1299T) and breast cancer (Sum159, Sum149) cell lines.

Presenter(s): Marietta Saldías Montivero, Macalester College
Session: Poster P1.20
Title: Accelerated differentiation of hiPSC into midbrain neuronal progenitor cells for the treatment of Parkinson's disease
Advisor(s): Patrick Walsh, Department of Neurosurgery, James R. Dutton, Department of Genetics, Cell Biology and Development, University of Minnesota; Randy Daughters, Biology Department, Macalester College

Abstract: Parkinson's Disease (PD) affects more than 50,000 people in the United State and this number will rise to 1.2 million by 2030. Stem cells are a prime candidate to address neurodegeneration in patients by replacing brain cells lost to PD. Current neural induction protocols for differentiation of human induced pluripotent stem cells (hiPSCs) into midbrain floor plate cells have considerable drawbacks, such as lengthy differentiations times and cumbersome culture conditions. Here, we report that modulation of the FGF, BMP, SHH, WNT pathways induced accelerated production of midbrain floor plate neuroepithelium (decreased from 20-25 days to 7 days) marked by the expression of the transcriptional factors OTX2, FOXA2 and PAX5. Accelerated differentiation of midbrain floor plate should facilitate the production of dopaminergic neurons and stem cell therapies for parkinson's disease.

Presenter(s): Nivedina Sarma, University of Chicago
Session: Oral I.A.1 (10:00)
Title: Biomedical Device to Target Electrical Disorders in Cardiomyocytes
Advisor(s): Bozhi Tian, Department of Chemistry, University of Chicago

Abstract: The Center for Disease Control reports that heart disease is the leading cause of death and myocardial infarction is the primary form of heart failure. Many treatments for myocardial infarction cause scar tissue to develop over coronary muscle, impeding regular

contraction and perpetuating risk of heart failure. Recent advances in cardiac tissue engineering promise materials that support hearts' contractile activity, and scaffolds prove to be more supportive than cardiac grafts. However, many scaffolds are limited by insulating materials and passive materials, thereby failing to provide cohesive beating between cell patches. We introduce a polymer-silicon nanowire mesh scaffold that provides mechanical and chemical cues for cardiac tissue support. Dynamic mechanical analysis shows that the scaffold pins water and will adhere to wet tissue through capillary action without requiring sutures or adhesives that would reintroduce risk of infarction. Photovoltaic p-i-n silicon nanowires embedded in the scaffold train cardiomyocytes to beat at target frequencies and a memory effect enables sustained synchronous beating. Cytotoxicity studies indicate that photostimulation does not induce cell death in adult rat hearts. This device promises a novel method of targeting electrical disorders in cardiomyocytes.

Presenter(s): Abigail Schmid, University of Chicago
Session: Oral I.D.3 (10:30)
Title: The infamous capsular polysaccharide loci of Bacteroides fragilis and their 'conserved hypervariability'
Advisor(s): A. Murat Eren, Department of Medicine, University of Chicago
Co-Author(s): Alon Shaiber, Mirae Lee, Yue Shan, Aretha Fiebig, Sean Crosson, Eugene B. Chang, A. Murat Eren

Abstract: The common human gut microbe Bacteroides fragilis evades host immune responses by producing capsular polysaccharides (CPS). B. fragilis populations typically carry eight distinct CPS genomic loci, each with about twenty genes. While the hypervariable nature of CPS-associated genes is widely appreciated, we have limited understanding of their phylogenetic, structural, and functional characteristics. Here we used public isolate genomes and gut metagenomic assemblies to create a database of 297 complete, non-redundant CPS loci from B. fragilis. We employed phylogenetic and pangenomic strategies to study variation among CPS-associated genes and found hypervariable genes follow non-random distributions within loci. We also employed metagenomic read recruitment strategies to study the distribution of CPS-associated genes across gut metagenomes. We detected every complete CPS locus from a specific isolate in at least one gut metagenome, but the occurrence of one locus was not predictive of the occurrence of other isolate loci in that metagenome. Thus, there probably exists a finite and randomly distributed collection of loci across B. fragilis populations. Interestingly, some genes that were rare across CPS loci were prevalent across metagenomes, suggesting targets to investigate gene incorporation events. Together, these insights reveal experimental targets to investigate how environmental selection shapes these cryptic genomic loci.

Presenter(s): Harini Shah, University of Chicago
Session: Oral II.G.2 (2:45)
Title: The role of CHOP transcription factor in EAE, a mouse model of multiple sclerosis
Advisor(s): Brian Popko, Department of Neuroscience, University of Chicago
Co-Author(s): Yulia Dzhashiashvili

Abstract: Multiple sclerosis (MS) is a chronic demyelinating disease of the central nervous system (CNS). It is characterized by the presence of inflammation, loss of oligodendrocytes, demyelination, and axonal degeneration. Current treatments target and only modestly tame the

immune response associated with the disease. There is no specific treatment to protect the central nervous system from loss of oligodendrocytes, which are myelinating glial cells inherent to the CNS that provide trophic support to neurons and promote axonal viability.

Endoplasmic reticulum (ER) stress occurs when unfolded or misfolded proteins accumulate in the ER. Oligodendrocytes in the CNS are especially sensitive to ER stress, given that they produce large quantities of plasma membrane proteins. ER stress has been implicated in MS lesion formation. The unfolded protein response (UPR), which is an adaptive mechanism that helps reduce ER stress, has been shown to be activated in MS and experimental autoimmune encephalomyelitis (EAE), a mouse model for MS. The UPR protein CHOP functions as a pro-apoptotic transcription factor that is activated in cells in response to prolonged ER stress. In this study, we analyzed the response of CHOP mutant and control littermate mice to EAE. Our results indicate that CHOP expression increases the sensitivity of oligodendrocytes to CNS inflammation.

