The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 1 & 2, 2019
Washington University in St. Louis

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 1

12:00 pm – 5:30 pm	**Registration**	**The Parkway Hotel Lobby**
6:00 pm	**Buffet Dinner**	**Eric P. Newman Educational Center (EPNEC) Great Rooms A and B**
7:00 pm	**Introductions and Comments** Michael Seymour, Director – Midstates Consortium for Math and Sciences	
7:10 pm	**Young Scientist Program Activity**	
8:00 pm	**Keynote Address** **Dr. Jason Weber** Professor of Internal Medicine – Molecular Oncology and Cell Biology & Physiology, Washington University in St. Louis ***Adding tools to your toolbox: the discovery of novel targets in cancer***	
Following lecture	**Group Picture**	**EPNEC**

Saturday, November 2
All Saturday events are at the Eric P. Newman Educational Center (EPNEC)

7:30 am - 8:30 am	**Breakfast** *If checking out from hotel, there is a locked room for luggage and posters at EPNEC.*	**EPNEC Lobby**
8:15 am - 8:30 am	**Check set-up for oral presentations I.A, I.B, I.C** **All speakers in each session**	**Great Room A, Seminar room A and B**
8:30 am – 9:40 am	**Session I Oral Presentations of Student Papers**	
	Session I.A: (4) *Moderator: Clara Kao*	Great Room A
	Session I.B: (4) *Moderator: Sasha Dmytrenko*	Seminar Room A
	Session I.C: (3) *Moderator: Rachel Johnston*	Seminar Room B

Saturday, November 2 (continued from previous page)

9:40 am -10:00 am	**Break, Set-up for Poster Session 1 (P1)**	**Lobby, Great Room B**
10:00 am - 11:00 am	**Poster Session P1**	**EPNEC Great Room B**
11:00 am – 11:10 am	**Set-up for Poster Session 2 (P2)**	**EPNEC Great Room B**
11:10 am – 12:10 pm	**Poster Session P2**	**EPNEC Great Room B**
12:10 pm - 12:40 pm	**Sandwich Buffet Lunch** *Take lunch to presentation of your choice*	**EPNEC Lobby**
12:40 pm - 1:30 pm	***Applying to Graduate School*** ***Graduate Student Panel*** ***Washington University in St. Louis*** *Moderator: Dr. Steve Mennerick* *Department of Psychiatry* **Graduate Student Panelists** *Michael (Mike) Fitzpatrick, Grinnell College ('16)* *Matthew Rosene, Luther College ('15)* *Oleksandr (Sasha) Dmytrenko, St. Olaf College ('16)* *Kelsy Cotto, Mercer University ('16)* *Rachel Johnston, University of Michigan-Ann Arbor ('16)*	**Seminar Room A**
12:40 pm – 1:30 pm	***Careers at Liberal Arts Colleges*** **Consortium Faculty Members** *Robin Shields-Cutler, Macalester College* *Tom Bultman, Hope College* *Katie Peterson, Gustavus Adolphus College* *Shane Heschel, Colorado College*	**Seminar Room B**
1:30 pm - 1:40 pm	**Check set-up for oral presentations II.D, II.E, II.F** **All speakers in each session**	**Great Room A,** **Seminar room A and B**
1:40 pm – 2:50 pm	**Session II Oral Presentations of Student Papers** Session II.D (4) *Moderator: Lisa McClellan* Session II.E: (3) *Moderator: Nicolette Laird* Session II.F: (3) *Moderator: Elena Tonc*	 Great Room A Seminar Room A Seminar Room B
2:50 pm - 3:10 pm	**Break, Set-up for Poster Session 3 (P3)**	**Lobby, Great Room B**
3:10 pm – 4:10 pm	**Poster Session P3**	**EPNEC Great Room B**
4:10 pm – 4:30 pm	**Meeting Concludes** Remove posters Complete evaluations – available online Boxed dinners to go	**EPNEC Lobby**

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
2019		Jill Dietz, Mathematics, Statistics & Computer Science, St. Olaf College

2019 Keynote Lecture

Adding tools to your toolbox: the discovery of novel targets in cancer

Jason D. Weber, PhD

Professor

Dept. of Medicine, Oncology Division; Dept. of Cell Biology and Physiology

Washington University School of Medicine, Saint Louis

Research Overview: The goal of the Weber laboratory is to understand the basic mechanisms behind tumor cell growth and proliferation. Cellular growth involves the production of ribosomes and translation of existing mRNAs into proteins. Numerous projects in the lab are aimed at understanding these basic processes and how they might impact tumor growth and progression. Dr. Weber has a broad background in molecular and cellular biology with an emphasis on tumor cell biology. He recently expanded his research to understand the processes of cell growth signaling, ribosome biogenesis and mRNA translation in breast cancer. His group has lately begun to identify interaction networks with these pathways using genetic, biochemical, and proteomic approaches. As PI on numerous grants, his lab has laid the foundation for how major tumor suppressors prevent tumor formation by targeting cellular growth pathways. They have been a leader in the field of alternate reading frame (ARF) tumor suppressor biology since its discovery and continue to seek information on how ARF functions in collaboration with p53.

Dr. Weber obtained his BS in Biotechnology at Bradley University and his PhD in Cell & Molecular Biology from St. Louis University. Following his PhD, he was a Postdoctoral Research Associate with the Howard Hughes Medical Institute, Tumor Cell Biology Lab at the St. Jude Children's Hospital. In 2001 he became a faculty member in the Departments of Medicine and Cell Biology & Physiology at Washington University in St. Louis where he continues to pursue his research in the areas of tumor cell growth and proliferation. The Weber lab has over 50 peer reviewed publications and Dr. Weber serves on numerous committees that guide cutting edge cancer research, including the Department of Defense-CDMRP for Breast Cancer Research, NIH -National Cancer Institute Study Section, and the Artemis 2020 Project. He was recognized by the American Cancer Society as an Honorary Corporate Hero in 2016 and has been a 10-time recipient of the Distinguished Service Teaching Award for the First Year Medical Students at Washington University.

ORAL SESSION I SCHEDULE

Session I.A: 8:30 am – 9:40 am Great Room A *Moderator: Clara Kao*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1 (8:30)	Bailey Underwood	Lawrence University	5-HT Receptor Subtype May Mediate Anxiety Response and CRH Production in Hypothalamus
I.A.2 (8:47)	Yueqi Du	Washington University in St. Louis	Analyzing the Role of the V1/V2 Region in HIV-1 Coreceptor Switching
I.A.3 (9:04)	Yige He	Beloit College	Quorum Sensing Affecting Nisin Gene Expression in L. lactis.
I.A.4 (9:21)	Kelly Hartigan	Washington University in St. Louis	Human iPSC-Derived Cerebral Organoids Establish Mutational Specificity in NF1

Session I.B: 8:30 am – 9:40 am Seminar Room A *Moderator: Sasha Dmytrenko*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1 (8:30)	Jay Fordham	Gustavus Adolphus College	Targeted applications of triclopyr to Fraxinus pennsylvanica to manage experimental plots
I.B.2 (8:47)	Melissa Wood	Knox College	Evidence of local adaptation in Helianthus annuus L. revealed through transcript mapping
I.B.3 (9:04)	Xinrui Yang	Lawrence University	Employing T cell subtyping to predict drug resistances and prognoses in DLBCL patients
I.B.4 (9:21)	Marie Crane	Macalester College	Using assembly graphs to analyze strain-level variation and identify novel phages in hot spring metagenomes

Session I.C: 8:30 am – 9:40 am Seminar Room B *Moderator: Rachel Johnston*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1 (8:30)	Irein Thomas	Knox College	Does moral framing of abortion increase highly-identified liberals' willingness to aggress against a conservative?
I.C.2 (8:47)	Gabriel Barrón	University of Chicago	Elucidating the effects of the microbiome on susceptibility to lung injury
I.C.3 (9:04)	Steven Traeger	Lawrence University	Early changes in innate and adaptive immunity are associated with resistance to ileocolitis

ORAL SESSION II SCHEDULE

Session II.D: 1:40 pm – 2:50 pm Great Room A *Moderator: Lisa McClellan*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.D.1 (1:40)	Saman Tabatabaee Zavareh	University of Chicago	Investigating the Contribution of Low-Complexity Domains to Repressive Activity of the ETS Transcription factor Yan
II.D.2 (1:57)	Victoria Shi	Washington University in St. Louis	SERPINB3 Expression Protects Cervical Cancer Cells from Radiation Induced Cell Death
II.D.3 (2:14)	Samantha Ardery	Carthage College	Don't stop your YAPing: How expressing constitutively active YAP affects retinal development and regeneration
II.D.4 (2:31)	Atreyo Pal	University of Chicago	Understanding fin development may lead to mechanism behind the fin-to-limb transition

Session II.E 1:40 pm – 2:50 pm Seminar Room A *Moderator: Nicolette Laird*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1 (1:40)	Ashley Hermans	Carthage College	A vision test for fish: Optokinetic response to assess functional recovery after optic nerve injury
II.E.2 (1:57)	Chineze Egwudo	University of Chicago	Optimizing microCT tractography for use as a potential diffusion MRI gold standard
II.E.3 (2:14)	Cody Leong	Colorado College	Fluorescence-based high throughput quantification of yeast mating efficiency in O. polymorpha

Session II.F 1:40 pm – 2:50 pm Seminar Room B *Moderator: Elena Tonc*			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1 (1:40)	Hanaa Alhosawi	Gustavus Adolphus College	Exploring the Function of MAD2 in Candida albicans through Drug Sensitivity
II.F.2 (1:57)	Eleanor Wettstein	Macalester College	Plakoglobin as a candidate gene for Wnt signaling misregulation in Arrhythmogenic Right Ventricular Cardiomyopathy
II.F.3 (2:14)	Isabel Shen	Washington University in St. Louis	The Role of Fibroblast Growth Factor 2 and FGF Receptors 1 and 2 in Group 3 Pulmonary Hypertension

POSTER SESSION P1

10:00 am – 11:00 am EPNEC Great Room B			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Zhengyue Li	Beloit College	Advanced Synthesis of Magnetic Barcoded Beads in High-throughput scRNA-seq
P1.02	Withdrawn		
P1.03	Rose Williams	Beloit College	Automated analysis of human intracranial EEGs for seizure detection in epilepsy
P1.04	Julissa Molina-Vega	Macalester College	Biguanide sensitivity of the nuclear pore complex in breast cancer: A potential therapeutic strategy
P1.05	Ariel Roghair	Macalester College	Activation of Microglia and Astrocytes in the Retina Following Traumatic Brain Injury
P1.06	Charlotte DiBiase	Colorado College	Maternal Floral Color, UV Protection, and Germination in Ipomopsis aggregata
P1.07	Byunghyun Ahn	St. Olaf College	Lipid storage in starved Tetrahymena thermophila
P1.08	Aaron Bao	Washington University in St. Louis	Optimization of disaggregase Hsp104 in solubilizing neurodegenerative-disease implicated protein aggregation
P1.09	Julian Moulton	Colorado College	Metabolism of the spring field cricket Gryllus veletis during freezing, thawing and recovery
P1.10	Melanie Nevins	St. Olaf College	MESP1 is Essential for Human Cardiovascular Development
P1.11	Jacob Amme	Washington University in St. Louis	Development of placental and fetal circadian rhythms in utero
P1.12	John Feigelson	Colorado College	The Effect of Experimental Warming on Plant-Pollinator Relationships in the Low Arctic
P1.13	Justine Shih	University of Chicago	Role of ASIC2b in Proprioception and Cognition
P1.14	Jacob Blum	Washington University in St. Louis	Decoding methylation profiles that silence tumor suppressor genes via a massively parallel reporter assay
P1.15	David Lynum, Torey Flint-Kjellgren	Gustavus Adolphus College	The Effect of Lovingkindness Meditation on Emotional Self-Regulation
P1.16	Nicholas Ornstein	University of Chicago	How do the mechanical properties of the skin shape our perception of texture?
P1.17	Shreeja Vachhani	Lawrence University	Neural correlates of maternal affection and empathic concern
P1.18	Tessa Dethlefs	Gustavus Adolphus College	Resource allocation in response to nitrogen availability in female white campion (Silene latifolia)

P1.19	Arielle Weinstein	University of Chicago	The evolution of allosteric inhibition in bacterial citrate synthase
P1.20	Neetij Krishnan	St. Olaf College	IL-17A and TNF-α promotes migration and proliferation of breast cancer cells in vitro
P1.21	Isabelle Matthews	Hope College	Benevolent sexism influences how we detect uses for objects
P1.22	Alissa Kunczt	University of Chicago	α7 Nicotinic Acetylcholine Receptors Relieve Pain Via Modulation of the Descending Pain Pathway
P1.23	Yutong Zou, Thomas Diaz	Hope College	Hazelnuts: Genetic Relationships and Secondary Compounds for Cancer Treatment
P1.24	Thomas Diaz, Yutong Zou	Hope College	Detecting cancer treatment compound Taxol in different species of Hazelnuts with HPLC

POSTER SESSION P2

11:10 am – 12:10 pm EPNEC Great Room B

Poster #	Presenter Name	Institution	Title of Presentation
P2.01	Rie Kaneko	Beloit College	Automated Analysis of human EEG
P2.02	Diego Morones	Knox College	Analysis of CRISPR-Cas loci and spacer conservation within Staphylococcus species
P2.03	Melanie Gucwa	Carthage College	Potential Roles of a NUP155 Protein Subdomain in Cardiac Electrophysiological Development
P2.04	Madison Byrne	Knox College	Examining the relationship between jaw muscle physiology and predation strategy in Centrarchid fishes
P2.05	Lidija Namike	Macalester College	The effect of partisanship on environmental action
P2.06	Nicholas Sucher	Carthage College	Transect-Free Transect Sampling of Coral Reefs in Roatán, Honduras
P2.07	Stella Matutina Ikuzwe	Macalester College	Prostate-specific G-protein-coupled Receptors Activate Oncogenic Mitogen-activated Protein Kinases in Prostate Cancer
P2.08	Alan Kim	University of Chicago	Eye dynamics in premenopausal and postmenopausal patients with female hypoactive sexual desire disorder (HSDD)
P2.09	Alexandra Shapiro	Colorado College	Cotyledon stomatal density differentiation and quantitative genetic analysis of seedling traits in Impatiens capensis ecotypes
P2.10	Margot Groskreutz	St. Olaf College	Does Residential Land Use Impact Water Chemistry?
P2.11	Daniel Berkovich	Washington University in St. Louis	A biochemical characterization of aspartate aminotransferases in plants

P2.12	Emily Vierling	Colorado College	Differences in call-types across the Northern Resident Orca matrilineal groups
P2.13	Yifan Mao	University of Chicago	Circulating Extracellular Vesicles of Sickle Cell Subjects Disrupt Endothelial Integrity
P2.14	Alicia Wilkening	Washington University in St. Louis	Epigenetic Dynamics in Pigment Cell Fate
P2.15	Anchalee Tantiviramanond	Grinnell College	Tannins, Herbivory, and Petal-spot Polymorphism
P2.16	Emily Watters	University of Chicago	Similarities and differences between *Ulva sp., Gracilaria sp.*, and seawater's microbiome in Little Sippewissett Marsh
P2.17	Jenna Kotz	Gustavus Adolphus College	Microbial Degradation of Herbicides
P2.18	Collin Carlson	Gustavus Adolphus College	The leaching of Dissolved Organic Carbon and Lead from a Peatland system
P2.19	Anne Havlik	University of Chicago	Early Neural Tube Development During Chick Embryogenesis
P2.20	Jillian Ward	Lawrence University	Constructing an ANG and RI Double-Knockdown in dCas9 HeLa Cells
P2.21	Skylar Sundquist	Hope College	Regulation of cellular proliferation by VACM-1/CUL5 is dependent on its posttranslational modifications by NEDD8
P2.22	Rohan Kremer Guha	University of Chicago	Stability of Anaerobic Salt-Marsh Microbial Consortia Over Time When Exposed to High Nitrate Concentrations

POSTER SESSION P3

3:10 pm – 4:10 pm EPNEC Great Room B			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Marit Simmons	Beloit College	Isolation of antibiotic-producing bacteria and capstone course design using the Tiny Earth research sequence
P3.02	*N/A*		
P3.03	Joy Layton, Azniv Khaligian	Carthage College	Play Behavior in Captive White-handed Gibbons (Hylobates lar)
P3.04	Neha Motwani	Knox College	Where should Adults with Congenital Heart Disease receive inpatient care?
P3.05	Hiywot Tulu	Macalester College	The Impact of Abca7 p.A693S mutation on Alzheimer's disease pathology
P3.06	Rosa Mallorson	Colorado College	Optimization of red-emitting carbon quantum dot sensors for measuring H^+ and Mg^{2+} in Dictyostelium discoideum

