The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 10 & 11, 2017
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 10

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	**Introduction, Welcome and Activity - Young Scientist Program**	
8:00 pm	**Keynote Address** **Dr. Guatam Dantas** Associate Professor of Pathology and Immunology Washington University in St. Louis School of Medicine *Combating Antibiotic Resistant Superbugs Across Diverse Habitats*	
Following lecture	**Group Picture**	**EPNEC**

Saturday, November 11

Begins at 7:00 am	**Breakfast for Hotel Guests** *If checking out, luggage can be stored at EPNEC*	**The Parkway Hotel**
7:30 am	**Breakfast for Wash U undergraduate presenters and graduate student moderators**	**EPNEC 308**
8:20 am – 8:40am	**Set-up for poster session 1** **Check computer set-up for oral presentations**	**EPNEC Great Room B**
8:50 am – 9:50 am **9:50 am**	**Poster Session P1** **Remove posters**	**Great Room B**
9:50 am - 10:10 am	**Break**	**Lobby**
10:10 am -11:30 am	**Oral Presentations of Student Papers** Session A: (4) Session B: (4) Session C: (4)	**EPNEC** Great Room A Seminar Room A Seminar Room B

11:30 am– 11:50 am	**Pick up box lunch** *Take lunch with you to the workshop of your choice*	**EPNEC Lobby**
11:50 am – 12:40 pm	***Applying to Graduate School*** ***Graduate Student Panel*** ***Washington University in St. Louis*** *Moderator: Dr. John Russell* *Interim Associate Dean of Graduate Education* **Graduate Student Panelists** Kelsy Cotto, Mercer University Michael Fitzpatrick, Grinnell College Andrew Menssen, St. Olaf College Jasmin Sponagel, Mannheim University	**Seminar Room B**
11:50 am – 12:40 pm	***Careers at Liberal Arts Colleges*** **Consortium Faculty Members** Nancy Wall, Lawrence College James Shulte, Beloit College Vince Eckhart, Grinnell College Sara Hanson, Colorado College	**Seminar Room A**
12:40 pm – 1:00 pm	**Break** **Set-up posters for session P2**	**Lobby** **Great Room B**
1:00 pm – 2:00 pm **2:00 pm**	**Poster Session P2** **Remove posters**	**Great Room B**
2:00 pm – 2:20 pm	**Break, Check computer set-up for oral presentations in respective rooms**	**Lobby**
2:20 pm – 3:20 pm	**Oral Presentations of Student Papers** Session D: (3) Session E: (3) Session F: (3)	**EPNEC** Great Room A Seminar Room A Seminar Room B
3:20 pm -3:40 pm	**Break** **Set-up for poster session P3**	**Lobby** **Great Room B**
3:40 pm – 4:40 pm **4:40 pm**	**Poster Session P3** **Remove posters**	**Great Room B**
4:40 pm – 5:00 pm	**Meeting Concludes** Complete evaluations – available online Boxed dinners to go	**EPNEC Lobby**

2017 Keynote Lecture: *Combating Antibiotic Resistant Superbugs Across Diverse Habitats*

Gautam Dantas, PhD
Associate Professor
Dept. of Pathology and Immunology, Dept. of Biomedical Engineering, Dept. of Molecular Microbiology, Center for Genome Sciences & Systems Biology
Washington University School of Medicine, Saint Louis

ABSTRACT: Antibiotic resistant infections currently claim over 700,000 lives globally. If current trends in resistance continue unchecked, this toll is projected to bloom to 10 million annual deaths by 2050, encoding a cumulative loss of $150 trillion to the global economy. While the most acute effects of increasing antibiotic resistance in pathogens are observed in clinical settings, it is becoming increasingly clear that the evolution and transmission dynamics of resistance gene dissemination is an ecological problem. Indeed, steady use and abuse of antibiotics over the past century in food animals, humans, and the environment has provided substantial selective pressure for enrichment of resistance genotypes in each of their associated microbiomes. An over-reliance on culture-based methods, the standard in the study of clinical resistance, has vastly underestimated these reservoirs of resistance genes (or 'resistomes'). To address this issue, we have recently developed high-throughput metagenomic functional selections, aided by next-generation sequencing, to characterize resistomes encoded by the microbiota of humans, animals, soils, and built-environments. By combining these analyses with 16S amplicon sequencing and deep shotgun sequencing, we model the impact of various anthropogenic perturbations on the transmission and evolutionary dynamics of microbial communities and their resistomes across time and habitats. Hundreds of resistance genes we identify from specific taxa in these different microbial communities are identical to resistance genes found in major human pathogens, indicating recent genetic exchange between these microbes. We also find thousands of functionally validated resistance genes which are genetically novel, but flanked by genes involved in horizontal gene transfer, including transposases and integrases. Together, these findings highlight the substantial antibiotic resistome encoded by microbes from diverse environments, which is available for exchange with pathogens, with the potential to severely exacerbate the problems with clinical resistance.

Dr. Dantas was awared a BA dgree in biology and chemistry from Macalester College in 2000. He received his PhD in biochemistry from the University of Washington under the guidance of Dr. David Baker, and post-doctoral training in microbial genomics from Harvard Medical School under the guidance of Dr. George Church. Dr. Dantas's research interests and training lie at the interface of microbial genomics, synthetic biology, systems biology, and computational biology. His current research focuses on understanding the evolution and exchange of antibiotic resistance amongst diverse microbial communities, on engineering improved probiotics to treat gastrointestinal disorders, and on engineering microbial catalysts to produce value chemicals such as biofuels. He is a recipient of the AAAS Newcomb Cleveland Prize, the Harvard University Certificate for Distinction in Teaching, the NIH Director's New Innovator Award, the Kenneth Rainin Foundation Breakthrough Award, the Edward Mallinckrodt Jr. Foundation Scholar Award, and the Academy of Science – St Louis Innovator Award. More information about the Dantas Lab can be found at http://www.dantaslab.org.

2017 Janet Andersen Lecture:

Research Without Borders: Research as Service

Professor Julie Legler

Professor of Statistics and Statistics Program Director
Department of Mathematics, Statistics and Computer Science
St. Olaf College

Abstract: Most of us would like to live a meaningful life; we'd like to be involved in work which makes the world a better place. When we think about lives that improve the world, we tend to think of people involved in heroic ventures such as Doctors Without Borders or the Peace Corps. However, researchers also play a critical role in dealing with crises. Here in the U.S., over 65,000 people overdosed on opioids this past year. Service providers such as social workers and ER doctors respond directly to this overwhelming epidemic, however researchers are working indirectly to battle it. At St. Olaf, student researchers and their mentor psychologist Shelly Dickinson are injecting rats with alcohol and cocaine to understand neuropharmacological mechanisms of drug abuse. Student researchers, like you, also have the potential to address pressing problems and arrive at answers that can contribute directly, or indirectly, to improve the world. Research can be a career that will provide you meaningful work for a lifetime

About Professor Legler: After completion of her Sc.D. in Biostatistics at the Harvard School of Public Health, Dr. Julie Legler spent 8 years with the National Institute of Health where much of her work was with the Cancer Surveillance Research Program. A colleague recalls that "Upon arriving at St. Olaf in 2001, she believed, rightfully, that undergraduate statistics students could (should) work in collaborative, interdisciplinary research teams modeled on the type she knew so well from her work at the NIH." Since then Julie has received almost $3 million from National Science Foundation grants to create and sustain the St. Olaf Center for Interdisciplinary Research (CIR). The CIR has provided a structure in which hundreds of students have been able to engage in meaningful – and often life changing – collaborative research with faculty and other students. While many projects are broadly health related, they have ranged from biology, psychology, and neuroscience to economics and political science, as well as many other areas. Julie herself has been personally involved in dozens of undergraduate research projects, including international collaborations with entities such as the World Health Organization in Geneva. Julie's work to inspire the next generation of leaders in STEM is exceptional.

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 of Award	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

Oral Sessions Schedule

SESSION A: 10:10 am – 11:30 am Room: Great Room A			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
A.1 (10:10)	Serena Dow	Knox College	The Effect of Oxytocin on Tactile Sensitivity in Male Rats
A.2 (10:30)	John Havlik	University of Chicago	Exploring a rat model of the Bystander Effect
A.3 (10:50)	Anqi Jiang	Macalester College	Development of color representation in infant monkey primary visual cortex
A.4 (11:10)	Madison Kasoff	Washington University in St. Louis	Investigating the processes underlying when smaller images enhance category learning

SESSION B: 10:10 am – 11:30 am Room: Seminar Room A			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
B.1 (10:10)	Nicholas Bone	Beloit College	Evidence of convergence in the lizard genera Liolaemus and Sceloporus
B.2 (10:30)	Michelle Noyes	University of Chicago	Genetics of Commercial Monarch Butterflies
B.3 (10:50)	Halie Ostberg	Gustavus Adolphus College	Identifying genes involved in Drosphila ovulation through genetic screens
B.4 (11:10)	Tiwonge Chirwa Lauren Knuckey	Luther College	Multi-drug resistant Staphylococci and E. coli in springs and streams in Northeast Iowa

SESSION C: 10:10 am – 11:30 am Room: Seminar Room B			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
C.1 (10:10)	Emily Goering	Washington University in St. Louis	Intracellular Localization of Staphylococcus aureus in Osteoclasts
C.2 (10:30)	Jaclyn Kline	Macalester College	Characterizing the local inflammatory microenvironment following repeated topical application of Methylisothiazolinone
C.3 (10:50)	Zoë Levine	University of Chicago	A potential role of carbohydrates in the anastomotic microenvironment for selection of Enterococcus faecalis population with tissue-destructive phenotype.
C.4 (11:10)	Kathleen Mills	University of Chicago	IL-5 signaling reduces edema to protect mice against mortality from acute lung injury

SESSION D: 2:20 pm – 3:20 pm Room: Great Room A

Session #	Presenter Name	Institution	Title of Presentation
D.1 (2:20)	Caroline Behling-Hess	Macalester College	Membrane Trafficking in Epithelial Cells
D.2 (2:40)	Timothy Burnette	Grinnell College	Do tissue water relations explain contrasting drought tolerance and distributions of closely related plants?
D.3 (3:00)	Charles Ofosu	Macalester College	What is in Areca? An investigation of the cholinergic and carcinogenic activities of molecules in areca

SESSION E: 2:20 pm – 3:20 pm Room: Seminar Room A

Session #	Presenter Name	Institution	Title of Presentation
E.1 (2:20)	Sara Graves	Gustavus Adolphus College	Nonsense-mediated mRNA decay regulates mRNA levels for kinetochore proteins in *Saccharomyces cerevisiae*
E.2 (2:40)	Mervenaz Koska	University of Chicago	Hedgehog Signaling Controls Gene Regulatory Networks for Early Cardiovasculogenesis
E.3 (3:00)	Alexis Stutzman	University of Chicago	Lamin A/C is required for maintaining the structure and function of mature cardiomyocytes

SESSION F: 2:20 pm – 3:20 pm Room: Seminar Room B

Session #	Presenter Name	Institution	Title of Presentation
F.1 (2:20)	Purujit Chatterjee	University of Chicago	Expression of Cell-Surface Proteins in the Drosophila Nervous System
F.2 (2:40)	Dustin Tillman	Washington University in St. Louis	Investigating the recognition and attachment of heme in prokaryotic cytochrome c biogenesis
F.3 (3:00)	John Wang	Grinnell College	Homocysteine-amplified Effects of Oxidative Stress at Mouse Neuromuscular Junction are mediated by Nitric Oxide Synthase

Poster Sessions Schedule

Poster Session 1: 8:50 a.m. – 9:50 a.m. Great Room B			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Emma Deihl	Luther College	Moral Foundations of the 2016 Presidential Election Voters
P1.02	Juana Delao	University of Chicago	Exploring the mechanisms of transcriptional dysregulation of human ETV6 in Drosophila melanogaster
P1.03	David Edholm	Gustavus Adolphus College	Bioinformatic characterization of the YHL018W gene in *Saccharomyces cerevisiae* with GFP and KO
P1.04	Rebecca Ferrer Laura Hurtado	St. Olaf College	Effects of controlled burns on structure of soil microbial communities in St. Olaf's restored prairies
P1.05	Zhiye Lu Carolyn Lorch	Grinnell College	Wee1 inhibition results in misoriented meiotic spindles with significantly decreased length in Xenopus laevis oocytes
P1.06	Mia Altenau	Colorado College	Investigation of How Different Growth Mediums Affect the Growth Curve and Morphology and Topography of Acinetobacter baylyi Using Atomic Force Microscopy
P1.07	Hailey Bomar	Lawrence University	Engaging communities in native bee research – Appleton Pollinator Project
P1.08	Kirstyn Buchholz	Carthage College	Mechanisms of Ventilatory and Neural Adaptations to Chronic Hypercapnia in Goats
P1.09	Benjamin Gentile	Beloit College	Comparison Transcriptomic Analysis of Uterine Tissue of the Northern Watersnake, Nerodia Sipedon
P1.10	Cady Greenslit	Lawrence University	Appleton Pollinator Project: Genetic exchange in Great Lake bumble bee populations identified through microsatellite techniques
P1.11	Rohit Kamath	Macalester College	Characterization of the immune responses to the hapten, dinitrofluorobenzene.
P1.12	Nathan Meshbesher	St. Olaf College	Exploring TonB-dependant Sucrose Transport In Caulobacter crescentus
P1.13	Jacob Peecher	Hope College	Genomic and Physiological Characteristics of Novel Escherichia Strains Isolated from Freshwater Sources
P1.14	Dulce Saenz	Beloit College	Carbon Cycling in Managed Turf and Restored Ecosystems
P1.15	Toluwalope Toluhi	St. Olaf College	Prenatal Stress and Bone Development

P1.16	Arun Velamuri	Gustavus Adolphus College	Analysis and characterization of protein with unknown function YGL101W.
P1.17	Connor Balfany	Gustavus Adolphus College	Role Identification of the YJL055W gene in Saccharomyces cerevisiae
P1.18	Haley O'Neill	Grinnell College	The Effect of Manure Application on the Presence of Multi-Antibiotic Resistant Bacteria
P1.19	George Nahass	Colorado College	Brazilin Inhibits Fibril Formation of Alpha-Synuclein in vitro
P1.20	Bijoya Basu	Washington University in St. Louis	Modeling 'addiction' from the perspective of neuronal homeostasis
P1.21	Katherine Alexander	Washington University in St. Louis	Changes in Immune Surveillance in Response to Antigenicity of Pancreatic Ductal Adenocarcinoma
P1.22	Carly Merritt	Colorado College	Co-localization of mTORC1 and hexokinase II favors OXPHOS phenotype in MPNST
P1.23	Anh Thu Doan	St. Olaf College	Evaluating the Role of CSF1R on Osteosarcoma Pathogenesis
P1.24	Shambhavi Upadhyaya	Beloit College	Action potential propagation in axons: the effect of electrotonic length on sodium conductance
P1.25	Juliet Fink	Colorado College	Regulation of Mitochondrial Mass Following Stimulation of the BCR, CD40 and Their Viral Mimics
P1.26	Divya Joshi	Washington University in St. Louis	A Human In Vitro Model to Study Genetic Influences on Morbidity in Traumatic Brain Injury
P1.27	Joseph Beggs	Grinnell College	Optimizing FRET spectroscopy to detect microtubule nucleation
P1.28	Peeta Li	Washington University in St. Louis	Strategic Prospective Memory Monitoring in Older Adults: The Time Course of Monitoring Deactivation and Reactivation
P1.29	Marta Williams	Luther College	Implications of Micra leadless pacemaker extraction for tricuspid valve integrity

Poster Session 2: 1:00 p.m. – 2:00 p.m. Great Room B			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Muhammad Rehman	Knox College	Enhancing the properties of the GBH-1 protein based hydrogel via deletion mutants
P2.02	Alicia Wilkening	Washington University in St. Louis	An Assay for Blood Parasite Detection in Golden Eagles (Aquila Chrysaetos)
P2.03	Micaela Wells Madison Buckner Emily Arendsen	Hope College	Edge Effects on Non-Native Plant and Microbial Communities
P2.04	Caitlin McCombe Cara Hull	Carthage College	Acoustic signatures as aids in monitoring longevity in wild roaming Gray Wolves (Canis lupus)
P2.05	Hyun Hwan An	Grinnell College	The Role of RNF4 in Maintaining Genome Stability
P2.06	Kylee Brimsek	Gustavus Adolphus College	Ecological assessment of a chronosequence of prairie restorations
P2.07	Chelsea Coleman	Beloit College	Genetic Similarities Between Reptiles and Mammals
P2.08	Chelsea Gosney	Lawrence University	A macrophage expressed gene (Mpeg) in Biomphlaria glabrata
P2.09	Luise Johannes	Luther College	Characterizing soil bacterial communities with and without buckthorn (Rhamnus cathartica) and prescribed fire.
P2.10	Yanzhuo Li	Grinnell College	RNF4 and its cancer associated mutant have effects on genome instability
P2.11	Mikael Mir	Gustavus Adolphus College	Bioinformatical analysis and characterization of open reading frame YGR021W from Saccharomyces cerevisiae
P2.12	Tanisha Perlmutter	Carthage College	Analysis of Pigment Cell Regeneration in a GNAQ Q209L zebrafish model of melanoma
P2.13	Matthew Schuiling	Hope College	Isolation and Identification of Fungistatic Compounds from Phytolacca americana and Phytolacca rivinoides
P2.14	Bethany Van Houten	Hope College	Temperature Effects and Mutants of Cluster K Mycobacteriophages
P2.15	Meredyth Wenta	Carthage College	Manipulation of Danio rerio Melanosome Dispersion By Targeting Second Messenger Systems
P2.16	Katherine Johnson	Beloit College	Green tea polyphenols effect on the concentration of live probiotics in non-dairy yogurt
P2.17	Bryce Gerrits	Lawrence University	Role of CXCL-14 on lateral line development in zebrafish by quantifying rheotaxis

P2.18	Lara Braverman	Knox College	Towards the synthesis of an iron dialkyl precatalyst for the hydrosilylation of 1-hexene
P2.19	Allison Leopold	Macalester College	Effects of Apical Resection Surgery on Heart Regeneration in Neonatal Mice
P2.20	Aidan Tirpack	Macalester College	Determining hyaluronan's effect on Idiopathic Pulmonary Fibrosis
P2.21	Amanda Eness	Carthage College	Biosolid education for open house at Kenosha Water; experimental results and environmental applications of biosolids
P2.22	Ngwe Sin Phyo	Beloit College	Effect of Distance from Soma on Sodium Conductance to Generate Action Potential Propagation in Axons
P2.23	Rachel Potter	University of Chicago	Disruption of the Antiviral RIG-I Pathway by JC Virus
P2.24	Samuel Mathai	Colorado College	Neuroguidin: a unique neuronal transcription factor
P2.25	Jack Jagielski	Luther College	SUDEP-7 and revised SUDEP-7 risk inventory prediction of mortality in epilepsy patients
P2.26	Natalie Sarver	Colorado College	Title: Identification of Active Competence Pili in Acinetobacter baylyi Imaged by Atomic Force Microscopy
P2.27	Ryan Hoopes, Nick Kosinski	Washington University in St. Louis	The Effect of Symbolic, Linguistic Information on Delay Discounting of Real Liquid Rewards
P2.28	Alexis Sienczak	Gustavus Adolphus College	Thalassa testudinum blade measurements in two different environmental stressor sites surrounding Drago Beach Panama