Presenter(s): Sara Siddiqui, University of Chicago
Session: Poster P3.24
Title: Effects of TPI-1 Inhibitor on Red Blood Cell Differentiation of Erythroleukemic Cells
Advisor(s): Amittha Wickrema, Hemacology/Oncology, University of Chicago

Abstract: Myelodysplastic syndromes (MDS), a group of malignant blood disorders, are caused by ineffective hematopoiesis. SHP-1, a novel target for cancer treatment, is inhibited by the tyrosine phosphatase inhibitor-1 (TPI-1). Erythroleukemic cells and hematopoietic stem/progenitor cells were treated with TPI-1 prior to and during differentiation into erythrocytes to determine whether the drug increases red blood cell (RBC) production. Erythropoietin (EPO) cytokines were added to activate the JAK2 signaling cascade that would stimulate differentiation of the RBC. At different days of differentiation, cells were cytospun and stained for hemoglobin. The hemoglobin positive percentage of the samples was analyzed as a representation of how the differentiation process was unfolding.

Results: Drug pre-treatment show higher hemoglobin positive percentages than the drug treatment during differentiation process. There are relatively low standard errors of 1-3 percentage points. There is either a dose-dependent increase (seen for Experiment 1, Day 5) in hemoglobin, or the percentages remain relatively constant. By Day 7, the hemoglobin percentages are similar regardless of inhibitor concentration.

Presenter(s): Sayira Silverio, Macalester College
Session: Poster P1.21
Title: Induction of Mechanical Hyperalgesia and Cytokine Production in a Murine Model of Localized Provoked Vulvodynia
Advisor(s): Devavani Chatterjea, Biology, Macalester College
Co-Author(s): Erica Arriaga-Gomez, Devavani Chatterjea

Abstract: Vulvodynia is a chronic vulvar pain condition that presents without any visual evidence of inflammation. It is estimated that 10-15% of women live with the condition. Although poorly understood, epidemiological studies have associated seasonal allergies with chronic vulvar pain. We have established a novel murine model of localized provoked vulvodynia using

Oxazolone to elicit pain and immune responses in the labiar skin. This model induces mechanical hyperalgesia and cytokine production that mimics what is seen in patients with vulvodynia. Methylisothiazolinone (MI) is a preservative found in household products, known for its ability to induce contact dermatitis. Because MI is an environmentally relevant allergen, we sought to investigate whether MI would elicit pain and immune responses. Furthermore, because the mucosal membrane of the vaginal canal of mice is more similar to human vestibular tissue, we investigated whether pain and immune responses in the vaginal canal would be observed. Here we used repeated administrations of MI and measured mechanical hyperalgesia and cytokine production in both vaginal canal and labiar skin. We found that MI-challenged mice developed mechanical hyperalgesia at 1-day post 10th challenge in the vaginal canal, and increased cytokine production at 5 days post 5th challenge in the labiar skin.

Presenter(s): Monica Smith, Beloit College
Session: Poster P2.23
Title: Effects of nitrates and phosphates on growth and leukocyte recruitment of Xenopus laevis
Advisor(s): Tawnya Cary, Biology, Beloit College
Co-Author(s): Olivia Ruffins and Tawnya Cary

Abstract: Approximately one third of amphibian species have experienced severe population declines since the 1970s. One explanation for amphibian declines is that pollutant exposure results in increased susceptibility to disease. In the Midwest, agricultural runoff is a pollutant of concern because it contains nitrates and phosphates; both known stressors in amphibians. Little is currently known about potential effects of these nutrients alone or in combination on growth or immune response. We exposed Xenopus laevis to environmentally relevant levels of nitrate (20 mg/L), phosphate (5 mg/L), and a combination of nitrate and phosphate for 18-19 days and measured leukocyte recruitment and snout-to-vent length (SVL). Neither nitrate nor phosphate affected SVL, nor was there a significant difference in leukocyte recruitment between the control and experimental groups. Additionally, there was no evidence for a synergistic effect between nitrate and phosphate as the combined treatment group was not statistically different from any other treatment group in both immune response and SVL. Based on our results, nitrates and phosphates at these concentrations did not have an effect on leukocyte recruitment or body size of X. laevis; however, due to the small sample size and variability in leukocyte recruitment, we propose further investigation.

Presenter(s): Shreya Sodhi, Washington University in St. Louis
Session: Poster P3.25
Title: The effects of exposure to diversity on children's racial thinking
Advisor(s): Lori Markson, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Lori Markson, Sarah Blair

Abstract: Understanding children’s racial attitudes is important for understanding the development of prejudice and bias before they become more fixed. Earlier findings show that white parents are less likely to talk about race with their children compared to parents of color. The present study investigates whether exposure to diversity through books as a form of racial socialization can affect the racial attitudes of 3- to 8-year-old children. The study examines

primarily white children living in homogeneous neighborhoods who typically have little exposure to diversity. Critically, we are also testing a similar population of children who were intentionally exposed to diverse books over a period of four months. Both groups of children are tested in a series of seven tasks designed to explore the racial attitudes and preferences of young children. To date, 70 children have participated and data collection is ongoing. Given the wide age range of children being tested across the two populations (experimental and control group), the current sample size is too small to provide conclusive findings, but initial observations will be discussed. The study has the potential to reveal whether mere exposure to racial diversity through children's books is sufficiently powerful to influence children's thinking about race.