P3.07	Manik Reddy	Macalester College	Optimization of an in situ hybridization protocol for C. elegans embryos
P3.08	Sarah Pan	University of Chicago	Toddlers' Cognitive Skill and Active versus Observational Object Learning
P3.09	Roberth Anthony Rojas Chavez	Colorado College	The effects of natural competence on the spatiotemporal evolution of Acinetobacter on antibiotic landscapes
P3.10	Liban Jama	St. Olaf College	Quantifying the Interactions between Bulged RNA and Cosolute
P3.11	Amy Kwan	Washington University in St. Louis	Identifying patterns of Foxl1 expression in mouse development
P3.12	Yuzhu Cheng	Colorado College	Investigating the Genetic Control of Nervous System Development Using Genome Editing
P3.13	Anna Von Duyke	St. Olaf College	Factors relating to Common Eider nest success and failure in Arctic Alaska
P3.14	Sahee Abdelmomin	Washington University in St. Louis	Real World Functioning, Cognition and Symptom Severity Predict Vocational Success in Individuals with Schizophrenia
P3.15	Rachel Snodgrass	Grinnell College	Causes and consequences of hydrologic microrefuges in an arid-land annual plant
P3.16	Madison Stamos	University of Chicago	Pharmacokinetic Tail Analysis of Long-Acting PrEP in HIV-negative, Low-risk Individuals
P3.17	Yumino Sasaki	Washington University in St. Louis	Characterization of residues required for coupling of chromophore isomerization and biological activation in bacterial phytochromes
P3.18	Maicy Vossen	Gustavus Adolphus College	CaMad2 promotes multiple aspects of genome stability beyond its direct function in chromosome segregation
P3.19	Magdalena Murray	University of Chicago	DNA Damage Repair in Neuroblastoma
P3.20	Jenna Kotz	Gustavus Adolphus College	Relationship between Personality and Likert Response Style
P3.21	Kevin Catalfano	Hope College	Use of Site-Directed Mutagenesis to Probe the Cystine Binding Site within System xc-
P3.22	Katherine Chiasson	University of Chicago	Investigating the Impact of Mucins on Wound Healing in Clytia hemisphaerica
P3.23	Natalie Sarver	Colorado College	Effect of Nutritional Signaling on Mating-Type Switching in O. polymorpha

Abstracts for all Sessions
Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, Washington University in St. Louis
November 1-2, 2019

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): Sahee Abdelmomin, Washington University in St. Louis
Session: Poster P3.14
Title: Real World Functioning, Cognition and Symptom Severity Predict Vocational Success in Individuals with Schizophrenia
Advisor(s): Deanna Barch, Psychological and Brain Sciences, Washington university in St. Louis
Co-author(s): Erin Moran, Deanna Barch

Abstract: Schizophrenia is a disorder characterized by delusions and hallucinations, blunted affect, anhedonia, and pervasive socio-economic downward drift. However, few well-powered studies have examined the relationship between employment status and cognitive performance across a range of cognitive domains. Data from 176 individuals with schizophrenia from the CNTRACS Consortium study was used to examine relationships between different aspects of cognition, symptom severity, real world functioning and employment outcome. Real-world functioning was calculated using years of education, social interaction and the UCSD Performance-Based Skills Assessment. Cognitive battery included assessment of working memory, episodic memory, cognitive control, processing speed, and reinforcement learning. Results suggest that participants with higher composite cognitive scores also had higher overall real world functioning scores. Further, the employed group (n= 58) showed significantly higher real-world functioning, processing speed, working memory and episodic memory. The unemployed group (n=115) had more severe anhedonia, depression, mania and disorganization symptoms. Thus, findings suggest that multiple factors are associated with employment status among individuals with schizophrenia. These finding help us understand which domains to enhance via treatment such as working memory, episodic memory, anhedonia and depression to provide more holistic improvement in patient outcome.

Presenter(s): Byunghyun Ahn, St. Olaf College
Session: Poster P1.07
Title: Lipid storage in starved Tetrahymena thermophila
Advisor(s): Laura Listenberger, Biology and Chemistry, St. Olaf College
Co-author(s): Hannah Nilsson, Laura Listenberger

Abstract: Lipid droplets are increasingly recognized as important and dynamic organelles in all cells. The pathways contributing to the formation and degradation of lipid droplets have been well-studied in a variety of organisms. Our experiments aim to determine the cellular pathways that contribute to lipid droplet homeostasis in Tetrahymena thermophila, a single-celled ciliate. In this study, we demonstrate an increase neutral lipid storage in Tetrahymena following

starvation. Pulse chase experiments using a fluorescent fatty acid analogue (Red C12) show that lipid trafficking to lipid droplets in starved Tetrahymena occurs along a similar time frame. We hypothesize that Tetrahymena mobilize lipids in lipid droplets to serve as substrates for beta oxidation. However, our results suggest that lipophagy does not play a role in this process. Monodansylcadaverine, a fluorescent label for autophagosomes, fails to colocalize with lipid droplets in starved Tetrahymena. Future studies will use inhibitors of cytosolic lipases and/or lipophagy to investigate the pathways of lipid droplet metabolism in Tetrahymena. We have also identified several novel lipid droplet-associated proteins from starved Tetrahymena following lipid droplet isolation, SDS-PAGE and mass spectrometry. Ongoing analysis of these proteins will provide further insight into mechanisms of lipid storage in starved Tetrahymena thermophila.

Presenter(s): Hanaa Alhosawi, Gustavus Adolphus College
Session: Oral II.F.1 (1:40)
Title: Exploring the Function of MAD2 in Candida albicans through Drug Sensitivity
Advisor(s): Dr. Laura Burrack, Biology,

Abstract: There are many causes of genome instability: these include unrepaired DNA damage, DNA replication errors, and chromosomal missegregation. These processes give genomic variation among cells in a population. In most cases, mutations and aneuploidy are deadly to cells. However, in specific stressful situations, mutations and aneuploidy can serve as a selective force. MAD2 is a gene that is critical to the function of the Mitotic Checkpoint Complex (MCC). MCC complex promotes accurate chromosome segregation, thus preventing aneuploidy. However, in some organisms, MAD2 also has other roles in the cell. To investigate and better understand the MAD2 gene in Candida albicans, we used different drugs and treatments as tools. We found that C. albicans lacking MAD2 have reduced growth on microtubule destabilizing drugs and DNA damaging agents, but increased growth on the antifungal drug fluconazole. Additionally, we looked at the localization of the Mad2 protein in the cells with and without drugs. Through this project, we found that MCC role is conserved in C. albicans, that Mad2 has additional functions beyond chromosome segregation to help cells respond to DNA damage, and that Mad2 localization is similar to other organisms.

Presenter(s): Jacob Amme, Washington University in St. Louis
Session: Poster P1.11
Title: Development of placental and fetal circadian rhythms in utero
Advisor(s): Erik D. Herzog, Department of Biology, Washington University in St. Louis
Co-author(s): Keenan Bates, Ronald McCarthy, Sarah K. England, Erik D. Herzog

Abstract: Women who undergo shift work during pregnancy have a 13-21% increase in risk for preterm birth. One possible cause of this increased risk is chronodisruption, or the disturbance of circadian rhythms. A circadian rhythm is any endogenous and entrainable biological process with an intrinsic period of approximately 24 hours. Circadian rhythms are generated through a transcriptional-translational feedback loop, which includes the Period 2 gene. Mammalian fetal and placental circadian rhythms have been observed in vitro in tissue explants. However, this has yet to be seen in vivo. As such, I tested the hypothesis that embryos expressing a reporter of PER2 protein levels (PER2::Luc) would display diurnal rhythms in utero. I crossed wild-type females with PER2::Luc male mice and imaged

bioluminescence starting at embryonic day 8.5 (E8.5). I found that the bioluminescence derived from the fetus and placenta increased in intensity as early as E10 and displayed a strong diurnal variation starting on E12. Thus, I conclude that embryonic PER2 circadian rhythms develop in utero beginning around E12. Next, I will use a two color PER2 luciferase reporter to distinguish between placental and fetal circadian rhythms to determine how these circadian systems interact during prenatal development and relate to birth outcomes.

Presenter(s): Samantha Ardery, Carthage College
Session: Oral II.D.3 (2:14)
Title: Don't stop your YAPing: How expressing constitutively active YAP affects retinal development and regeneration
Advisor(s): Steve Henle, Biology, Carthage College

Abstract: Zebrafish (Danio rerio) have the capability to regenerate their optic nerve after injury. Understanding the molecular and genetic mechanisms that allow zebrafish to regenerate their optic nerve will help to develop therapies for treating optic nerve damage in humans. This is due to the fact that the zebrafish eye closely models the human eye in the developmental process. The Yes-associated protein (YAP) has been previously shown to be involved in the process of eye development and tissue regeneration. Understanding the role of YAP in development can improve the comprehension of the regeneration pathway as well. In order to study the role of YAP in development and regeneration, transgenic zebrafish with a UAS:constitutively active YAP (CA-YAP) gene have been mated with zebrafish with Isl2b:gal4 markers to express CA-YAP and an RFP in the cells of the optic nerve. Confocal microscopy was used to characterize the development of the optic nerve in the presence of CA-YAP. In the future, expression of how CA-YAP affects optic nerve regeneration in adult zebrafish will be monitored. CRISPR will also be used to label the wildtype YAP gene with GFP in order to localize expression and activation of YAP in optic nerve development.

Presenter(s): Aaron Bao, Washington University in St. Louis
Session: Poster P1.08
Title: Optimization of disaggregase Hsp104 in solubilizing neurodegenerative-disease implicated protein aggregation
Advisor(s): Dr. Meredith Jackrel, Chemistry, Washington University in St. Louis

Abstract: Many neurodegenerative disorders such as Alzheimer's, Huntington's, ALS, and Parkinson's arise due to the formation of insoluble protein aggregates, often caused by protein misfolding. These protein aggregates are extremely stable and resilient to forms of denaturation, which makes finding a direct, curative treatment difficult.

We combat the misfolding and aggregation of toxic proteins by utilizing yeast protein Hsp104, which natively acts as a disaggregase that solubilizes protein aggregates within the cell by unfolding them and allowing them to refold into proper conformation. However, wild-type Hsp104 fails to solubilize many disease-implicated protein aggregates such as FUS, TDP, and alpha-synuclein. Thus, more potent forms of HSP104 are needed to disaggregate these proteins. Our lab engineers Hsp104 variants that exhibit enhanced disaggregase function, specifically toward disease-associated protein aggregates. We create mutational libraries of

Hs104 variants, where we hope to observe relationships between protein structure and substrate specificity. Given the intimate relationship between protein aggregation and neurodegenerative disorders, the solubilization of such aggregates could help lead to curative treatments for these debilitating disorders.

Presenter(s): Gabriel Barrón, University of Chicago
Session: Oral I.C.2 (8:47)
Title: Elucidating the effects of the microbiome on susceptibility to lung injury
Advisor(s): Anne Sperling, Immunology, University of Chicago
Co-author(s): Cara Hrusch, Na Fei, Kathleen A. M. Mills, Maile Hollinger, Vanessa Leone, Jack Gilbert, Anne Sperling

Abstract: Acute respiratory distress syndrome (ARDS) is a lung pathology that manifests pulmonary edema and barrier dysfunction of the epithelium. ARDS, along with the fibrotic aspect of idiopathic pulmonary fibrosis, is often modeled in mice by administering the chemotherapy drug, bleomycin (BLM). In humans, BLM treatment results in lung fibrosis only within a fraction of those who are treated, which raises the question: why do some patients develop pulmonary fibrosis while others do not? These studies posit that the microbiome, and its influence on immunological responses, is responsible for this discrepancy—and these studies seek to elucidate microbiome-dependent mechanisms of lung injury. My recent studies show gnotobiotic mice conventionalized to the microbiomes of two different housing facilities show differential weight loss, survival and collagen in the lungs. While the microbiome has been implicated in immune training, the data presented here is early evidence of the gut microbiota influencing the expansion of specific T helper subsets that protect against lung injury. Supported by the University of Chicago.

Presenter(s): Daniel Berkovich, Washington University in St. Louis
Session: Poster P2.11
Title: A biochemical characterization of aspartate aminotransferases in plants
Advisor(s): Joseph M. Jez, Biology, Washington University in St. Louis

Abstract: In addition to functioning as a component of proteins in all living organisms, the amino acid aspartate also participates in a variety of plant metabolic processes, including the assimilation of nitrogen via a transamination reaction. This reaction is catalyzed by the enzyme aspartate aminotransferase (AAT), of which five differentially-localized isoforms exist in model plant Arabidopsis thaliana. While the general reaction mechanism of these enzymes is known, they have yet to be fully characterized structurally or kinetically. In this research, comparisons of AAT amino acid sequences to that of the related prephenate aminotransferase (PAT) revealed the critical residues for the AAT reaction and its substrate specificity. Steady-state kinetics were then implemented to analyze the feedback regulation and substrate specificity of AAT isoforms and of several site-directed mutants.

Presenter(s): Jacob Blum, Washington University in St. Louis
Session: Poster P1.14
Title: Decoding methylation profiles that silence tumor suppressor genes via a massively parallel reporter assay
Advisor(s): John R. Edwards, Internal Medicine, Washington University in St. Louis

Abstract: Irregular levels of DNA methylation are known to play a significant role in carcinogenesis. Conventionally, it is thought that methylation of a tumor suppressor gene results in the decrease of that gene's expression, increasing a cell's likelihood of becoming cancerous. However, it still remains unclear if gene expression is repressed simply by the increase in DNA methylation across the entire promoter, or if methylation of specific CpG dinucleotides within the promoter are required in order to inhibit gene expression. Understanding which methylation changes are significant is critical to determining the pathological consequences of DNA methylation. In order to evaluate important methylation, we developed an experimental approach to determine the functional effects of millions of methylation patterns within the same gene in parallel. This massively parallel reporter assay (MPRA) first utilizes fluorescence-activated cell sorting to categorize individual cells by expression of a randomly methylated promoter-reporter cassette. Sorted cells are bisulfite sequenced to reveal which methylation patterns silenced expression. Our initial results have demonstrated proof-of-concept for the approach. Future experiments using this method are underway to determine the significance of different DNA methylation patterns, ultimately allowing us to build computational models for predicting the consequences of methylation changes in clinical epigenomic data.

Presenter(s): Madison Byrne, Knox College
Session: Poster P2.04
Title: Examining the relationship between jaw muscle physiology and predation strategy in Centrarchid fishes
Advisor(s): Nicholas Gidmark, Biology, Knox College
Co-author(s): Janki Bhalodi, Jeri Rosenbloom, Nicholas J Gidmark

Abstract: Prey capture in fishes spans a continuum between ram- and suction-feeding. Ram feeders approach their prey at high speeds, snapping the jaw shut to secure their meal, whereas suction feeders rapidly expand the buccal cavity, forcing their food and the water around it into the mouth. A fish's predation strategy can fall anywhere on this ram-suction continuum, but each feeding mode demands a different kind of performance. An organisms' ability to be successful in prey capture in the wild is determined partially by jaw-closing force and jaw-closing velocity; these organismal metrics are in turn directly limited by muscle performance, such as the physiological limits of muscle's instantaneous length and shortening velocity. We empirically tested the interplay of jaw-closing velocity, force, and gape angle across five Centrarchid species that represent multiple points, including the extremes, of the ram-suction spectrum. We found that ram-feeding fishes (largemouth bass and green sunfish) have faster jaw-closing muscles at a given force, and faster muscles overall than suction feeders (bluegills, redear sunfish). Our goal is to examine where variation occurs in the muscle physiology of different fishes, as well as how this variation correlates to the ram-suction index.

Presenter(s): Collin Carlson, Gustavus Adolphus College
Session: Poster P2.18
Title: The leaching of Dissolved Organic Carbon and Lead from a Peatland system
Advisor(s): Jeff Jeremiason, Environmental studies, Gustavus Adolphus College

Abstract: Peatlands in northern Europe and North America have long been studied to understand the cycling and retention of dissolved organic carbon (DOC) and lead in these systems. One long-term study site is the S2 ombrotrophic peatland in the Marcell Experimental Forest (MEF), a research facility located in northern Minnesota. Ombrotrophic peatlands depend on the atmosphere for water and nutrients. They can also provide long-term records of atmospherically derived pollutants such lead. With this long-term study conducted at this site, it has been found that lead and DOC concentrations are highly correlated within this system. One aspect of this study is to understand some of the factors that effect the trends of DOC and lead flow in this peatland system. To conduct a study on this system, peat cores were taken from S2 peatland. The goal of this study was to test if it is possible to replicate the trends of DOC and lead at MEF within a lab setting. Another goal of this research was to use historical data to study the historical levels of lead and DOC. With the results found, it shows that these columns can replicate an ombrotrophic peatland system within a lab since the data from these columns follows the same trends found in MEF.

Presenter(s): Kevin Catalfano, Hope College
Session: Poster P3.21
Title: Use of Site-Directed Mutagenesis to Probe the Cystine Binding Site within System xc-
Advisor(s): Leah Chase, Biochemistry, Hope College

Abstract: The Chase lab studies System xc-, a SLC7 heterodimeric transporter that exchanges extracellular cystine for intracellular glutamate. The transporter is comprised of xCT, which is the catalytic subunit, and 4F2HC. This substrate specificity is novel among the SLC7 transporters, therefore, the goal of this project is to identify the amino acids within xCT that are important for substrate binding and exchange. We used PyRx to dock cystine and glutamate in xCT, and selected residues within the apparent binding pocket for mutagenesis visualized with PyMol. We created the following point mutations S181A, R135A, T376A, H373A, Y244F in xCT using a PCR-based approach. We plan to test the transport efficiency of these mutants with a spectrophotometric assay, which employs glutamate dehydrogenase, once the transport assay is standardized. We hypothesize that mutants which lead to diminished transport activity or changes in substrate affinity are important in substrate binding and/or translocation.