Poster Session 3: 3:40 p.m. - 4:40 p.m. Great Room B			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Jacob Cantrell	Washington University in St. Louis	Driving gene expression in the heterochromatic environment of the fourth chromosome of D. melanogaster
P3.02	Kelly Hartigan, Margaret Gaggioli	Washington University in St. Louis	Improving genome assemblies and gene annotations of Drosophila Muller F and D elements
P3.03	Kim Nguyen	Hope College	Drug Discovery: An Interdisciplinary Approach
P3.04	Savannah Fuqua, Erin Carroll	Washington University in St. Louis	The role of soil microbes and plant diversity in pollination and soil carbon sequestration
P3.05	Jada Royer, Ryann Felton	Hope College	Establishing the Validity of a Novel Animal Model for Bipolar Disorder Through Behavioral Testing
P3.06	Josey Muske, Stefanie Huttelmaier	Carthage College	Characterization of cell surface markers on cancer cells cultured in atmospheric vs normoxic oxygen
P3.07	Leah Barkema	Luther College	PI3K/Akt signaling influences neuronal function in C. elegans
P3.08	Zachary Brown	Gustavus Adolphus College	Functional analysis of the uncharacterized open reading frame YPL247C in Saccharomyces cerevisiae
P3.09	Brian Dahlberg	Beloit College	An Automated EEG Scoring Method Based on Wavelet Decomposition and Line-Length Calculation
P3.10	Tristan Grams	Carthage College	Assessing the ability of a microgravity environment to promote the transfer of antibiotic resistance genes between bacteria
P3.11	Soo Kyong Joo	Macalester College	Optimizing CGRP+ nerve staining in murine model of DNFB-induced contact hypersensitivity
P3.12	Edward Lopatto	Grinnell College	Abundance of resistance and virulence genes following manure application
P3.13	Spencer Morgan	Hope College	The effects of diet, obesity and predisposition on anxiety-like behaviors in Sprague Dawley rats.
P3.14	Kelsie Pos	Knox College	Evolutionary history versus dietary niche both shape pharyngeal jaw skeletal structure in cyprinid fishes
P3.15	Geordan Stukey	Hope College	Cluster K Mycobacteriophages May Have a Natural Growth Advantage at Lower Temperatures

P3.16	Joel Vargeese	Knox College	Large bite forces maintained across gapes may evade length-tension constraints due to the muscular dynamics in the masticatory system of the primate Macaca mulatta
P3.17	Luke Zimmerman	Beloit College	An analysis of soil bacterial communities of different stages of prairie succession in southern Wisconsin
P3.18	Trevor Kao	Luther College	Assessing the influence of PI3K/Akt signaling integrity on metabolic and oxidative activity in Caenorhabditis elegans
P3.19	George Nahass	Colorado College	High Yield Bacterial Expression of Alpha-Synuclein via Escherichia Coli
P3.20	Qiu Chang Wu	Colorado College	Construction and Characterization of a Noise Rheostat Using Small Molecule Induction in HEK293T Cells
P3.21	Shutian Lu, Kaylyn Nicole Billmeyer	St. Olaf College	The Preferential Destabilization of GC-rich RNA Duplexes by L-Proline Explained
P3.22	Jean-Baptiste Reynier	University of Chicago	Developing Clytia Hemispherica as a model for single-cell wound healing
P3.23	Kai Gui	Grinnell College	Repurposing disulfiram, a drug used to treat alcohoism, to target non-small-cell lung cancer
P3.24	Yizhe Tang	Beloit College	Action Potential Propagation in Axons: How Sodium Conductance Can Linearly Estimate Propagation
P3.25	Brandon Wolfe	Colorado College	The Role and Localization of RNY1 Under Carbon Starved Conditions in S. cerevisiae
P3.26	Ellen Wu	Washington University in St. Louis	Analysis of Drug Resistant HIV-1 Evolving in the Presence of Co-receptor Antagonist
P3.27	Zoe Moffett	Colorado College	Pollination Ecology and Natural History of Pedicularis groenlandica
P3.28	Tamia Phifer	Knox College	Comparison of MicroRNAs expressed by the parasitic plant, *Cuscuta campestris*, in response to different hosts
P3.29	Elizabeth Cordell	University of Chicago	The role of miR122 in SHC1-mediated invasion in triple-negative breast cancer

Abstracts for all Sessions

Biological Sciences and Psychology

MCMS Undergraduate Research Symposium, Washington University in St. Louis

November 10-11, 2017

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

Presenter(s): Katherine Alexander, Washington University in St. Louis
Session: Poster P1.21
Title: Changes in Immune Surveillance in Response to Antigenicity of Pancreatic Adenocarcinoma
Advisor(s): David G DeNardo, Department of Medicine; Integrating Communications within the Cancer Environment (ICCE) Institute; Department of Pathology and Immunology, Washington University School of Medicine; Siteman Cancer Center
Co-Author(s): Samarth Hegde

Abstract: Even in its earliest stages, pancreatic ductal adenocarcinoma (PDAC) remains a highly lethal disease, with a 5-yr survival rate of < 8%. Current treatment options provide little clinical benefit to patients, and recent efforts to utilize T-cell directed immunotherapy have failed to induce significant response in PDAC. This is especially puzzling, given the known presence of neoantigens that should be acted upon by the host adaptive immune response. Using a genetically engineered mouse model of PDAC that recapitulates human PDAC progression and produces a moderately immunogenic epitope, we investigated changes in the immune infiltrate in response to neoantigen exposure. This was done using immunofluorescent staining and image quantitation, which revealed that T cell, B cell and granulocyte infiltration did increase in tumors expressing the antigen. These findings provide some insight into an active host immune response against neoantigens during early PDAC progression and may further support why advances in immunotherapy have yet to yield results in treating patients with pancreatic cancer. Subsequent correlation of immune cell infiltration in early PDAC progression to quantitation in later stage tumors will aim to characterize how this response becomes dysfunctional in later stages of the disease.

Presenter(s): Mia Altenau, Colorado College
Session: Poster P1.06
Title: Investigation of How Different Growth Mediums Affect the Growth Curve and Morphology and Topography of Acinetobacter baylyi Using Atomic Force Microscopy
Advisor(s): Pheobe Lostroh, Biology, Colorado College
Co-Author(s): Pheobe Lostroh, Kristine Lang

Abstract: Cell morphology and topography is variable among cells of the same species. However, the exact molecular mechanisms that regulate cell shape and surface texture are currently only theorized. Since it is very likely that environment plays a role in the cell's regulation of morphology, our lab investigated how different molecular forms of carbon in media affects cell growth rate and cell morphology and topography in order to further understand the relationship between cell regulation of morphology and environmental factors that influence growth. We cultured samples of Acinetobacter baylyi in mediums containing different forms of carbon, determined growth curves for the cells grown in each medium, and then used those growth curves to isolate a second set of experimental samples at the same growth stage according to their respective medium. We are currently examining the cells using Atomic Force Microscopy (AFM). The remaining data is scheduled to be collected and analyzed by Monday, October 9th. The results collected thus far are promising in the respect that several nutrient conditions have resulted in the growth of cells with different morphologies compared to the control group (cells grown in LB).

Presenter(s): Hyun Hwan An, Grinnell College
Session: Poster P2.05
Title: The Role of RNF4 in Maintaining Genome Stability
Advisor(s): Yee Mon Thu, Biology, Vanderbilt University
Co-Author(s):

Abstract: RNF4 is a SUMO-targeted ubiquitin ligase known to play a role in DNA damage repair and maintaining genome stability. A mutation within the ligase domain of RNF4 (G138*) has been identified in some cancer tissues. To confirm whether the G138* mutation negatively affects genome stability by preventing RNF4 from participating in DNA repair processes, we transformed budding yeast cells with wild-type and mutant RNF4. We show that incorporation of the G138* mutation may impair genome stability. Additionally, we overexpressed RNF4 in breast cancer cell lines MCF-7 and MDA-MB-468 to observe if RNF4 alleviates the stress of genome instability and thus promotes cell proliferation. We hypothesized that RNF4 is able to share the functions of its homolog heterodimer, Slx5/Slx8, which provides survival advantage under conditions of genome instability in budding yeast. We show that the data for MDA-MB-468 supports our hypothesis but the data for MCF-7 does not.

Presenter(s): Connor Balfany, Gustavus Adolphus College
Session: Poster P1.17
Title: Role Identification of the YJL055W gene in Saccharomyces cerevisiae
Advisor(s): S. Brookhart Shields, Biology, Gustavus Adolphus
Co-Author(s): S. Brookhart Shields

Abstract: Although an incredible amount of work has been done to sequence the genome of Saccharomyces cerevisiae (baker's yeast), approximately 10% of the possessed genes have unknown functions. These 'open reading frames' (ORF's) are the focus of the ORFan project, which seeks to understand the function of these genes by utilizing bioinformatic methods to characterize previously unexplored stretches of genome. One such gene is YJL055W, a hypothesized putative protein that is thought to contribute to the metabolism of purine and pyrimidine base analogues. The YJL055W sequence was analyzed to identify similarity to known proteins, conserved sequence motifs, and potential active sites on the unknown protein. By analyzing highly similar sequences, a hypothesis was created to predict the function of the gene, which was then tested by performing knock-outs to remove the YJL055W gene of to observe the effect of its removal from Saccharomyces cerevisiae. By cross referencing the unknown stretch of basepairs in YJL055W to other known coding regions, and performing in lab knock-outs to generate a modified yeast, a more complete picture of the function of YJL055W and its role on organismal development can be obtained.

Presenter(s): Leah Barkema, Luther College
Session: Poster P3.07
Title: PI3K/Akt signaling influences neuronal function in C. elegans
Advisor(s): Stephanie Fretham, Biology, Luther College
Co-Author(s): Marta Williams, Stephanie Fretham

Abstract: Active cells such as neurons must mitigate the cost of high energy demands. Cells can accomplish this is via the phosphatidylinositol 3-kinase (PI3K)/Akt signaling pathway which integrates external and internal cues such as nutrients, energy levels, and oxidative stress. Disrupted signaling has been identified in several neurological conditions. To understand how this contributes to neuronal function this study assessed neuronal function in wild type (WT) and mutant Caenorhabditis elegans, a nematode model system with a well characterized nervous system and PI3K/Akt pathway. Strains were cultured on standard or iron supplemented agar. Iron is essential for many metabolic enzymes

but accumulates in the nervous system in several neurodegenerative conditions. In standard conditions PI3K/Akt mutants demonstrated an inverse relationship between pathway activity and lifespan. Excess iron reduced lifespan in WT animals and mutants with increased PI3K/Akt signaling but not in mutants with decreased signaling. Furthermore there was an inverse relationship between PI3K/Akt activity and dopamine-dependent behaviors. Excess iron resulted in further impairment of these behaviors in PI3K/Akt mutants suggesting optimal dopaminergic function depends on PI3K/Akt integrity and that PI3K/Akt integrity may be disrupted by iron dyshomeostasis.

Presenter(s): Bijoya Basu, Washington University in St. Louis
Session: Poster P1.20
Title: Modeling 'addiction' from the perspective of neuronal homeostasis
Advisor(s): Yehuda Ben-Shahar, Department of Biology, Neurosciences Program, Washington University in St. Louis
Co-Author(s): Ross McKinney

Abstract: Although genetics and heritability play a major role in its etiology, the molecular and cellular mechanisms underlying addiction are largely unknown. Although current dogmas stipulate that addiction is specifically associated with the dopaminergic reward system, emerging data suggest that this model cannot explain all physiological aspects of the phenotype. We propose the alternative hypothesis that addiction is a direct product of modulation of neuronal homeostasis in response to constant exposure to drugs. To test our hypothesis, we are investigating the effects of long-term exposure of Drosophila to nicotine, an acetylcholine receptor agonist, on the neuronal homeostatic response to stress. Preliminary data indicate that withdrawal after long-term nicotine exposure leads to impaired behavioral responses to acute heat stress. These data suggest that neural adaptations may occur in response to chronic exposure to an excitatory neural stimulation. We hypothesize that both intrinsic and synaptic mechanisms exist to compensate for extended nicotine exposure and are currently examining the exact mechanisms on the molecular and cellular levels that may explain the role of neuronal homeostasis in addiction.

Presenter(s): Joseph Beggs, Grinnell College
Session: Poster P1.27
Title: Optimizing FRET spectroscopy to detect microtubule nucleation
Advisor(s): Keisuke Hasegawa, Physics, Grinnell College
Co-Author(s): Joy Suh

Abstract: Microtubules are tubulin-based protein filaments that compose the mitotic spindle, a macromolecular machine that divides duplicated chromosomes during mitosis. Proper formation of microtubules and the mitotic spindle is essential for normal cell division. However, interactions between tubulin heterodimers such as microtubule nucleation are not visible with optical microscopy. Consequently, microtubule nucleation is not well understood. There is currently no technique for detecting microtubule nucleation in real time.

To better understand microtubule nucleation, a protocol for Förster Resonance Energy Transfer (FRET) was developed to observe microtubule formation in vitro. We identified the optimal pair of fluorophores for FRET by writing a code that calculates the Förster distance and spectral bleed through (SBT) values of numerous FRET pairings. After labelling our purified tubulin from porcine brains with these fluorophores, we tested FRET by preparing labelled samples that mimic intracellular tubulin and nucleating microtubules. Our pair, ATTO542 and ATTO647N, had minimal SBT with greater contrast between samples than previously tested pairs.

Presenter(s): Caroline Behling-Hess, Macalester College
Session: Oral D.1 (2:20)
Title: Membrane Trafficking in Epithelial Cells
Advisor(s): Jean M. Wilson, Cellular and Molecular Medicine, University of Arizona

Abstract: Differential membrane trafficking establishes and maintains cellular polarity in epithelial cells -- this trafficking is controlled in part by Rab proteins, a family of small GTPases that serve as molecular switches to control downstream effectors. Rab14 has been shown to be involved in the establishment of epithelial polarity and in lumen formation, but how it interacts with other trafficking machinery is unknown. Here we report the colocalization of Rab14 with Rab22 in endosomes of Madin Darby Canine Kidney (MDCK) cells. Interestingly, at cell:cell interfaces, Rab22 is present but Rab14 is only observed in adjacent endosomes. Overexpression of Rab22 in Rab14 knockdown (KD) cell pairs rescued the multi-lumen phenotype otherwise characteristic of these cells. However, there does not appear to be a change in distribution of Rab22 after Rab14 KD, suggesting that Rab14 controls the activity of Rab22, not its localization. Overexpression of Rab22 in Rab14 KD cells, but not in control cells, results in the production of Rab22-positive retraction fibers, cellular components involved in the establishment and maintenance of polarity. Both the production of retraction fibers in the absence of Rab14, and the rescue of the single-lumen phenotype, suggest that Rab22 lies downstream of, and perhaps is regulated by Rab14.

Presenter(s): Hailey Bomar, Lawrence University
Session: Poster P1.07
Title: Engaging communities in native bee research – Appleton Pollinator Project
Advisor(s): Israel Del Toro, Biology, Lawrence University

Abstract: The Appleton Pollinator Project (APP) was founded in 2017 and aims to increase native bee diversity in urban green spaces in the Fox Valley. The project installed native bee habitat across the Fox Valley and organized outreach events that engaged community members, with the goal of improving immediate conditions for bees and increasing long-term species success through community awareness. The success of an endeavor like APP requires communication with different audiences to protect sampling arrays and habitat. In addition, native bee populations depend on human communities to modify behaviors that are harmful to their success. A survey was implemented to develop a benchmark for community perceptions regarding the project and general knowledge about bees. Initial results indicated that over 55% of respondents were unafraid of bees, and 80% maintained bee habitat on their property. 25% of participants were familiar with APP, but less than half of those participants had received information directly. Responses were analyzed to determine correlations between demographic factors and knowledge of the project, identifying target areas for future outreach efforts. Outreach efforts on behalf of the project must be relevant to the community to accomplish the goals of the project and increase native bee awareness.

Presenter(s): Nicholas Bone, Beloit College
Session: Oral B.1 (10:10)
Title: Evidence of convergence in the lizard genera Liolaemus and Sceloporus
Advisor(s): James Schulte II, Biology, Beloit College

Abstract: Body size differentiation between sexes in the same species has been correlated with a multitude of traits, which presents an excellent opportunity for comparative studies. The independently derived lizard genera Sceloporus and Liolaemus are ecological analogues widely distributed in North and South America, respectively, that vary greatly in sexual size dimorphism (SSD). We compared

SSD evolution using a phylogenetic tree for 149 species utilizing the program SURFACE to reconstruct evolutionary convergence for this trait. Convergence was found both within and between genera using this method.

Presenter(s): Lara Braverman, Knox College
Session: Poster P2.18
Title: Towards the synthesis of an iron dialkyl precatalyst for the hydrosilylation of 1-hexene
Advisor(s): Helen M. Hoyt, Chemistry, Knox College

Abstract: An iron(II) dialkyl precatalyst bearing the dppBIAN ligand (BIAN = bis(imino)acenaphthene; dpp = diisopropylphenyl) was prepared by combining 2 equivalents of $LiCH_2SiMe_3$ with py_4FeCl_2 to form $py_2Fe(CH_2SiMe_3)_2$ in situ, followed by addition of the dppBIAN ligand to form the iron dialkyl precatalyst dppBIANFe$(CH_2SiMe_3)_2$. The resulting compound was analyzed using 1H NMR spectroscopy. Preliminary hydrosilylation results were achieved using 1-hexene and phenylsilane as substrates and 2 mol% catalyst. Ongoing focuses for this project are to improve purification methods and hydrosilylation results as compared to related iron dibromide precatalysts, as well as expanding catalysis to include 4,5-fused rings.

Presenter(s): Kylee Brimsek, Gustavus Adolphus College
Session: Poster P2.06
Title: Ecological assessment of a chronosequence of prairie restorations
Advisor(s): Amy Kochsiek, Biology, Gustavus Adolphus College
Co-Author(s): Sarah Anderson, Amy Kochsiek

Abstract: There is less than 2% of native prairie remaining in Minnesota; thus, attempts to restore this ecosystem are critical. We examined a chronosequence of prairie restorations in comparison to a native site to assess the efficacy of restoration efforts in these sites, and how long it may take to function similarly to a native prairie. We measured plant diversity, above and belowground productivity, and soil structure characteristics at three prairie restoration sites and one native site. We found that the restored site with consistent burning and a more diverse seed mix in initial seeding efforts was significantly more diverse than other restored sites regardless of site age ($p < 0.0001$). Above and belowground productivity recovered to native levels rapidly as all sites were fairly similar except for the restored site on sandy loam soil. Generally, sandy soil leads to less water availability and lower productivity. The native site had significantly higher amounts of macro and microaggregates, as well as course and fine intra-particulate organic matter in soil ($p < 0.0001$). The increasing trend in these soil structure measurements with restoration age suggests that the legacy of plowing lasts for many years, but recovery is possible.

Presenter(s): Zachary Brown, Gustavus Adolphus College
Session: Poster P3.08
Title: Functional analysis of the uncharacterized open reading frame YPL247C in Saccharomyces cerevisiae
Advisor(s): S. Brookhart Shields, Biology, Gustavus Adolphus College

Abstract: Approximately 10% of open reading frames (ORF) in the Saccharomyces cerevisiae genome are considered uncharacterized in function. One example, YPL247C, codes for a protein of unknown function. Through the bioinformatics based ORFan workflow, established by the Yeast ORFan Gene Project, we investigate the structure of this gene and corresponding protein, and hypothesize potential functions the protein may exhibit in the cell. Exploration of the ORF includes

using numerous bioinformatics software to look at physical and genetic interactions and expression (e.g. GeneMania, SPELL), structure-based evidence for function predictions (e.g. TIGRFAM, PDB), and cellular localization data (e.g. TMHMM, Philius). Using these observational data, we formulate and test a hypothesis about YPL247C cellular localization and function, using GFP-tagging and analyzing knockout (YPL247CΔ) phenotypes.

Presenter(s): Kirstyn Buchholz, Carthage College
Session: Poster P1.08
Title: Mechanisms of Ventilatory and Neural Adaptations to Chronic Hypercapnia in Goats
Advisor(s): Paul Martino, Biology, Carthage College
Co-Author(s): Kirstyn Buchholz; Nick Burgraff; Suzanne Neumueller; Hubert V. Forster

Abstract: Prior studies investigating chronic exposure to hypercapnia show that changes in the temporal pattern of ventilation cannot be described by changes in arterial or cerebrospinal fluid [H^+] or PCO_2. We hypothesize neuroplastic events may occur within the respiratory control network of the brainstem during chronic hypercapnia, contributing to the temporal pattern of ventilation observed and further extend into the cortex, impairing cognitive function. Goats were exposed to elevated inspired CO_2 (6%) for 30-days. Physiological parameters and chemosensitivity were measured for 3-hours, every 4-days. Cognitive function was determined by shape discrimination tests. Brains were extracted for immunohistochemistry to determine neuroadaptations within medullary respiratory nuclei. In the hypercapnic goat, minute ventilation increased by 446% on Day 1 then decreased to 273% above control levels on Day 2. Following Day 2, ventilation remained elevated throughout the remaining period. During hypercapnia, pH initially increased then returned to control levels, while $PaCO_2$ and CO_2 chemosensitivity continually increased. Immunohistochemistry revealed decreases in TPH+ neurons and trends for increased receptor density of AMPA/NMDA receptor subtypes in the hypercapnic goat. Cognitive function was impaired by hypercapnia. In conclusion, physiological and neurochemical adaptations occurred during chronic hypercapnia. Future studies are needed to increase the sample size to confirm our findings.