Presenter(s): Senait Solomon, Washington University in St. Louis
Session: Poster P1.22
Title: The Effects of Social Media on Self-Esteem and Eating Concern in Adolescent Military Dependents
Advisor(s): Mary Katherine Higgins, Department of Medical and Clinical Psychology, Uniformed Services University
Co-Author(s): M. K. Higgins Neyland, Natasha L. Burke, Abigail Pine, Mary Quattlebaum, and Marian Tanofsky-Kraff

Abstract: Research has shown a relationship between social media use and psychological functioning, but there are limited data on this relationship among adolescents at high risk for eating disorders and obesity. We studied 146 adolescent (14.4 ± 1.6y; 53.4% girls; 46.2% Non-Hispanic White; BMIz, 1.98 ± .44) military dependents prior to entry into a larger study to investigate the links between social media use, self-esteem, and disordered eating. Participants were included if they endorsed loss of control (LOC) eating and/or elevated anxiety. The Eating Disorder Examination (EDE) assessed restraint, eating, and weight and shape concern, a global score, and LOC presence. The Rosenberg Self-Esteem Scale measured self-esteem, and the Kaiser Family Foundation's measure assessed social media use. Analyses of variance were used, with age, sex, and BMIz considered as covariates. A significant main effect was found for self-esteem, such that those who did not use social media had significantly higher self-esteem than those who did, $F(1, 96) = 3.97$, $p = .049$. A trend was found such that those who used social media had higher eating concern scores than those who did not, $F(1, 96) = 3.64$, $p = .059$). Among youth at high risk for eating disorders and obesity, those who use social media appear to have lower self-esteem, and possibly greater eating concern, than those who do not. Future data are needed to determine how social media use impacts psychological functioning prospectively.

Presenter(s): Jessica Song, Colorado College
Session: Poster P2.24
Title: Thermodynamics of magnesium ion binding to trinucleotide bulged TAR RNA
Advisor(s): Neena Grover, Chemistry and Biochemistry, Colorado College
Co-Author(s): Neena Grover

Abstract: TAR RNA is the sequence between positions +1 and +59 of HIV-1 RNA and contains a UCU bulge at positions 23-25. Bulges within RNA sequences often act as sites for inter- and intramolecular binding and recognition. The trinucleotide bulge in TAR RNA interacts with the

Tat protein, in complex with cyclin T1, to increase the rate of transcription by nearly 100-fold. Crystallization studies of HIV-1 TAR RNA have shown four Ca^{2+} binding sites that induce an alternative conformation of TAR RNA that is not predicted to bind to Tat. However, magnesium ions have been found to stabilize TAR RNA in a different way than Ca^{2+} and Na^{+}. Magnesium ions can effectively neutralize the phosphate backbone of RNA and allow a sequence to fold into a compact secondary structure. In this study, the thermodynamics of magnesium ion binding to the TAR RNA sequence was investigated by employing isothermal titration calorimetry, in which a RNA construct was modeled after the TAR sequence and titrated with a magnesium. ITC results show this is an endothermic reaction, supporting the results from UV-visible thermal denaturation experiments previously done on TAR RNA.

Presenter(s): Aparna Srinivasan, University of Chicago
Session: Oral II.F.3 (3:00)
Title: Investigating recovery from the heat shock response in S. cerevisiae
Advisor(s): D. Allan Drummond, Biochemistry and Molecular Biology, University of Chicago
Co-Author(s):

Abstract: Heat stress in the fungus S. cerevisiae causes the upregulation of heat shock protein (hsp) transcripts by up to 1000-fold the amount present in cells during optimal growth conditions. This poses the question of how cell returns to basal transcript levels, and the consequences on cellular fitness if this process is impeded. I observe that in S. cerevisiae cells that are heat shocked for 10 minutes, two heat shock proteins, SSA4 and HSP26 are induced to high levels within ten minutes, and recede to basal levels within about 90 minutes after heat stress has subsided. The data provide a reference timeframe to investigate whether a selective mechanism exists to degrade hsp transcripts after heat stress has passed, or whether cells rely solely on non-selective mRNA degradation and cell division to return to basal transcript levels. A possible mechanism may be through XRN1, a 5'-3' mRNA degradation enzyme that only degrades mRNA with 5' monophosphate. Experiments to determine the localization and state of XRN1 during varying severities of heat shock and the effect of XRN1 deletion or inactivation on return to basal mRNA levels after stress within the cell forthcoming.

Presenter(s): Skylar Sundquist, Hope College
Session: Poster P3.26
Title: The Regulation of Cellular Proliferation by VACM-1/CUL5 is Dependent on its Posttranslational Modifications by NEDD8
Advisor(s): Maria Burnatowska-Hledin, Biology Department & Chemistry Department, Hope College
Co-Author(s): Si Eun Lee