Presenter(s): Yuzhu Cheng, Colorado College
Session: Poster P3.12
Title: Investigating the Genetic Control of Nervous System Development Using Genome Editing
Advisor(s): Darrell Killian, Molecular Biology Department, Colorado College
Co-author(s): Patrick Ende

Abstract: The nervous system is composed of neurons – cells with cellular extensions called axons and dendrites – whose complexity of morphology and interconnection dictates neuronal

function. The nanos gene is important for dendrite development in the fruit fly. However, other species have more than one nanos-related gene, which complicates genetic analyses. In C. elegans there are three nanos-related genes (nos-1, nos-2, and nos-3) and loss of any one or two has minimal effects on dendrite branching. This suggests that the three nanos-related genes play genetically redundant roles in dendrite development. To test this hypothesis, we used CRISPR-Cas9 genome editing to create a triple mutant, which we are now analyzing for defects in dendrite development. Another gene, rbm-39, has suspected roles in dendrite branching in both fruit flies and C. elegans based on experiments that reduced rbm-39 activity. To further investigate the role of rbm-39, we aimed to delete the gene using CRISPR-Cas9. Molecular evidence suggests that genome editing was successful, but we are still working to obtain animals homozygous for the deletion.

Presenter(s): Katherine Chiasson, University of Chicago
Session: Poster P3.22
Title: Investigating the Impact of Mucins on Wound Healing in Clytia hemisphaerica
Advisor(s): Jocelyn Malamy, MGCB, University of Chicago

Abstract: The cnidarian Clytia is an up-and-coming model organism, partially for its ability to heal wounds at an advanced rate. Understanding how wound healing developed in this simple organism may provide key insights into wound healing in more complex creatures. One area that has not been fully explored is the role of mucus in wound healing in Clytia. Mucus is composed of heavily glycosylated proteins called mucins which interact to form a polymer gel. There are two types of mucins- secreted and membrane associated mucins- but only the secreted mucins form gels. Since mucus covers much of the epithelial surface and acts as a protective and selective barrier in many organisms[1], it has been theorized that mucus is involved in the wound healing process, possibly by aiding water retention or signaling a wound for healing[2].

Over the past three months, I initiated experiments to identify, image, and probe the function of mucins in the jellyfish genome, focusing on epithelial wound healing in the medusa of Clytia. Using the conserved domains in mucins, I identified two potential secreted mucins in the Clytia genome predicted to be expressed in the medusa.

To assess where these putative mucins are expressed, we designed specific probes to perform in situ hybridizations. Despite some complications, I confirmed that both mucins were expressed in the medusa, and made some initial observations about differential expression within the animal.

Furthermore, I piloted an approach to visualize mucus in live animals using wheat germ agglutinin (WGA) to bind to the sugar molecules in the mucosal proteins. My tests confirmed that mucins were present and concentrated around wounds. They also showed that this method should allow us to watch the changes in mucus distribution during wound healing, as the dye will track the movement and flow of the stained mucus.

Presenter(s): Marie Crane, Macalester College
Session: Oral I.B.4 (9:21)
Title: Using assembly graphs to analyze strain-level variation and identify novel phages in hot spring metagenomes
Advisor(s): Mihai Pop, Computer Science, University of Maryland
Co-author(s): Kassie Wang, Jacquelyn Meisel, Harihara Muralidharan

Abstract: Assembly graphs are often used in genomic assembly, to form a consensus sequence from many individual sequences. However, in the context of metagenomics, valuable information is lost when complex assembly graphs are collapsed into a single consensus sequence. This study explored the use of assembly graphs to analyze strain-level variation and identify potential novel phages in metagenomic data. Samples were collected from Mushroom and Octopus hot springs in Yellowstone National park across a temperature gradient and sequenced with Illumina shotgun sequencing. Metagenomes were assembled and assigned taxonomic annotations. Assembled contigs were scaffolded and bubble motifs in the resulting assembly graphs were identified and characterized. Unannotated bubble motifs were identified as potentially novel elements and were clustered. Genes were predicted from these clusters and searched against a phage database, anticipating integrase genes as indicators of the presence of phages. Many bubble motifs were observed in assembly graphs, the majority of which were “simple” 4-node bubbles, suggesting high diversity at the strain level in these samples. Many “indel” 3-node bubbles were also observed, which suggest the presence of potential phages. Unannotated bubble clustering produced 60 clusters, potentially containing phage elements.

Presenter(s): Tessa Dethlefs, Gustavus Adolphus College
Session: Poster P1.18
Title: Resource allocation in response to nitrogen availability in female white campion (Silene latifolia)
Advisor(s): Cristina Portales Reyes, Ecology, Evolution and Behavior, University of Minnesota
Co-author(s): Cristina Portales Reyes

Abstract: Soil nitrogen conditions can have differing impacts on resource allocation in plants. Silene latifolia is a dioecious forb, and due to potential sex differences in resource allocation, we only focused on female individuals. To investigate whether changes in soil nitrogen availability affect resource allocation in female S. latifolia, we analyzed its aboveground biomass harvested from experimental plots that differed in amount of nitrogen supplementation. Samples were compared based on metrics that indicate relative allocation of resources to vegetative versus reproductive structures (i.e., fruit capsules and seeds). Interestingly, females grown under high nitrogen conditions produced significantly smaller reproductive structures compared to those grown under control and low nitrogen conditions ($p<0.01$). Our data suggest that female S. latifolia direct resources toward growth rather than reproduction under excess nitrogen, and this shift in resource allocation may function to counter abundant aboveground competition in high nitrogen conditions. This finding is consistent with other studies that have examined the impacts of nitrogen addition on vegetative growth versus reproductive effort in dioecious plant species.

Presenter(s): Thomas Diaz and Yutong Zou, Hope College
Session: Poster P1.24
Title: Detecting cancer treatment compound Taxol in different species of Hazelnuts with HPLC
Advisor(s): Jianhua Li, Biology, Hope College
Co-author(s): Yutong Zou, Brittany Henkin, Jianhua Li, Kenneth Brown

Abstract: Paclitaxel (brand name Taxol) is an elusive chemotherapy drug originally discovered in Taxus brevifolia, or the Pacific Yew Tree. In order to get enough Taxol for one dose, an entire Taxus specimen must be destroyed. This poses obvious environmental concerns, but paclitaxel is in extreme demand as it targets and destroys many cancers efficiently. Nowadays, paclitaxel is produced from semi-synthesis using precursors, such as 10-deacetylbactin-III, extracted from Yew needles. Recent studies have shown that paclitaxel is present in the leaves and shells of various Corylus species. This study aims to prove the presence of the cancer panacea in hazelnut leaves and compare the different concentration between species.

Presenter(s): Charlotte DiBiase, Colorado College
Session: Poster P1.06
Title: Maternal Floral Color, UV Protection, and Germination in Ipomopsis aggregata
Advisor(s): M. Shane Heschel, Organismal Biology and Ecology, Colorado College

Abstract: Scarlet gilia (Ipomopsis aggregata) is a red to pink flowering plant which shows floral color plasticity within populations on the eastern slope of the Rocky Mountains. Anthocyanin is the red flavonoid pigment which gives these petals color and has been shown to act as protection from UV damage in plants by shielding chloroplasts and acting as an antioxidant. This study was conducted on seeds from 24 plants from Manitou Experimental Forest (12 dark with dark petals, 12 with light petals). After being counted and weighed, seeds were germinated in a growth chamber over the course of 23 days and were censused for germination rate every other day. Photosystem efficiency, anthocyanin content, chlorophyll content, and biomass were measured on germinated seedlings after the census was completed. Dark-flowering maternal plants yielded seeds and seedlings with higher biomass than light-flowering ones. Seeds from darker maternal plants also germinated faster than those from light maternal plants and had higher anthocyanin content. The hereditary nature of anthocyanin content thus suggests that higher anthocyanin levels are linked to measures of fitness such as higher seed weight, germination rate, and seedling biomass, indicating that UV protection provided by anthocyanins potentially increases the realized fitness of maternal plants.

Presenter(s): Yueqi Du, Washington University in St. Louis
Session: Oral I.A.2 (8:47)
Title: Analyzing the Role of the V1/V2 Region in HIV-1 Coreceptor Switching
Advisor(s): Lee Ratner, Molecular Oncology, Washington University in St. Louis

Abstract: HIV entry is a dynamic process that requires binding to CD4 and a coreceptor, either CCR5 or CXCR4, on helper T-cells. CCR5 antagonists are a class of antiretrovirals that block CCR5 (R5)-tropic virions from binding by inducing a conformational change in CCR5 chemokine receptor. Our earlier study focused on the development of CCR5-antagonist resistance of R5 strains in two patients in a Vicriviroc (VCV) phase 2b clinical trial (PMID: 30787151). Notably, our genotypic and functional assays identified significant changes in the first three variable domains (V1/V2 and V3) in dual-tropic variants, suggesting that the V1/V2

region also plays a role in co-receptor switching. Changes in V1/V2 led to increased IC50 concentrations for CCR5-antagonist resistance, consistent with a model of competitive resistance. Previous studies have established that the V3 region on the viral envelope protein (Env) is a key determinant in coreceptor specificity. More recently, it is believed that other regions may also affect tropism. In our current work, we focused on understanding the role of the V1/V2 in the emergence of CXCR4 (X4)-using virus under CCR5-antagonist therapy. We analyzed five patient samples from the same cohort and whose quasispecies switched fully from R5 to DM. Next generation sequence analysis identified distinct differences between R5 and X4 strains from each subject. Genotypic analysis of single clones isolated from the patient samples showed significant V1/V2 domain differences between baseline and virologic failure (VF) after CCR5-antagonist therapy, suggesting that the V1/V2 regions may also contribute to tropism switching. This work will contribute to the development of a new genotypic prediction tool to guide therapy in HIV positive patients.

Presenter(s): Chineze Egwudo, University of Chicago
Session: Oral II.E.2 (1:57)
Title: Optimizing microCT tractography for use as a potential diffusion MRI gold standard
Advisor(s): Patrick Rivere, Department of Radiology, University of Chicago
Co-author(s): Scott Trinkle, Patrick Rivere

Abstract: Diffusion MRI is the only way to noninvasively acquire information about white matter connectivity in-vivo, making it a valuable tool for clinical practice and biomedical research [1] Tractography applies fiber-tracking algorithms to processed diffusion MRI images to connect voxel-wise orientation estimates and represent fibers as 3D images[2, 3]. However, these algorithms are limited by the low resolution of MRI voxels, which makes it difficult to delineate fiber position and orientation. [2, 3]. The tracking process also requires users to define tracking parameters, which leads to variability among final tract reconstructions.

Ex-vivo synchrotron microCT images show high isotropic, spatial resolution across the whole mouse brain with improved detection of multi-oriented fibers. Using orientation distribution functions (ODFs) derived from structure tensor analysis as the basis for whole-brain tractography with greater tracking precision, more accurate reconstructions could possibly encourage the use of microCT as a validation tool for dMRI.

For this project, we explored different tractography algorithm parameters in order to understand the differences between x-ray and MRI tractography performance. Tracer data from the mouse brain Allen Atlas was used as a ground-truth data set in order to assess the accuracy of the final fiber reconstructions and their sensitivity to different algorithm parameters [4].

Presenter(s): John Feigelson, Colorado College
Session: Poster P1.12
Title: The Effect of Experimental Warming on Plant-Pollinator Relationships in the Low Arctic
Advisor(s): Roxaneh Khorsand, Organismal Biology and Ecology, Colorado College

Abstract: In the Arctic, climate change is having a pronounced effect on seasonality and life cycles of tundra plants. As the air warms and snow melts earlier in the spring, growth of many species begins earlier. Despite their importance in ecosystem function, the basic natural history and reproductive ecology of low Arctic tundra plant communities is not well understood. This

lack of understanding carries over to insect life cycles, as well. If insects and plants experience different life cycle responses to climate change, an asynchronous relationship can develop, resulting in plant-pollinator mismatch and potential fitness losses for both groups of organisms. Our work on the North Slope of Alaska investigates the potential for phenological mismatch between plants and pollinators. Using an experimental warming treatment, we observed floral visitors, tracked plant phenology, and tested for pollen limitation in multiple tundra species. Preliminary results suggest that (1) Dipterans, or flies, were the most common floral visitors; (2) Polygonum bistorta received a higher proportion of floral visitors than any other plant species; and (3) pollen limitation occurred in Ledum palustre, Cassiope tetragona, and Polygonum bistorta. These findings imply that while pollinators are not necessary for fruit set, a potential plant-pollinator mismatch would result in reduced plant reproductive output across the plant community. This research provides important insight into the reproductive ecology of tundra plant species and allows us to predict how plant-pollinator relationships could change as the climate warms.

Presenter(s): Jay Fordham, Gustavus Adolphus College
Session: Oral I.B.1 (8:30)
Title: Targeted applications of triclopyr to Fraxinus pennsylvanica to manage experimental plots
Advisor(s): Stuart Wagenius, Biology, Northwestern University

Abstract: Woody encroachment of Fraxinus pennsylvanica (green ash) in Western tallgrass prairie have become an increasing problem for prairie researchers, especially within common garden plots. Without protocol for a targeted application of herbicide there is not an effective way to manage experimental plots. In order to address this problem, I designed an experiment that tested three applications of triclopyr. I found stem senescence for stump applications of triclopyr where trees were cut down to 10 cm from the ground line was significantly greater than the foliar application. For all treatments, there was an assessment of herbicide drift within experimental plot. No evidence was found.

Presenter(s): Margot Groskreutz, St. Olaf College
Session: Poster P2.10
Title: Does Residential Land Use Impact Water Chemistry?
Advisor(s): Meredith Holgerson, Biology and Environmental Studies, St. Olaf College
Co-author(s): Katie Hoffman, Meredith Holgerson

Abstract: Freshwater ponds, one of Earth's most abundant resources, could be altered by the global increase in residential land use. In this study, we evaluated how residential land use affected the water chemistry and mixing dynamics of 11 ponds in south-central Minnesota. We selected ponds along a residential land use gradient, with completely forested and highly residential watersheds represented. We analyzed how water chemistry, such as pH and conductivity, changed with watershed land use by using GIS land cover data. We found that the water chemistry was influenced by characteristics of the watershed and the pond. Specifically, we found that the percent of pavement in a watershed increased conductivity (indicative of road salts), while yard cover increased nitrogen concentrations (possibly from fertilizers). Other pond characteristics, specifically increased depth and conductivity, appeared to decrease pond mixing frequency. Pond mixing occurs when pond water rotates throughout

the water body, allowing benthic and surface waters to switch locations. This aids in nutrient cycling and impacts greenhouse gas emissions. Overall, both watershed and pond characteristics influenced water chemistry with residential areas tending to have higher nutrient and conductivity levels. We recommend that future studies evaluate the impact of road salts and fertilizers on pond ecology.

Presenter(s): Melanie Gucwa, Carthage College
Session: Poster P2.03
Title: Potential Roles of a NUP155 Protein Subdomain in Cardiac Electrophysiological Development
Advisor(s): Randolph S. Faustino, Genetics and Genomics, Sanford Research
Co-author(s): Melanie E. Gucwa, Tyler A. Bradley, Riley J. Leonard, Claudia C. Preston, Ruby Hawks, Randolph S. Faustino

Abstract: Cardiovascular Disease (CVD) is the number 1 cause of death globally and accounts for 31% of deaths. One form of CVD are arrhythmias which causes irregular beating of the heart. Atrial Fibrillation (AF) is a specific class of arrhythmia that can lead to stroke, other heart related complications, and death. Recent studies have illustrated a connection between AF and proteins called nucleoporins (nups). These proteins make up the nuclear pore complexes embedded throughout a cell's nuclear membrane. The NPC's main function is to allow for transport of macromolecules between the nucleus and the cytoplasm. Mutations found in one of the nups, NUP155, have been clinically found in patients with AF. The mutation in NUP155 that predicted to have the highest pathogenicity is the R672G point mutation found in the alpha helical region. In this project, we performed the CRISPR/Cas9 method of genome editing to introduce the NUP155 R672G mutation in human dermal fibroblasts, human-induced pluripotent stem cells (hiPSCs), and premature hiPSC-derived cardiomyocytes. We then utilized the human stem cell models for cardiac differentiation to study the effects of the NUP155 R672G mutation on developing cardiomyocytes of these various cell lines.