Presenter(s): Timothy Burnette, Grinnell College
Session: Oral D.2 (2:40)
Title: Do tissue water relations explain contrasting drought tolerance and distributions of closely related plants?
Advisor(s): Vincent Eckhart, Biology, Grinnell College
Co-Author(s):

Abstract: Physiological underpinnings of drought tolerance in relation to niche differentiation and species success at various biological and ecological levels is largely unexplored. To examine differences in physiological processes allowing for drought tolerance, I conducted pressure-volume analyses on four coexisting congeners native to the dry Southern Sierra Nevada of California: *Clarkia xantiana ssp. xantiana*, *Clarkia cylindrica*, *Clarkia unguiculata*, and *C. speciosa*. I found that the species differed in their drought tolerance, specifically in their relative water contents at the turgor loss point and the saturated water content. Based on my findings, *C. xantiana* may tolerate drought, and *C. cylindrica* and *C. unguiculata* are likely less tolerant of drought. While no evidence of drought tolerance was found in tissue water relations for *Clarkia speciosa*, it is possibly drought tolerant through other traits such as germination or root structure and function.

Presenter(s): Jacob Cantrell, Washington University in St. Louis
Session: Poster P3.01
Title: Driving gene expression in the heterochromatic environment of the fourth chromosome of D. melanogaster
Advisor(s): Elena Gracheva, Sarah C. R. Elgin, Biology, Washington University in St. Louis
Co-Author(s):

Abstract: Genomes of higher eukaryotes can be divided into two fundamental and dynamic subtypes: euchromatin and heterochromatin. In general, genes that are active in a euchromatic environment are silenced when transposed to heterochromatin, resulting in a variegating phenotype (PEV). However, heterochromatin is not devoid of actively functioning genes. The main goal of our project is to identify gene regulatory elements that drive transcription of heterochromatic genes. Insertion of an *hsp70-white* transgene, which exhibits a uniform red eye phenotype in euchromatin, into a heterochromatic region on the fourth chromosome results in PEV. We replaced the *hsp70* promoter of *hsp70-white* with a genomic fragment of a highly expressed fourth chromosome (heterochromatic) gene, *Rad23*. Insertion of the *Rad23-white* transgene into the same location switched the *hsp70-white* PEV phenotype to a uniform red eye, suggesting that the *Rad23* fragment is sufficient to drive strong expression of the euchromatic *white* reporter. A series of experiments with reporter constructs containing fragments of varying lengths of the *Rad23* promoter region have identified a minimal *Rad23* promoter fragment that drives *white* expression. Additional experiments manipulating the motifs of the transgenic promoter region are underway to identify the essential elements of the 5'noncoding regulatory region of *Rad23*.

Presenter(s): Purujit Chatterjee, University of Chicago
Session: Oral F.1 (2:20)
Title: Expression of Cell-Surface Proteins in the Drosophila Nervous System
Advisor(s): Robert Carrillo, Department of Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s):

Abstract: In order to generate a functional nervous system, the developing neurons must form highly specific synaptic connections. Thus, elucidating the underlying molecular mechanisms of synaptic specificity is essential to our understanding of nervous system function, and the neurological diseases associated with connectivity errors such as autism spectrum disorder. Two subfamilies of the immunoglobulin superfamily, the defective proboscis extension response proteins (Dprs) and the Dpr-interacting proteins (DIPs), are known to play roles in synapse function and specificity at the neuromuscular junction and visual system of Drosophila melanogaster, respectively. To begin to test our hypothesis that Dpr and DIP interactions allow synaptic partners to recognize each other, we characterized the expression profiles of Dprs and DIPs by utilizing the GAL4-UAS system. Further we monitored their expression at critical stages of development in order to gain insights into the functions of their interactions. We found that each Dpr and DIP analyzed thus far is expressed in unique subsets of neurons throughout the nervous system. Utilizing the powerful genetic tools available in Drosophila, we plan to investigate roles for Dpr-DIP interactions in establishing synaptic specificity in various circuits.

Presenter(s): Tiwonge Chirwa, Lauren Knuckey, Luther College
Session: Oral B.4 (11:10)
Title: Multi-drug resistant Staphylococci and E. coli in springs and streams in Northeast Iowa
Advisor(s): Eric Baack, Biology Department, Luther College
Co-Author(s): Kristine Luebbe, Lauren Knuckey, Max Eness, Elijah Kane, Joel Denney, Kayla Ingvalson, Luke Von Eschen

Abstract: Many Iowa rivers and streams are impaired due to high bacteria levels, particularly following heavy rain, and higher bacteria levels are linked to increased risk of illness and infections. We investigated levels of drug resistance in E. coli and Staphylococcus bacteria found in streams in springs in NE Iowa. E. coli counts frequently exceeded recommended limits in springs around Decorah especially during rainy season and this can be explained by the karst topography in NE Iowa. Staphylococcus resistant to methicillin were commonly found, and many of these were resistant to other antibiotics, including vancomycin. Levels of multidrug resistance varied among springs in the Decorah area. Using qPCR we were able to confirm that the E. coli in our samples are coming from human and bovine sources and that levels of drug resistance increased as bovine proportions increased. Identifications of Staphylococcus species have been made using tuf and 16s genes in PCR. So far, drug resistant Staph have included Staph aureus and related species including Staph sciurus, S. succinus, and S. lentus.

Presenter(s): Chelsea Coleman, Beloit College
Session: Poster P2.07
Title: Genetic Similarities Between Reptiles and Mammals
Advisor(s): Dr. James Schulte, Biology, Beloit College
Co-Author(s): James Schulte

Abstract: Innate immunity plays a key role in pregnancy by regulating the body's immune response to the embryo. Reptiles, such as snakes, share significant genetic similarities with mammals. This study will compare innate immunity genes expressed in humans to genes expressed in a group of snakes with live birth. Genes will be collected from uterine transcriptomes of water snakes and garter snakes at different stages of pregnancy and those associated with innate immunity will be compared with those found in the human reproductive systems. We hypothesize that the reproductive genes related to innate immunity are similar between mammals and reptiles.

Presenter(s): Elizabeth Cordell, University of Chicago
Session: Poster P3.29
Title: The role of miR122 in SHC1-mediated invasion in triple-negative breast cancer
Advisor(s): Geoffrey L. Greene, The Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Ya-Fang Chang, Geoffrey L. Greene

Abstract: Triple-negative breast cancer (TNBC) accounts for 15-20% of breast cancer cases and is more common in young women and African American women. TNBC is highly metastatic and difficult to treat due to a lack of targeted therapy. Src Homology 2 Domain Containing Transforming Protein 1 (SHC1) is often overexpressed in breast cancer. Although its mechanism of action is not well known, SHC1 has been shown to affect tumor invasiveness and drug resistance in ER+ breast cancer. Similarly, in TNBC, preliminary work has shown that knockdown of SHC1 significantly decreases invasion in vitro. RNA-seq analysis comparing TNBC cell lines before and after SHC1 knockdown indicates that miR-122 could be a possible target of SHC1. In the current study, we found that knocking down SHC1 decreased miR-122 expression, suggesting that miR-122 is a downstream

target of SHC1. Additionally, overexpression of miR-122 increased the invasiveness of TNBC cell lines in vitro. From these data, we hypothesize that inhibiting miR-122 will reduce invasion while overexpressing miR-122 will reverse invasion inhibited by siSHC1. Overall, our studies may suggest that SHC1 mediates tumor invasion through miR-122 in TNBC. Therefore, SHC1 and/or miR-122 may be potential novel therapeutic targets. Future studies will investigate the effect of miR-122 on drug response in TNBC.

Presenter(s): Brian Dahlberg, Beloit College
Session: Poster P3.09
Title: An Automated EEG Scoring Method Based on Wavelet Decomposition and Line-Length Calculation
Advisor(s): Rachel Bergstrom, Biology, Beloit College
Co-Author(s): J.Z. Alex Cheong, Everett Baxter, Rachel Bergstrom

Abstract: Roughly 150,000 people are diagnosed with epilepsy each year, most of them via electroencephalogram (EEG). The EEG must be read ("scored") by a neurologist, which carries several disadvantages – this process is slow, expensive, and subject to poor interobserver reliability. An automated scoring method would retain the core advantages of EEG whilst eliminating these disadvantages.

This work proposes such an algorithm, based on the murine algorithm of Bergstrom et al. 2013. Patient records were obtained from an online, NIH-funded repository (ieeg.org) and scored manually, with interobserver reliability monitored via Cohen's kappa (median = 0.69). The algorithm utilized a Daubechies wavelet transform and line length calculation to characterize the signal. A line length threshold was used to identify events, which were then sorted into spikes (<5 s) and seizures (>5 s) based on duration. The optimal threshold value was explored via a Receiver Operating Characteristics (ROC) curve (1.0-1.5 σ above mean). With modification, the algorithm could be applied towards real-time monitoring in clinical settings.

Presenter(s): Emma Deihl, Luther College
Session: Poster P1.01
Title: Moral Foundations of the 2016 Presidential Election Voters
Advisor(s): David Njus, Psychology, Luther College
Co-Author(s): David Njus

Abstract: The current study focuses on moral foundation differences among Trump, Clinton, and Johnson voters in the 2016 presidential election. Moral foundations include: Care/Harm and Fairness/Cheating (the individualizing foundations) and Loyalty/Betrayal, Authority/Subversion, and Sanctity/Degradation (the binding foundations, which focus on maintenance of groups and values prized by those groups). We also examined a potential sixth foundation, liberty, which assesses autonomy/freedom as the basis for a moral foundation.

Participants (232 males and 534 females) were 2016 voters obtained online from Amazon MTurk. They completed the Moral Foundations Questionnaire (MFQ30), a 32-item measure that taps five moral foundations. Subjects also completed the 11-item Liberty scale, which measures economic/governmental and lifestyle liberty, and which has been proposed as a possible sixth moral foundation.

According to our findings, Trump, Clinton, and Johnson voters differed on their moral foundations. Consistent with previous research on liberals and conservatives, Trump voters scored slightly lower than Clinton voters on the individualizing foundations and higher than Clinton voters on the binding foundations. Trump voters also scored higher than Clinton voters on Economic/Governmental Liberty.

Presenter(s): Juana Delao, University of Chicago
Session: Poster P1.02
Title: Exploring the mechanisms of transcriptional dysregulation of human ETV6 in Drosophila melanogaster
Advisor(s): Ilaria Rebay, Ben May Department of Cancer Research, University of Chicago
Co-Author(s): Matt Hope, Ilaria Rebay

Abstract: Many human cancers are driven by mutations in transcription factors (TFs), yet how such mutations deregulate gene expression is not well understood. TEL/ETV6 is an evolutionarily conserved polymerizing TF that regulates blood development in mammals. It contains a Sterile Alpha Motif (SAM) that mediates polymerization and an E-Twenty Six (ETS) DNA binding domain that is regulated by two adjacent auto-inhibitory helices. Chromosomal translocations that fuse the TEL SAM to the DNA binding domain of another TF leads to leukemia. How these converted polymerizing TFs disrupt endogenous transcription is not understood nor is it known how the strength of polymerization, which impacts polymer length, modulates transcriptional output during either normal or oncogenic development. To answer these questions, I am developing a model system in which I overexpress mammalian TEL in the developing eye of the fruit fly, Drosophila melanogaster, and then assess the consequences of modulating SAM-SAM affinity with respect to gene expression, cell fate specification, and overall tissue patterning. My results show a positive correlation between SAM-SAM interaction strength and the severity with which TEL expression disrupts the normally well-organized eye. These effects require higher order TEL polymers, as dimers are insufficient to recapitulate these phenotypes.

Presenter(s): Anh Thu Doan, St. Olaf College
Session: Poster P1.23
Title: Evaluating the Role of CSF1R on Osteosarcoma Pathogenesis
Advisor(s): David Largaespada, Masonic Cancer center, University of Minnesota
Co-Author(s): Nicholas Slipek

Abstract: Osteosarcoma (OS) is a very aggressive bone cancer that primarily affects children and young adults. Tumors develop on bones within the body and current treatment options limited to surgical resection and highly toxic chemotherapy. Using an osteoblast specific Sleeping Beauty transposon system, our lab previously identified a set of genes predicted to be involved in OS. One of the top candidates identified from this screen is CSF1R. CSF1R is an oncogene that can enhance tumor cell growth. The role of this study is to characterize the role of CSF1R in promoting OS and evaluate the effectiveness of anti-cancer drug provided by Plexxikon Co. We genetically engineered the Hos cell line to both overexpress CSF1R and knock out its expression. By using different assay methods, we evaluated the growth of OS cells in the presence of the receptor's ligand and the receptor specific kinase inhibitor. Finally we performed early preclinical drug testing in an othotopic mouse model. The study showed that CSF1R acts as an oncogene, driving the development of osteosarcoma cells. The drug provided by Plexxikon Co was proved to be effective in decreasing the growth of tumor in vitro and in vivo.

Presenter(s): Serena Dow, Knox College
Session: Oral A.1 (10:10)
Title: The Effect of Oxytocin on Tactile Sensitivity in Male Rats
Advisor(s): Heather Hoffman, Neuroscience, Knox College
Co-Author(s): Heather Hoffman

Abstract: One common symptom of autism spectrum disorder (ASD) is restricted and repetitive behaviors, which can be expressed as hypo- and hyper-reactivity to sensory input. These sensory deficits can cause avoidance and negative emotions towards sensory engagement in hyper-reactive

individuals. Oxytocin (OT) is a neuropeptide that has a wide range of psychological and physiological effects. Past studies have found an abnormality in the OT receptor gene, which indicates that an abnormality in OT signaling could lead to ASD symptoms. Recent research demonstrated therapeutic effects of OT by decreasing social impairments and repetitive behaviors for individuals with autism. However, none of these studies investigated the effects of OT on tactile sensitivity. In the present study, we injected twelve male rats with OT and twelve male rats with saline. We then measured the rodent's paw withdrawal threshold using von Frey hairs and the SUDO method. OT administration significantly reduced tactile sensitivity in male rodents. OT acts both peripherally and centrally and can impact a range of behaviors. The precise mechanism for the observed effect is unclear. However, this finding suggests that oxytocin could become a possible pharmaceutical therapy for sensory alterations in autism, as well as chronic pain and other sensory disorders.

Presenter(s): David Edholm, Gustavus Adolphus College
Session: Poster P1.03
Title: Bioinformatic characterization of the YHL018W gene in *Saccharomyces cerevisiae* with GFP and KO
Advisor(s): S. Brookhart Shields, Biological Sciences, Gustavus Adolphus College

Abstract: Approximately 10% of the yeast genome is comprised of uncharacterized regions known as open reading frames (ORFans), or genes with unknown functions. Understanding the function of ORFans in key to protein structure and functional understanding, protein-protein interactions, and genetic analysis in yeast, and humans. Using bioinformatic analysis tools: BLAST, CDD, PFAM, PDB, SUPERFAMILY, GENE3D, PANTHER, T-COFFEE, TMHMM, PSORT II, and TARGETP, YHL018W was hypothesized to regulate gene transcription in the cytoplasm and localize to the mitochondria. This hypothesis was then tested with GFP-localization and phenotypic assays in KO.

Presenter(s): Amanda Eness, Carthage College
Session: Poster P2.21
Title: Biosolid education for open house at Kenosha Water; experimental results and environmental applications of biosolids
Advisor(s): Sarah Rubienfeld , Environmental Science, Carthage College
Co-Author(s):

Abstract: Biosolids are a soil amendment produced as a byproduct of the Kenosha wastewater treatment process; biosolids are a sustainable alternative to chemical fertilizers. While improving the physical property of soil, it provides essential nutrients such as: nitrogen, phosphorus, sulfur, and a range of micronutrients. They are organically bound in a slow releasing form and continue to supply nutrients throughout the growing season. Soil amendments are known to have lower risk of nutrient runoff and leaching. Kenosha Water produces class A exceptional quality biosolid that complies to strict pathogen and heavy metal limits set by the EPA. The purpose of this study was to grow Kentucky bluegrass in a sand mixture with Kenosha biosolid utilized as a soil amendment to educate the community on biosolids positive potential uses. The results confirmed Kenosha biosolid is comparable to commercially available biosolid products such as milorganite. Application rates where determined according to nitrogen, phosphorus and potassium rates; nutrient content for Kenosha biosolid were 4.0 total nitrogen, 6.0 total phosphorus as P2O5, and 0.1 potassium as K20. Overdosing application rates were also determined. All information was collected and presented at the Kenosha public open house to inform the community of the environmental benefits of biosolids.

Presenter(s): Rebecca Ferrer, Laura Hurtado, St. Olaf College
Session: Poster P1.04
Title: Effects of controlled burns on structure of soil microbial communities in St. Olaf's restored prairies
Advisor(s): Jean Porterfield, Biology, St. Olaf College
Co-Author(s): Laura Hurtado, Jean Porterfield

Abstract: St. Olaf College has restored prairies that are maintained by periodic controlled burns. While this management technique is well-researched, less is known about its effects on soil microbial communities. Soil microbes use enzymes to carry out chemical reactions in the nitrogen cycle, thus influencing large-scale ecological variables, such as nitrogen availability, water runoff pollutants, and production of the greenhouse gas nitrous oxide. In this study, we assessed the abundance of nitrogen-relevant microbial genes in the soils of two St. Olaf restored prairies burned at different times. We extracted DNA from 30 soil samples taken from the two sections, used PCR to amplify six nitrogen-related genes, as well as the 16s rRNA gene, and measured the intensity of the PCR products as a proxy for gene abundance. There was no significant difference in 16s gene abundance between the two prairie sections, but most nitrogen-related genes had greater abundance in soil from the more recently burned section. Multivariate analyses suggested that gene abundance varied more widely in more recently burned soils. Overall, the two restored prairie sections did not markedly differ in microbial community structure as assessed by gene abundance at the time and scale studied.

Presenter(s): Juliet Fink, Colorado College
Session: Poster P1.25
Title: Regulation of Mitochondrial Mass Following Stimulation of the BCR, CD40 and Their Viral Mimics
Advisor(s): Olivia Hatton, Molecular Biology, Colorado College
Co-Author(s): Olivia Hatton

Abstract: B lymphocytes generate antigen-specific responses and are activated through the B cell receptor (BCR) and CD40 by interaction of antigen and CD40 ligand, respectively. Following activation, B cells undergo energetically demanding processes of proliferation and differentiation. A relative of B cells – T lymphocytes – require a metabolic change to aerobic glycolysis following activation to support function and memory differentiation. Due to the similarities of these two cells, we hypothesized that a metabolic change must also occur in B cells to allow for their proliferation and differentiation to memory cells. Specifically, we examined alterations in mitochondrial mass to indicate a metabolic transition after activation. We previously demonstrated that mitochondrial mass increased following stimulation through the BCR and CD40 in Ramos cells – a germinal center-like Burkitt's Lymphoma B cell line. We repeated these experiments in BL41, another Burkitt's Lymphoma B cell line. We found no increase in mitochondrial mass in BL41 following stimulation through BCR and CD40. We also asked whether a viral CD40 mimic – the Epstein-Barr Virus (EBV) protein LMP1 – can regulate mitochondrial mass in BL41 cells; LMP1 signaling did not increase mitochondrial mass. These results could motivate future studies investigating the mechanism through which mitochondrial mass increases in Ramos cells in response to BCR and CD40 activation, using BL41 as a negative control.

Presenter(s): Savannah Fuqua, Erin Carroll, Washington University in St. Louis
Session: Poster P3.04
Title: The role of soil microbes and plant diversity in pollination and soil carbon sequestration
Advisor(s): Scott Mangan, Biology, Washington University in St Louis
Co-Author(s): Erin Carroll, Claudia Stein, Scott Mangan

Abstract: It is well-established that an ecosystem's functioning, and thus the services it provides us, is related positively to its biodiversity. Further, it is known that soil microbial communities play an important role in maintaining this relationship between plant diversity and ecosystem functioning. How the relationship between soil microbes, plant diversity and ecosystem functioning will be affected by a changing climate, however, remains unclear. In order to explore these interactions we examine how pollination and soil carbon sequestration, two important metrics of ecosystem function, are affected by plant community diversity, drought, and soil microbial communities within the context of native tallgrass prairies. Specifically, as previous data has shown that soil microbes have a strong influence on the fecundity of individual plant species in this system, we attempt to determine whether this is through a direct effect on plant fitness or an indirect effect by mediating plant-pollinator interactions. Additionally, as our lab has shown with past data that systems with live soil microbial communities continue to sequester carbon under drought conditions better than systems with sterile soil, we examine how the same measurements are affected by different gradients of plant community diversity.