Abstract: VACM-1/CUL5 acts as the scaffold protein in the E3 ligase complex in the ubiquitin-dependent protein degradation pathway. The overexpression of VACM-1/CUL5 is known to inhibit proliferation, whereas inhibition of VACM-1/CUL5 expression induces cellular proliferation. Thus, VACM-1/CUL5 is implicated in cancer pathways. The effect of VACM-1/CUL5 on cellular proliferation is dependent on its post-translational modification (PTM) by the protein NEDD8 (neddylation). The relationship between NEDD8 and VACM-1/CUL5 is important for cell cycle regulation and offers a target for cancer therapy. This work explores the

relationship between VACM-1/CUL5 and NEDD8, specifically investigating the structure function relationship of VACM-1/CUL5 and its neddylation sites. VACM-1/CUL5 was mutated at three potential neddylation sites, Lysine (K) 724, 727, and 728, and referred to as the 3K mutant. Our previous work suggests that the expression of the 3K mutant decreases the antiproliferative effect of VACM-1/CUL5. Our current work focuses on characterizing cells transfected with the mutated VACM-1/CUL5 cDNA to better understand the importance of neddylation at these sites. Interestingly, Western Blot analysis indicates that the 3K VACM-1/CUL5 mutant is still neddylated, which suggests that VACM-1/CUL5 may be neddylated at additional lysine sites.

Presenter(s): Pietro Tardelli Canedo, Macalester College
Session: Poster P1.23
Title: Novel findings on the morphology and phylogeography of Neopurcellia salmoni in New Zealand
Advisor(s): Sarah L. Boyer, Biology, Macalester College
Co-Author(s): Eliza J. Passereau, Rina Morisawa, Sarah L. Boyer

Abstract: Neopurcellia is a monotypic genus of harvestmen endemic to New Zealand. These dispersal-limited organisms have a poorly understood and unusually widespread distribution across the West coast of the South Island. Most morphological diagnostic characters are found on the ventral side of the body; therefore, little attention has been given to dorsal morphology. This research analyzes the phylogeography of the genus, and describes a surprising level of within-species morphological variation in their dorsal anatomy not yet described in literature and unique amongst mite harvestmen. We reconstructed the phylogeographic relationships between Neopurcellia salmoni populations using DNA sequence data from the fast-evolving locus COI. Phylogenetic analyses revealed two distinct and well-supported clades occupying distinct geographical regions without any overlap. It further displayed a deep split between the southernmost specimen and the rest of the southern clade. Major lineage divergences are hypothesized to be the result of isolation in allopatric forest refugia during the Last Glacial Maximum. Scanning electron microscopy of the dorsal anatomy revealed larger granules and pores on the sulci between different tergites for some but not all of the male specimens. There was not a significant geographic or phylogenetic pattern in the distribution of dorsal pores and larger granules.

Presenter(s): George Valladares, Beloit College
Session: Poster P2.25
Title: FINDING THETA OSCILLATIONS USING ECoG & ICA
Advisor(s): Erin Munro, Mathematics, Beloit College

Abstract: The goal is to determine whether non-REM sleep cycles as depicted in an ECoG exhibit theta oscillations. Theta oscillations are predicted to play a role in emotional processing and learning. These oscillations were previously thought to only be found in the REM stage of the sleep cycle. However, new developments have pointed to the possibility of theta oscillations existing in non-REM sleep cycles. It is predicted theta oscillations will become prevalent in the latter stages of sleep because the slow-wave amplitudes will decrease over time.

Presenter(s): Diane Vargas, St. Olaf College
Session: Poster P1.24
Title: Investigating Local Adaptation in Common Milkweed
Advisor(s): Emily Mohl, Biology and education,
Co-Author(s): Emily Mohl

Abstract: Milkweed plants are essential for the life cycle of monarch butterflies, which lay their eggs on milkweed leaves. Recent declines in monarch abundance may be linked to reduced availability of milkweed plants. Conservation biologists are encouraging communities to plant milkweed, but there may be risks involved; it is unknown whether milkweed display patterns of local adaptation (LA). If so, seeds transplanted to a novel environment, may perform poorly. Factors like climate and herbivory vary across sites, and studies of LA in milkweed are necessary. This study investigated LA in common milkweed (Asclepias syriaca) through the use of transplant experiments. Pesticide treatments were added to randomized plants to test the influence of biotic factors on patterns of LA. Local milkweed populations and pesticide-treated plants tended to have higher average growth. Studying LA in milkweed will allow for good conservation science.

Presenter(s): Tiffany Vaughan, University of Chicago
Session: Poster P2.26
Title: Cellular and Molecular Mechanisms of Neural Tube Closure
Advisor(s): Timothy Sanders, Department of Pediatrics, Neonatology, University of Chicago

Abstract: Neural tube defects (NTDs) are birth defects that affect the development of the nervous system. In the posterior nervous system, these defects are collectively termed spina bifida, a condition that leads to lifelong morbidity. A wide spectrum of NTDs arise from disturbances to neurulation, the process in which the neural plate rolls, folds, or bends into the neural tube that then comprises the entire adult central nervous system. Compared to the early neurulation stages, the last step of neural tube closure is not as well understood. Here we show the cellular and molecular behavior of proper posterior neural tube closure in the chick embryo model organism. Our studies show that the chick embryo serves as an excellent model for visualizing the stages of neural tube closure, as it can be preserved in a healthy state for many stages of development and visualized easily using advanced microscopy. Various cell populations from both sides of the posterior neural tube form connections with each other, underscoring the importance of specific cell-to-cell communication. These results demonstrate that proper morphogenetic movements allow the neural tube to develop correctly. The findings lead us one step closer to unraveling the origins of NTDs and possible intervention strategies.