Presenter(s): Kelly Hartigan, Washington University in St. Louis
Session: Oral I.A.4 (9:21)
Title: Human iPSC-Derived Cerebral Organoids Establish Mutational Specificity in NF1
Advisor(s): David Gutmann, Neurology, Washington University

Abstract: Neurofibromatosis type 1 (NF1) is a common neurogenetic condition caused by germline mutations in the NF1 gene. While all germline NF1 gene mutations have traditionally been regarded as equivalent loss-of-function alleles, emerging evidence from population-based studies now suggests that the germline NF1 gene mutation may be one factor underlying the clinical variability in this condition. In order to determine whether NF1 gene mutations have mutation-specific effects on human brain development, we have employed an isogenic series of human induced pluripotent stem cell (hiPSC) lines CRISPR/Cas9-engineered to harbor distinct patient NF1 germline gene mutations. From these hiPSC lines, we derived three-dimensional cerebral organoids to analyze mutation-specific effects on neural progenitor cell, astrocyte, and neuron maturation. All experiments employed numerous biological replicates from two independently generated hiPSC clones. While all mutations resulted in increased glial cell growth and whole-organoid RAS activity, we observed striking NF1 mutation-specific effects on neural progenitor cell proliferation, death, and

neuronal differentiation within the ventricle-like zones of developing cerebral organoids. These findings provide the first evidence of NF1 mutational specificity operative at the cellular and tissue levels, supporting population-based genotype-phenotype correlations, relevant to their applications to risk assessment and targeted therapeutics for a disorder characterized by clinical heterogeneity.

Presenter(s): Anne Havlik, University of Chicago
Session: Poster P2.19
Title: Early Neural Tube Development During Chick Embryogenesis
Advisor(s): Timothy Sanders, Department of Neurobiology, University of Chicago

Abstract: Scientists are still uncertain of the mechanisms by which the neural tube closes as the vertebrate embryo develops. Recognizing this, I began to further elucidate neural tube closure during chick embryogenesis. As the neural tube develops, an array of complex morphogenetic movements leads to changes in cell morphology and cell fate. These changes result in epithelial fusion of opposing neural folds, leading to the creation of a neural tube and a non-neural ectoderm. Through both fixed embryo staining and live embryo injection of targeted membrane specific dyes followed by electroporation, pathways of injected neural progenitor cells were followed and imaged over early embryonic development. Bright-field microscopy, fluorescence stereomicroscopy, and computational clearing, paired with the use of several different dyes and trials, allowed for the mechanistic imaging and delineation of cellular architecture of neural tube closure. I established a novel experimental paradigm to collect and image the developing embryo to further delineate the process of early nervous system development in chick embryos. This study is useful for furthering the understanding of one of the most common birth defects in humans, known as neural tube defects (NTDs), that affect human nervous system function in over 300,000 live births per year.

Presenter(s): Yige He, Beloit College
Session: Oral I.A.3 (9:04)
Title: Quorum Sensing Affecting Nisin Gene Expression in L. lactis.
Advisor(s): Amy Briggs, Biology, Beloit College
Co-author(s): Kellyn Tippins, McKensie Finan and Amy Briggs

Abstract: This experiment aims to determine if interspecies quorum sensing can affect the nisin production of Lactococcus lactis. Nisin is the autoinducer used by L. lactis for quorum sensing. Because of its antibiotic effect, nisin is commonly used in food preservation industry. Nisin expression was analyzed by using q-PCR to compare nisin RNA transcription rate with reference gene 23s RNA transcription rate. The result shows V. anguillarum and B. subtilis can robustly increase nisin gene expression rate of L. lactis.

Presenter(s): Ashley Hermans, Carthage College
Session: Oral II.E.1 (1:40)
Title: A vision test for fish: Optokinetic response to assess functional recovery after optic nerve injury
Advisor(s): Steven Henle, Neuroscience, Carthage College
Co-author(s): Ashley Franklin, Sophia Tajnai

Abstract: Zebrafish, unlike humans, can regenerate their optic nerve after injury. Optokinetic response (OKR) may be useful in determining the rate of optic nerve regeneration. OKR is the reflexive tracking of movements across the visual field to preserve the visual acuity of moving objects. This movement is consistent and reproducible, allowing the behavior to be quantified as a vision test. The OKR Vision Test entails placing the zebrafish in a 3D printed drum pulled by a motor controlled by an Arduino to elicit the OKR, a significantly cheaper alternative to previous methods. After eliciting an OKR, fish eye angles can be measured to create a graph depicting the OKR. Finding a baseline speed at which a wild type zebrafish can first no longer see the drum turn will help set a standard for normal vision prior to an optic nerve injury. In the future, performing optic nerve crush and measuring daily OKRs, the rate of functional regeneration of the optic nerve can be found and compared to the baseline. This will allow us to both better understand the process of optic nerve regeneration and provide a new assay for measuring optic nerve regeneration that doesn't require sacrificing the animal.

Presenter(s): Stella Matutina Ikuzwe, Macalester College
Session: Poster P2.07
Title: Prostate-specific G-protein-coupled Receptors Activate Oncogenic Mitogen-activated Protein Kinases in Prostate Cancer
Advisor(s): Guangyu Wu, Pharmacology and Toxicology, Augusta University

Abstract: Prostate cancer is the second most common cancer and sixth leading cause of cancer death in men. It has been found that olfactory receptors (ORs), which are part of the G-protein coupled receptor (GPCR) family are not only expressed in the sensory neurons of the olfactory epithelium but also in other human tissues like the colon, sperm, blood cells and so on. Additionally, It has also been found that these ORs are highly expressed in cancer cells such as prostate cancer. One of these cancer-related receptors is OR51E2, also known as prostate-specific G protein-coupled receptor (PSGR). The activation of PSGR with its agonist β-ionone have been found to increase the severity and metastasis of prostate cancer.
However, a lot is still unknown about the underlying mechanism of the signaling pathway involved in the cell proliferation and invasiveness of prostate cancer through these receptors. Therefore, we became interested in further studying these receptors in prostate cancer and their underlying mechanism with hope of identifying potential targets for new therapeutics and their potential of being used as new biomarkers of prostate cancer.

Presenter(s): Liban Jama, St. Olaf College
Session: Poster P3.10
Title: Quantifying the Interactions between Bulged RNA and Cosolute
Advisor(s): Jeff Schwinefus, Chemistry, St. Olaf College
Co-author(s): Amy imdieke

Abstract: Aqueous environments influence the stability of the three-dimensional structure of biopolymers. Past research has characterized the cosolutes urea, glycine betaine, and proline as denaturants of nucleic acid secondary and tertiary structure due to favorable interactions with functional groups exposed in the single stranded state. In this study, thermal denaturation experiments were performed in aqueous urea, glycine betaine, and proline solutions using four trinucleotide bulged RNA duplexes, in the context of HIV-1 TAR RNA, to determine how the bulge sequence affects RNA stability and its interactions with specific cosolutes. The trinucleotide bulges were constructed to determine the effect of cytosine and uracil-based codons on nucleic acid stability and interactions with cosolutes. Our results showed that urea served as an effective denaturant for the CCU and CCC trinucleotide bulges, glycine betaine for the CCU bulge, and proline for the CCU and UUU bulges all relative to an RNA duplex lacking a trinucleotide bulge. Our work suggests that these three cosolutes are sensitive enough to chemically probe solvent accessible surface area changes as small as those from trinucleotide bulges.

Presenter(s): Rie Kaneko, Beloit College
Session: Poster P2.01
Title: Automated Analysis of human EEG
Advisor(s): Rachel Bergstrom, ,
Co-author(s): Rose Williams, Chelsea Coleman

Abstract: Primary analysis of EEG is typically performed by visual inspection of the signal by expert observers. However, visual inspection is very time consuming and has the potential for lack of reproducibility of EEG interpretation because of observer bias and error. An automated algorithm for EEG signals can reduce time consumption and bias of individual observers.
Our algorithm combines line length with wavelet transformation to detect spike or seizures. One can capture very minute details, such as sudden changes and similarities in the EEG signals, using Wavelet Decomposition. Line length is defined as the sum of the absolute values of the differences between neighboring data points over a specified time interval. We can detect a spike or seizure event observing the increases in the line length.

Our automated method for EEG signals of mice identified epileptiform activity with high fidelity. We predict that we can use this automated method for EEG signals of human brains as well. We did visual scoring and compared the algorithm to that visual scoring. Our algorithm detected seizures. However, our algorithm was more strict than manual scoring. There is still more to be done to optimize this for human EEGs.

Presenter(s): Alan Kim, University of Chicago
Session: Poster P2.08
Title: Eye dynamics in premenopausal and postmenopausal patients with female hypoactive sexual desire disorder (HSDD)
Advisor(s): Stephanie Cacioppo, Department of Psychiatry and Behavioral Neuroscience, University of Chicago
Co-author(s): Erika Kaske, Wasuwat Siewsrichol, Jon Grant, Stephanie Cacioppo

Abstract: In our previous study, we have established that the visual patterns of patients with hypoactive sexual desire disorder (HSDD) follow the top-down neurofunctional self-attention-model (SAM) of desire and HSDD, which suggests that self-evaluation of oneself before or during sexual activities interferes with sexual desire. Little is known, however, whether menopause causes differences in visual patterns among female patients with HSDD. A total of 33 premenopausal and 11 postmenopausal female patients who met DSM-V criteria of HSDD were presented with a series of stimuli in our standard behavioral task i.e., the Desire Intention Task (DIT). Eye movements were recorded during DIT, and measures were calculated for two visual regions of interest, face and torso. As demonstrated in previous experiments, female patients with HSDD, regardless of menopausal state, were more likely to first orient to the torso than the face, but also looked away from the torso more quickly, therefore spending less time on average looking at the torso than the face. These results suggest that a) premenopausal and postmenopausal women with HSDD report similar visual-attentional patterns in relation to sexual desire-associated visual stimuli, and b) HSDD may be characterized by an aversion of such stimuli that is mediated by self-attention.

Presenter(s): Jenna Kotz, Gustavus Adolphus College
Session: Poster P2.17
Title: Microbial Degradation of Herbicides
Advisor(s): Amanda Nienow, Chemistry, Gustavus Adolphus College
Co-author(s): Amanda Nienow

Abstract: Many herbicides are used to kill undesired weed growth, but all have a wider impact on the surrounding ecosystem. While abiotic factors, such as photodegradation, can be significant contributors to the degradation of herbicides in soil and rivers, biotic factors also play a large role. There has been some research into the biotic degradation of Dicamba, identifying few species capable of utilizing the compound as a sole carbon source. Other studies have identified many herbicides and microorganism species capable of degradation This experiment will focus on specific herbicides including Dicamba and Bromoxynil and microbes found in farmland soils in Minnesota.

Presenter(s): Jenna Kotz, Gustavus Adolphus College
Session: Poster P3.20
Title: Relationship between Personality and Likert Response Style
Advisor(s): Madeline Harms, Psychology, Gustavus Adolphus College
Co-author(s): Goldina Lee, Kayla Thoen

Abstract: Likert scales are a common format found within opinion-based questionnaires. However, research shows correlations between response styles on these Likert scales and personality traits, which may skew data. Previous research has found that extraversion and

neuroticism are correlated with extreme response styles such as responding with “Strongly Agree” rather than “Agree”. Studies also show differences in public self-expression between introverted and extroverted people. Based on these findings, we hypothesized that extraversion would correlate positively and neuroticism would correlate negatively with extreme responses on a self-related survey and non-self related survey. 56 undergraduate students participated in a study that was conducted through three online surveys: a personality survey, a self-related survey, and a non-self related survey. There was a positive correlation with extraversion and extreme response style on the self-related survey ($r=0.288$, $p=0.031$); however, neuroticism was not correlated with response style. These findings suggest that extraverted people are more likely to respond with extreme answers to Likert Scales. This may skew studies conducted through Likert Scale surveys, and future studies may consider accounting for the correlation between personality and extreme responses.

Presenter(s): Rohan Kremer Guha, University of Chicago
Session: Poster P2.22
Title: Stability of Anaerobic Salt-Marsh Microbial Consortia Over Time When Exposed to High Nitrate Concentrations
Advisor(s): Joseph Vallino, Ecosystems Center, Marine Biological Laboratory
Co-author(s): Ashley Bulseco, Joseph Vineis, Jennifer Bowen, Joseph Vallino

Abstract: Most microbial communities change over time in response to environmental perturbations and neighboring bacterial communities. Dynamic changes may occur in taxonomy, nutrient uptake, metabolic output and abundance. This dynamism is often caused by division of labor within these communities including symbiotic relationships affecting waste, food, and toxic waste removal. Little is known about stability and response to perturbations in bacterial sub-communities in salt marshes. We hypothesized that consortia, representing sub-populations of a community, isolated from other communities and exposed to high concentrations of nutrients, will remain stable over time. We collected consortia from soil cores in a salt marsh on Plum Island in Newburyport, MA. Three flasks containing marine broth and nitrate feed were inoculated with equal quantities of the consortium, with a fourth consortium-free flask as control. Pumped nitrogen gas maintained anaerobic conditions. Over two weeks, 300 mL samples extracted every three days, were analyzed for metabolic activity (CO_2 output), taxonomy/diversity (16S rRNA sequencing), bacterial abundance (DAPI counts), and nutrient utilization (NO_3 levels). Sequencing results indicated that the consortia were contaminated. However, overall dynamics observed in this experiment suggest that the community as a whole was stable over time. Further experimentation is needed to support our hypotheses.

Presenter(s): Neetij Krishnan, St. Olaf College
Session: Poster AM P1.20
Title: IL-17A and TNF-α promotes migration and proliferation of breast cancer cells in vitro
Advisor(s): Helen Piwnica-Worms, Department of Experimental Radiation Oncology, MD Anderson Cancer Center
Co-author(s): Vidya Sinha, Amanda Rinkenbaugh, Helen-Piwnica-Worms

Abstract: Ductal carcinoma in situ (DCIS) is a pre-cancerous growth of indeterminate prognosis within the breast. At least 60% of women diagnosed with DCIS will not develop invasive cancer, but they are still exposed to the toxic side effects of cancer therapeutics due

to the indiscriminate nature of treatment. Breast cancer cells require assistance from the microenvironment to become invasive; immune cells associated with invasive lesions display upregulation of signaling targets associated with interleukin-17A (IL-17A), a cytokine associated with inflammation and recruitment of immunosuppressive cells.

Therefore, IL-17A is of interest as a candidate driver of invasiveness within in situ breast lesions and as a possible biomarker for predicting progression. We applied IL-17A and TNF-α (a key IL-17 synergist) in vitro to murine and human breast cancer cell lines with varying degrees of invasiveness, evaluating rates of proliferation and migration between vehicle-treated and cytokine-treated populations.

Our findings implicate IL-17A as a contributor to an invasive phenotype in early breast lesions. Multiple non-invasive and invasive cancer cell lines exhibited increased proliferation and migration upon cytokine exposure. We plan to use this methodology to evaluate other metrics for progression, including expression of immune-modulating and angiogenic cytokines, invasion within 3D culture, and organoid formation.

Presenter(s): Alissa Kunczt, University of Chicago
Session: Poster P1.22
Title: α7 Nicotinic Acetylcholine Receptors Relieve Pain Via Modulation of the Descending Pain Pathway
Advisor(s): Daniel McGehee, Department of Anesthesia & Critical Care, University of Chicago

Abstract: Over 20% of adults in US suffer from chronic pain conditions, highlighting the need for effective and sustainable treatments. Specific neural pathways mediate pain sensitivity, including ascending sensory circuitry and descending modulatory pathways. Descending pathways include the ventrolateral periaqueductal grey (vlPAG) and rostroventromedial medulla (RVM). Manipulation of vlPAG activity elicits pain relief, which is a mechanism of opioid induced analgesia. In addition to opioid receptors, vlPAG neurons express α7 nicotinic acetylcholine receptors (nAChRs). Our lab has shown that α7 nAChR agonists can relieve tonic inflammatory pain. Using behavioral tests for somatic and affective components of pain in mice, we found that α7 nAChR agonists relieve both of these measures. We also monitored neuronal activity in the vlPAG in vivo using an intracellular calcium sensor with fiber photometry and found that vlPAG neuronal activity increased during painful experience and decreased with α7 nAChR agonist administration. Finally, we used optogenetic methods to either increase or decrease activity of α7 nAChR-expressing neurons in the vlPAG during a pain state and found that only inhibition of these cells was analgesic. Together, these data provide novel insights into the physiology of α7 nAChRs in the vlPAG, which may lead to better treatments for pain.

Presenter(s): Amy Kwan, Washington University in St. Louis
Session: Poster P3.11
Title: Identifying patterns of Foxl1 expression in mouse development
Advisor(s): Klaus Kaestner, Genetics, University of Pennsylvania
Co-author(s): Ayano Kondo, Hannah Kolev

Abstract: The mammalian gastrointestinal epithelium is highly regenerative and completely self-renews every three to five days. This self-renewal is regulated by local niche cells, which surround intestinal crypts and provide signals that promote stem cell proliferation. One population of cells required for proliferation is the mesenchymal FOXL1-expressing cells.