Presenter(s): Benjamin Gentile, Beloit College
Session: Poster P1.09
Title: Comparison Transcriptomic Analysis of Uterine Tissue of the Northern Watersnake, Nerodia Sipedon
Advisor(s): James Schulte II, Biology, Beloit College
Co-Author(s): Chelsea Coleman

Abstract: One question of particular interest in evolutionary biology is the evolution of viviparity (live birth) from oviparity (egg laying). Reptiles make good model systems for studying this transition for multiple reasons, among them are the fact that a multitude of reptilian clades have independently evolved viviparity throughout time, viviparous species often have at least relatively closely related oviparous members, and that research has shown evidence for convergent evolution, particularly in the formation of placental membranes, between mammals and reptiles. For this study the Northern Watersnake (Nerodia sipedon), a viviparous member of the Natricinae subfamily, was chosen as our study organism, and our interest was in how uterine gene expression rates changed as pregnancy progressed. This was studied by isolation, sequencing, and annotating of the uterine transcriptomes (a suite of mRNA molecules in a tissue at a time). After transcriptomes were sequenced and annotated, comparative expression tests were run to identify genes that significantly varied between timepoints. After this Panther software was used to determine gene function, as well as gene functional class, for our identified genes.

Presenter(s): Bryce Gerrits, Lawrence University
Session: Poster P2.17
Title: Role of CXCL-14 on lateral line development in zebrafish by quantifying rheotaxis
Advisor(s): Nancy Wall, Biology Department and Neuroscience Program, Lawrence University
Co-Author(s):

Abstract: During embryogenesis, a complex molecular framework delineates the characteristics that comprise an organism. For example, many signaling pathways are highly conserved in different animal groups, allowing the use of a model organism, such as zebrafish, to elucidate ancient

molecular signals in vertebrates. I am studying a signaling molecule, CXCL-14, and its role in the formation of a mechanosensory structure in the lateral line system. To assess lateral line function, I constructed a flow chamber to quantify rheotaxis (orientation in a stream of fluid). I plan to microinject a morpholino to knockdown CXCL-14 expression. CXCL-14 knockdown zebrafish will be compared with untreated negative control fish and chemically treated positive control fish without functional neuromasts. To generate positive control animals an aminoglycoside antibiotic, Neomycin, was used to damage the neuromasts of the lateral line. This causes significant reduction in rheotaxis. Overall, levels of rheotaxis will be used to determine CXCL-14's effect on the development of functional lateral line neuromasts.

Presenter(s): Emily Goering, Washington University in St. Louis
Session: Oral C.1 (10:10)
Title: Intracellular Localization of Staphylococcus aureus in Osteoclasts
Advisor(s): Deborah Veis Novack, Division of Bone and Mineral Diseases, Washington University School of Medicine
Co-Author(s): Jennifer Krauss

Abstract: Osteomyelitis (OM) is infection-driven inflammatory disease of the bone primarily caused by Staphylococcus aureus (S. aureus). New research has shown that S. aureus is internalized into osteoclasts, the cells that destroy bone, and avoids cellular defense mechanisms to remain alive intracellularly. The purpose of this study was to investigate how S. aureus evades the cellular defense system by studying the endocytic vesicles where S. aureus resides within osteoclasts over time. To determine the location of S. aureus within osteoclasts, we infected primary murine osteoclasts and their precursors with the GFP-expressing MRSA strain USA300 to assess the degree of co-localization of bacteria with acidified vesicles marked with the fluorescent dye Lysotracker over time. We found that over half of S. aureus are localized to lysosomes in osteoclasts and osteoclast precursors within 6 hours of infection, with no significant differences in localization between osteoclasts and osteoclast precursors. However, at 18 hours of infection all S. aureus are localized to lysosomes in osteoclast precursors while less than 5% of S. aureus is localized to lysosomes in differentiated osteoclasts. This indicates that S. aureus may avoid the cellular defense system by avoiding progression of endocytic vesicles to lysosomes or escaping the endocytic vesicle system in osteoclasts.

Presenter(s): Chelsea Gosney, Lawrence University
Session: Poster P2.08
Title: A macrophage expressed gene (Mpeg) in Biomphlaria glabrata
Advisor(s): Judith Humphries, Biology, Lawrence University
Co-Author(s):

Abstract: Macrophage expressed genes (Mpegs) have been shown to punch holes in the membrane of pathogens as a defense mechanism in various species but have not been widely studied in the freshwater snail Biomphlaria glabrata. B. glabrata is studied due to its role as the host for the parasite Schistosoma mansoni, a human trematode mainly found in the southern hemisphere. A previous study demonstrated that following exposure to S. mansoni, an Mpeg-like partial transcript increased in B. glabrata. The change in expression level lead to the hypothesis that a Mpeg-like protein played a role in the immune system of B. glabrata. Our lab found multiple Mpeg genes in the genome and we are currently focusing on one Mpeg. This His-tagged protein was expressed in E. coli and purified under denatured conditions. Following this, antimicrobial assays are underway to look at the ability of B. glabrata Mpeg on defending against E. coli and S. aureus to gain insight on how Mpeg works within B. glabrata's immune system.

Presenter(s): Tristan Grams, Carthage College
Session: Poster P3.10
Title: Assessing the ability of a microgravity environment to promote the transfer of antibiotic resistance genes between bacteria
Advisor(s): Andrea Henle, Biology, Carthage College
Co-Author(s): Camilla Urbaniak , Andrea Henle , and Kasthuri Venkateswaran

Abstract: Anti-microbial resistance (AMR) is a major concern worldwide, which prompted the World Health Organization (WHO) this year to publish the first list of antibiotic resistant "priority pathogens" that pose the greatest threat to human health. While AMR is a serious problem on Earth, it is a bigger issue in space, as astronauts become immune-compromised and therefore more prone to infection. This, coupled with the fact that bacteria become more virulent and antibiotic resistant when grown in space, make the study of AMR under microgravity a high priority. We believe the increase in antibiotic resistance could be due to increased horizontal gene transfer (HGT) of AMR genes leading to a gain of function when these bacteria are exposed to microgravity.
To carry out our hypothesis, S. aureus, isolated from the ISS, will be incubated with A. pitti, which carries OXA75 and OXA421, under simulated microgravity using the High Aspect Ratio Vessel (HARV). Transfer of these genes to S. aureus will be assessed by PCR using primers against the A. pittii OXA genes. Functionality of these genes will be assessed by growing on plates supplemented with oxacillin. Determining the cause of increased AMR will help protect astronauts on future long-term space missions.

Presenter(s): Sara Graves, Gustavus Adolphus College
Session: Oral E.1 (2:20)
Title: Nonsense-mediated mRNA decay regulates mRNA levels for kinetochore proteins in *Saccharomyces cerevisiae*
Advisor(s): Jeffrey N. Dahlseid, Biology and Chemistry, Gustavus Adolphus College
Co-Author(s): Jeffrey N. Dahlseid

Abstract: Nonsense-mediated mRNA decay (NMD) is best known as a cell surveillance pathway that recognizes and targets aberrant mRNAs for accelerated decay. NMD also targets numerous wild-type mRNAs, thereby contributing to the regulation of gene expression. We have identified three wild-type mRNAs seemingly affected by NMD in *Saccharomyces cerevisiae*. The *CTF13*, *SKP1*, and *CEP3* mRNAs encode proteins that bind centromere DNA to assemble the centromere-binding factor 3 (CBF3) complex of the kinetochore, which promotes proper chromosome segregation during mitosis. Our lab has shown that the stability of *CTF13* mRNA is directly affected by NMD. We aimed to determine if NMD similarly affects the stability of *SKP1* and *CEP3* mRNAs. To study this, we engineered *SKP1* and *CEP3* genes to express their wild-type mRNAs under the control of the carbon-source dependent regulator, Gal4p. As expected, both showed dextrose-based suppression and galactose-based induction. *CEP3* mRNA, but not *SKP1* mRNA, accumulates in cells lacking NMD. Using carbon-source control, we will measure rates of decay from steady-state for these mRNAs in yeast with and without NMD. In future work, we aim to elucidate how any confirmed wild-type mRNA substrates of NMD are recognized for accelerated decay.

Presenter(s): Cady Greenslit, Lawrence University
Session: Poster P1.10
Title: Appleton Pollinator Project: Genetic exchange in Great Lake bumble bee populations identified through microsatellite techniques
Advisor(s): Israel del Toro, Biology, Lawrence University
Co-Author(s): Israel del Toro

Abstract: The Appleton Pollinator Project is a multifaceted research effort with the goal of understanding more about the native bee populations in the Appleton area, and possible ways to help conserve these populations and the pollination services they provide. The fieldwork component is done by student researchers using sampling 16 locations in the Appleton area for native bee specimens. This data is used for a community ecology survey that analyzed environmental covariates that correlate with bee biodiversity. There's also a community outreach component to complement the field and laboratory experiments. My focus in this project is looking at microsatellite loci of bumble bees (Bombus ssp.) to understand inter-population dynamics of bumble bees. Microsatellites are DNA segments that are highly variable within a population. The goal of this project is to create a map that demonstrates areas of genetic flow between populations around Lake Michigan. Specimens where obtained via net collection throughout the summer of 2017. This will highlight areas of importance for habitat protection to maintain bumble bee populations, by identifying areas in which genetic exchange is taking place. Genetic exchange between populations is essential for species survival over time because without it deleterious mutations can arise due to genetic drift.

Presenter(s): Kai Gui, Grinnell College
Session: Poster P3.23
Title: Repurposing disulfiram, a drug used to treat alcohoism, to target non-small-cell lung cancer
Advisor(s): Douglas R. Spitz, Free Radical Radiation Biology Program, Department of Radiation Oncology, The University of Iowa
Co-Author(s): Kelly C. Falls, Douglas R. Spitz

Abstract: New and improved therapies are needed to treat lung cancer, the leading cause of cancer death in the US. Because drug development is a long and expensive process, repurposing existing drugs for novel therapies may have merit. Disulfiram, an FDA approved drug for the treatment of alcoholism, has been shown to kill many cancers in a copper-dependent fashion, but the specific mechanisms for disulfiram/copper toxicity are not well understood. The following experiments show that in non-small-cell lung cancer, disulfiram toxicty can be attributed to the generation of reactive oxygen species as well as increased Cu-mediated redox cycling.

Cu is a redox-active metal known to participate in Fenton-like reactions - generating reactive oxygen species (ROS) by cycling between Cu(II)/Cu(I) oxidation states. Under normal conditions, the production of ROS can serve important cellular processes such as cell signaling, but elevated levels of ROS may lead to damage to DNA, lipids, and proteins. In this way, DSF cancer cell cytotoxicity may be explained by increased levels of intracellular copper. In this study the mechanisms involved in cancer cell specific cytotoxicity of DSF are investigated in NSCLC and normal non-transformed lung epithelial cells.

Presenter(s): Kelly Hartigan, Margaret Gaggioli, Washington University in St. Louis
Session: Poster P3.02
Title: Improving genome assemblies and gene annotations of *Drosophila* Muller F and D elements
Advisor(s): Sarha CR Elgin, Department of Biology , Washington University in St. Louis
Co-Author(s): Kelly Hartigan, Margaret Gaggioli, Frank Chen, Mitchell Grinwald, Mikayla Johnson, Kendra Woodruff, Christopher D. Shaffer, Wilson Leung, Sarah C.R. Elgin

Abstract: The *Drosophila melanogaster* Muller F element provides a good platform for understanding how chromatin packaging affects gene expression: surprisingly, it is almost entirely heterochromatic but contains ~80 genes that are widely expressed. In order to use phylogenetic footprinting to identify regulatory factors that facilitate F element gene expression, we must first produce high quality assemblies and gene annotations for the F elements and euchromatic reference regions from the D elements of multiple *Drosophila* species. We used Consed to analyze nine gaps on the *D. ficusphila* and *D. eugracilis* F and D elements, resolving five gaps via bioinformatics approaches plus genomic PCR and sequencing. Using the Apollo annotation editor, we reconciled 1,354 gene models produced by students participating in the Genomics Education Partnership to create reference gene sets for the F and D elements of three *Drosophila* species. Analysis of these reconciled gene models shows that F element genes have distinct characteristics compared to D element genes (*e.g.*, larger coding spans, more coding exons). The improved sequences and gene annotations produced in this study facilitate research into the evolution of the F element, which could enhance our understanding of how chromatin packaging affects gene expression. Supported by NSF grants #1431407, #1517266.

Presenter(s): John Havlik, University of Chicago
Session: Oral A.2 (10:30)
Title: Exploring a rat model of the Bystander Effect
Advisor(s): Peggy Mason, Ph.D., Department of Neuroscience, University of Chicago
Co-Author(s): Maura Clement

Abstract: The Bystander Effect is a phenomenon which has been observed and studied in humans for over fifty years. The most prominent hypothesis on why the Bystander Effect occurs is that there is a “diffusion of responsibility” across groups of humans in emergency scenarios. Using an arena-restrainer paradigm, we examined the possibility of the effect occurring in rats by placing a trapped rat in a restrainer which could only be opened from the outside to create an effective distress scenario (Bartal et Al., 2011). We observed a strong Bystander Effect in the form of increased time taken to open a restrainer door for a trapped rat by a free rat when experimental confederates dosed with an anxiolytic were present in the arena than when these confederates were absent. The presence of a strong Bystander Effect in rats calls into question the validity of the "diffusion of responsibility" hypothesis, which depends on higher cognitive function. We propose the effect occurs because rats and humans take the judgments of a group into account and integrate these judgments with their own reasoning when making decisions. More simply, a rat’s decision to help another rat is informed by the perceived decisions and actions of other rats present.

Presenter(s): Ryan Hoopes, Nick Kosinski, Washington University in St. Louis
Session: Poster P2.27
Title: The Effect of Symbolic, Linguistic Information on Delay Discounting of Real Liquid Rewards
Advisor(s): Leonard Green, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Nick Kosinski

Abstract: We continually face situations that involve choices between outcomes that differ in amount and delay to their receipt. Previous research articulates the occurrence of delay discounting in affecting those choices, in which the subjective value of a reward decreases as the time to its receipt increases, and both humans and non-human animals discount delayed outcomes. Interestingly, an amount effect has been observed only with humans: Larger, delayed rewards are discounted less

steeply than smaller ones. Non-human animals, in contrast, appear to discount different amounts of a delayed reward at similar rates. It is undetermined whether this observation represents a species difference in decision-making, a difference in experimental conditions (the use of linguistic symbolism with humans), or a difference in type of reward (real for animals versus hypothetical for humans). In the present study, participants are asked to choose between smaller, immediate amounts and larger, delayed amounts of a preferred liquid under one of two conditions: Symbolic, involving numerical values for the delay to and amount of liquid administered, and Non-symbolic, involving no linguistic information. The results will determine whether the observed amount effect is due to experimental differences or unique characteristics of humans.

Presenter(s): Jack Jagielski, Luther College
Session: Poster P2.25
Title: SUDEP-7 Risk Inventory Predicts Mortality in Individuals with Epilepsy
Advisor(s): Erik K. St. Louis, Neurology, Sleep Medicine, Mayo Clinic
Co-Author(s): Emma L. Veum, Aradhana Sahoo, Mykhaylo Krushelnytskyy, Paul C. Timm, Anna Myburgh, Tanya Bredesen, Rabe Alhurani, Keerthi Jaliparthy, Akil Sherif, Virend Somers, Anwar A. Chahal, Erik K. St. Louis

Abstract: Assembled from independently validated risk factors for Sudden Unexpected Death in Epilepsy (SUDEP), the relationship between the SUDEP-7 Risk Inventory and mortality in patients with epilepsy, independent of consideration for seizure semiology or eventual cause of death, has not yet been tested. Retrospective chart review was used to determine SUDEP-7 and revised SUDEP-7 scores for 394 deceased epilepsy patients at the date of initial seizure presentation, date of last follow up, and midpoint date (whenever dates of presentation and last follow up were at least 12 months apart and a midpoint date was available in the medical records). The Kaplan-Meier method was used to determine survival from initial presentation based on mean SUDEP-7 and revised SUDEP-7 scores. For both the original SUDEP-7 and revised SUDEP-7 scoring methods, Kaplan-Meier analysis of patients with average scores ≥ 2 showed increased mortality compared to those with average scores < 2 ($p<0.001$, Log Rank test). Mean SUDEP-7 Risk Inventory scores ≥ 2 (regardless of scoring method) predict increased mortality in epilepsy patients over a 15-year time frame. SUDEP-7 risk factors should be considered by clinicians at first seizure or suspected seizure presentation and actively monitored on a long-term basis for patients with epilepsy.

Presenter(s): Anqi Jiang, Macalester College
Session: Oral A.3 (10:50)
Title: Development of color representation in infant monkey primary visual cortex
Advisor(s): Anna W. Roe, Neuroscience, Oregon Health & Science University
Co-Author(s): Robert M. Friedman, Derek Zaraza, Mykyta M. Chernov, Anna W. Roe

Abstract: Human and nonhuman primates have poor spatial vision and no color vision at birth, which improve over a period of months. A question is: Is this visual development related to changes in cortical circuitry? In this study we examined how color domains (“blobs”) in primary visual cortex (V1) fine tune to color and eye-specific stimuli during development. We used intrinsic optical imaging, with its spatial resolution on the order of tens of microns, to examine the responses of color domains in macaque monkeys ranging in age from 8 to 77 days old (N=9). We presented as visual stimuli color (red and green) and monochromatic moving gratings to either the left or right eye. Overall (N=7), color blobs in V1 exhibited an increase in signal preference to color over monochromatic stimuli as infants grew older. Two cases did not show clear color functional domains in V1, pointing to the importance of individual differences. We also observed that early on color blobs responded to binocular visual signals, but gradually showed stronger preference to one eye until becoming monocular as adults. In line with the general understanding of brain development, visual cortex fine tunes the modular domains that process visual features.

Presenter(s): Luise Johannes, Luther College
Session: Poster P2.09
Title: Characterizing soil bacterial communities with and without buckthorn (Rhamnus cathartica) and prescribed fire.
Advisor(s): Molly McNicoll, Biology, Luther College
Co-Author(s): Molly McNicoll

Abstract: European buckthorn (Rhamnus cathartica) is associated with altered ecosystem properties, including greater soil carbon and nitrogen cycling. These changes may be associated with altered microbial communities, although the causal or response nature of these feedbacks is unclear. Microbial communities alter rates of decomposition, mineralization, and nutrient loss, and may differ among areas with and without R. cathartica. We assessed the soil bacterial community in areas with and without buckthorn, and in areas where prescribed fire had been used to manage R. cathartica invasion. Soil samples were collected in two separate experimental designs, the first comparing the bacterial community under individual R. cathartica (x6) with a paired sample 3 m away. Additionally, we collected soil samples along 100 m transects in invaded, uninvaded, burned, and unburned regions of an oak-hickory forest, with pooled samples for three replicates per transect. Soil samples were processed using Ecoplates to assess the community-level physiological profile of the bacterial community by quantifying metabolism of different carbon sources. The results from this analysis will be presented and discussed in light of our predictions that bacterial communities would differ based on state of R. cathartica invasion and whether prescribed fire had been applied to the site.

Presenter(s): Katherine Johnson, Beloit College
Session: Poster P2.16
Title: Green tea polyphenols effect on the concentration of live probiotics in non-dairy yogurt
Advisor(s): Amy Briggs, Biology, Beloit College
Co-Author(s):

Abstract: Yogurt has been a popular food across many cultures and is increasing in popularity as a health food. Yogurt is made using a starter culture of lactic acid bacteria, namely two genuses: Lactobacillus and Streptococcus. Lactic acid bacteria also includes probiotics. Probiotics are healthy bacteria that live in the human gastrointestinal tract. The two most important genuses of probiotics are Lactobacillus and Bifidobacteria. The focus of this study was to determine whether two types of popular non-dairy milks, soy and coconut, were capable of not only growing probiotic bacteria, but growing sufficient colony forming units (CFU) to impart of healthy effect on the human body. Additionally, green tea polyphenols which have been shown to increase the CFU of probiotics in fermented milk products. Yogurts made from a whole milk control, soy, and coconut milk were infused with green tea polyphenols to determine their effect on probiotic growth in the yogurt. This study found that soy and coconut milk yogurts were capable of sustaining probiotic bacteria, however whole milk was the only yogurt capable of sustaining a beneficial amount of lactic acid bacteria. However, these results showed that tea polyphenols increase the viability of probiotic bacteria. Further studies investigating the effectiveness of non-dairy yogurt and polyphenol infusions should be explored.