Presenter(s): Maicy Vossen, Gustavus Adolphus College
Session: Oral I.C.2 (10:15)
Title: Modeling the Consequences of Increased Kinetochore Protein Levels in Cancer using Yeast
Advisor(s): Laura Burrack, Biology, Gustavus Adolphus College

Abstract: Cancer is a disease of uncontrolled cell division, which is caused by problems within the cell cycle. Factors that disrupt the cell cycle include DNA mutations and aneuploidy resulting in abnormal amounts of proteins in the cell. In certain types of cancer, there is an increased amount of a protein called CENP-A, and CENP-A overexpression correlates with

poor patient prognosis. CENP-A is a protein in the kinetochore complex that is essential for microtubule attachment and chromosome segregation. To begin to understand why CENP-A overexpression has such severe consequences, a yeast model, C. albicans, was used to monitor growth differences using genetic and pharmacological approaches. We found that there was no significant difference between the growth rates of C. albicans with and without CENP-A overexpression. However, our results showed that alterations of the CENP-A protein levels changed how cells responded to cyclosporine, a proposed anti-cancer drug. Currently, we are characterizing the mechanism of how CENP-A overexpression may alter the effectiveness of cyclosporine.

Presenter(s): Sunny Vuong, St. Olaf College
Session: Poster P3.27
Title: Identifying Proteins in Alcoholic Fatty Liver Disease
Advisor(s): Laura Listenberger, Biology and Chemistry, St. Olaf College

Abstract: Fatty liver is an early and consistent morphological feature of alcohol-related liver injury, and with continued alcohol consumption, can progress to cirrhosis and liver failure. Our experiments explore the mechanisms that contribute to the over-accumulation of hepatic lipid droplets in alcoholic fatty liver disease. We have shown that culturing AML12 mouse liver cells in choline-deficient media alters the phospholipid composition of lipid droplets in these cells. Similar changes to the phospholipid composition of lipid droplets have been observed in alcoholic fatty liver disease. Here, we examine whether changes to the phospholipid surface of hepatic lipid droplets impacts the number and/or types of lipid droplet-associated proteins. We used a protein assay to determine the concentration of total lipid droplet proteins in control and choline-deficient AML12 cells. We used SDS-PAGE and western blotting to visualize the concentration of candidate lipid droplet proteins. The results of our study show that three proteins (perilipin 1, perilipin 2, and CIDEC) are more prevalent on lipid droplets under cell culture conditions that model alcoholic fatty liver disease. Future work will assess the role that these proteins play in the development of alcoholic fatty liver disease and may lead to a more accurate diagnosis or treatment options for this disease.

Presenter(s): Sara Warrington, University of Chicago
Session: Poster P1.25
Title: TdT labeling of DNA double strand breaks to probe DNA damage signaling and repair
Advisor(s): Stephen Kron, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s): Julian Lutze

Abstract: DNA double-strand breaks (DSBs) are the most serious DNA lesions created by DNA damaging agents. When unrepaired, DSBs can result in chromosomal instability and translocations, which can cause carcinogenesis. DSBs are repaired mainly through homologous recombination and non-homologous end joining. Repair of breaks is complicated by the compaction of DNA into chromatin, which makes broken DNA ends inaccessible to repair machinery. Cells therefore respond to DNA damage by recruiting chromatin remodelers to increase DSB accessibility, which triggers the downstream recruitment of damage signaling and repair proteins. However, our lab has recently shown that chromatin modifications and signaling proteins at DSBs can be decoupled from repair. To track DSB repair independent of chromatin modification and signaling proxy markers, we identified conditions under which terminal deoxynucleotidyl transferase (TdT) labels DNA ends with biotinylated nucleotides in

situ. We then verified that these conditions labeled DSBs by using immunofluorescence microscopy to confirm co-localization of label loci with DSB markers such as γH2AX and 53BP1. Finally, we used streptavidin beads to directly isolate the DNA and proteins adjoining DSBs by immunoprecipitation. We confirmed that labeling was TdT and damage dependent, and observed robust enrichment of γH2AX from irradiated, labeled cells, indicating specificity.

Presenter(s): Meredith Wells, University of Chicago
Session: Poster P2.27
Title: Limited Changes in Impedance and Current with Constant Voltage in Patients with Bilateral DBS
Advisor(s): Tao Xie, Department of Neurology, University of Chicago
Co-Author(s): Huiyan Yu, Matthew Burns, Mahesh Padmanaban, Tao Xie

Abstract: There exists an ongoing debate about the modification of constant voltage or constant current stimulation and their effects on long term changes in impedance in studies evaluating the use of Deep Brain Stimulation (DBS) over time in patients with Parkinson's and Essential Tremor. As a common practice, modifications in voltage are used to better control the motor symptoms of patients, however, other modifications to stimulating parameters are also made to improve the motor symptoms or reduce the side effects during patient visits. This study looks to analyze whether the impedance changes with time if the conditions of the additional stimulating parameters remain unchanged. Understanding if there exists a necessity for changing modifications from constant voltage to constant current is essential for the quality of long-term treatment for patients with Parkinson's Disease and Essential Tremor using DBS. Based on data collected at the University of Chicago Medical Center Neurology Department, impedance and current are very stable over the long period of time studied to a given unchanged voltage/stimulating parameters. Conclusions can be drawn that changes from constant voltage to constant current would not yield a large difference, as long as the impedance remains largely stable, according the Ohm's law.