FOXL1 is a winged helix transcription factor that functions during embryonic villus development in conjunction with bone morphogenic protein (BMP) and Hedgehog signaling. While the role of FOXL1 in the adult gut has been well-characterized, the dynamics of FOXL1 expression throughout development remains unknown. To address this gap, we performed immunofluorescent staining for FOXL1 at various time points in embryonic mouse intestine, kidney, and lung. FOXL1+ cells were detected as early as E8.5 in the developing gut tube and tightly bordered the gut epithelium throughout development. By E18.5, FOXL1+ cells drastically decrease in number and become uniformly distributed throughout the subepithelial layer of the intestine. Interestingly, FOXL1+ cells were also found surrounding kidney and lung epithelial tissue at E13.5, which has never been shown previously. These findings suggest that FOXL1 expression may be involved with mesenchymal-epithelial crosstalk during embryonic development. Further study of FOXL1 will help elucidate mechanisms of organogenesis in mammalian systems.

Presenter(s): Joy Layton and Azniv Khaligian, Carthage College
Session: Poster P3.03
Title: Play Behavior in Captive White-handed Gibbons (Hylobates lar)
Advisor(s): Angela Dassow, Biology, Carthage College
Co-author(s): Azniv Khaligian

Abstract: White-handed gibbons have a diverse vocal repertoire comprised of tonal and frequency-modulated sounds. Recently, an acoustically distinct sound was discovered. The focus of this research is to characterize this novel vocalization, which sounds akin to a bleat, and to determine its function. Our hypothesis is that the “bleat” serves as a distress or stop signal during play. Audio and visual data on play vocalizations and behavior were collected from two captive lar gibbons for eight weeks during summer 2019. Data analysis was conducted using Adobe Audition and Open Shot Video Editor. A change in the frequency of previously described gestural behaviors occurred during play versus non-play behaviors. Additionally, a few novel gestural behaviors associated with play were identified. Play behavior was more commonly initiated by the female gibbon, who is younger than the male gibbon. Acoustically, the “bleat” vocalization has a lower amplitude than the rest of the gibbons’ vocal repertoire. Future research will examine whether play behavior occurs in other captive or wild lar gibbons, as well as whether the play behaviors are present in other species of gibbon.

Presenter(s): Cody Leong, Colorado College
Session: Oral II.E.3 (2:14)
Title: Fluorescence-based high throughput quantification of yeast mating efficiency in O. polymorpha
Advisor(s): Sara Hanson, Molecular Biology, Colorado College

Abstract: The yeast species Ogataea polymorpha is an important model organism for the study of the evolution of sexual reproduction, as well as many other aspects of cellular biology. However, the scope and scale of current studies are limited due to a lack of efficient methods for examination and quantification mating efficiency, with current methods requiring large amounts of time and laboratory resources. O. polymorpha is capable of existing in two haploid mating types, which mate to form a diploid cell through fusion. We constructed plasmids that contained one of two fragments of green fluorescent protein (GFP), which will be transformed

into the genome of O. polymorpha. Once created, these strains will produce a complete functional protein after a successful mating between two haploid cells. Using the method of flow cytometry, we can then determine mating efficiency by counting fluorescent diploid cells. In the course of the research period, one of the two fragments of GFP was successfully integrated into O. polymorpha, and proof of concept was established for the process of transforming DNA fragments into similar strains of yeast.

Presenter(s): Zhengyue Li, Beloit College
Session: Poster P1.01
Title: Advanced Synthesis of Magnetic Barcoded Beads in High-throughput scRNA-seq
Advisor(s): Wenqi Zhu, Singleron Biotechnologies Co , Ltd, R&D, Southeast University

Abstract: Due to the increasing needs of human genome study, research in high-throughput and low-cost scRNA-seq platform has been pushed further to the forefront. Instead of averaging the results of multiple cells via traditional cell sequencing, single-cell RNA sequencing could narrow down the result to single-cell mutation and provide us explicit details for further bioinformatics analysis, especially for cancer diagnosis. Despite the fact that previous research has mainly been done with the streptavidin-coated beads and hydrosol-based beads, magnetic beads coated with carboxyl groups were chosen for further synthesis due to their outstanding high-temperature resistance and PCR stability. Even though ligation-based barcoding synthesis has been the most popular synthesis method, it has reached its bottleneck in the past few years. In order to achieve a higher cDNA capture efficiency, this research tries to improve the ligation-based synthesis with extension-based synthesis methodology via three rounds of split-pool synthesis. Reverse complement oligo FAM coated with fluorescence was applied to the research product for further quality checks.

Presenter(s): David Lynum and Torey Flint-Kjellgren, Gustavus Adolphus College
Session: Poster P1.15
Title: The Effect of Lovingkindness Meditation on Emotional Self-Regulation
Advisor(s): Marie Walker, Psychological Science, Gustavus Adolphus College
Co-author(s): Torey Flint-Kjellgren, Marie Walker

Abstract: We continued our exploration on the effect of lovingkindness and body scan meditation on emotional self-regulation, expecting increased self-compassion in a loving kindness meditation, and positive effects of both meditation types on emotional self-regulation compared to neutral visualization. Across conditions, men had marginally higher positive and lower negative affect than women. Lovingkindness was shown to elicit slightly higher positive affect, while body scan led to lower levels of suppression. Self-compassion was shown to be marginally higher in the neutral visualization condition compared to lovingkindness and body scan.

Presenter(s): Rosa Mallorson, Colorado College
Session: Poster P3.06
Title: Optimization of red-emitting carbon quantum dot sensors for measuring H^+ and Mg^{2+} in Dictyostelium discoideum
Advisor(s): Murphy Brasuel, Chemistry and Biochemistry, Colorado College

Abstract: The facile synthesis of fluorescent, non-toxic, and stable red-emitting carbon quantum dots were optimized as nano-ion sensors. Medically important compound protonation and diseases states in eukaryotic cells are altered by H^+ and Mg^{2+} ion transduction pathways. Dictyostelium discoideum indicate ion concentration shifts in these pathways, most notably apparent in their endosomes during periods of aggregation that increase intracellular H^+ concentration. Carbon source, steric stabilizer, carbonization acid dilution, temperature, and dialysis reagent were varied. Mixed carbon sources with amine groups and variable oxygen content, dilute acid, low temperature, and dialysis in neutral solution were optimal to develop red-emitting dots either containing or omitting a steric stabilizer with ethylene glycol. A longer synthesis, up to 48 hours, results in a greater yield of red-emitting dots. Red-emitting dots are less polar than shorter- wavelength emitting dots and exhibit a direct correlation between emission intensity and acidity. Combined with a passivating long-chain carboxylic acid and fluorescein isothiocyanate or coumarin 343 dye to measure H^+ and Mg^{2+} respectively, a ratiometric analysis of dye to red-emitting dot peak facilitates real-time monitoring of intracellular ion flux. A decrease in H^+ in Dictyostelium discoideum upon addition of caffeine was observed. Optimization of coumarin 343/dot constructs will enable Mg^{2+} tracking.

Presenter(s): Yifan Mao, University of Chicago
Session: Poster P2.13
Title: Circulating Extracellular Vesicles of Sickle Cell Subjects Disrupt Endothelial Integrity
Advisor(s): Eric C. Beyer, Pediatric Hematology/Oncology, The University of Chicago
Co-author(s): Yifan Mao, Joanna Gemel, Gianna Sparks, Gabrielle Lapping-Carr, and Eric C. Beyer

Abstract: BACKGROUND: Small cell-derived extracellular vesicles (EVs) can affect endothelial function. We previously found that patients with sickle cell disease (SCD) have increased numbers of circulating EVs, which differentially disrupt endothelial integrity in vitro. Because endothelial disruption is a critical component of acute chest syndrome (ACS), we hypothesized that EVs isolated during ACS would induce greater endothelial damage than those isolated at baseline.

METHODS: Nine pediatric subjects had plasma isolated at baseline and during ACS. Cultured microvascular endothelial cells were treated with EVs and then studied by immunofluorescence microscopy to localize VE-cadherin and F-actin.

RESULTS: The EVs had a diameter of 95 nm. They contained CD63 and flotillin, which were increased in SCD patients (5-13-fold compared to control) and further increased between baseline and during ACS (24-57%). The EVs contained hemoglobin, glycophorin A, and ferritin. Treatment with baseline EVs caused modest separation of endothelial cells, while ACS EVs caused substantial disruptions of the endothelial cell monolayers. EVs from subjects with ACS also caused a 50% decrease in levels of VE-cadherin.

CONCLUSIONS: These results suggest that circulating EVs can modulate endothelial integrity contributing to the development of ACS in SCD patients by altering cadherin-containing intercellular junctions.

Presenter(s): Isabelle Matthews, Hope College
Session: Poster P1.21
Title: Benevolent sexism influences how we detect uses for objects
Advisor(s): Benjamin Meagher, Psychology, Hope College
Co-author(s): Benjamin Meagher

Abstract: Ideas about gender extend to the interpretation of objects. This research aimed to examine the relationship between a person's gender, their beliefs about gender, and how they determine the functions of objects associated with the opposite gender. An online survey with 173 participants was used to collect mouse-tracking data. On each trial, a specific action was described to participants (e.g., tying twigs together in a bundle), and they had to decide whether each object shown to them could or could not be used for that action. Each object was either functional or non-functional and pre-tested to be culturally masculine, neutral, or feminine. Mouse-movements to "Yes" or "No" were recorded in order to measure their maximum deviation away from the correct answer. Participants then self-reported on scales measuring in-group identification, bio-gender essentialism, and ambivalent sexism. A mixed-effects regression analysis revealed that both men and women who were high in benevolent sexism showed significantly higher deviation when presented with a functional object associated with the opposite gender, relative to men and women who were low in benevolent sexism. These results illustrate how sexist mindsets can inhibit people's cognition, specifically how they solve creative and critical thinking problems.

Presenter(s): Julissa Molina-Vega, Macalester College
Session: Poster P1.04
Title: Biguanide sensitivity of the nuclear pore complex in breast cancer: A potential therapeutic strategy
Advisor(s): David A. Potter, Department of Medicine, University of Minnesota
Co-author(s): Zhijun Guo, David A. Potter

Abstract: Cancer cell-intrinsic enzyme cytochrome P450 3A4 (CYP3A4) promotes tumor progression through epoxyeicosatrienoic acid biosynthesis. CYP3A4 localizes to mitochondria in estrogen receptor positive (ER+) breast cancer cells, where it is required for tumor growth. Structure-based design led to the discovery of N1-hexyl-N5-benzyl-biguanide (HBB), which binds to and inhibits CYP3A4 arachidonic acid epoxygenase activity. HBB was discovered to inhibit nuclear localization of RagC, an important component of the mTORC1 complex, which is required for biomass assembly in cancer. Since HBB restrains nuclear transport of regulatory proteins, we hypothesized that HBB modulates the nuclear pore complex (NPC) to influence nuclear transit of transcription factors, including estrogen receptor alpha (ERα). ER+ breast cancer cells (MCF-7 and ZR-75) were seeded on petri dishes and treated with vehicle or HBB for varied periods of time. Using immunofluorescence confocal microscopy, it was determined that HBB reduced nuclear translocation of ERα as well as RagC in both cell lines, correlating with reduced cell proliferation. This suggests that HBB can be utilized to inhibit the growth of

ER+ breast cancer cells by inhibiting nuclear transit of regulatory proteins through the NPC and may provide a new therapeutic strategy for combined ERα and mTORC1 inhibition in breast cancer therapy.

Presenter(s): Diego Morones, Knox College
Session: Poster P2.02
Title: Analysis of CRISPR-Cas loci and spacer conservation within Staphylococcus species
Advisor(s): Matthew Jones-Rhoades, Biology, Knox College
Co-author(s): Matthew Jones-Rhoades

Abstract: In bacteria and archaea, CRISPR arrays consist of tandem arrays of "spacers" that are derived from the DNA of bacteriophage and other foreign genetic elements. CRISPR arrays are thought to change quickly over evolutionary time, as new spacers are acquired and older spacers are lost. Since CRISPRs evolve so rapidly, it is common to observe highly divergent CRISPR arrays in genomes of very closely related organisms. Here we present a counterexample in which two strains of Staphylococcus, SA1 and SS1, have shared spacers despite being distantly related by most measures. These shared spacers are not present in other Staphylococcus genomes that are closely related to either SA1 or SS1, implying that a recent horizontal gene transfer event is responsible for the observed similarity of CRISPR spacers between SA1 and SS1.

Presenter(s): Neha Motwani, Knox College
Session: Poster P3.04
Title: Where should Adults with Congenital Heart Disease receive inpatient care?
Advisor(s): Angela Yetman, Pediatric Cardiology and Divisions of Cardiology and Cardiothoracic Surgery, University of Nebraska Medical Center
Co-author(s): Angela Yetman, Kim Duncan, Jonathan Cramer, Carolyn Coons, David Danford

Abstract: Background: Adults with congenital heart disease (ACHD) may be admitted to an adult or pediatric hospital for inpatient care. There are proponents of both systems. We sought to characterize a cohort of ACHD patients requiring hospitalization and determine the frequency and type of consultations required.

Methodology: A retrospective chart review of all inpatient records (2015-2019) was performed. Correlates of number of consultations, as well as unanticipated adverse outcomes were sought.

Results: During the period 2015-2019, there were 586 hospitalizations for 368 ACHD patients. There were 262 females (44%). Mean age at hospitalization was 39.1±13.7 years. Most patients were in AHA ACHD complexity class II (58%). The median length of stay was 5 days (1-117). Median number of consults per patient was 4 (0-15) including nephrology consults in 60%, infectious diseases in 59%, and gastroenterology in 33%. There were 40 (7%) unanticipated in-hospital adverse. Clinical correlates of greater number of consults included older age ($p<0.0001$), and longer length of stay ($p<0.0001$). Adverse outcome was not related to age ($p=0.37$), AHA complexity ($p=0.43$) or gender ($p=0.53$).

Conclusions: Adult congenital patients often have several non-cardiac co-morbidities. Need for other adult medical specialty input during cardiac hospitalizations is frequent.

Presenter(s): Julian Moulton, Colorado College
Session: Poster P1.09
Title: Metabolism of the spring field cricket Gryllus veletis during freezing, thawing and recovery
Advisor(s): Emilie Gray, Organismal Biology and Ecology, Colorado College
Co-author(s): Brent Sinclair, Kurtis Turnball

Abstract: Freeze-tolerant insects can survive a substantial proportion of their body water being converted to ice. However, the mechanisms underlying the capacity to prevent or recover from freeze-induced damage are poorly understood. I measured carbon dioxide (CO_2) production in the spring field cricket (Gryllus veletis) as a proxy for metabolic rate after freezing and thawing and compared the metabolic costs associated with recovery from freezing and chilling. I hypothesized that freezing and thawing do not induce active responses, and that long-term recovery from freezing is metabolically costly. I observed a burst of CO_2 release at the onset of freezing in all crickets that froze, and that the expulsion of CO_2 upon freezing is due to the liberation of CO_2 that was buffered in the hemolymph. Additionally, the metabolic rates of crickets that froze were elevated at 72 hours of recovery relative to crickets that had been chilled (but not frozen). Thus, recovery from freezing and the repair of freeze-induced damage is metabolically costly in G. veletis, and this cost persists for several days after thawing. Understanding how freeze-tolerant insects manage these energetic demands during recovery from freezing may reveal mechanisms underlying natural variation in insect freeze tolerance.

Presenter(s): Magdalena Murray, University of Chicago
Session: Poster P3.19
Title: DNA Damage Repair in Neuroblastoma
Advisor(s): Susan Cohn, Pediatrics, University of Chicago
Co-author(s): Alexandre Chlenski, Marija Dobratic, Helen Salwen, Susan Cohn

Abstract: Neuroblastoma is a cancer of the sympathetic nervous system. Previously, we showed a correlation between high Maternal Embryonic Leucine Zipper Kinase (MELK) expression and poor prognosis in neuroblastoma patients. We also demonstrated synergy between a MELK inhibitor (OTS167) and Camptothecin (CPT), a DNA damaging agent. In CPT-treated cells, OTS167 inhibited DNA damage repair (DDR), implicating MELK in DDR.
Recently, we showed that MELK physically interacts with MYCN, an oncogene frequently amplified in neuroblastoma, as well as with Enhancer of Zeste Homolog 2 (EZH2), a methyltransferase implicated in DDR.

To assess DDR efficiency, we treated cells with CPT to induce DNA damage and subsequently quantified levels of two DDR markers: phosphorylated histone H2AX and phosphorylated replication protein A (pRPA).
First, we genomically inhibited MELK using CRISPR-Cas9. We then treated MELK knockouts and controls with CPT. MELK knockouts exhibited lower levels of DDR markers.

Next, we pharmacologically inhibited EZH2 using an inhibitor, EPZ6438. Preliminary data indicate that EZH2 inhibition decreases levels of pRPA in CPT-treated cells.

Due to the lack of inhibitors, we overexpressed MYCN. CPT-treated cells overexpressing MYCN had increased levels of DDR markers compared to controls. All together, these results indicate that the MELK/EZH2/MYCN complex promotes neuroblastoma DDR.