Presenter(s): Soo Kyong Joo, Macalester College
Session: Poster P3.11
Title: Optimizing CGRP+ nerve staining in murine model of DNFB-induced contact hypersensitivity
Advisor(s): Devavani Chatterjea, Biology, Macalester College
Co-Author(s):

Abstract: Vulvodynia is a condition characterized by chronic vulvar pain with no identifiable cause. Epidemiological studies have shown that women with a history of allergies have an increased risk of developing this condition. One clinical characteristic is hyper-innervation in vestibular biopsies. We

have shown that nerve density in female ND4 mice is increased after repeated exposure to the hapten dinitrofluorobenzene (DNFB) in our murine model of vulvodynia. Density of Calcitonin Gene-Related Peptide (CGRP), a protein produced from peripheral neurons commonly used in pain studies, was measured in the labiar tissue. CGRP+ nerve staining is a common immunofluorescent (IF) assay that identifies sensory fibers due to their expression of the peptide. IF assays are a quintessential part of clinical research of chronic pain condition as it can visualize and quantify the change in the density of nerve fibers. Here, we demonstrated the optimization process of CGRP+ nerve IF staining in samples from a novel murine model of DNFB-induced contact hypersensitivity. Producing a reliable and successful IF nerve staining protocol will support the study of chronic pain conditions and thus aid the understanding of intersection between allergen exposure and chronic pain conditions.

Presenter(s): Divya Joshi, Washington University in St. Louis
Session: Poster P1.26
Title: A Human In Vitro Model to Study Genetic Influences on Morbidity in Traumatic Brain Injury
Advisor(s): Colin Franz, Neurology, Northwestern University
Co-Author(s): Colin Franz, Sydney Sherman, Jack Phillips, Shreya Udani, Evangelos Kiskinis, John D. Finan

Abstract: Traumatic brain injury outcomes have suggested a dependency on genetic factors. Human induced pluripotent stem cells (hiPSCs) can be used to retain the genetic identity of that donor without the inconsistencies across patients that exist in clinical studies. Clinical phenotypes of traumatic injury can be reproduced in iPSC-derived brain cells using a custom built in vitro trauma model. A transparent, elastic, silicone layer was covalently bonded to a conventional 96 well plate top to create a flexible growth substrate, which was then stretched at a clinically relevant speed and magnitude by a custom device, simulating neuronal injury. Motor neurons with an SOD1 mutation, one of the causal factors of ALS, as well as their isogenic controls were stretched and compared to one another and their non-stretched controls for cell viability and reduced neurite length. It was seen that applying injury decreased the cell viability and produced neuritic beading, the hallmark of traumatic axonal injury. This in vitro model produces clinically relevant quantifiable injury phenotypes in neurons derived from human iPSCs. Future directions include the addition of stretchable electrodes to the substrate to simulate neuronal over activity, another potential contributing factor to neurodegenerative disorders.

Presenter(s): Rohit Kamath, Macalester College
Session: Poster P1.11
Title: Characterization of the immune responses to the hapten, dinitrofluorobenzene.
Advisor(s): Devavani Chatterjea, Biology, Macalester College
Co-Author(s):

Abstract: In order to understand the effects of repeated topical exposure to the hapten, 1-Fluoro-2,4-dinitrobenzene (DNFB), in the local immune environment, we profiled the changes in the iliac lymph nodes of female ND4 swiss mice after repeated DNFB exposure. Tissue collected from mice challenged with the hapten show higher numbers of CD4+ T cells, CD8+ T cells, and B cells, when compared to tissue collected from mice challenged with 0.9% saline. We then characterised the immune response to this chemical in the skin tissue of these mice, and found that there is an upregulation of activation markers in CD4+ T cells. In order to strengthen our findings, replications of these experiments will be carried out. However, these findings indicate a role for these adaptive immune cells in the immunological responses to the hapten, DNFB.

Presenter(s): Trevor Kao, Luther College
Session: Poster P3.18
Title: Assessing the influence of PI3K/Akt signaling integrity on metabolic and oxidative activity in Caenorhabditis elegans
Advisor(s): Stephanie Fretham, Biology and Neuroscience, Luther College
Co-Author(s): Tanner Gibbons

Abstract: Altered energy metabolism is hallmark of neurological diseases. Several neurological diseases are associated with aberrant insulin/insulin-like signaling including DJ-1 and PINK1 mutations in Parkinson's Disease. This study used Caenorhabditis elegans (C. elegans), a small nematode model system to examine roles of phosphatidylinositol 3-kinase (PI3K)/Akt, a downstream effector of insulin/insulin-like receptor signaling, in regulating cellular metabolism and oxidative state. The PI3K/Akt signaling cascade integrates extracellular and intracellular signals including nutrient availability, growth factor signaling, and ATP levels regulating cellular metabolism and gene expression. Synchronous populations of wild type (WT) and PI3K/Akt mutant young adult C. elegans were cultured on NGM agar plates seeded with OP-50 E. coli and collected for metabolic assessment. Mutants with reduced upstream PI3K/Akt signaling displayed elevated ATP levels relative to WT animals. Conversely, increased PI3K/Akt activity mutants exhibited decreased ATP levels relative to WT. Furthermore, total glutathione and MTT reduction potential were altered by mutations in the PI3K/Akt/FOXO pathway, however these oxidative alterations were not consistent patterns relative to PI3K/Akt activity. These observations suggest in standard culture conditions ATP levels and oxidative status depend on PI3K/Akt signaling integrity.

Presenter(s): Madison Kasoff, Washington University in St. Louis
Session: Oral A.4 (11:10)
Title: Investigating the processes underlying when smaller images enhance category learning
Advisor(s): Mark A. McDaniel, Psychological and Brain Sciences, Washington University in St. Louis
Co-Author(s): Toshiya Miyatsu & Mark A. McDaniel

Abstract: Past research in our laboratory has suggested that some natural categories, such as tropical fish, are learned better with small (100 px) rather than large (1000 px) images, even though learners predict and postdict that large pictures are better for learning. Across four experiments encompassing seven conditions, we demonstrate the reliability of the finding and examine the plausibility of three potential mechanisms supporting the advantages that smaller images provide for learners. *The general desirable difficulty hypothesis* suggests that small images create difficulty in the learning process, which subsequently improves performance (Bjork, 1994). *The focus shift hypothesis* suggests that learners' attention shifts from the local elements (e.g., color of particular parts) to the global elements (e.g., overall shape and pattern, critical features when categorizing fish) as the image becomes smaller, a prediction based on a well-developed psychological literature of global precedence. *The ease of shape extraction hypothesis* proposes that shapes are easier to extract for smaller images because the entire shape is within learners' visual contour, whereas larger images require gaze shifting during the shape extraction process. Current findings are supportive of the general desirable difficulty hypothesis.

Presenter(s): Jaclyn Kline, Macalester College
Session: Oral C.2 (10:30)
Title: Characterizing the local inflammatory microenvironment following repeated topical application of Methylisothiazolinone
Advisor(s): Devavani Chatterjea, Biology, Macalester College
Co-Author(s): Beebie Boo

Abstract: Vulvodynia is a chronic vulvar pain condition affecting 8-16% of women today, yet its etiology and pathophysiological mechanisms are poorly understood. Clinically, increases in CD4+ T cell densities and levels of proinflammatory cytokines are characteristics of vulvodynia. An association

has been established between a history of allergies and vulvodynia risk. We used an established model of hapten-driven contact hypersensitivity to investigate the allergic and inflammatory effects of Methylisothiazolinone (MI), an environmentally ubiquitous preservative in cosmetic and household products, on outbred rodents. Ten daily applications of 0.5% MI on the labiar skin of previously sensitized ND4 Swiss mice induced increased local levels of mRNAs encoding proinflammatory cytokines IL-6, IL-1β and IFN-γ. Using flow cytometric analysis, we saw a significant increase in activated CD4+CD44+, CD8+CD44+, and resident memory CD8+CD103+ T cells at one day after ten daily applications of MI. We are currently investigating whether changes in these inflammatory molecules can be mapped on MI-induced changes in tactile sensitivity in the affected skin and serve to elucidate possible mechanisms underlying the intersection of allergies and chronic pain.

Presenter(s): Mervenaz Koska, University of Chicago
Session: Oral E.2 (2:40)
Title: Hedgehog Signaling Controls Gene Regulatory Networks for Early Cardiovasculogenesis
Advisor(s): Ivan Moskowitz, Departments of Pediatrics, Pathology and Human Genetics, University of Chicago
Co-Author(s): Alexander Guzzetta, Megan Rowton, Jeff Steimle, Andrew Hoffman, Junghun Kweon, Ivan P. Moskowitz

Abstract: Congenital heart disease is the most common birth defect, yet its cause is poorly understood. Our lab attempts to address this issue by investigating the underlying molecular and developmental mechanisms for cardiac morphogenesis. Currently, we focus on hedgehog (hh) signaling, which has been shown to be critical for secondary cardiac morphogenesis. Our initial observations demonstrated that complete removal of the hh signaling through ablation of smoothened (Smo) led to severe defects in primary cardiac morphogenesis resulting in hypoplasia and early embryonic lethality; therefore, we focused on this poorly known role of hh signaling in primary cardiac morphogenesis. We utilized the Cre-Lox system to induce conditional removal of Smo in different domains and found its requirement to be restricted to the early mesoderm. A fate map for hh-receiving cells revealed that cardiac precursors do not receive the hh signal directly—implicating the requirement of an intermediate signaling pathway. To address this, we profiled hh-deficient mesoderm using RNA-seq and observed the most significant disruption in the fibroblast growth factor (fgf) signaling pathway, which plays a vital role in mesoderm development. This has led us to implicate a master regulatory role for hh signaling in mesoderm development and the allocation of cardiac precursors.

Presenter(s): Allison Leopold, Macalester College
Session: Poster P2.19
Title: Effects of Apical Resection Surgery on Heart Regeneration in Neonatal Mice
Advisor(s): Jop van Berlo, Department of Cardiology, University of Minnesota
Co-Author(s):

Abstract: The adult human heart cannot regenerate substantial amounts of functional cardiac tissue[1,4]. Thus, when a heart attack occurs, important functional tissue is lost and the heart becomes less effective at pumping blood[1]. However, we know that younger hearts have a greater ability to regenerate than those of adults[1,4]. Here, we use neonatal mice to model young mammalian hearts. Mice can exhibit significant regeneration of cardiac tissue during the first seven days of their lives[4]. In this experiment, we test this notion using an apical resection model to mimic the effects of a heart attack; then we gauge the success of the tissue regeneration with a combination of paraffin sectioning and Masson Trichrome staining. For day one operated mice, the imaging data showed successful

restoration of cardiac tissue. For day seven operated mice, we observed little to no regeneration of tissue and a persistent fibrotic scar. Thus, we conclude that the potential for regeneration of cardiac tissue is great in young hearts, and we can now further examine genetic manipulations of this phenomenon.

Presenter(s): Zoë Levine, University of Chicago
Session: Oral C.3 (10:50)
Title: A potential role of carbohydrates in the anastomotic microenvironment for selection of Enterococcus faecalis population with tissue-destructive phenotype.
Advisor(s): John Alverdy, Surgery, University of Chicago
Co-Author(s): Nathaniel Hubert, Emma Koropp, Olga Zaborina, and John Alverdy

Abstract: The important role of microbiota in colonic surgery is well appreciated. Microbial species with the ability to cleave collagen and activate host metalloproteinase-9 (MMP9) exhibit a tissue destructive phenotype (TDP). These species, including Enterococcus faecalis, have been shown to impair anastomotic healing.

Recent comparative genetic analysis between TDP- and non-TDP E. faecalis isolated post-operatively and prior to colonic surgery demonstrated no differences in the fsr-gelEsprE locus responsible for collagenase production, but numerous differences in phosphotransferase systems responsible for metabolism of carbohydrates. We suggest carbohydrates may play a role in the differential regulation of collagenolytic activity in TDP and non-TDP E. faecalis.

In our current study, we determined the ability of TDP and non-TDP strains to metabolize carbohydrates by a phenotypic microarray analysis performed in a Biolog system. We found that pre-operative non-TDP strains preferentially metabolize carbohydrates. By performing qRT-PCR analysis, we found that non-TDP strains responded to carbohydrates with a profound increase in expression of gelE encoding collagenase in E. faecalis.

These data indicate regulation of metabolism and virulence by carbohydrates differs between TDP and non-TDP strains of E. faecalis. Further work assessing carbohydrate changes in the microenvironment may delineate their effect on the colonization of TDP strains at anastomosis.

Presenter(s): Peeta Li, Washington University in St. Louis
Session: Poster P1.28
Title: Strategic Prospective Memory Monitoring in Older Adults: The Time Course of Monitoring Deactivation and Reactivation
Advisor(s): Julie Bugg, Psychological & Brain Science, Washington University in St.Louis

Abstract: Prospective memory refers to remembering to perform intended actions upon encountering environmental targets. Strategic monitoring refers to using contextual information to increase or decrease attention (i.e., monitoring) in context in which targets are or are not expected to occur, respectively. Prior research has shown that younger adults are able to strategically monitor, as evidenced by a quick monitoring deactivation after the first trial followed by a monitoring reactivation across the last few trials in blocks of trials in which targets were not expected. However, to date no research has examined the time course of strategic monitoring in older adults. In the present study, we investigated older adults' ability to strategically monitor by examining the time course of monitoring deactivation and reactivation. Experiment 1 showed that older adults could quickly identify unexpected contexts and deactivate monitoring following the first trial, similar to previous research with younger adults. Experiment 2, however, showed no evidence for monitoring reactivation in preparation for the upcoming block in which targets were expected. These findings suggested that strategic inhibitory processes generally remain intact with increased age whereas strategic preparatory processes may not.

Presenter(s): Yanzhuo Li, Grinnell College
Session: Poster P2.10
Title: RNF4 and its cancer associated mutant have effects on genome instability
Advisor(s): Yee Mon Thu, Biology, Vanderbilt University
Co-Author(s): Yee Mon Thu

Abstract: Maintaining stable genome is essential for the existence of life. RNF4 is one of the key proteins that regulates genome stability because of its role in DNA damage repair and cell cycle regulation. Since genome instability is one hallmark of cancer, it is not surprising that mutations in RNF4 have been identified in cancer tissues. However, the contribution of these mutations to tumorigenesis remains unclear. We studied one cancer associated mutation of RNF4 to understand its role under DNA damage conditions. Using yeast as a genomic model, we demonstrated that this mutation may impair wild type's ability to provide survival advantage when the integrity of the genome was compromised. Concurrently, we also asked if cancer cells rely on RNF4 since these malignant cells constantly experience the stress of unstable genome. Using breast cancer cell lines, we demonstrated that RNF4 over-expression may increase micronuclei formation which is an indication of unstable genome.

Presenter(s): Edward Lopatto, Grinnell College
Session: Poster P3.12
Title: Abundance of resistance and virulence genes following manure application
Advisor(s): Shannon Hinsa-Leasure, Biology, Grinnell College
Co-Author(s):

Abstract: Manure from concentrated animal feeding operations (CAFOs) may disseminate antibiotic resistance and virulence genes when applied to soil. This study quantified the abundance of three antibiotic resistance genes and one mobile element gene (ermB, sul1, strB and int1) in soil before manure application, manure, manure injection line, and soil adjacent to manure injection samples from a swine CAFO relative to the 16S rRNA gene using quantitative PCR. The abundance of ermB, int1, sul1, and strB all significantly increased in soil after manure application. Additionally, this study determined the presence of stx1, stx2, eaeA, spvC, mecA, and tetB in all samples utilizing PCR. mecA and tetB were the only PCR target genes detected in the manure samples, and none were detected in the soil samples.

Presenter(s): Zhiye Lu, Carolyn Lorch, Grinnell College
Session: Poster P1.05
Title: Wee1 inhibition results in misoriented meiotic spindles with significantly decreased length in Xenopus laevis oocytes
Advisor(s): Joshua Sandquist, Biology, Grinnell College
Co-Author(s): Carolyn Lorch

Abstract: Meiosis, a fundamental biological process in eukaryotic cells, produces haploid gametes, thus enabling sexual reproduction and the perpetuation of genetic diversity. The successful assembly of the meiotic spindle is essential for proper distribution of genetic material in meiosis, and errors may result in infertility or birth defects. Recent data suggest that the tyrosine kinase Wee1 may perform the novel function of stabilizing the mitotic spindle through interaction with myosin-10, an actin-based motor protein, and we suspect that this interaction may also have an impact on meiosis. To characterize the effect of Wee1 on the meiotic spindle, we treated Xenopus laevis oocytes with

PD166285, a Wee1 small molecule inhibitor, at various concentrations, and examined the spindle phenotype via confocal microscopy. Wee1 inhibition results in significantly shorter spindles that are also significantly more deviated from perpendicularity to the cell membrane than control spindles. These phenotypes are expected to negatively impact normal meiotic divisions. Our results suggest a novel role for Wee1 in regulating the structure and/or function of the meiotic spindle.

Presenter(s): Shutian Lu, Kaylyn Nicole Billmeyer , St. Olaf College
Session: Poster P3.21
Title: The Preferential Destabilization of GC-rich RNA Duplexes by L-Proline Explained
Advisor(s): Jefferey Schwinefus, Department of Chemistry , St. Olaf College
Co-Author(s): Kaylyn Nicole Billmeyer, Jefferey Schwinefus

Abstract: To understand the role of L-proline as a probe of biopolymer conformational changes in vitro, the temperature dependence of proline interactions with the RNA dodecamer duplex surface exposed during unfolding was quantified using thermal and isothermal titration denaturation monitored by uv-absorbance. The m-value, which quantifies these interactions between proline and the RNA duplex surface area exposed (ΔASA) after unfolding, was measured using RNA duplexes with GC content ranging from 17-83%. The m-values from thermal denaturation decreased (became more negative) with increasing GC content indicating increasingly favorable proline interactions with the exposed RNA surface area. However, m-values from isothermal titration denaturation at 25.0 °C were independent of GC content and less negative than those from thermal denaturation. The m-value from isothermal titration denaturation for the 50% GC RNA duplex decreased as the temperature increased and was in nearly exact agreement with the m-value from thermal denaturation. Since RNA duplex transition temperatures increased with GC content and m-value was observed to be independent of GC content, the more favorable proline interactions with the higher GC content duplex surface areas observed from thermal denaturation resulted from the temperature dependence of proline interactions rather than the RNA chemical composition. The enthalpy contribution to the m-value was positive yet small (indicating a slight increase in duplex unfolding enthalpy with proline) while the entropic contribution to the m-value was positive and increased significantly with temperature. Our results will facilitate the use of proline as a probe of the Δ ASA during biochemical reactions at different reaction temperatures.

Presenter(s): Samuel Mathai, Colorado College
Session: Poster P2.24
Title: Neuroguidin: a unique neuronal transcription factor
Advisor(s): Darrell Killian, Molecular Biology, Colorado College
Co-Author(s):

Abstract: Dendrites are the structures in the nervous system that receive information from outside the neuron itself. Proper dendrite formation is required for many roles of the central nervous system such as cognition, memory, and learning. Dendrite malformation is implicated in neurodevelopmental disorders that affect these areas. Here we investigated the role of lpd-2/neuroguidin in dendrite formation in the PVD neuron of C. elegans as model for neuron development. By labeling the PVD neuron of C. elegans with a fluorescent tag and knocking down expression of lpd-2 using RNAi, we have identified a neural phenotype caused by the under expression of lpd-2.

Presenter(s): Caitlin McCombe, Cara Hull, Carthage College
Session: Poster P2.04
Title: Acoustic signatures as aids in monitoring longevity in wild roaming Gray Wolves (Canis lupus)
Advisor(s): Angela Dassow, Biology, Carthage College

Abstract: Current monitoring of gray wolves utilizes invasive trapping and radio-collaring methods to study their population dynamics. Previous research has found that vocalizations can be used to determine individual identity on high quality recordings from captive animals and thus offers an opportunity for non-invasive monitoring of packs. In this study, wild wolves were recorded in Central Wisconsin in order to determine whether low quality recordings can be analyzed with similar feature selections as the captive animals. Preliminary results have demonstrated that acoustic features relating to frequency at the middle of the call, duration and patterns of change throughout the howl are the most useful features. Additional analyses were performed to verify which features are most useful in identifying individual wolves in the wild. The data collected during this study will be compared to data collected during the 2018 field season. Upon completion of additional testing, a novel and non-invasive method for monitoring gray wolves will be available for use in wildlife management.