Presenter(s): Madeleine Welt, Beloit College
Session: Poster P3.28
Title: Is petting your plants good for them? Thigmomorphogenesis and transplant shock in peas (*Pisum sativum)*
Advisor(s): Yaffa Grossman, Biology, Beloit College

Abstract: Transplant shock is the stress plants undergo when uprooted and moved. A variety of methods are being examined to mitigate this phenomenon, including thigmomorphogenesis, which is physical change in response to tactile stimulation. In some plants, touching or stroking can cause dwarfism, and has a variety of other epigenetic effects. I subjected 20 pea (*Pisum sativum*) plants to daily stroking and transplanted them with a stress period to assess whether thigmomorphogenesis had any effect on plants' abilities to cope with transplanting. For the next several days, I monitored the health of the plants, determined by stem water pressure, and measured their length from soil level to the second-to-last set of leaves. After three days in the transplanted environment, nearly all the plants had died or lost their primary stems. There was no significant difference in plant health between the treated plants and the control plants, but treated plants had significantly less length loss due to withering, and some even continued growing. Examining the effect of touch on peas and post-transplant health requires larger, more long-term studies.

Presenter(s): Eleanor Wettstein, Macalester College
Session: Poster P1.26
Title: Contribution of Membrane Proteins and Composition to Microbial Robustness
Advisor(s): Randy Daughters, Biology, Macalester College
Co-Author(s): Miguel Chavez-Santoscoy, Laura Jarboe

Abstract: Bacterial membranes are composed of proteins embedded in a lipid matrix. Bacteria survive in a range of environments due to their ability to maintain membrane stability, achieved by adjusting abundance of various proteins and phospholipids. Membrane lipid composition is modulated by modifying pre-existing phospholipids and manufacturing different types of fatty acids. The use of microbial processes to produce biorenewable chemicals and biofuels has been growing; however, most industrially useful chemicals are inhibitory to bacteria, limiting efficiency of these bioprocesses. One strategy to improve microbial productivity is engineering bacteria to tolerate higher concentrations of toxic chemicals, in turn producing desired metabolites at higher rates. The goal of my project is to explore relationships between protein sequence variations and microbial characteristics. This was accomplished by testing the tolerance of several genetically modified strains of E. coli to a variety of desirable compounds and chemical precursors. We found that knocking out or overexpressing certain genes had different effects depending on the microbial strain and inhibitor tested, and that certain genetic variations tended to alter an engineered strain's growth in specific inhibitors. Ultimately, this will help advance the goal of engineering microbes for optimal resilience and utility in bioenergy applications.

Presenter(s): Rebecca Williams, Washington University in St. Louis
Session: Poster P2.28
Title: Correlations between delay discounting and cognitive functions
Advisor(s): Leonard Green, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Yanjie Zhou, Yu-Hua Yeh

Abstract: Delay discounting refers to the decrease in the subjective value of an outcome as the time until its occurrence increases. Previous studies suggest that there is a relation between delay discounting, assumed to be a measure of impulsivity, and cognitive functions, but these findings typically have been based on limited sample sizes and have included few facets of cognition. The present effort systematically evaluates the correlation between degree of delay discounting and performance on numerous cognitive tasks. We use data collected from 1187 young adults, 22-35 years old, from the Human Connectome Project. Of the many cognitive tasks evaluated, only a few proved to be significantly, albeit weakly correlated with delay discounting, specifically fluid intelligence, reading decoding, and vocabulary comprehension. Other measures of cognition (e.g., episodic memory, sustained attention, working memory) were not significantly correlated with degree of discounting. These findings argue for caution in assuming that steep discounting is a hallmark of impulsivity that negatively affects cognitive functioning.

Presenter(s): Savannah Wilson, Luther College
Session: Poster P3.29
Title: Forest communities of Finch Memorial Hardwoods, Winneshiek County, IA
Advisor(s): Beth Lynch, Biology department, Luther College
Co-Author(s): Beth Lynch

Abstract: The objective of this research was to identify and describe deciduous forest communities in a 70-ha preserve located in Winneshiek County, IA. The preserve contains several plant rare communities, including algific talus slope, balsam fir forest, and a white pine stand. We used 20 10 x10 m plots to determine species composition and structure in the hardwood forests. We also measured light, slope, aspect, soil depth and organic matter. We used ordination to group plots sharing similar species composition and compared the resulting groups with previously described native forest communities of southern MN. We identified three community types in the preserve: mesic maple-basswood forest, dry-mesic oak forest, mesic oak-basswood forest. The mesic maple-basswood forest occurs on steep north-facing slopes and on rocky slopes at the base of the limestone escarpment. This community is characterized by relatively high abundances of Adiantum pedatum, Anemone acutiloba, Mitella diphylla, Ostrya virginiana, and Acer saccharum. The dry-mesic oak forest plots are on steep slopes near the bluff tops; important plant species include Ageratina altissima, Circaea luteiana, Laportea canadensis, Osmunda claytoniana, and Ribes missouriense. Southern mesic oak-basswood forest plots are on flatter upland sites; species with relatively high abundance in these sites include Celtis occidentalis, Geranium maculatum, Sanicula odorata, Quercus rubra and Acer saccharum.

Presenter(s): Sophie Wulfing, Colorado College
Session: Poster P1.27
Title: Effects of sediment characteristics on carbon and methane production in a lake system
Advisor(s): Shane Heschel, Organismal Biology and Ecology, Colorado College
Co-Author(s): Leandra Praetzel

Abstract: Bodies of water play a major role in the Earth's cycling of greenhouse gases mainly due to the creation and release of these gasses by microbes digesting organic matter in the sediment layer. This is especially prominent in inland lakes, where high levels of nutrient cycling accounts for about half of all carbon and methane release among earth’s bodies of water.
Different forms of sediment also play a role in the amount of carbon and methane production, such as lake depth, sediment age, amount and type of organic material, and nutrient content. In this study, we look at the effects of these sediment characteristics on the production of carbon and methane on two lakes in Northern Germany. We found significant increases in production rates with the addition of new material, the amount of organic material, and the decomposition of plant matter. However, we found no significant increases due to distance from lakeshore.