Presenter(s): Lidija Namike, Macalester College
Session: Poster P2.05
Title: The effect of partisanship on environmental action
Advisor(s): Christie Manning, Environmental Science / Psychology, Macalester College
Co-author(s): Christie Manning

Abstract: The current study focuses on how personal and collective political identities shape how conversations on climate change are perceived. It aims to observe how participants' response to climate change is affected differently by implicit versus explicit mentions of climate change (e.g. phrasing it as "environmental destruction" versus "climate change"). Since the explicit phrase "climate change" has become the root of this often heated partisan debate, this research aims to observe the differences that occur in climate change belief and concern when the phrase is either implicitly or explicitly mentioned, whether it be by a Republican or a Democrat elite cue (Feldman & Hart, 2018).

It has been shown that the rift between Republican and Democrat climate change concern is not actually about climate change (as most Republicans do believe that climate change is a problem), but rather a result of partisan identity alliance (Van Boven et al., 2018). This research aims to break down and bypass the climate change phrasing barrier, and thus clarify individual perception. Our goal is to understand how to increase motivation to combat climate change in all individuals through message framing. We are particularly interested in examining how concern and motivation changes for self-identified Republicans/Conservatives.

Presenter(s): Melanie Nevins, St. Olaf College
Session: Poster P1.10
Title: MESP1 is Essential for Human Cardiovascular Development
Advisor(s): Sunny Chan, Division of Blood and Marrow Transplantation, Department of Pediatrics, University of Minnesota
Co-author(s): Jacqueline Penaloza

Abstract: Cardiomyocyte death following a heart attack can lead to heart failure and eventually death. With the advent of pluripotent stem cell technology, healthy cardiomyocytes can be grown in a lab and transplanted to repair the damaged heart. However, there is great variability in the efficiency of cardiomyocyte differentiation in existing protocols. A better understanding of transcription regulation will allow for its manipulation to improve the efficiency of cardiomyocyte differentiation across cell lines. We are studying the MESP family of genes, which have been implicated in mice as major players in cardiovascular development, by assessing the ability of MESP1 and MESP2 knockout human pluripotent stem cell lines to differentiate into cardiomyocytes and by determining the effects of reintroducing MESP1 into the knockout cells during differentiation.

Presenter(s): Nicholas Ornstein, University of Chicago
Session: Poster P1.16
Title: How do the mechanical properties of the skin shape our perception of texture?
Advisor(s): Sliman Bensmaia, Organismal Biology and Anatomy, University of Chicago
Co-author(s): Charles Greenspon

Abstract: We are exquisitely sensitive to texture: We can tell the difference between satin and silk and can discern features as small as 10 nanometers. While much is known about the neural mechanisms that mediate texture perception, the role of skin in shaping the textural percept

remains elusive. Indeed, many surfaces comprise compliant elements, which not only deform the skin but are themselves deformed by it, a mechanical interaction that is very difficult to characterize analytically. In the present study, we adopted an empirical approach to the problem. Specifically, we developed a transparent silicone elastomer gel that mimics the mechanical properties of human skin. We indented textured surfaces onto this elastomer and visualized in vivid detail the patterns of deformation produced in the elastomer by the surface using a laser profilometer. We then used these measurements to understand how the skin deforms when we interact with a textured surface and interpreted previously measured patterns of neuronal activity in the context of these hitherto invisible patterns of skin deformation. This study contributes to a growing literature on neuromechanics that seeks to elucidate how biomechanics – in this case of the skin – shape our perception of and interactions with the external world.

Presenter(s): Atreyo Pal, University of Chicago
Session: Oral II.D.4 (2:31)
Title: Understanding fin development may lead to mechanism behind the fin-to-limb transition
Advisor(s): Anindita Basu, Neil Shubin, Section of Genetic Medicine, Organismal and Evolutionary Biology, University of Chicago

Abstract: The homologous structures in tetrapod limbs and fish fins exhibit a range of shape diversity and have a shared evolutionary history. However, understanding of fin diversity and the fin-to-limb transition remain hampered by a lack of genomic and developmental studies of fins outside of model taxa. We performed a comparative developmental and transcriptomic study using high-throughput, droplet-based single cell RNA-sequencing (scRNA-seq) called Dropseq and leveraged morphological diversity between fin types across the two species zebrafish (Danio rerio) and little skate (Leucoraja erinacea) to study fin development. Implementation of trajectory inference in conjunction with scRNA-seq gave us a "developmental tree" or “Devtree” of the fin samples that combines genetic and cell differentiation information in a single figure. Based on these trees, we used common developmental patterns to draw conclusions about how disparate morphologies are built and learn the molecular mechanisms behind the fin-to-limb transition.

Presenter(s): Sarah Pan, University of Chicago
Session: Poster P3.08
Title: Toddlers’ Cognitive Skill and Active versus Observational Object Learning
Advisor(s): Amanda Woodward, Psychology, University of Chicago
Co-author(s): Natalie Brezack, Riley Abeles, Amanda Woodward

Abstract: While much of an infant’s early learning experience is through observing others perform actions, as children develop they may benefit from acting on objects themselves. However, few studies have compared active and observational learning against one another directly. A recent semi-naturalistic study found that when learning from a caregiver, toddlers’ active experience boosted learning, while viewing demonstrations did not.

Here, we experimentally examined whether active or observational teaching styles benefitted 22-26-month-olds’ complex object learning and learning transfer. 48 toddlers were taught to build one novel, multi-step toy through active experience and another through observational experience. Children were then tested on their learning of the taught toys and generalization

skills on similar toys. Toddlers' parents also taught them to use a toy, and children's cognitive skills were measured (Bayley Cognitive Scales). Analyses will compare children's active and observational learning to the instructional styles toddlers receive from their respective caregivers. We will also test whether children's cognitive skills affected learning from the instructional conditions. This study has implications for understanding how children learn to use objects, both experimentally and in everyday interactions with adults.

Presenter(s): Manik Reddy, Macalester College
Session: Poster P3.07
Title: Optimization of an in situ hybridization protocol for C. elegans embryos
Advisor(s): Mary Montgomery, Biology, Macalester College
Co-author(s): Mew Soisangwan, Mary Montgomery

Abstract: Early embryonic development in C. elegans is influenced by stage-specific asymmetric localization of key proteins and maternally transcribed mRNAs. However, the mechanisms by which the aforementioned spatial and temporal distributions are generated remain poorly understood. Since in situ hybridization (ISH) allows visualization of specific mRNAs within cells and tissues, an ISH protocol optimized for C. elegans embryos may help elucidate the expression patterns and post-transcriptional regulation mechanisms of critical developmental genes. We worked to optimize a C. elegans whole-mount embryo ISH protocol from Seydoux & Fire (1994) in order to improve tissue fixation and reduce non-specific background staining. ISH was performed with different combinations of fixative and primary antibody, using DNA probes specific to the mRNA of the early embryonic regulator mex-3. Three fixatives (3.7% formaldehyde, Histochoice™, or Streck™ fixative, which is no longer commercially available) and two primary antibodies (sheep anti-DIG-rhodamine Fab fragment and sheep anti-DIG-AP Fab fragment) were tested. Mex-3 mRNA localization detected by our modified procedures corresponded to previously reported mex-3 embryonic mRNA distributions (e.g. Draper et al. 1996). Cumulatively, our results indicate that optimal ISH in whole-mount embryos may be achieved by a combination of Histochoice™ fixation and anti-DIG-AP exposure.

Presenter(s): Ariel Roghair, Macalester College
Session: Poster P1.05
Title: Activation of Microglia and Astrocytes in the Retina Following Traumatic Brain Injury
Advisor(s): Alexander Bassuk,
Co-author(s): Lucy Evans, William Castonguay, Nicole Hehr, Anne-Sophie Wattiez, Brittany Todd, Polly Ferguson, Elizabeth Newell, Levi Sowers, Matt Harper, Alexander Bassuk

Abstract: Traumatic brain injury (TBI) causes about 30% of all injury-related deaths in the United States and those that survive suffer from permanent deficits including a range of visual dysfunctions. After the initial injury, ongoing inflammation causes tissue damage in the brain. As the retina is an extension of the central nervous system, we hypothesized that the retina would also experience inflammation after TBI injury. We utilized a blast TBI (bTBI) and weight drop (WD) mouse model to examine retinal inflammation after injury. A compressed air-driven shock tube system was used to expose mice to a blast pressure wave three times, or a weight was dropped vertically to the skull three times, to stimulate repetitive injury. RT-PCR revealed increased inflammatory cytokines (IL-1a, IL-1B, IL-6, and TNFa) four hours post bTBI when

compared to the shams. One-week post both blast and WD we observed morphological changes in microglia, indicating activation of the cells in response to injury. Additionally, astrocyte activation was seen throughout the retinal layers. This increase in retinal inflammatory cytokines in the acute period post injury could lead to the activation of pro-inflammatory microglia and astrocytes, which are currently being pharmacologically targeted to ameliorate the detrimental effects on vision.

Presenter(s): Roberth Anthony Rojas Chavez, Colorado College
Session: Poster P3.09
Title: The effects of natural competence on the spatiotemporal evolution of Acinetobacter on antibiotic landscapes
Advisor(s): C. Phoebe Lostroh, Molecular Biology, Colorado College
Co-author(s): C. Phoebe Lostroh

Abstract: Acinetobacter baylyi is capable of twitching motility and natural transformation using a Type IV pilus [1]. Natural transformation allows for foreign DNA acquisition, which helps drive evolution within a population [2].

We are using a spatiotemporal analysis in antibiotic landscapes to visualise the effects of natural competence in strain ADP1. We are observing evolution of tetracycline resistance using an adapted microbial evolution growth arena (MEGA)-plate in which very large dishes with substantial antibiotic gradients are inoculated with ADP1 at one end, allowing them to twitch and selecting for increasingly resistant mutants. To see an animation of our plate design, please see https://tinyurl.com/Megaplate2.

We are comparing the emergence of resistant mutants in wild type populations with that in comA populations because while cells lacking comA have a mild twitching defect, they are not at all transformable. ComA forms the inner membrane channel that allows DNA to enter the cytoplasm. We hypothesize that the evolution of comA mutants will likely be similar to that observed for non-transformable E. coli, whereas the evolution of wild type cells will be different because of the movement of genes that confer resistance.

Presenter(s): Natalie Sarver, Colorado College
Session: Poster 3.23
Title: Effect of Nutritional Signaling on Mating-Type Switching in O. polymorpha
Advisor(s): Sara J. Hanson
Co-author(s): Sara J. Hanson

Abstract: The response to nutritional signaling is a homeostatic mechanism in the function of cells in all organisms. Here, we examined the nutrient response of the yeast Ogataea polymorpha and its role in sexual processes. Haploid cells of O. polymorpha undergo mating-type switching, a process that causes a 19-kilobase DNA region to invert, placing either the MATa or MATa genes under centromeric repression of transcription. Nitrogen starvation induces this reversible change in the structure of a chromosome. Previous work demonstrated that in a nutrient-deprived media, O. polymorpha can undergo mating-type switching, while the addition of ammonium sulfate suppressed this response. We wanted to better understand the effect of nutritional signaling on mating-type switching by extracting DNA from O. polymorpha that had grown in media with other nitrogen sources, as well as media with rapamycin and

cyclic-AMP. Most nitrogen sources were found to suppress switching. The rapamycin and cyclic-AMP were shown to induce and suppress switching, respectively. These data provide insights into the specific signaling pathways that underlie the mating-type switching response in O. polymorpha.

Presenter(s): Yumino Sasaki, Washington University in St. Louis
Session: Poster P3.17
Title: Characterization of residues required for coupling of chromophore isomerization and biological activation in bacterial phytochromes
Advisor(s): Richard Vierstra, Biology, Washington University in St. Louis
Co-author(s): Ernest Burgie

Abstract: Phytochromes are photoreversible protein switches that regulate various photomorphogenic processes by interconverting between a red-light absorbing Pr state that is biologically inactive and an active far-red light absorbing Pfr state.

The phytochrome photosensory module comprises a sequential array of PAS, GAF, and PHY domains, where the GAF domain envelops the photoactive biliverdin chromophore, and a hairpin motif extends from the PHY domain to interact with the GAF domain. These regions harbor residues essential for propagating structural changes during photoconversion and maintaining stabilization of the Pr or Pfr states. Using the photosensory module of Deinococcus radiodurans bacterial phytochromes, site-directed mutations of residues within the hairpin motif were structurally assayed, identifying key determinants of the connection between chromophore isomerization and phytochrome activation. The phytochromes were found to conform to one of two space groups corresponding to the active or inactive forms. Mutants known to stabilize the Pfr state such as W451G, G452E, G453E, and F469W crystallized in the same space groups as the active wild type Pfr form even while the biliverdin chromophore was presumably in the Pr state, highlighting the sensitive balance to maintain either state and the appropriate coupling of structural states and photostates.

Presenter(s): Alexandra Shapiro, Colorado College
Session: Poster P2.09
Title: Cotyledon stomatal density differentiation and quantitative genetic analysis of seedling traits in Impatiens capensis ecotypes
Advisor(s): M. Shane Heschel, Organismal Biology and Ecology, Colorado College

Abstract: The contiguous distribution of Impatiens capensis, from New England to Colorado, indicates that this species has evolved to inhabit a wide variety of ecosystems. Physiological, morphological, and phenological plasticity in this species facilitate drought responses in these regionally specific ecotypes. These drought responses include changes in stomatal density, stomatal conductance, ABA production, and leaf growth. This study focuses on comparing stomatal density and conductance of Impatiens seedlings and their parents, respectively, from both Colorado and Pennsylvania populations, and includes a quantitative genetic analysis of Impatiens plants from both these populations. Stomatal density of cotyledons was measured using a Scanning Electron Microscope (SEM). Stomatal conductance was also measured on the parent plants of the seedlings used for stomatal density analysis. It was found that region was a predictor of stomatal density, but not of conductance. Contrary to previous studies on adult Impatiens, high stomatal densities in Colorado ecotypes indicate a hereditary drought

escape strategy in seedlings that is not correlated to transpiration rates of parents. The quantitative genetic analysis of seedling physiological traits here provides an indication of the evolutionary potential of progeny traits across the geographic range of this species.

Presenter(s): Isabel Shen, Washington University in St. Louis
Session: Oral II.F.3 (2:14)
Title: The Role of Fibroblast Growth Factor 2 and FGF Receptors 1 and 2 in Group 3 Pulmonary Hypertension
Advisor(s): David Ornitz, Developmental Biology, Washington University in St. Louis

Abstract: Group 3 pulmonary hypertension (PH), is caused by hypoxemia resulting from chronic obstructive pulmonary disease and bronchopulmonary dysplasia. Fibroblast Growth Factor 2 (FGF2) and FGF Receptors 1 and 2 (FGFR1/2) levels are elevated in PH patients and in mice exposed to hypoxia. Endothelial cell (EC) FGFR1/2 signaling is important for response to injury. We hypothesize that FGF2 and endothelial FGFR1/2 signaling promotes endothelial cell signals that protect against PH.

Mice that lack FGFR1/2 in endothelial cells (DCKO), or mice that can be induced to express a constitutively active FGFR1 in endothelial cells (caFGFR1) were challenged with hypoxia (10% O2) for 2 weeks, followed by cardiac catheterization to assess PH. Compared to control littermates, DCKO mice in hypoxia developed worse PH. Mice with endothelial overexpression of caFGFR1 showed catherization results similar to control mice in normoxia. Human umbilical vein endothelial cells (HUVECs) were placed in hypoxia (1% O2) for 48 hours and compared to normoxia controls. Hypoxia induced a smooth muscle cell (SMC) morphology whereas normoxia controls retained their cobblestone appearance, suggesting an endothelial-to-mesenchymal transition (EndoMT). SMC and EndoMT markers were elevated, while endothelial cell markers were decreased in hypoxia-challenged HUVECs cultured in FGF2-deficient media compared to media with FGF2.

We conclude that loss of endothelial FGFR1/2 worsens hypoxia induced PH in vivo and augments EndoMT in vitro. We show that overexpression of caFGFR1 in endothelial cells prevents hypoxia induced PH in vivo. Our data suggests that endothelial FGF signaling regulates EndoMT and protects against Group 3 PH, the opposite of what is reported in Group 1 PH.

Presenter(s): Victoria Shi, Washington University in St. Louis
Session: Oral II.D.2 (1:57)
Title: SERPINB3 Expression Protects Cervical Cancer Cells from Radiation Induced Cell Death
Advisor(s): Stephanie Markovina, Radiation Oncology, Washington University in St. Louis

Abstract: Previous literature has indicated elevated serum squamous cell carcinoma antigen (SCCA) levels as strong prognostic indicator for cervical cancer. While we have previously shown that CRISPR knock-out of SERPINB3 increases radiation sensitivity in cervical cancer cells, it is unknown if increased SERPINB3 expression protects tumor cells from cell death. We hypothesize that SCCA (SERPINB3) protects tumor cells from radiation-induced death by inhibiting lysosomal cysteine proteases. To test this, the SERPINB3-WT gene was inserted into two cervical cancer cell lines (C33A and SiHa) with low baseline SERPINB3 expression

through a constitutively expressed lentiviral vector. A mutant (SERPINB3-p14mut) gene was also inserted to see if radiation protection requires the protease inhibition function of SERPINB3, as this point mutant renders SERPINB3 incapable of inhibiting target proteases. Clonogenic survival assays were used to analyze the effect of the inserted genes on radiation resistance. In both cell lines, the SERPINB3-WT-expressing cells demonstrated a higher survival fraction than both control and p14-mutant-expressing cells, demonstrating radiation protection. No difference in surviving fraction between the control and mutant cells indicates the protease inhibition function of SERPINB3 is required. Our results suggest that targeting SERPINB3 represents a novel approach to improve treatment outcomes for patients with cervical cancer.