Presenter(s): Carly Merritt, Colorado College
Session: Poster P1.22
Title: Co-localization of mTORC1 and hexokinase II favors OXPHOS phenotype in MPNST
Advisor(s): Brian Van Tine, Division of Medical Oncology, Washington University
Co-Author(s): Bethany Prudner

Abstract: Malignant peripheral nerve sheath tumors (MPNSTs) are rare, but highly aggressive Ras driven tumors that often occur in NF1 patients (~50%) or sporadically (50%). Currently, surgical resection and radiation are the only treatments, but are largely ineffective, resulting in a five-year survival rate between 20 and 50 percent. Understanding MPNST's unique metabolism may lead to the development of effective therapies. Preliminary studies show that oxidative phosphorylation (OXPHOS) is the preferred energy source over glycolysis in MPNSTs. We hypothesize that the MTORC 1/2 spatial and temporal function within this subset of tumors results in the preference of OXPHOS over glycolysis for energy production. Additionally, Arginine aids in the translocation of mTORC to the mitochondria where mTORC is capable of binding to hexokinase II resulting in an OXPHOS phenotype. Importantly, arginine succinate dehydrogenase I (ASSI), an enzyme necessary for arginine synthesis, is suppressed in most sarcomas. This causes the cells to become reliant on extracellular arginine. By utilizing an arginine deprivation drug, ADI-PEG20, extracellular arginine is removed. We further hypothesize that by depleting MPNST of arginine by ADI-PEG20, mTORC is unable to be localized to the mitochondria rendering the MPNST OXPHOS phenotype vulnerable. Within this study, the mechanism of MPNST OXPHOS was examined by utilizing immunofluorescence and immunoprecipitation to identify the localization of MTORC 1/2 in both ADI-PEG20 treated and untreated MPNSTs. We found that mTORC activation by phosphorylation decreases with ADI-PEG20 treatment and that mTORC localization changes from punta to dispersed. This change in localization and function may allow for new therapies to be developed in conjunction with ADI-PEG20 treatment.

Presenter(s): Nathan Meshbesher, St. Olaf College
Session: Poster P1.12
Title: Exploring TonB-dependant Sucrose Transport In Caulobacter crescentus
Advisor(s): Lisa Bowers, Biology, St. Olaf College
Co-Author(s): Nathan Meshbesher, Meryl Nath, Lisa Bowers

Abstract: An organism's ability to acquire nutrients is essential to its survival. Caulobacter crescentus, an aquatic gram-negative bacterium, lives in nutrient poor environments. It relies on a set of 65 surface proteins called TonB Dependent Receptors that actively transport nutrients into the cell.

This study focuses on one TonB dependant receptor, encoded by the cc1136 gene. Several of the neighboring genes have roles in sucrose metabolism so we hypothesized that this receptor is involved in sucrose transport. Previous work in the lab showed that the expression of cc1136 increases in the presence of sucrose. Here we show that cells with a knockout of cc1136 have a decreased growth rate when sucrose is used as the carbon source. These results support our hypothesis that the cc1136 gene encodes a sucrose transporter.

Presenter(s): Kathleen Mills, University of Chicago
Session: Oral C.4 (11:10)
Title: IL-5 signaling reduces edema to protect mice against mortality from acute lung injury
Advisor(s): Anne I. Sperling, Department of Medicine, University of Chicago
Co-Author(s): Donna M. Decker, Dana Bryazka, Catherine A. Bonham, Kelly M. Blaine, Stephenie T. Manns, Anne I. Sperling, Cara L. Hrusch

Abstract: Acute respiratory distress syndrome (ARDS) is a clinical diagnosis of acute lung injury (ALI) with a mortality rate of 20-40% and no specific treatment. ARDS is characterized by airway edema, bilateral pulmonary cellular infiltrates, and impaired gas exchange. In a bleomycin model of ALI, we have shown that ICOS-/- mice have decreased survival in addition to low IL-5 production. However, these mice can be rescued from death by treatment with exogenous IL-5. We hypothesized that IL-5 signaling is necessary for survival from ALI. Therefore, we obtained mice deficient in the high-affinity IL-5 receptor (IL-5Rα). Strikingly, these mice have increased mortality and lung edema after bleomycin challenge. They have severely impaired eosinophilia, which we also found in ICOS-/- mice. We also examined Treg expansion in both mouse strains as they have been shown to limit inflammation to protect mice from ALI. While Tregs failed to expand in ICOS-/- mice, they were activated and expanded normally in the IL-5Rα-/- mice, suggesting Tregs are not sufficient to promote survival during ALI. Thus, our data indicate an important role for IL-5 and its receptor in ALI, possibly through an eosinophil-regulated pathway.

Presenter(s): Mikael Mir, Gustavus Adolphus College
Session: Poster P2.11
Title: Bioinformatical analysis and characterization of open reading frame YGR021W from Saccharomyces cerevisiae
Advisor(s): S. Brookhart Shields, Biology, Gustavus Adolphus College
Co-Author(s): S. Brookhart Shields

Abstract: The open reading frame (ORF) YGR021W is an uncharacterized orphan gene (ORFan) in Saccharomyces cerevisiae with a known DNA sequence but an unknown function. Genomic data taken from the Saccharomyces Genome Database (SGD) was used to run various bioinformatical modules in which the ORFan's genomic and protein sequence were characterized. The function of the ORFan was hypothesized using various bioinformatic techniques such as conserved domain database (CDD) analysis, TIGRFAM and Pfam protein family sequencing, multiple sequence alignment, and cellular localization procedures. This data led to the hypothesis that YGR021W is homologous to YebC, a transcriptional regulatory protein, and localizes to the mitochondria within the cell. Specific knockouts were performed for YGR021W in order to determine the exact localization of the protein in addition to phenotypical changes. YGR021WΔ cells were imaged with GFP and confocal microscopy, and gene knockout phenotypes were observed.

Presenter(s): Zoe Moffett, Colorado College
Session: Poster P3.27
Title: Pollination Ecology and Natural History of Pedicularis groenlandica
Advisor(s): Shane Heschel, Organismal Biology and Ecology, Colorado College
Co-Author(s):

Abstract: Arctic and alpine ecosystems have been found to be highly susceptible to changes caused by shifts in global climate trends. For this reason, it is important to study both the plants and the pollinators within these vulnerable ecosystems in order to best hypothesize how their mutualistic relationships may be affected by predicted, future climates. This study focuses on exploring the natural history and reproductive strategies of Pedicularis groenlandica (little elephanthead or elephantella). Through various pollination treatments, it was found that pollen may be limiting to the seedset of these flowers. Flowers that were hand-pollinated with extra pollen tended to have slightly heavier seeds than those which were naturally pollinated by bees alone. Microphones were used to record the acoustics of bumblebee flight buzzes in order to see how the number of buzzes within a patch of flowers related to the seedset of those flowers. When controlled for factors of visibility (such as the number of inflorescences within the patch), the number of recorded buzzes predicted the average seed weight of the flowers within that patch. These findings, combined with past studies on P. groenlandica, indicate the importance of bumblebees, and their evolved buzz-pollination behaviors, to populations of this species of wildflower.

Presenter(s): Spencer Morgan, Hope College
Session: Poster P3.13
Title: The effects of diet, obesity and predisposition on anxiety-like behaviors in Sprague Dawley rats.
Advisor(s): Peter J. Vollbrecht, Biology, Hope College
Co-Author(s): Peter J. Vollbrecht, Jager Haan

Abstract: According to the Center for Disease Control, obesity is a growing epidemic with more than one third of the U.S. adult population being obese. Recently, studies have suggested a link between anxiety and obesity, and are often found to be comorbid. However, it has yet to be determined whether anxiety-like phenotypes and their underlying causes lead to obesity, or whether obesity may lead to anxiety-like behaviors. Here we utilized two distinct model systems in an attempt to further understand the relationship between anxiety-like behaviors and obesity. In order to study interactions between diet and anxiety development, outbred rats were given a junk-food (JF) diet which does not produce obesity. To examine interactions between obesity and anxiety development outbred rats were given a high fat (HF) diet to cause obesity. Finally, selectively bred rats were utilized to explore whether anxiety-like behaviors exist prior to obesity development. Our data suggest that anxiety-like behaviors are dependent on both genetic predisposition to obesity as well as actual obesity development.

Presenter(s): Josey Muske, Stefanie Huttelmaier, Carthage College
Session: Poster P3.06
Title: Characterization of cell surface markers on cancer cells cultured in atmospheric vs normoxic oxygen
Advisor(s): Andrea Henle, Biology, Carthage College
Co-Author(s): Stefanie Huttelmaier, Andrea M. Henle

Abstract: Cancer research is often conducted in vitro using cells cultured in flasks at atmospheric O_2, but this is not truly representative of in vivo conditions. This hyperoxic environment could influence the results obtained in in vitro experiments. To best study the interactions between immune cells and cancer cells, we must first understand the physiology and profiles of cancer cells in “normoxic”

conditions, similar to the in vivo setting. Celartia developed Petaka plates to closely mimic in vivo conditions by reducing O_2 levels to normoxic levels typically found in tissues. In this study, a panel of 9 cell lines representing both primary and metastatic uveal melanoma and colon carcinoma were used to investigate cell surface marker expression in atmospheric and reduced O_2. Cells were grown in T75 flasks or Petaka plates and the expression of 8 markers was analyzed by flow cytometry. The levels of upregulation or downregulation of cell surface markers was determined for each cell type in normoxic vs atmospheric O_2. Future research will be conducted to ensure consistent replication of cell growth periods and culture conditions, and to determine the mechanism by which different O_2 levels cause changes in cell surface marker expression.

Presenter(s): George Nahass, Colorado College
Session: Poster P1.19
Title: Brazilin Inhibits Fibril Formation of Alpha-Synuclein in vitro
Advisor(s): Jan Bieschke, Biomedical Engineering, Washington University in St.Louis
Co-Author(s): Niraja Kedia, Yuanzi Sun, Kevin Spehar

Abstract: Parkinson's Disease is the second most common neurodegenerative disorder caused by fibrils of alpha-synuclein (aS). Brazilin, a drug derived from Red Cedarwood trees in Brazil was shown to reduce fibrillogenesis of amyloid-beta in Alzheimer's Disease. To test if Brazilin has a similar effect on aS, we tested its effects in kinetic aggregation assays. aS (50 μM) was incubated with Brazilin at 0x, 1x, and 10x molar ratios. Samples were retrieved at 0, 24, 72, 168hr and imaged using Atomic Force Microscopy(AFM). The time courses of aggregate formation were analyzed by ThT fluorescence as described by Lam et al. (Biochemistry 2016) on aS treated with Brazilin in various concentrations (.1x, .5x, 1x, 2x, 10x). aS showed reduced formation of fibrils in AFM and reduced ThT fluorescence when treated with Brazilin. Circular Dichroism showed the absence of beta sheet structure, which is the hallmark of toxic amyloids. Ultracentrifugation and SDS-PAGE experiments showed that Brazilin treated protein stayed soluble. ThT aggregation assays were performed in the presence of 5% fibrillar aS, which showed Brazilin delayed the growth rate of aS fibrils. These findings indicate that Brazilin effectively delays aS fibril formation giving it potential as a neuroprotective and therapeutic agent for Parkinson's Disease.

Presenter(s): George Nahass, Colorado College
Session: Poster P3.19
Title: High Yield Bacterial Expression of Alpha-Synuclein via Escherichia Coli
Advisor(s): Jan Bieschke, Biomedical Engineering, Washington University in St. Louis

Abstract: Fibrillization of alpha-synuclein (aS) is a hallmark of Parkinson's disease and other synucleinopathies. Here, we've optimized a method of producing and purifying alpha-synuclein (aS) from E. Coli at high yield and high purity. We optimized bacterial density prior to induction and the protocol for bacterial lysis by allowing the bacteria to grow to an OD600 of 1.1, increasing sonication times, and lowering the volume of lysis buffer used. The optimized expression protocol yielded ~3x as much usable protein in the same time frame (~5 days) compared to the standard purification protocol. The reproducibility of aS fibrillization was tested via kinetic aggregation assays using thioflavin-T (ThT) fluorescence. Automated ThT assays were performed in a fluorescence microplate reader at aS concentrations from 15-90 uM. The concentration dependence of aS aggregation yielded similar results to aS purified by the previous protocol, the only difference being a slightly higher fluorescence signal shown with the new protein. Fibril morphologies of old and new protein were tested using Atomic Force Microscopy which showed consistent fibrils between preparations. We conclude aS made from this procedure can be used for all ranges of in vitro protein experimentation while vastly decreasing the time spent on protein purification.

Presenter(s): Kim Nguyen, Hope College
Session: Poster P3.03
Title: Drug Discovery: An Interdisciplinary Approach
Advisor(s): Maria Burnatowska-Hledin, Biochemistry and Molecular Biology, Chemistry, Hope College
Co-Author(s): Nicholas Parliament

Abstract: It is hypothesized that out of the 25,000-30,000 protein encoding genes in the human genome, approximately 3,000 genes are "druggable", meaning that their protein products may be modulated by small molecule compounds. Identifying small molecule modulators for these genes remains a pronounced goal of the scientific community, which could expand treatment options for countless pathologies.

Here, we present a vision for an interdisciplinary project that will expose undergraduate students to the fields of computer science, organic chemistry, and cellular biology in the context of novel drug development. Additionally, we present results from screening the anticancer potential of seven organic compounds as an example of one phase of this proposal. Our screens demonstrate the feasibility of this approach at the biological level, and future efforts may lead to the development of promising new anticancer agents.

Presenter(s): Michelle Noyes, University of Chicago
Session: Oral B.2 (10:30)
Title: Genetics of Commercial Monarch Butterflies
Advisor(s): Marcus Kronforst, Evolution and Ecology, University of Chicago

Abstract: The company Educational Science sells North American migratory monarch butterflies, but a previous experiment has shown that these commercial butterflies do not exhibit migratory behavior (Tenger-Trolander, 2017). In order to understand why these butterflies do not migrate, and what implications their release may have on local migratory populations, I am working to identify to which source populations the Educational Science butterflies are most closely related. I took fifteen Educational Science monarchs and had their DNA sequenced, and then, comparing to a reference genome, I identified variants (single nucleotide polymorphisms, or SNPs) in each DNA sequence. Next, using genomes of eighty-nine previously studied monarchs from populations around the world (Zhan et al., 2014), I can use the program Admixture (Alexander et al., 2009) to compare their variants with those of the Educational Science monarchs. Admixture will allow us to estimate the percentage of the genome that shares variants with a source population, such that we can match these individuals with their source populations. This process is still ongoing, but in several weeks I should know these butterflies' origins. Based on whether these butterflies are related to migratory or non-migratory populations, I can make further conclusions about why they do not migrate.

Presenter(s): Haley O'Neill, Grinnell College
Session: Poster P1.18
Title: The Effect of Manure Application on the Presence of Multi-Antibiotic Resistant Bacteria
Advisor(s): Shannon Hinsa-Leasure, Biology Department, Grinnell College
Co-Author(s): Kai Vorhies

Abstract: Industrial agriculture can contribute to the growing threat of antibiotic resistance via environmental exposure to fertilizer containing antibiotic resistant bacteria (ARB) and genes (ARGs). Such agriculture usually includes confined animal feeding operations (CAFOs), which concentrate animals in high densities, and require antibiotic administration to prevent and treat disease and to maintain weight gain. Antibiotic exposure occurs through treated feed and water and injections; 25-75% of antibiotics enter the environment in undigested forms. This environmental presence exposes

humans and surrounding environments to ARBs and ARGs, posing health threats. This study aims to quantify the presence of antibiotic resistance bacteria across time spans and sample types using community isolate characterization to determine how manure-based fertilizer impacts the presence and spread of ARGs and ARBs in unexposed and exposed environments. High rates of multi-antibiotic resistance bacteria were found across all sample times and conditions with an impressive amount of resistance within pre-manure soil samples and manure samples. Possibly pathogenic resistant bacteria were reported in manure exposed soil samples. These results illustrate the importance of similar research for suggest environmental and human health and prompt future analyses of antibiotic degradation time periods and the impacts of seasonality on degradation.

Presenter(s): Charles Ofosu, Macalester College
Session: Oral D.3 (3:00)
Title: What is in Areca? An investigation of the cholinergic and carcinogenic activities of molecules in areca
Advisor(s): Roger L. Papke, Department of Pharmacology and Therapeutics, University of Florida

Abstract: Commonly referred to as Betel nut, areca is consumed by about 600 million people worldwide. It is the 4th most widely-used addictive substance in the world and its consumption has been linked with an increased risk of oral diseases and cancers. In fact, the International Agency for Research on Cancer (IARC) lists betel quid—areca nut wrapped in betel leaves with added condiments—as a Group 1 carcinogen.

Previous work by the Papke Lab has shown arecoline, which is one of the 4 main alkaloids in the areca nut, to be a partial agonist to α4-sub-unit containing nicotinic acetylcholine receptors (nAChRs). These receptors are most closely linked to nicotine dependence. Recent discoveries by the lab point to the whole areca extract having even greater activity on α4- and α7-sub-unit containing nAChRs and muscarinic AChRs, more than arecoline by itself. These imply there is more to areca than the known alkaloids.

My project in the Papke lab was, therefore, to investigate what in areca caused such electrophysiological effects on these receptors. Voltage clamp analyses of the areca extract point to the inhibitory ingredient being in the high molecular weight fractions obtained from the dialysis, ultra-filtration and gel filtration chromatography of aqueous areca broths.

Presenter(s): Halie Ostberg, Gustavus Adolphus College
Session: Oral B.3 (10:50)
Title: Identifying genes involved in Drosphila ovulation through genetic screens
Advisor(s): Margaret Bloch Qazi, Biology, Gustavus Adolphus College
Co-Author(s): Elizabeth Knapp, Jianjun Sun

Abstract: Ovulation is the release of an oocyte from the ovary into the oviduct for fertilization, made possible by the proteolytic degradation of the layer of somatic follicle cells that surround the mature oocyte. In humans, ovulation is closely tied to multiple ovulatory disorders, including polycystic ovary syndrome (PCOS), infertility, and ovarian cancer. To better treat and prevent these disorders, the complex genetic regulation of ovulation must be understood. Recent work demonstrates that the follicle rupture process during ovulation is largely conserved between flies and mammals. In flies, this rupture process is induced by octopamine (OA), a neuromodulator similar to norepinephrine in mammals, which leads to the degradation of posterior follicle cells, the release of the oocyte, and the formation of corpus luteum. Such conserved mechanisms, along with high fecundity and a wealth of available genetic tools, make Drosophila a fitting model organism to explore ovulation mechanisms. In the present study, we seek to determine which genes are required for follicle rupture, and therefore for successful ovulation. Four genes expressed in the follicle cells of mature egg chambers were investigated for ovulation defects through in vivo and ex vivo ovulation assays, and all four were found to have ovulation involvement.

Presenter(s): Jacob Peecher, Hope College
Session: Poster P1.13
Title: Genomic and Physiological Characteristics of Novel Escherichia Strains Isolated from Freshwater Sources
Advisor(s): Aaron Best, Biology, Hope College
Co-Author(s): Kim Nguyen, Amy Olgers, Jacob Peecher, Adam Slater, Shannon Smith, Matthew Hughes, Chelsea Payne, Shay Pritchard, Luke Ragon and Aaron A. Best

Abstract: Escherichia coli is commonly viewed primarily as a commensal of the mammalian gut, but this view has begun to change with the recognition of "naturalized" populations of Escherichia found in non-host associated, secondary environments. We have produced 101 high quality draft genome sequences of Escherichia isolates from freshwater sources as part of a longitudinal survey of microbial communities in a watershed with high sediment pollution. We have placed our isolates into context with publicly available sequenced Escherichia strains using core genome phylogenetic inference and in silico multi-locus sequence typing. We found that 98 of the watershed strains fall within the traditional E. coli clade, while only three fall within the non-traditional environmental clades. We have used in silico methods to screen the 101 watershed strains for virulence factors and antibiotic resistance genes. Few differences were observed between watershed and reference strains. We conducted physiological experiments to test for metabolic activity of selected watershed strains at temperatures as low as 2°C, finding that many of the watershed isolates metabolize glucose at 8°C. Together, these data expand the available knowledge of potentially naturalized E. coli strains, allowing us to explore the genomic diversity of the Escherichia genus found in freshwater environments.