All of these factors play a major role in the lake’s overall greenhouse gas emission, demonstrating a need for more thorough research of the chemistry of inland lakes in order to have a more precise view of their contribution to the global carbon and methane budget.

Presenter(s): Ellie Xu, University of Chicago
Session: Poster P2.29
Title: Protective Factors Fail to Moderate the Association between the Dysregulation Profile and Impairment
Advisor(s): Rhonda Boyd, Child and Adolescent Psychiatry & Behavioral Sciences, University of Pennsylvania & Children's Hospital of Philadelphia
Co-Author(s): Jason Jones, Laura Butler, Tami Benton, Rhonda Boyd

Abstract: Severe mood dysregulation (SMD) occurs in 1-3.5% of youth. Though difficult to characterize, SMD has been captured by the Child Behavior Checklist – Dysregulation Profile (CBCL-DP). This dysregulation profile is based on significantly elevated scores on the Aggressive Behavior, Anxious/Depressed, and Attention Problems (AAA) subscales of the Child Behavior Checklist. Relative to their peers, youth who fit this dysregulation profile face greater difficulties with functioning in childhood and in later life. Protective factors for dysregulated youth are understudied. We conducted the present study with the following aims: (1) to examine how children's dysregulation relates to their social skills, attributional style, and impairment, and (2) to test if children's social skills or attributional style moderate the association between dysregulation and impairment. We extracted data from an existing registry of 7- to 18-year-old patients referred for an evaluation at a mood specialty behavioral outpatient clinic. We conducted correlations and hierarchical linear regressions, and found that dysregulation was significantly associated with social skills, attributional style, and impairment. Though social skills and positive attributional style were not protective factors for dysregulated youth, social skills are a protective factor on impairment for non-dysregulated youth. Future research can further explore protective factors of youth dysregulation on impairment.

Presenter(s): Xiaochan Yang, University of Chicago
Session: Poster P3.30
Title: Effects of Anxiety and Depression on Smoking Cessation Outcomes in a Minority Sample
Advisor(s): Anne Henly, Psychology Department, The University of Chicago

Abstract: Depressive and anxiety symptoms in smokers have been shown to correspond to significantly poorer smoking cessation outcomes. Less is known about how depression/anxiety moderates smoking behaviors among minority smokers. This report considers the extent to which negative emotional states of depression, anxiety and stress predict smoking cessation outcomes in an African American sample.

Data was collected as part of a study on smoking intervention for non-treatment seeking African American smokers (n=194) in the Chicago area. Participants were randomized to one of two conditions: Treatment as Usual (self-help smoking cessation materials), or Enhanced Care (brief counseling and optional nicotine replacement therapy starter kit). We used DASS-21 to measure depression, anxiety and stress levels, and scored all participants on a Fagerström Test for Nicotine Dependence, a cessation fatigue scale, and a contemplation ladder. All participants completed a 1-month follow-up interview after their initial visit.

Using data from Enhanced Care participants, we found that participants who score higher totals on DASS-21 tend to score lower on the contemplation ladder (p=-0.02) and report fewer quit attempts (trending significance) in 1-month follow-up interviews. Further analysis will look into how cessation outcomes varies with depression, anxiety and stress respectively, as well as a 6-month follow-up interview.

Presenter(s): Mahmoud Yousef, University of Chicago
Session: Poster P1.28
Title: Quantifying Homogeneity for Pangenomic Gene Clusters
Advisor(s): A. Murat Eren, Department of Medicine, The University of Chicago

Abstract: Pangenomics is a commonly used computational approach to organize genes across microbial genomes - typically based on shared sequence homology - into 'gene clusters'. This technique can reveal evolutionary relationships between genomes de novo, and enable researchers to assess differences between closely related taxa by observing accessory gene content. The magnitude of sequence homology across genes within a single gene cluster could also reveal clues of their evolutionary history; however, effective computational strategies are lacking. To address this gap, here we introduce an algorithm that quantifies 'functional' and 'geometric' agreement between amino acid sequence alignments within each gene cluster. The 'functional homogeneity index' estimates the extent of agreement between amino acid residues based on the similarity of their biochemical properties. The 'geometric homogeneity index' only considers the binary distribution of alignment gaps and residues to quantify compositional homogeneity. These two complimentary indices offer efficient estimates of homogeneity within gene clusters by intrinsic properties of amino acid sequence alignments and provide broad insights into processes that likely govern heterogeneity within homologous genes across distinct genomes. Our algorithm improves the utility of pangenomics by introducing numerical assessments that could identify genes affected by evolutionary processes. Such insight could support hypothesis-driven investigations of microbial adaptation.