Presenter(s): Justine Shih, University of Chicago
Session: Poster P1.13
Title: Role of ASIC2b in Proprioception and Cognition
Advisor(s): Chih Cheng-Chen, Institute of Biomedical Sciences, Taipei, Taiwan
Co-author(s): Cheng-Han Lee, Robert Midence

Abstract: Acid-sensing ion channels, or ASICs, expressed in peripheral sensory neurons, play a variety of physiological roles in the body. Among the many types of ASICs, it was previously established that ASIC3 is involved in sensory mechanotransduction and contributes to cognitive function in the central nervous system. ASIC2, with two splice variants ASIC2a and ASIC2b, was also previously found to be involved with mechanotransduction, motivating research into whether ASIC2a or 2b plays roles in cognition and proprioception, the awareness of body position and movement. To understand how peripheral sensing is involved in central nervous system cognition, we hypothesize that ASIC2b may contribute to proprioception. My goal is to validate whether ASIC2b-/- mice show deficits in proprioception, motor function, or cognition by performing a series of behavioral assays.

In proprioceptive tasks, ASIC2b-/- mice showed a larger print length in gait analysis as well as a significant increase in foot faults on the grid walk, but normal behavior on the balance beam, indicating a proprioceptive defect. On the rotarod, male ASIC2b-/- mice displayed a lower latency to fall, indicating some motor coordination hinderance. In cognitive tasks, ASIC2b-/- mice spent a larger percent of the time in the central field and showed higher exploration rates in the open field test, but no sign of repetitive behavior in the marble burying test. Male ASIC2b-/- mice also showed a lack of preference for social novelty in the 3-chamber assay. Results seem to suggest anxiolytic and autism-like behavior. Taken together, the behavioral assays conducted paint a preliminary picture of the important role ASIC2b may play in proprioception, cognition, and motor coordination.

Presenter(s): Marit Simmons, Beloit College
Session: Poster P3.01
Title: Isolation of antibiotic-producing bacteria and capstone course design using the Tiny Earth research sequence
Advisor(s): Kristin Labby, Chemistry, Beloit College
Co-author(s): Krisin Labby, Koleman Lund, Brenda Martinez-Flores

Abstract: The prevalence of antibiotic-resistant pathogenic bacteria has become a global health threat and innovative approaches are now essential in combating these pathogens. The

development of new antibiotics through natural product chemistry— in which the substances naturally produced by bacteria are extracted and engineered into effective antibiotics— has emerged as a promising approach. Tiny Earth is an initiative which seeks to involve a wide network of college instructors and students in this type of preliminary antibiotic research, with the goal of crowdsourcing antibiotic discovery from soil microbes. In this study, the Tiny Earth research sequence was used to isolate 50 unique bacteria with antimicrobial properties, characterize them through 16s rRNA PCR and gene sequencing, and extract their secondary metabolites. Our discovery of new antibiotic-producing bacteria is an exciting addition to the known database of bacterial strains which may now be used in future antibiotic development. This research also involved the development of a curriculum plan for a new laboratory-based biochemistry capstone course which will be taught Spring semester of 2020 at Beloit College, centered around this research sequence. Protocols were optimized and adapted for classroom use and a preliminary course schedule and materials were prepared.

Presenter(s): Rachel Snodgrass, Grinnell College
Session: Poster P3.15
Title: Causes and consequences of hydrologic microrefuges in an arid-land annual plant
Advisor(s): Vincent Eckhart, Biology, Grinnell College

Abstract: Hydrologic microrefuges may expand the geographic extent of a species' range in arid regions by creating patches of suitable habitat in areas where the species would otherwise be unable to exist. I studied the effects of possible biotic (hydraulic redistribution by shrubs) and abiotic (runoff from exposed rock) sources of locally high soil water on plant density, physiological water status, stomatal conductance, and soil water potential in the southern Sierra Nevada annual plant, *Clarkia xantiana*, during the annual terminal drought in June. Overall, benefits of shrubs and rocks were more evident in populations near the arid eastern edge of the species' range, though effects were highly variable in direction and magnitude among populations. The rarity of strong effects on plant water relations, despite shrub- and rock-associated distributions, suggest that hydrologic refuge mechanisms operate mainly at life stages other than flowering. Diurnal cycles in soil water potential were more dramatic near shrubs, characteristic of hydraulic lift from deep soil, but they were offset in time from the simplest expectation. Findings reinforce the importance of including microenvironmental variation in species distribution models and projections, as well as identifying key mechanisms and life stages.

Presenter(s): Madison Stamos, University of Chicago
Session: Poster P3.16
Title: Pharmacokinetic Tail Analysis of Long-Acting PrEP in HIV-negative, Low-risk Individuals
Advisor(s): Deborah Donnell, Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center
Co-author(s): Madison Stamos, Brett Hanscom, Sue Li, Deborah Donnell

Abstract: HPTN077 was a phase 2a trial analyzing the safety and tolerability of long-acting cabotegravir (CAB-LA), an injectable form of PrEP, in low-risk, HIV-uninfected participants in the U.S., Malawi, Brazil, and South Africa. We analyzed tail phase (8-72 weeks post-terminal injection) log10 CAB-LA concentration elimination rates; persistent CAB-LA post-terminal injection could leave participants susceptible to drug-resistant mutations. We used a two-stage

least-squares regression, stratified by dosing schedule (DS) (DS1: n=46, DS2: n=43). First, we fit a log-linear regression with log10 concentration as the outcome and time since last injection (t) as the independent variable. Second, we ran a weighted least-squares regression with tail phase slope (coefficient on t) as the outcome against clinically relevant independent variables, weighted with the standard error of t. Women on birth control (BC) experienced slower CAB-LA elimination rates vs. women not on BC (DS1: 23.0-28.2ng/mL/week slower, DS2: 25.5-35.2ng/mL/week slower, $p<0.01$). Women not on BC had faster elimination in DS1 compared to men (30.3ng/mL/week faster, $p<0.01$), but not in DS2 (0.381ng/mL/week slower, $p>0.05$). This study provides evidence that CAB-LA elimination rate differences can be attributed to interactions between CAB-LA and BC, not sex. BC-CAB-LA interaction analyses will be incorporated into the phase 3 CAB-LA trial HPTN084.

Presenter(s): Nicholas Sucher, Carthage College
Session: Poster P2.06
Title: Transect-Free Transect Sampling of Coral Reefs in Roatán, Honduras
Advisor(s): Scott Hegrenes, Biology, Carthage College

Abstract: Transect sampling is a method of assessing the distribution and abundance of organisms along a physical, linear line placed along the ground. Due to conservation measures, this physical line cannot always be placed along the surface of the study area. This study attempted to acquire a sample along an invisible transect to assess the distribution of life on a protected coral reef, utilizing various depths as transects. Through the use of scuba diving, this study counted the presence of reef life forms along invisible transects along two reef walls in Roatán, Honduras. The species of focus in this study include the common sea fan, sea plumes, azure vase sponge and the blue chromis fish. This study occurred at a scuba-diving resort, which allowed for multiple transects to be applied on the same reef walls over the course of a week. The corals appear to have a reciprocal relationship with one another where the soft corals were of greater abundance in shallower depths and the hard corals were more abundant at greater depths. This study was not intended to study the spatial distribution of reef life, but instead was testing the feasibility and use of transect-free transect sampling.

Presenter(s): Skylar Sundquist, Hope College
Session: Poster P2.21
Title: Regulation of cellular proliferation by VACM-1/CUL5 is dependent on its posttranslational modifications by NEDD8
Advisor(s): Maria Burnatowska-Hledin, Biology and Chemistry, Hope College

Abstract: VACM-1/CUL5 acts as the scaffold protein in the E3 ligase complex in the ubiquitin proteasome system. The overexpression of VACM-1/CUL5 inhibits cellular proliferation, whereas inhibition of VACM-1/CUL5 expression induces cellular proliferation. The effect of VACM-1/CUL5 on cellular proliferation is dependent on its post-translational modification (PTM) by NEDD8 protein (neddylation). The relationship between NEDD8 and VACM-1/CUL5 is important for cell cycle regulation and offers a target for cancer therapy. VACM-1/CUL5 was mutated at the putative neddylation site Lysine (K) 724 and at three potential neddylation sites, K724, K727, and K728 (3K mutant). The expression of the K724 mutant induces cellular proliferation whereas expression of the 3K mutant does not affect cellular proliferation. Further analysis indicates that 3K VACM-1/CUL5 mutant is still neddylated. Current work focuses on

characterizing the mutant forms of VACM-1/CUL5 to determine if additional neddylation sites are present.

This work was supported by the Arnold and Mabel Beckman Foundation Scholar Award to S. Sundquist and by Schaap Endowed Fund for Undergraduate Research.

Presenter(s): Saman Tabatabaee Zavareh, University of Chicago
Session: Oral II.D.1 (1:40)
Title: Investigating the Contribution of Low-Complexity Domains to Repressive Activity of the ETS Transcription factor Yan
Advisor(s): Ilaria Rebay, Ben May Department for Cancer Research, University of Chicago

Abstract: Drosophila Melanogaster's Yan is a transcriptional repressor downstream of RTK signaling in the retinal development. The overexpression of Yan in the salivary glands of the fly, where it is not normally expressed, produces nuclear puncta characteristic of liquid-liquid phase separated condensates. Canonically, Yan aggregation has been attributed to its protein binding domain SAM, with which Yan homotypically polymerizes. Here, I try to investigate the role of low complexity domains (LCDs) in the biological activity of Yan. In the sequence of Yan, there are eight predicted LCDs. To assess the contribution of each Low complexity domain, ΔLCD mutants were created and their subcellular localization and repressive activity was observed in S2 cells. Using Luciferase transcription assay and immunofluorescent imaging, one LCD containing a polyglutamine stretch was detected that decreases Yan's nuclear stability. By expressing this mutant in the salivary glands of the fly, I hope to disrupt Yan's LCD interactions and observe the effects on Yan aggregation. Furthermore, by tuning the SAM affinity along with the LCD disruption, I would like to characterize the interplay between these two mechanisms of aggregation, and the significance of the presence of LCD interactions.

Presenter(s): Anchalee Tantiviramanond, Grinnell College
Session: Poster P2.15
Title: Tannins, Herbivory, and Petal-spot Polymorphism
Advisor(s): Vince Eckhart, Biology, Grinnell College
Co-author(s): Vince Eckhart

Abstract: Flower color evolution is not only affected by animal pollinator behavior, but also by indirect associations with other fitness components. *Clarkia xantiana* ssp. *xantiana* is polymorphic for spotted and unspotted petals. This polymorphism is thought to be maintained by various selective pressures, including herbivory. Spotted individuals appear to contain higher tannin concentrations than unspotted individuals; tannins may reduce palatability and thus act as a defense against herbivory. To identify links between petal-spotting polymorphism, tissue tannin concentrations, and mammal herbivory, I carried out inflorescence translocation experiments in the field and analyzed tannin concentrations in fruit tissue samples. The translocation experiments were conducted between six populations in the field, where inflorescences were placed in their site of origin as well as a site beyond the range edge where herbivory rates are notably high. At home sites, herbivores showed no significant preference for either phenotype. At the cafeteria site, overall herbivore damage and petal-clipping by leaf-cutter bees were associated with unspotted phenotypes. Fruits from spotted individuals

contained significantly higher tannin concentrations than those from unspotted individuals, though this association was not absolute. Full analysis of whether tannins act as a defense against herbivory must wait until the remaining 83% of samples receive assays.

Presenter(s): Irein Thomas, Knox College
Session: Oral I.C.1 (8:30)
Title: Does moral framing of abortion increase highly-identified liberals' willingness to aggress against a conservative?
Advisor(s): Tim Kasser, Psychology, Knox College
Co-author(s): Tim Kasser

Abstract: Research has shown that liberals and conservatives favor different moral foundations and that liberals primarily care about harm-related issues. The current study examined how framing abortion as harmful would affect highly-identified liberals' willingness to aggress against a conservative in a moral disagreement. Participants (N =19) were asked to respond to either a harm-framed or neutral prompt on their opinion on women's access to abortion, and afterwards, participants received a conservative's response to the prompt. Participants were given an opportunity to aggress against the conservative in a taste test by dropping hot sauce into a cup of water that the conservative would have to drink. Results indicate that there was not a significant difference between groups in aggression towards the conservative, $t(19) = -0.105$, $p = .108$.

Presenter(s): Steven Traeger, Lawrence University
Session: Oral AM I.C.3 (9:04)
Title: Early changes in innate and adaptive immunity are associated with resistance to ileocolitis
Advisor(s): Calvin Williams, Department of Pediatrics, Medical College of Wisconsin
Co-author(s): Calvin Williams, Christopher DeCiantis

Abstract: Following birth, the gastrointestinal tract becomes rapidly colonized with microbes. Innate and adaptive immune responses develop simultaneously, resulting in stable bacterial communities and a balanced inflammatory response that protects the host from tissue invasion. Perturbations in these developmental processes that occur during a critical early time window create dysbiosis and may lead to disease susceptibility. We used a new spontaneous mouse model of ileocolitis, where only half of the mice develop disease, to examine biomarkers of innate and adaptive immune responses and to correlate these with outcome. In 100 day old mice, chromogenic in situ hybridization (RNAscope) was used to quantify and localize gut expression of the genes encoding the antimicrobial peptides Reg3g and Lyz1. Sections of the large and small bowel were also stained for IgA expression. Early results indicate that there are clear differences in both the pattern and level of expression of Reg3g and IgA which correlate with disease resistance. These data support the notion that early life immune responses that originate in the gastrointestinal tract and shape the microbiome are prerequisites for a healthy gut.

Presenter(s): Hiywot Tulu, Macalester College
Session: Poster P3.05
Title: The Impact of Abca7 p.A693S mutation on Alzheimer's disease pathology
Advisor(s): Takahisa Kanekiyo, Department of Neuroscience, Mayo Clinic

Abstract: Alzheimer's disease (AD) is the leading cause for dementia characterized by amyloid-β (Aβ) deposition, neurofibrillary tangle formation, and neurodegeneration. Recent genome-wide association studies (GWAS) and genome sequencing studies identified the associations of ABCA7 gene variants with the increased risk for AD. While ATP-binding cassette subfamily A member 7 (ABCA7) mainly regulates the homeostasis of phospholipids and cholesterol, accumulating evidence has demonstrated that ABCA7 loss of function leads to the exacerbated Aβ pathology. In this study, the functional effects of an AD risk Abca7 p.A693S mutation as well as Abca7 deficiency on AD pathology were investigated in amyloid AD model 5xFAD mice. By crossing Abca7 knockout mice or Abca7 p.A693S knockin mice with 5xFAD mice, we investigated Aβ pathology and microglial activation in the hippocampus and cortex at the age of 3-4 months. When amyloid plaque burden and brain Aβ levels were assessed, we found that neither Abca7 p.A693S mutation nor Abca7 deficiency affected Aβ pathologies in 5xFAD mouse brains. Nonetheless, Iba-1 immunostaining revealed that Abca7 p.A693S mutation, but not Abca7 deficiency, accelerated microglial activation in those mice. Together, our results suggest that Abca7 p.A693S mutation and Abca7 deficiency may contribute to the increased AD risk through different pathogenic pathways.

Presenter(s): Bailey Underwood, Lawrence University
Session: Oral AM I.A.1 (8:30)
Title: 5-HT Receptor Subtype May Mediate Anxiety Response and CRH Production in Hypothalamus
Advisor(s): Nancy Wall, Biology, Lawrence University
Co-author(s): Nancy Wall

Abstract: Increased levels of corticotropin releasing hormone (CRH) are associated with anxiety, as are decreased levels of serotonin (5-HT). Do serotonin levels influence CRH production and anxiety? The ventral hippocampus is associated with anxiety behavior, contains cells expressing 5-HT receptors (including 5HT7R), and extends axons into CRH producing regions of the hypothalamus. Therefore, 5-HT responsive neurons may play a role in the anxiety response and CRH production. To analyze how 5-HT may influence anxiety, 5dpf Danio rerio were examined following application of a 5-HT7R agonist (AS-19) and antagonist (SB-258179). A C-turn assay was used to assess physical manifestations of anxiety response. It is hypothesized that separate application of 5-HT7R agonist and antagonist should result in a decrease and increase in the anxiety response, respectively. Furthermore, it is hypothesized CRH levels should increase or decrease in an inverse manner.