Presenter(s): Tanisha Perlmutter, Carthage College
Session: Poster P2.12
Title: Analysis of Pigment Cell Regeneration in a GNAQ Q209L zebrafish model of melanoma
Advisor(s): Andrea M. Henle, Biology, Carthage College
Co-Author(s): Josey Muske and Andrea M. Henle

Abstract: Transgenic GNAQQ209L zebrafish express a hyperactive, mutated Gα gene in their pigmented cells, melanocytes. This mutation is associated with human uveal melanoma and may cause increased proliferation and/or survival of melanocytes. We used zebrafish to study the role of GNAQQ209L during pigment regeneration. We amputated the caudal fin to analyze pigmentation changes and determine the origin of melanocytes during regeneration. We asked whether pre-existing melanocytes from adjacent tissue migrate into new tissue post-amputation, or whether unpigmented melanocyte precursors proliferate in regenerated tissue. This study used phenylthiourea to block formation of new pigment and address these two possible outcomes. Pigmentation in the regenerating caudal fin was analyzed weekly until week 7. We found no significant difference in the area of pigmentation pre- and post-amputation, but did find that expression of GNAQQ209L increased the total pigmented area compared to wild type zebrafish. Our results suggest that pigmentation in regenerating tissues in both GNAQQ209L and wild type zebrafish arises from unpigmented melanocyte precursors rather than migration of pre-existing melanocytes. This provides a better understanding of how GNAQQ209L affects melanocyte development and regeneration. Future research could identify downstream signaling pathways in diseases in which melanocytes are hyperproliferative, such as cutaneous melanoma or uveal melanoma.

Presenter(s): Tamia Phifer, Knox College
Session: Poster P3.28
Title: Comparison of MicroRNAs expressed by the parasitic plant, *Cuscuta campestris*, in response to different hosts
Advisor(s): Michael Axtell, Plant Biology, Pennsylvania State University
Co-Author(s): Saima Shahid1,2, Gunjune Kim3, Nathan R. Johnson1,2, Eric Wafula2, Feng Wang1,2,4, Ceyda Coruh1,2,5, Vivian Bernal-Galeano3, Claude W. dePamphilis1,2, James H. Westwood3, and Michael J. Axtell1,2

Abstract: Dodders are parasitic plants that infest many crops and wild plants. During a dodder infestation, cross-species RNA transfer occurs, with messenger RNAs and other regulatory RNAs exchanged between the parasite and host. In this experiment, we measured microRNA abundance within the dodder (Cuscutacampestris) and infested host plants (Arabidopsis thaliana and Nicotiana benthamiana). We collected tissue from 1) the interface between the host and parasite, 2) the host stem immediately above the interface, and 3) the parasite tissue adjacent to the interface. We extracted total RNA from each sample and prepared libraries for high-throughput sequencing of expressed small RNAs.

Presenter(s): Ngwe Sin Phyo, Beloit College
Session: Poster P2.22
Title: Effect of Distance from Soma on Sodium Conductance to Generate Action Potential Propagation in Axons
Advisor(s): Erin Munro Krull, Mathematics, Beloit College
Co-Author(s): Erin Munro Krull, Yizhe Tang, Shambhavi Upadhyaya

Abstract: Realistic axons are complex. This makes it difficult to predict the behavior during action potential (AP) propagation. It is often assumed that APs successfully propagate down the axon. When previous literature investigated APs in axons, it predicted AP propagation in electronically symmetric axons. Yet, we cannot predict propagation in electronically asymmetric axons. In this study, we looked at the sodium conductance (g_{Na}) of the axon, which determines the axon's excitability. We initiated APs in a collateral branch and tested if it successfully propagates to the end of the axon. The simplest model we used was a neuron with maximum three collateral branches. We simulated our neurons, varying the distance of the collateral branches along the axon and studying the threshold g_{Na} required for APs to propagate. From this research, we would like to develop a theory to predict AP propagation. That, in turn, we hope will tell us more about how neurons compute. Since the neurons are basic blocks of our nervous system, we also hope this will help future studies to improve treatment for neurological disorders.

Presenter(s): Kelsie Pos, Knox College
Session: Poster P3.14
Title: Evolutionary history versus dietary niche both shape pharyngeal jaw skeletal structure in cyprinid fishes
Advisor(s): Nicholas J Gidmark, Biology, Knox College
Co-Author(s): Matthew A Kolmann, Nicholas J Gidmark

Abstract: Minnows (Family Cyprinidae) are a trophically diverse clade, with species that specialize on myriad prey: plants, snails, insects or detritus; their evolutionary history is also well known. This makes minnows a phenomenal model system for studying the interplay between diet and evolutionary history in shaping anatomy. The anatomy of this family has only been marginally investigated in published literature (only 3% of species have been imaged), but these studies show tight correlation

between anatomy of the pharyngeal jaw and dietary specialization. We used micro-CT of 315 species of North American minnows (98% of species diversity) to evaluate how evolutionary history and dietary ecology have shaped this clade's trophic diversity. Preliminary results show high rates of trophic convergence and immense variation in several morphological aspects: 1) muscle attachment area; 2) relative size of the ligament spanning hemi-mandibles; and 3) tooth robustness. For example, herbivorous and durophagous species show large muscle attachment areas and robust ligaments compared to lean, thin-ligamented jaws seen in insectivores. This variation is consistent but less prominent within closely-related species, suggesting that phylogenetic history is important, and that relatively small changes in skeletal anatomy between congeners can accompany large shifts in diet.

Presenter(s): Rachel Potter, University of Chicago
Session: Poster P2.23
Title: Disruption of the Antiviral RIG-I Pathway by JC Virus
Advisor(s): Michaela U Gack, Microbiology, University of Chicago
Co-Author(s): Cindy Chiang

Abstract: The first line of antiviral defense is the body's innate immune response, which acts within hours of the pathogen entering the body. Many viruses have developed mechanisms to evade the innate immune response to establish infection. JC virus is a polyomavirus, a double-stranded DNA virus without a protein coat, present in over half of the human population. In healthy individuals, the virus is kept in check by the immune system, although in immunocompromised individuals the virus can progress to cause progressive multifocal leukoencephalopathy (PML). In both healthy and immunocompromised individuals, the immune system does not clear JC virus, allowing it to establish persistent infection. However, the molecular mechanisms by which JC virus evades innate immunity are not well understood. Mass Spectrometry revealed that JC's Small t Antigen protein binds to the innate immune protein TRIM25, which is an upstream activator of the viral RNA sensor RIG-I that is responsible for the detection of many RNA viruses as well as some DNA viruses. Furthermore, protein-binding assays reveal that Small t decreases non-degradative K63-linked ubiquitination of RIG-I, resulting in an overall inhibition of the pathway. This research highlights that viruses from different families have independently developed similar mechanisms to avoid RIG-I detection.

Presenter(s): Muhammad Rehman, Knox College
Session: Poster P2.01
Title: Enhancing the Properties of the GBH-1 Protein Hydrogel via Deletion Mutants
Advisor(s): Andrew Mehl, Biochemistry, Knox College
Co-Author(s):

Abstract: GBH-1 is an artificial protein biopolymer capable of forming a stable hydrogel under conditions of basic or neutral pH at low temperatures. This construct was derived from work on a mutant of the GrpE protein, whose alpha helix motif was found to form tetrameric species. Replication of this motif on either end of the GBH protein resulted in a protein network that in turn gave rise to a hydrogel. In order to obtain a more robust hydrogel that might have a greater range of applications, we created a range of mutant proteins with truncated spacer regions, which we theorize will form denser networks and as such result in a more robust product. In order to investigate this, preliminary thermal studies were conducted on the wild type GBH protein and a truncated mutant, which indicate that although our mutant is not more robust it may be able to form a protein network faster. We are currently working on, and hope to present a more complete analysis with thermal studies of more of our mutants. We also hope to have CD spectra to confirm the presence of alpha helical secondary structure and thus proper folding for all our samples.

Presenter(s): Jean-Baptiste Reynier, University of Chicago
Session: Poster P3.22
Title: Developing Clytia Hemispherica as a model for single-cell wound healing
Advisor(s): Jocelyn E. Malamy, Department of Molecular Genetics and Cell Biology, The University of Chicago
Co-Author(s): Jeanne Cardenas, Harry Kyriazes, Jocelyn E. Malamy

Abstract: The epithelium, which protects the surfaces of organs, is constantly subject to stress: micro-wounds between cells often occur, and the cells themselves also endure membrane tears. In vitro models do not allow for a complete understanding of the healing mechanisms in the cellular context of the intact organism. We therefore asked whether the jellyfish Clytia hemisphaerica, a new model organism with exceptional healing capabilities, could allow for in vivo studies of epithelial repair at the cellular level. Using the pressure of a cover slip to wound the animal, one can easily observe the healing of holes both inside and on the border of cells with DIC and fluorescent microscopy. Staining with CellMask indicates that the holes go through both membranes of the cell, though plasma membrane debris is present in some of the wounds. Surprisingly, the healing of the micro-wounds recapitulates the fundamental steps of multi-cellular wound healing: lamellipodia come together, adhere to one another, and a contraction of the wound ensues, extruding any cellular debris present in the wound. Phalloidin staining shows that actin recruitment at the wound is necessary for healing. This initial research demonstrates that Clytia is a powerful new tool to study single-cell wound healing.

Presenter(s): Jada Royer, Ryann Felton, Hope College
Session: Poster P3.05
Title: Establishing the Validity of a Novel Animal Model for Bipolar Disorder Through Behavioral Testing
Advisor(s): Leah Chase-Wallar, Biology, Hope College
Co-Author(s): Ryann Felton, Anna Lunderberg

Abstract: Bipolar disorder (BD) is a disorder that causes shifts in mood, changes in activity levels, and affects the ability to complete normal tasks. Previous experiments provided evidence of face validity for a BD rat model created by early postnatal exposure to homocysteic acid (HCA). Recently, we sought to test the predictive validity of this model by examining the effects pharmacological intervention on HCA-treated rats. Last summer, we observed lithium, a common treatment of BD, treated the manic behaviors, but not the depressive behaviors displayed by the HCA rats. Here, we investigated the effects of ketamine, a rapid acting antidepressant. We observed ketamine increased the time to the first passive behavior in the forced swim test and increased social interaction of HCA-treated rats, but it had no effect on the manic behaviors. Collectively these data suggest HCA treatment leads to a truly mixed manic/depressive state as predicted for BD.

Presenter(s): Dulce Saenz, Beloit College
Session: Poster P1.14
Title: Carbon Cycling in Managed Turf and Restored Ecosystems
Advisor(s): Chantal Koechli, Biology, Beloit College
Co-Author(s): Luke Zimmerman

Abstract: Microbial communities play an essential role in the soil carbon cycle. In the process of decomposing of organic matter, microbes produce CO_2, a greenhouse gas, as a by-product. Soil microbial community function may impact whether soils are sinks or sources of CO_2, potentially impacting the magnitude of climate change. I studied the carbon cycling and microbial communities in turf and native soil ecosystems along the Rock River in Beloit, WI, where restoration of native plants was recently done to prevent erosion. I hypothesized that the native soil would have greater CO_2

respiration than the grass soil. Replicate soil cores in the grass and native sites were taken and geochemical analyses, including soil moisture, water holding capacity, soil organic matter content, and pH, were done. I also measured soil CO_2 respiration over the course of five days. Geochemical properties of soil were not significantly different between the two treatments, but respiration did differ significantly. The turf soil respired more CO_2 than the native soil, which may indicate that carbon is more accessible to microbial communities in the turf soil than in the native soil.

Presenter(s): Natalie Sarver, Colorado College
Session: Poster P2.26
Title: Identification of Active Competence Pili in Acinetobacter baylyi Imaged by Atomic Force Microscopy
Advisor(s): Kristine Lang, Phoebe Lostroh , Physics, Molecular Biology ,
Co-Author(s): Sara L. Worsham, Natalie A. Sarver, Caroline M. Boyd, Kristine M. Lang, C. Phoebe Lostroh

Abstract: Many bacteria are able to take exogenous DNA from the environment and incorporate it into their own genome through the mechanism of transformation. Acinetobacter baylyi (ADP1) is a Gram negative bacterium that can acquire DNA this way. This soil bacterium utilizes appendages for the functions of motility, adhesion, and transformation. We are interested in active transformation appendages also known as Type IV Pili (T4P). In order to view T4P, ADP1 is exposed to DNA attached to nanoparticle gold spheres. Thus, appendages attached to gold spheres via the DNA are categorized as T4P, because they are in contact with DNA. In our lab, we utilize atomic force microscopy (AFM) to image and analyze appendages with spherical gold nanoparticles attached. In order to conduct further in-depth analysis of T4P and gold spheres, preliminary research was conducted to determine the specific parameters of gold balls as well as appropriate sampling populations.

Presenter(s): Matthew Schuiling, Hope College
Session: Poster P2.13
Title: Isolation and Identification of Fungistatic Compounds from Phytolacca americana and Phytolacca rivinoides
Advisor(s): K. Greg Murray and Dr. Elizabeth Sanford, Biology, Hope College
Co-Author(s): K. Greg Murray and Dr. Elizabeth Sanford

Abstract: The seeds of temperate and especially tropical pioneer plants must often survive in the soil despite threats from mammalian, arthropod, and microbial seed predators. Despite these challenges, seeds of some pioneer species such as *Phytolacca americana* and *Phytolacca rivinoides* have been known to remain dormant and viable in the soil for decades. Not until a canopy gap arises overhead do surviving dormant seeds germinate. Our research seeks to identify the chemicals that may protect seeds from fungal attack while they lie dormant in the soil. To isolate possible anti-fungal components of Phytolacca *Americana,* methanol seed extracts were prepared and then separated using preparative thin layer chromatography. We used poisoned-medium bioassays with pathogenic fungi on the separated fractions to further identify the compounds of interest. Once the most potent antifungal component was identified, it was purified and identified via proton nuclear magnetic resonance (^{1}H-NMR). We determined that the most toxic fractions from both species of *Phytolacca* had ^{1}H-NMR spectra very similar to that of a previously identified compound, Isoamericanin A.

Presenter(s): Alexis Sienczak, Gustavus Adolphus College
Session: Poster P2.28
Title: Thalassa testudinum blade measurements in two different environmental stressor sites surrounding Drago Beach Panama
Advisor(s): Alyson Dagang, School for International Training

Abstract: Marine ecosystems consist of a plethora of organisms and ecological mechanisms. Seagrass beds are regulators of climate change and provide homes for marine organisms. The effects of shade and excess nutrient have the ability to alter seagrass environments. Across three different sites in Drago Beach, Panama seagrass beds were examined based on different environmental stressors. Shade was found to have the most effect of blade measurement of Thalassa testudinum.

Presenter(s): Geordan Stukey, Hope College
Session: Poster P3.15
Title: Cluster K Mycobacteriophages May Have a Natural Growth Advantage at Lower Temperatures
Advisor(s): Joseph Stukey, Biology, Hope College

Abstract: Mycobacteriophages are viruses that infect mycobacterial hosts. About 1400 mycobacteriophages have been organized into at least 34 distinct groupings or clusters based on genomic sequence similarity. Some mycobacteriophages from Clusters A and K can also infect Mycobacterium tuberculosis, a distinction of potential medical importance. Recently, Hope College SEA-PHAGES students have been isolating predicted Cluster K phages at a higher frequency (≥ 2x) after changing the isolation temperature from 37°C to 32°C. We hypothesized that 32°C-isolated Cluster K phages (relative to non-cluster K phages) possess growth properties that give them a relative growth advantage at lower temperatures. To test our hypothesis, we used one-step growth assays to measure two key growth characteristics of a non-Cluster K and several PCR-supported Cluster K mycobacteriophages: 1) the latent period (time it takes to complete one full lysis cycle) and 2) the burst size (amount of phage released at time of lysis). The results were consistent with our hypothesis; 32°C-isolated presumptive Cluster K phages show higher burst size with no or minimal reduction in latent period at 32°C. Our findings provide insight into the growth behaviors of Cluster K phages at different temperatures that may be relevant to Cluster K mycobacteriophage environmental population dynamics.

Presenter(s): Alexis Stutzman, University of Chicago
Session: Oral E.3 (3:00)
Title: Lamin A/C is required for maintaining the structure and function of mature cardiomyocytes
Advisor(s): Ivan Moskowitz, Department of Pediatrics, University of Chicago
Co-Author(s): Kohta Ikegami, Ivan Moskowitz

Abstract: Point mutations to LMNA, the gene encoding the nuclear lamina component Lamin A/C, are responsible for laminopathies, a class of phenotypically diverse diseases that often affect the heart and whose molecular pathogenesis is unknown. Besides its well-characterized role as a structural component of the nuclear envelope, Lamin A/C have recently been implicated in gene regulation by directly interacting with chromatin. We hypothesize that Lamin A/C plays a critical role in regulating the gene expression program of cardiomyocytes. To define its role in the heart, we deleted Lmna in developing and adult mouse cardiomyocytes. The absence of Lmna during heart development resulted in severe growth retardation and postnatal death by 22 days of age. Strikingly, adult mice invariably died 4 weeks after Lmna deletion. Both postnatal and adult Lmna-null hearts exhibited

severe ventricular wall thinning, ventricular chamber dilation, and alteration of cellular and nuclear structures. Collectively, this indicates a requirement for Lamin A/C in maintaining the structure and function of the adult and postnatal hearts. We will aim to define the mechanisms underlying these phenotypes by examining the impact of Lmna-deletion on gene expression and identifying the direct chromatin targets of Lamin A/C in the heart.

Presenter(s): Yizhe Tang, Beloit College
Session: Poster P3.24
Title: Action Potential Propagation in Axons: How Sodium Conductance Can Linearly Estimate Propagation
Advisor(s): Erin Munro Krull, Mathematics, Beloit College
Co-Author(s):

Abstract: Predicting when an action potential can propagate in neuronal axons is a long-outstanding problem in both mathematics and neuroscience. Previous related research showed when an axon is electrotonically symmetric, the action potential propagation can be predicted. However, most axons are not electrotonically symmetric. This research uses simulation to provide evidence by looking at a key parameter: the sodium conductance of the axon. We hope to generate a fundamental theory to predict the action potential propagation linearly that can be used for different axon geometries.

We looked at different cases with some same parameters at certain values based on the simple neuron model that we constructed. In particular, I tested the cases by adding a sub-branch and varying the electrotonic length of the sub-branch the extra collateral branch. I looked at four parameters, the electrotonic length of the sub-branch, the electrotonic length of collateral branch, the distance of the sub-branch from the main axon and the distance of the parent branch from the soma. We may approximate propagation by looking at different combinations of these four parameters..

Presenter(s): Dustin Tillman, Washington University in St. Louis
Session: Oral F.2 (2:40)
Title: Investigating the recognition and attachment of heme in prokaryotic cytochrome c biogenesis
Advisor(s): Robert G. Kranz, Biology, Washington University in St. Louis
Co-Author(s):

Abstract: Cytochromes c (cyt c) play an essential role in many electron transport chains (e.g. respiration), making it important to understand how this protein is matured. Cyt c maturation occurs when heme is covalently attached, via two thioether bonds, to the cysteine thiols of a conserved CXXCH motif. Three pathways, two prokaryotic (Systems I and II) and one eukaryotic (System III), can mature cyt c. System II is proposed to utilize two integral membrane proteins (CcsBA) that transport heme from the cytoplasm to the periplasm and attach it to apocyt c via the conserved CXXCH motifs. A di-heme cyt c (cyt c4) with two CXXCH motifs was used to investigate the recognition capabilities of CcsBA. We conclude that full length cyt c cannot be matured at wildtype levels when either motif is mutated and that variation of one motif does not prevent attachment of heme to the other motif. These results demonstrate, for the first time, that the order of heme attachment is not fixed and that CcsBA has stringent recognition requirements. Similar variants and experimental techniques will be used to explore recognition requirements for the System I synthetase (CcmF/H).