Presenter(s): Carolina Yu, University of Chicago
Session: Poster P3.08
Title: Functional triplet motifs underlie accurate predictions of single-trial responses in V1 neurons
Advisor(s): Jason MacLean, Neuroscience, University of Chicago
Co-Author(s): Maayan Levy

Abstract: Our understanding of how information is represented at a circuit level in the neocortex is far from complete. Here we summarize visually evoked activity in groups of up to 350 neurons as functional networks constructed by partial correlation across the imaged neuronal population. Partial correlation coefficients are computed from calcium fluorescence changes in primary visual cortex of an awake mouse to summarize pairwise covariability, and we cross correlate to find directionality. We find the network to be highly bidirectional, meaning pairs of neurons are strongly correlated in the same imaging frame. Using directed weights from the networks, a simple linear encoding model can predict moment to moment activity of a neuron near optimally. We find that certain properties of the functional networks, such as bidirectional edges, play a disproportionally large role in generating near optimal predictions. We then parsed the data to compare functional networks driven by structured and unstructured visual stimuli. For each functional graph, we find increased counts of a specific functional triplet motif result in the best predictions, suggesting a signature of informative correlations in V1 cortical circuits. In summary, we show a circuit perspective and identification of functional groups of neurons, summarized as a functional network.

Presenter(s): Adam Zabner, University of Chicago
Session: Poster P3.31
Title: Stimulation Changes the Actin Architecture of the Presynaptic Terminal
Advisor(s): Elizabeth Jonas, Internal Medicine, Yale school of Medicine
Co-Author(s): Shobana Subramanian, Jessica Xia, Leonard K. Kaczmarek, Elizabeth A. Jonas

Abstract: The readily releasable pool of docked synaptic vesicles is depleted when neurons fire; therefore the pool must be renewed after stimulation. Actin is known to be key in the endocytosis of fused vesicles, but changes in actin architecture after stimulation have not previously been investigated using super resolution microscopy. We hypothesize that the actin architecture of neurons must change after stimulation to for endocytosis and renewal of vesicle pools. This study was performed in brain slices from young rats containing medial and lateral nuclei of the trapezoid body (MNTB). Stimulated and control slices were imaged for the synaptic vesicle marker synaptophysin and for f-actin using confocal microscopy. In non-stimulated slices, actin fingers wrap around clusters of synaptic vesicles. In stimulated slices, more colocalization of synaptophysin and actin is present as this structural confinement of vesicles by actin is lost. Additionally, stimulated slices have thinner actin rings at the point of highest focus, indicating that stimulation leads to depolymerization of f-actin. These preliminary data suggest that actin is important in renewal of the readily releasable pool of neurotransmitter-containing vesicles, but further study is needed to explain how the change in actin dynamics is regulated.

Presenter(s): Qianchen Zhang, University of Chicago
Session: Poster P1.29
Title: Prediction of Latrophilin-1/ADGRL1 Biased Signaling Through Statistical Coupling Analysis
Advisor(s): Demet Araç, Department of Biochemistry and Molecular Biology, University of Chicago
Co-Author(s): Qianchen Zhang

Abstract: Adhesion G-protein coupled receptors (aGPCRs) are the second largest class of GPCRs and play critical roles in many physiological functions. aGPCRs are characterized by a GPCR auto-proteolysis inducing (GAIN) domain in their extracellular region (ECR) and seven transmembrane helices forming the 7TM domain. The diversity and complexity of their extracellular domains hamper functional studies and prevents transmembrane domain targeting drug developments common for other families of GPCRs. ADGRL1, also known as latrophilin-1, is an evolutionarily conserved aGPCR with critical functions of the nervous system of humans and is one of the most studied aGPCRs. However, the molecular signaling mechanism of latrophilin-1 remains unclear. Here we present an evolution-based biostatistics method that produces accurate predictions of residue locations in the 7TM of latrophilin-1 responsible for biased signaling. We applied a variant of Statistical Coupling Analysis (SCA) on a multiple sequence alignment of the 7TM domain of latrophilin-1 to generate a list of residue locations with high coupling energies. We discovered that the list of residues predicted through SCA coincides with experimentally determined biased signaling inducing residues. Our results

establish the possibility of utilizing statistics-based methods that take advantage of the growing protein databases to predict residue locations responsible for biased signaling in aGPCRs, creating a valuable tool for informing the experimental design of future mutagenesis screens and paving the way to elucidating the signaling mechanism of aGPCRs.

Presenter(s): Patricia Zulueta, University of Chicago
Session: Poster P3.09
Title: Structural Determination of METTL3-METTL14 Complex by Cryo-Electron Microscopy
Advisor(s): Minglei Zhao, Biochemistry & Molecular Biology, The University of Chicago
Co-Author(s): Chang Liu

Abstract: The N6-Methyladenosine (m6A) modification of eukaryotic RNA is installed by a methyltransferase (MTase) enzyme, which post-transcriptionally adds a methyl group at the N6 position of adenine. This epigenetic modification affects the conformation of RNA, which in turn influences protein synthesis and various biomolecular interactions within the cell. The MTase that carries out the m6A methylation is a heterodimer composed of two proteins: methyltransferase-like-3 (METTL3) and methyltransferase-like-14 (METTL14). Although both METTL3 and METTL14 exhibit methylation activity on their own, their complex acts as a much more efficient methyltransferase.

Researchers have commonly used x-ray crystallography in their attempts to elucidate the C-terminal catalytic core structure of METTL3-METTL14, but often fail to crystallize and visualize the entire complex with the N-terminal zinc finger domain and/or with an RNA substrate. Because the flexible zinc finger motif has an indispensable role in RNA substrate recognition, it is essential that the entire METTL3-METTL14 structure containing this domain be characterized. Cryo-electron microscopy (cryo-EM) is a more ideal technique for viewing macromolecules in their natural living state. As a result, cryo-EM will be utilized to shoot a more complete view of the METTL3-METTL14 structure and clarify its RNA substrate recognition and catalysis mechanisms.

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