Presenter(s): Shreeja Vachhani, Lawrence University
Session: Poster AM P1.17
Title: Neural correlates of maternal affection and empathic concern
Advisor(s): Sasha L. Sommerfeldt , Department of Psychology , UW-Madison
Co-author(s): Sasha L. Sommerfeldt, Richard J. Davidson

Abstract: This study investigated the neural correlates of maternal affection and empathic concern, considering that empathy is a crucial component of human emotional experience and social interaction. Based on previous research, empathic concern is an adaptive trait that is positively correlated with maternal affection. We were interested in studying changes in hippocampal volume (part of the limbic system) since maternal affection likely influences the child's empathy through changes in brain regions. The role of the hippocampus towards social emotions such as empathy has not been systematically investigated thus far. We used the Midlife in the United States (MIDUS) dataset (N = 138) in relation to our two measures: maternal affection and empathic concern. Data were collected through self-administered questionnaires on both measures. For the hippocampal volume, MRI data were collected and processed through FreeSurfer. We found no significant interaction between maternal affection and empathic concern, maternal affection and child's hippocampus, and child's hippocampal volume and their level of empathic concern. Additionally, there were no gender interactions. The lack of significance may be explained by a low sample size, unreliability of participants' self-reports and the exclusion of other brain regions. Further research could look into other brain regions involved in empathy development.

Presenter(s): Emily Vierling, Colorado College
Session: Poster P2.12
Title: Differences in call-types across the Northern Resident Orca matrilineal groups
Advisor(s): Emilie Gray, Organismal Biology and Ecology, Colorado College

Abstract: This study isolated acoustics used by the Northern Resident Orca matrilines to determine whether or not specific call types had evolved to differentiate across matrilines. Six different matrilines were selected to be acoustically analyzed: the A30s and A12s, part of the A1 pod from the A Clan, the A23s and A25s, part of the A5 pod from the A clan and the I15s and the I35s, part of the GI pod from the G Clan. 22 different call-types were selected for analysis and 44 different call samples (two samples for each call-type) were gathered from the six different matrilines. The call samples were collected at OrcaLab, a small land-based whale research station on Hanson Island, BC, from six different hydrophones covering 61 square kilometers of recordable space in the Johnstone Strait area. Calls were then categorized, inputted into Audacity, and their average frequency and average call-length were calculated. Major differences were observed between the A30 and A12 N3 calls and between the I15 and I35 pings, suggesting those two call-types have evolved to become distinct to their matrilineal groups. The other calls studied do not show substantial differences and minor variances could be explained by sample error during collection.

Presenter(s): Anna Von Duyke, St. Olaf College
Session: Poster P3.13
Title: Factors relating to Common Eider nest success and failure in Arctic Alaska
Advisor(s): Beth Pettitt, Biology, St. Olaf College
Co-author(s): Rebecca McGuire

Abstract: Common Eiders (*Somateria mollissima*) occupy a rapidly changing arctic environment and are more closely tied to arctic marine habitats than any other sea duck. From June 19 to August 8, 2019, Common Eider nests (*n* = 417) were monitored by the Wildlife Conservation Society's Arctic Beringia program as an important part of efforts to conserve and manage this species and its habitat. This work occurred on barrier islands near Icy Cape, AK at Kasegaluk Lagoon. Nests were visually monitored after being initially found through a systematic search of the islands. Nest success was determined from physical evidence found in the nest (e.g., hatched eggs). Overall, this nesting colony had a successful breeding season, with a total of 87% (*n* = 369) of monitored nests successfully fledging young. Of the remaining 48 nests, the fate of 19 could not be determined based on the available evidence, whereas 29 appeared to have failed due to predation, abandonment, or weather. We assessed several factors that may be associated with breeding success, including observer effects (nest checks, cameras), nesting density, proximity to water, and predator density.

Presenter(s): Maicy Vossen, Gustavus Adolphus College
Session: Poster P3.18
Title: CaMad2 promotes multiple aspects of genome stability beyond its direct function in chromosome segregation
Advisor(s): Laura S. Burrack, Biology, Gustavus Adolphus College
Co-author(s): Hanaa M. Alhosawi, Katherine J. Aney, and Laura S. Burrack

Abstract: Cells undergo a highly regulated cell division process called mitosis. During mitosis, the DNA-containing chromosomes copy, and the two copies are pulled into the resulting cells by microtubules that attach to a complex at the center of the chromosomes, called the kinetochore. Mad2 is a protein that is a central component of the spindle assembly checkpoint required for accurate chromosome segregation. Additionally, in some organisms, Mad2 has roles in preventing mutations and recombination through DNA damage responses. In the fungal pathogen Candida albicans, CaMad2 has previously been shown to be required for accurate chromosome segregation, survival in high levels of hydrogen peroxide, and virulence in a mouse model of infection. In this work, we showed that CaMad2 promotes genome stability through its well-characterized role in promoting accurate chromosome segregation as well as through reducing smaller scale chromosome changes due to recombination and DNA damage repair. Deletion of MAD2 decreased cell growth, increased marker loss rates, increased sensitivity to microtubule-destabilizing drugs, and increased sensitivity to DNA damage inducing treatments. Furthermore, deletion of MAD2 increases growth on fluconazole, and fluconazole treatment elevates whole chromosome loss rates in the mad2D/D strain suggesting that CaMad2 may be important for preventing fluconazole resistance via aneuploidy.

Presenter(s): Jillian Ward, Lawrence University
Session: Poster AM P2.20
Title: Constructing an ANG and RI Double-Knockdown in dCas9 HeLa Cells
Advisor(s): Kimberly Dickson, Biology, Lawrence University
Co-author(s): Claire Vinopal

Abstract: Ribonuclease inhibitor (RI) is a protein that binds to ribonucleases and renders them inactive. The activity of angiogenin (ANG), a ribonuclease with implications in cancer and neurodegenerative diseases, needs to be studied, but RI can interfere. The aim of this work is to construct double-knockdown HeLa cells with sgRNAs to both ANG and RI to allow mutant ANG to be introduced and studied without inhibition by RI. Herein I have evaluated the efficacy of guide RNAs to ANG and RI in knockdown cells. Reduction in gene expression was analyzed using RT-qPCR and using Western Blots. ANG and RI sgRNAs showed varying degrees of knockdown. Current work is aimed at further quantification of decreases of protein expression in ANG and RI. We have identified highly effective sgRNAs that will be co-expressed in HeLa cells.

Presenter(s): Emily Watters, University of Chicago
Session: Poster P2.16
Title: Similarities and differences between *Ulva sp., Gracilaria sp*., and seawater's microbiome in Little Sippewissett Marsh
Advisor(s): Elena Lopez Peredo, The Ecosystems Center, Marine Biological Laboratory

Abstract: Microbial communities are diverse and dynamic forces within ecosystems, and microbial composition differs based on its host organism and environment. As such, this project seeks to further understand the microbiome of seawater, *Gracilaria sp*., and *Ulva sp.* from the marsh in Little Sippewissett Marsh in Falmouth, Massachusetts. I hypothesized that seawater will have more richness and phylogenetic diversity than both genera of algae because of the seawater's flow and freestanding environment, and that *Ulva sp.* and *Gracilaria sp.* will be more even than the seawater because of its rooted environment. However, using 16S sequencing and data analysis in Qiime2, I found that microbial community composition between seawater, *Gracilaria sp.*, and *Ulva sp.* might be more similar than originally thought. Specifically, there was no significant difference in the richness, phylogenetic diversity, and evenness between *Ulva sp.* and *Gracilaria sp.*, and only marginally significant differences between the seawater and both genera of algae.

Presenter(s): Arielle Weinstein, University of Chicago
Session: Poster P1.19
Title: The evolution of allosteric inhibition in bacterial citrate synthase
Advisor(s): Joseph W. Thornton, Department of Ecology and Evolution, University of Chicago
Co-author(s): Georg K.A. Hochberg, Joseph W. Thornton

Abstract: Enzymes allosterically regulated by the binding of effector molecules are observed across a range of protein families, but the genetic basis of allostery and how it evolved are poorly understood. The goal of this project is to trace the evolution and determine the genetic basis of allosteric inhibition in bacterial citrate synthase (CS) by the effector molecule NADH. CS are ubiquitous enzymes that catalyze the first reaction of the Krebs cycle, and in most Gram-negative bacteria, are homohexamers arranged as triangular rings of dimers. Some of

these hexamers are allosterically inhibited by NADH. Using ancestral sequence reconstruction, we experimentally characterized ancient CS and identified the phylogenetic interval over which CS evolved allosteric inhibition by NADH. To determine which of the 42 amino acid substitutions that occurred along this interval are necessary for allostery, we reverted groups of residues in the allosteric ancestor to the sites of the non-allosteric ancestor. We found that no more than 14 substitutions are necessary for CS to be inhibited by NADH. We are currently investigating whether these same substitution groups confer NADH sensitivity to the non-allosteric ancestor. This project is expected to provide the first detailed explanation of the evolution of allostery by small-molecule binding.

Presenter(s): Eleanor Wettstein, Macalester College
Session: Oral II.F.2 (1:57)
Title: Plakoglobin as a candidate gene for Wnt signaling misregulation in Arrhythmogenic Right Ventricular Cardiomyopathy
Advisor(s): Randy Daughters, Biology, Macalester College

Abstract: Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC) is a genetic disease characterized by fibrofatty replacement of heart muscle, resulting in cardiac dysfunction. Several genes have been found with pathogenic variants that can cause ARVC. These genes encode proteins involved in desmosomes, specialized junctions that facilitate intercellular connections. Breakdown of desmosomes is thought to cause nuclear relocalization of the desmosomal protein plakoglobin (JUP), which may interfere with the Wnt pathway – a signaling pathway that regulates several crucial cellular processes. To model the desmosomal dysfunction of ARVC, we used induced pluripotent stem cells to generate cardiomyocytes in vitro and transfected them with a desmoplakin (DSP) knockdown plasmid. We collected cytoplasmic and nuclear protein from control and DSP knockdown cardiomyocytes, and assessed JUP for nucleocytoplasmic distribution via Western blot and immunostaining methods. To determine the effect on the Wnt pathway, we quantified Wnt target genes involved in adipogenesis using real time quantitative polymerase chain reaction (qPCR). Compared to control cardiomyocytes, those with desmosome knockdown exhibited irregular JUP localization patterns and increased expression of adipogenic genes. These results suggest that pursuing the relationship between desmosome integrity and plakoglobin localization will facilitate better understanding of molecular mechanisms underlying ARVC and potentially lead to identification of therapeutic targets.

Presenter(s): Alicia Wilkening, Washington University in St. Louis
Session: Poster P2.14
Title: Epigenetic Dynamics in Pigment Cell Fate
Advisor(s): Ting Wang, Genetics, Washington University in St. Louis
Co-author(s): Hyo Sik Jang, Yujie Chen, Jiaxin Ge, Mikayla Choi, Rebecca Lowdon, Hyungjoo Lee, Yiran Hou, Stephen L. Johnson, Ting Wang

Abstract: Resolving the genetic and epigenetic forces that mold a pluripotent stem cell into the diverse cell types in adult organisms is a longstanding goal of developmental biology. In zebrafish (Danio rerio), neural crest cells are multipotent cells that differentiate into numerous morphologically distinct cells, including pigment cells. Previous work from our lab analyzed epigenetic dynamics, DNA methylation and chromatin accessibility across pigment cell differentiation, and identified transcription factors and enhancer-like regions possibly

responsible for driving iridophore (reflective pigment cells) cell fate. With a CRISPR/Cas9 knock out, we identified one transcription factor, alx4a, necessary for iridophore development. On-going work uses an enhancer assay to validate predicted enhancer-like regions, defined as cis-acting regulatory regions that increase transcription of nearby genes. In summary, we identify one transcription factor necessary for iridophore development, alx4a, as well as many putative enhancer-like regions, which we are in the process of validating. While we observe that alx4a interacts with pigment cell development in D. rerio, the human ortholog is associated with craniofacial and bone defects. Thus, our results demonstrate a previously unrecognized functional diversification of a conserved developmental system, shedding light on how the flexibility of these developmental systems aided in the evolution of life's vast diversity.

Presenter(s): Rose Williams, Beloit College
Session: Poster P1.03
Title: Automated analysis of human intracranial EEGs for seizure detection in epilepsy
Advisor(s): Rachel A Bergstrom, Biology, Beloit College
Co-author(s): Chelsea Coleman, Rie Kaneko

Abstract: The diagnosis of epilepsy can be confirmed with an electroencephalogram (EEG). Normal brain activity is shown as a fairly constant waveform, with small changes in frequency and amplitude. Abnormal activity is characterized as drastic changes in amplitude and or frequency for several seconds to minutes. Currently, EEGs are analyzed by doctors manually. This process has a low inter-rater reliability and is time consuming. We aim to validate an automated method to analyze epileptic EEGs, ultimately improving the precision, accuracy, and speed of EEG analysis. This allows for a shortened diagnosis time. A code developed in Matlab first sets a baseline of the normal frequency and amplitude for each channel individually. The signal is then compared to this threshold and any outlier events are categorized into either seizure, spike, or abnormal. This algorithm was shown to be successful in identifying abnormal epilepsy-related signal in a mouse model. We applied this same algorithm to a human model using intracranial EEG data obtained through IEEG.org, specifically Mayo Clinic patient 038. The algorithm has shown an ability to detect seizures, but it is not ready for clinical use and is in need for further optimization.

Presenter(s): Melissa Wood, Knox College
Session: Oral I.B.2 (8:47)
Title: Evidence of local adaptation in Helianthus annuus L. revealed through transcript mapping
Advisor(s): Mark Welch, Department of Biological Sciences, Mississippi State University
Co-author(s): Andy Perkins, Mark Welch

Abstract: Helianthus annuus L., known as the common sunflower, has many applications in agriculture as a crop for its seed, oil, forage for livestock, and aesthetics. It is grown across many latitudes, which makes it an ideal plant for studying genetic variation, and thus phenotypic variation between populations spanning different geographical and climatic regions. Heritable differences such as growth rate, leaf size and bloom time are observed in changing latitudes. We obtained high quality RNA-seq data from 95 individual sunflowers from a total of 6 distinct populations at 2 different latitudes, Oklahoma and Kansas, grown in a common garden experiment. Using read coverage tables and a differential expression plot created in mapping these data to the sunflower reference genome, differences between the transcriptomes and

gene expression of the two sets of populations were analyzed. Transcriptomic variation observed in this study may, upon further investigation, lead to a deeper understanding of genetic adaptation and selection for H. annuus populations spanning many climates.

Presenter(s): Xinrui Yang, Lawrence University
Session: Oral AM I.B.3 (9:04)
Title: Employing T cell subtyping to predict drug resistances and prognoses in DLBCL patients
Advisor(s): Mu Yang, , Sichuan Cancer Hospital & Institute

Abstract: Diffuse Large B Cell Lymphoma (DLBCL) is a common non-Hodgkin lymphoma (NHL). Constituting around 30% - 40% of all reported NHL cases worldwide, DLBCL is characterized as a malignant cancer where patients would often experience rapid tumor progression at multiple nodal or extranodal sites. Currently, treatments of DLBCL patients rely on blood infusion of R-CHOP, a rituximab based immunochemotherapy plan. However, besides experiencing heavy side effects from therapy, DLBCL patients are also suffering from ineffectiveness of R-CHOP. Studies report that over 30% of the DLBCL patients experienced either ineffective treatments or quick relapses following administrations.
From the peripheral blood of patients, I utilized flow cytometry to quantify the percentage of effector, memory, memory precursor and effector memory T cells within CD8 cells as well as helper 1, helper 2 and regulatory T cells within CD4 cells. By monitoring the fluctuations of T cell percentages along the R-CHOP treatment and combining this data with clinical feedback, I aim to establish a mathematical model for predicting R-CHOP effectiveness, and potentially, prognoses for DLBCL patients.

Presenter(s): Yutong Zou and Thomas Diaz, Hope College
Session: Poster P1.23
Title: Hazelnuts: Genetic Relationships and Secondary Compounds for Cancer Treatment
Advisor(s): Jianhua Li, Biology, Hope College
Co-author(s): Jianhua Li, Kenneth Brown, Brittany Henkin, Thomas Diaz, Yutong Zou

Abstract: Paclitaxel is a cytotoxic chemotherapy drug, it is originally found in Taxus brevifolia. It is used to fight against breast, ovarian, lung and many other solid carcinoma. Due to its use in treating various cancers, the demand for this drug has been increased throughout the years. The way that taxol is traditionally extracted, people have to take the entire tree apart and extract from the bark. On average, one tree only produces one dose of taxol. Because of the complexity of the extraction procedure, taxol is very expensive on the market. Therefore, due to the high demand and the price of this drug, people have been seeking other ways to produce taxol. Recent studies have presented that people have successfully extracted taxol from the shell and the leaves of Corylus avellana. Because hazelnuts are more widely available and the shells and leaves are byproducts for hazelnut production, it is both an inexpensive and eco-friendly way to extract taxol. Our research focuses on discovering more species in Corylus that possibly contain taxol. Based on our results, we were able to detect paclitaxel from leaves of four species of Corylus and the taxol concentrations are similar to Taxus brevifolia. However, further analysis are needed to verify the presents and quantity with the amount of paclitaxel in Corylus.

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