Presenter(s): Aidan Tirpack, Macalester College
Session: Poster P2.20
Title: Determining hyaluronan's effect on Idiopathic Pulmonary Fibrosis
Advisor(s): Jeremy Herrera, Peter Bitterman, Craig Henke, Department of Minnesota, University of Minnesota
Co-Author(s): Jeremy Herrera, Peter Bitterman, Craig Henke

Abstract: Idiopathic Pulmonary Fibrosis (IPF) is a progressive lung disease of unknown cause. IPF is characterized by the accumulation of fibroblasts depositing extracellular matrix (ECM) within the alveolar wall leading to impairment of gas exchange. Unfortunately, the drivers of IPF fibrotic progression remain incompletely understood. We have previously identified the fibrotic ECM itself as a driver of fibrotic progression. We have discovered that when fibroblasts are cultured on decellularized IPF-ECM, ECM synthesis is activated through the deregulation of microRNA-29 (miR-29), a master negative regulator of ECM synthesis. We have found that Dicer1, a key regulator of microRNA processing machinery, is suppressed in IPF leading to deregulation of miR-29. Left unanswered is the mechanism by which IPF-ECM regulates Dicer1 expression. Hyaluronan (HA) is upregulated in IPF and increases fibroblast collagen synthesis. However, a direct link between HA and Dicer1 has not yet been described. To assess the effect of HA on Dicer1 expression we treated fibroblasts cultured on plastic, and examined Dicer1 expression by Western Blot analysis. Our findings indicate that HA, which is enriched within the fibroblastic core, can regulate Dicer1 expression. Further work is required to fully elucidate the effect of HA on Dicer1 expression.

Presenter(s): Toluwalope Toluhi, St. Olaf College
Session: Poster P1.15
Title: Prenatal Stress and Bone Development
Advisor(s): Sarah Amugongo, Biology, St. Olaf College
Co-Author(s): Cecelia Sagona

Abstract: Undisturbed fetal development is ideal for the future health of an organism. It is hypothesized that long term bone health can be negatively impacted by harmful alterations in in-utero developmental environment. Pregnant rats were subjected to the stress of immobilization three times daily for a randomly assigned week. Their pups were raised under normal laboratory conditions to remove other confounding stressors from their environment. The pups were sacrificed at four, eight, twelve, or sixteen weeks of development. Their bones were analyzed to see if the increase in cortisol released into their developmental environment impacted their bones. Preliminary results show by the age of 12 weeks, rats that experienced prenatal stress had lower cross-sectional thickness and medullary area of cortical bone compared to controls. However by the age of 16 weeks, there was no significant difference in cortical bone parameters between in-utero stress exposed and control rats. Trabecular number and thickness was also lower in experimental groups with no recovery by the age of 16 weeks. More analysis is underway. Our preliminary results indicate high doses of cortisol negatively alter the balance between bone cells, decreasing mineralization, osteocyte, and osteoblast function while increasing osteoclast activity. This leads to compromised bone structure.

Presenter(s): Shambhavi Upadhyaya, Beloit College
Session: Poster P1.24
Title: Action potential propagation in axons: the effect of electrotonic length on sodium conductance
Advisor(s): Erin Munro Krull, Mathematics, Beloit College
Co-Author(s): Yizhe Tang and Ngwe Sin Phyo

Abstract: Previous research has attempted to study action potential (AP) propagation in neuronal axons. However, significant results have only been produced for electronically symmetrical axons that are quite unlike realistic axons. Therefore, all possible geometrical irregularities in these have to be individually assessed. On the other hand, sodium conductance is a linear parameter in the Hodgkin-Huxley formula, and therefore it provides a simplification to this long-standing problem. We use this key parameter in our research, along with simulations and mathematical equations, to provide evidence that propagation in neocortical cells can be linearly predicted. That is, we model a collection of neurons with varying electrotonic lengths of their side branches, and check for the threshold sodium conductance in each case. The threshold sodium conductance required for propagation in different branches may then be simply added together to give the total axonal sodium conductance required for propagation. Typically, the physical makeup of a cell may completely change neuronal behavior. For example, brain injuries may lead to extra branches in axons, consequently affecting neuron computation. The results from our research therefore have an important role in determining how neurons compute, and how we may better diagnose and treat neurological conditions.

Presenter(s): Bethany Van Houten, Hope College
Session: Poster P2.14
Title: Temperature Effects and Mutants of Cluster K Mycobacteriophages
Advisor(s): Joseph Stukey, Biology, Hope College
Co-Author(s): Geordan Stukey

Abstract: Mycobacteriophages are viruses that infect mycobacterial hosts. Over 1400 mycobacteriophages have been organized into over 34 distinct groupings or clusters based on genomic sequence similarity. Some mycobacteriophages from Clusters A and K can infect Mycobacterium tuberculosis, a distinction of potential medical importance. Recently, Hope College SEA-PHAGES students have been isolating predicted Cluster K phages at a higher frequency (≥ 2x) after changing the isolation temperature from 37°C to 32°C. Additionally, these phages were unable to propagate at 42°C. PCR analysis supported Cluster K classification for many (11/16) predicted Cluster K phages isolated at 32°C, but few (3/23) isolated at 37°C. We hypothesized that Cluster K phages have a relative growth advantage at lower temperatures and that key growth properties relevant to that advantage are compromised at 42°C. To explore this hypothesis, we examined two characteristics that can influence the rate of infection initiation – phage stability and host adsorption at 42°C – of several known and PCR-supported Cluster K mycobacteriophages. For most tested 32°C PCR-supported K phages, stability at 42°C and host adsorption kinetics appeared largely unaffected. Our findings provide insight into the growth behaviors of Cluster K mycobacteriophages at different temperatures that may be relevant to their population dynamics in nature.

Presenter(s): Joel Vargeese, Knox College
Session: Poster P3.16
Title: Large bite forces maintained across gapes may evade length-tension constraints due to the muscular dynamics in the masticatory system of the primate Macaca mulatta
Advisor(s): Nicholas J. Gidmark, Biology, Knox College
Co-Author(s): Courtney P. Orsbon, Callum F. Ross, Nicholas J. Gidmark

Abstract: Bite force is important for the fitness of an animal. It is comprised of muscular force input (by the jaw-closing muscle) and jaw mechanics (skeletal morphology). We investigated how the force-length relationship of a jaw-closing muscle (masseter) relates to bite force across various gapes in

two Rhesus macaque (*Macaca mulatta*) monkeys during direct, supra-maximal nerve stimulation. The female we tested varied in biting force by 35% across gapes, whereas the male varied by 25% across gapes. This variation in muscular input is surprisingly small, given 18% and 55% length change of the MTU (muscle-tendon unit) in the female and male, respectively. We found that intermediate gape widths produced the highest bite force, and extreme gapes (both large and small) produced lower bite forces. We implanted radiopaque markers in the masseter muscle, skull, and mandible of each individual and filmed with x-ray video during the experimental stimulation events for XROMM analysis. At higher gapes, the muscle fibers rotated such that they were more in line with the line of action of the muscle-tendon unit (which we attribute to a decrease in pennation angles) and produced less lateral bulging. We propose that both active and passive mechanisms produce muscle bulging.

Presenter(s): Arun Velamuri, Gustavus Adolphus College
Session: Poster P1.16
Title: Analysis and characterization of protein with unknown function YGL101W.
Advisor(s): S. Brookhart Shields, Biology, Gustavus Adolphus College

Abstract: Though first sequenced over 20 years ago, 10% of Saccharomyces cerevisiae open reading frames, or ORFs, are uncharacterized. Characterization of these ORFs and potential proteins require mining of yeast bioinformatic data, that then allows for the development of suitable hypotheses on protein function. YGL101W is a yeast protein of unknown function that interacts with DNA Helicase Hpr5p and has a paralog from whole genome duplication, YBR242W. YGL101W was first tested for sequence similarity comparisons utilizing the BLAST algorithm to determine the presence of a viable protein. Structure based evidence was then accumulated and multiple sequence alignment searches were run to formulate predictions on function through homology between YGL101W and different protein families and motifs. Cellular localization data algorithms were used to predict protein membrane topology and cellular localization. The yeast deletion collection and YGL101W-deleted genetic and physical interaction and expression data were also for any viable information to further characterize protein function. Structure based evidence has revealed potential functioning of YGL101W as a phosphohydrolase with homology to the HD domain. This hypothesis was then tested by GFP localization, gene knockout tests, and other lab tests to determine its validity.

Presenter(s): John Wang, Grinnell College
Session: Oral F.3 (3:00)
Title: Homocysteine-amplified Effects of Oxidative Stress at Mouse Neuromuscular Junction are mediated by Nitric Oxide Synthase
Advisor(s): Clark Lindgren, Biology, Grinnell College

Abstract: Amyotrophic lateral sclerosis is a neurodegenerative disease which causes a progressive loss of motor ability resulting in muscle atrophy in patients. Its early etiology has yet to be characterized, but the endogenous amino acid homocysteine has been observed at elevated levels in many ALS patients. Thus, our goal is to elucidate the role of homocysteine in neurodegenerative diseases through using the mouse neuromuscular junction as a model to test the synergistic effects of homocysteine and oxidative stress on neurotransmitter release. Homocysteine was found to amplify the effects of oxidative stress at the neuromuscular junction; its effects were characterized by a significant decrease in quantal content and miniature end-plate potential (MEPP) frequencies. Furthermore, it was found that upon applying L-NAME, a nitric oxide synthase (NOS) blocker, the neuromuscular junction was rescued from the effects of oxidative stress. These results suggest that the synergistic effect of homocysteine and oxidative stress at the neuromuscular junction is mediated through nitric oxide as blocking its synthesis restored quantal content and MEPP frequencies back to control levels. Further work will investigate the critical target of nitric oxide and may thereby provide insight into the cellular mechanisms active during early stages of amyotrophic lateral sclerosis.

Presenter(s): Micaela Wells, Madison Buckner, Emily Arendsen, Hope College
Session: Poster P2.03
Title: Edge Effects on Non-Native Plant and Microbial Communities
Advisor(s): Kelvin Greg Murray, Thomas Bultman, Jianhua Li, Biology, Hope College
Co-Author(s): Madison Buckner, Emily Arendsen, Jennifer Fuller

Abstract: In forests across the planet, fragmentation creates extensive edge habitat in which light availability and soil composition differ from those of the forest interior. These edge habitats are known to increase the potential for non-native plants to establish in forest communities. We used protocols established by EREN (Ecological Research as Education Network) to construct permanent forest plots in a deciduous forest in southwest Michigan, in which we compared plant species composition, soil microbe activity, and various abiotic factors between edge and interior habitats. We found that edges had significantly greater abundance of non-native plants than did interior habitat. We also compared the ability of soil microbes to metabolize 31 different substrates, and found that aside from broad similarity in the functional diversity of edge and interior soils, 11 of the 31 substrates were metabolized more poorly in the presence of invasive non-natives. Some similarities and differences in non-native plant abundance among our plots seemed to derive more from location than from edge vs. interior locations, which may reflect land use history; our study area contains forests that have been recovering from agricultural use. These results highlight the need for managing forest edges to minimize competition between native species and non-natives.

Presenter(s): Meredyth Wenta, Carthage College
Session: Poster P2.15
Title: Manipulation of Danio rerio Melanosome Dispersion By Targeting Second Messenger Systems
Advisor(s): Andrea M. Henle, Biology, Carthage College
Co-Author(s): Andrea M. Henle

Abstract: Zebrafish pigmentation is caused by the presence of melanin-containing chromatophores called melanophores (Jensen, 2016). Melanin within these cells is packaged into organelles called melanosomes. Melanosomes move within the cell on microtubules, altering the pigment within cells. Dispersal of melanosomes darkens the cell, while condensation causes lightening (Jensen, 2016). Along the microtubules, melanosome movement is activated by the Ca2+ and cAMP second messenger systems (Jensen, 2016). Thus, dispersal of cellular pigmentation can be used to indicate activation of second messenger systems. To test this, melanosomes found in the caudal fins of Danio rerio were analyzed for movement before and after exposure to agonists and antagonists. Caudal fins from wild type (WT) and Tg(mitfa:GNAQQ209L) fish were placed in a wet mount of Ringer's solution, and melanosome dispersal was documented. Each caudal fin was subject to drug or chemical treatment, and then the melanosome movement was documented. Twelve treatments were tested on each line of zebrafish. In the recombinant cell line, epinephrine showed a slight decrease in pigment dispersion, indicating a condensing of melanosomes. Caudal fins from WT fish showed minimal variation with chemical treatment. Although epinephrine did cause a slight decrease in WT pigment dispersion, the value was not significant.

Presenter(s): Alicia Wilkening, Washington University in St. Louis
Session: Poster P2.02
Title: An Assay for Blood Parasite Detection in Golden Eagles (Aquila Chrysaetos)
Advisor(s): Eric Hayden, Biological Sciences, Boise State University
Co-Author(s): Alicia Wilkening; Stephanie Hudon; Julie Heath; Benjamin M. Dudek; Eric J. Hayden

Abstract: Birds contain greater diversity of Haemosporidian parasites than any other vertebrate and these parasites are most notably represented by three genera: Plasmodium, Haemoproteus, and Leukocytozoon. Recent studies revealed that while many birds infected with these parasites are

asymptomatic, their fitness is impacted, especially when the infection is coupled with a second infection or environmental stressors. The two common methods of screening for these parasites are nested PCR and blood-film microscopy, both of which are time and resource consuming as well as low throughput. This study employed an innovative use of quantitative PCR (qPCR) to screen for these three parasite genera with a single assay in golden eagles. We then adapted the assay to screen for specific strains and amplify the product for sequencing. This study determined that use of qPCR provides a sensitive, high throughput, and easily adaptable method to not only screen for infection but help determine the strain of the infecting parasite and the relative parasite load.

Presenter(s): Marta Williams, Luther College
Session: Poster P1.29
Title: Implications of Micra leadless pacemaker extraction for tricuspid valve integrity
Advisor(s): Paul A. Iaizzo, Visible Heart Lab, University of Minnesota
Co-Author(s): Alex Mattson, Paul A. Iaizzo

Abstract: The leadless pacemaker is a promising new technology that eliminates or reduces many of the complications associated with transvenous pacing systems. While clinical experience in leadless pacemaker extraction is limited, the increasing number of implants will invariably necessitate these procedures. To date, as the first-generation Medtronic Micra leadless pacemaker has no designated retrieval feature, off-the-shelf solutions have been devised to extract these devices: e.g., solutions that involve pulling exposed fixation tines through the tricuspid valve before sheathing them into a cup introducer. This study used formalin-preserved and fresh swine hearts to determine the forces required for tricuspid valve chordae tendineae rupture and leaflet penetration, and the forces produced by engaging chordae or leaflets with the Micra device. Statistically significant differences between the forces required to rupture tricuspid valve chordae tendineae and the forces produced by disengaging Micra device tines were observed. Additionally, statistically significant differences in the forces required for rupture were found between chordae of different types and in different locations. These data indicate that Micra leadless pacemaker extractions are likely to be safe in regards to maintaining tricuspid valve integrity.

Presenter(s): Brandon Wolfe, Colorado College
Session: Poster P3.25
Title: The Role and Localization of RNY1 Under Carbon Starved Conditions in S. cerevisiae
Advisor(s): Jennifer Garcia, Molecular and Cellular Biology, Colorado College

Abstract: Autophagy is a self-degradative process utilized by cells in nutrient limiting conditions. Using S. cerevisiae, we investigated the role of autophagy in mRNA degradation. Recent work has shown that autophagy may represent a novel degradation pathway for mRNAs, which results in mRNAs being shuttled to the vacuole for their subsequent degradation. A dysfunction in this pathway has been implicated in the neurodegenerative disease, Amyotrophic Lateral Sclerosis. This led us to further understand the function of RNY1, which is an RNase that catalyzes the degradation of RNA and is suspected to be localized to the vacuole. Furthermore, RNY1 seems to be regulating mitochondrial function under nutrient limiting conditions because our previous work suggests that mRNAs that encode mitochondrial proteins are specifically degraded by RNY1. To test this, we genetically removed RNY1 and observed if the number of functional mitochondria per cell was affected by flow cytometry. The results show a small but insignificant change between wild type and mutant strains lacking rny1. Next, we sought to determine the localization of RNY1 as experimental evidence suggests that RNY1 can leave the vacuole to degrade tRNAs. Therefore, we suspect that RNY1 may also have the ability to leave the vacuole to degrade mRNAs. To determine RNY1's localization we used CRISPR-Cas9 and replaced genomic rny1 with rny1 containing an internal GFP tag. This will allow us to visualize whether RNY1 localizes to the vacuole or mitochondria to degrade mRNAs that encode for mitochondrial proteins.

Presenter(s): Qiu Chang Wu, Colorado College
Session: Poster P3.20
Title: Construction and Characterization of a Noise Rheostat Using Small Molecule Induction in HEK293T Cells
Advisor(s): Hana El-Samad, Department of Biochemistry and Biophysics, University of California San Francisco
Co-Author(s): Joao Pedro Fonseca, Alain Bonny, Hana El-Samad

Abstract: Cellular heterogeneity is often overlooked in the study of molecular biology. In isoclonal cell populations in uniform environments, gene expression of the same gene varies across the population. Such variation phenomenon is described by noise biologist as gene expression noise. In recent years, gene expression noise has been shown to have a functional role in cell fate decisions and HIV latency reactivation. While efforts have been made to measure noise, less is known about how to control noise. Here, we present our efforts in developing a noise control system in the form of a genetic circuit which we call a noise rheostat. The basic architecture of the circuit involves two small molecule inducible transcription systems linked in series, driving expression of the green fluorescent protein gene. The in-series architecture has been shown by the El-Samad laboratory to be effective in controlling noise in *S. cerevisiae*. Using a human embryonic kidney cell line (HEK293), we performed transient transfections and characterized the system through drug dosage experiments using flow cytometry. Data was analyzed using MATLAB and revealed a promising first working prototype of a mammalian noise rheostat by demonstrating that gene expression variance may be dialable while maintaining the gene expression mean. Further experiments are required to ensure that such system may control endogenous gene expression noise. We suggest that the mammalian noise rheostat will be a useful tool in the study of noise biology.

Presenter(s): Ellen Wu, Washington University in St. Louis
Session: Poster P3.26
Title: Analysis of Drug Resistant HIV-1 Evolving in the Presence of Co-receptor Antagonist
Advisor(s): Lee Ratner, Molecular Oncology, Washington University in Saint Louis

Abstract: In recent years, co-receptor antagonists show promising potential for the treatment of HIV patients. However, the high genetic variability of HIV allows the virus can easily mutate and evade the effects of these drugs. Therefore, it is important that physicians characterize the viral tropism to determine whether or not this course of treatment will be effective for a patient. There are two major ways tropism can be determined: (1) phenotypic and (2) genotypic. Phenotypic methods are considered the gold standard, but genotypic methods are cheaper and faster. In this study, we have combined genotypic and phenotypic tropism determination methods to analyze patient samples from a co-receptor antagonist clinical trial. In one particular patient, we have isolated two distinct populations of drug evasion. We hope to identify key genetic sequences that are associated with drug resistance, and to use this information to construct more accurate tropism predictive algorithms to better direct the treatment of patients.

Presenter(s): Luke Zimmerman, Beloit College
Session: Poster P3.17
Title: An analysis of soil bacterial communities of different stages of prairie succession in southern Wisconsin
Advisor(s): Chantal Koechli, Biology, Beloit College
Co-Author(s): Dulce Saenz

Abstract: Agriculture disrupts soil, impacting microbe-mediated soil carbon cycling and resulting in reduced soil fertility and affecting the microbial ecology. We compared soil characteristics and microbial communities in soils at different stages of prairie succession in southern Wisconsin to

address how agricultural disturbance of the soil has affected soil properties. Soil geochemistry and microbial respiration was measured for undisturbed native prairie, restored prairie, and recently used agricultural fields of the same soil type. We found that there are significant differences in the geochemical properties, rates of respiration, and total abundance of microbial communities between the agricultural field and the native prairie sites. The restored prairie showed significant differences with the native prairie in microbe abundance and water holding capacity, and with the agricultural field in microbe abundance and soil respiration. We concluded that utilizing these soils for agriculture has had a long-term impact on the ecology of the soil, with smaller abundances of microbes in the agricultural and restored prairie sites. Our results indicate that, despite superficial similarities like plant communities at the sites, the restored prairie showed greater similarity to the agricultural field in terms of geochemistry suggesting a prolonged transition (several decades) back to native prairie-like soil properties.

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