Midstates Consortium for Math and Science

Undergraduate Research Symposium in the Biological Sciences & Psychology

University of Chicago

November 11-12, 2016

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

Midstates Consortium for Math and Science
Undergraduate Research Symposium
Biological Sciences & Psychology
The University of Chicago
November 11 – 12, 2016

Program Schedule

Friday, November 11	All Friday evening events are at the La Quinta Inn & Suites: Lakeshore 4900 S Lake Shore Dr., Chicago, IL 60615
5:30 – 6:30 pm	**Registration**
6:30 – 7:30 pm	**Dinner buffet**
7:15 – 7:30 pm	**Greetings** Victoria Prince and Beatrice Fineschi The University of Chicago Michael Seymour Midstates Consortium for Math and Science Hope College
7:30 – 8:45 pm	**Keynote Lecture** **Dr. Jack Gilbert** Faculty Director, The Microbiome Center Professor, the University of Chicago Department of Ecology and Evolution Department of Surgery
8:45 – 9:00 pm	**Group Picture**

Saturday, November 12 Gaylord and Dorothy Donnelley Biological Sciences Learning Center (BSLC)
924 E. 57th St, Chicago, IL 60637

6:30 – 8:00	**Breakfast at La Quinta Hotel**	
8:00 – 8:15 am	**Load bus & vans – depart at 8:15 am sharp for University of Chicago campus** Groups with cars or vans will drive themselves; bus transportation is for everyone else. If not staying at the hotel Saturday night, please bring your luggage.	**Meet in LaQuinta lobby**
8:30 – 9:00 am	**Poster session 1 set-up**	**BSLC mezzanine**
9:00 – 10:00 am	**Oral Presentations of Student Papers** **Session A room 109, Session B Room 115** 9:00 - A.1, B.1 9:20 - A.2, B.2 9:40 - A.3, B.3	**BSLC**
10:00 – 10:15 am	**Break**	**BSLC lobby**
10:15 – 11:15 am	**Oral Presentations of Student Papers** **Session C room 109, Session D Room 115** 10:15 - C.1, D.1 10:35 - C.2, D.2 10:55 - C.3, D.3	**BSLC**
11:15 – 12:15 pm	**Poster Presentations – Session 1, P1.01 – P1.21**	**BSLC mezzanine**
12:15 – 1:00 pm	**Lunch buffet** Poster session 2 set-up	**BSLC lobby** BSLC mezzanine
1:00 – 1:30 pm	**Panel discussions** Graduate School Information Session Careers at Liberal Arts Institutions	**BSLC** Room 109 Room 115
1:30 – 2:30 pm	**Poster Presentations – Session 2, P2.01 – P2.20**	**BSLC mezzanine**
2:30 – 3:30 pm	**Oral Presentations of Student Papers** **Session E room 109, Session F Room 115** 2:30 - E.1, F.1 2:50 - E.2, F.2 3:10 - E.3	**BSLC**
3:30 – 3:45 pm	**Break – set up poster session 3**	
3:45 – 4:45 pm	**Poster Presentations – Session 3, P3.01 – P3.18**	**BSLC mezzanine**
4:45 – 5:00 pm	**Concluding Remarks** Complete evaluations & pick up dinner to go, if applicable	
5:15 pm	Bus leaves for La Quinta Inn	

Keynote Speaker: Jack Gilbert, PhD

Professor Jack A Gilbert earned his Ph.D. from Unilever and Nottingham University, UK in 2002, and received his postdoctoral training at Queens University, Canada. He subsequently returned to the UK in 2005 to Plymouth Marine Laboratory at a senior scientist until his move to Argonne National Laboratory and the University of Chicago in 2010. Currently, Professor Gilbert is the Director of the Microbiome Center and a Professor of Surgery at the University of Chicago. He is also Group Leader for Microbial Ecology at Argonne National Laboratory, Research Associate at the Field Museum of Natural History, and Scientific Fellow at the Marine Biological Laboratory. Dr. Gilbert uses molecular analysis to test fundamental hypotheses in microbial ecology. He has authored more than 250 peer reviewed publications and book chapters on metagenomics and approaches to ecosystem ecology. He is currently working on generating observational and mechanistic models of microbial communities in natural, built and human ecosystems. He is also on the advisory board of the Genomic Standards Consortium (www.gensc.org), and is the founding Editor in Chief of mSystems journal. In 2014 he was recognized on Crain's Business Chicago's 40 Under 40 List, and in 2015 he was listed as one of the 50 most influential scientists by Business Insider, and in the Brilliant Ten by Popular Scientist. In 2016 he won the Altemeier Prize from the Surgical Infection Society, and the WH Pierce Prize from the Society for Applied Microbiology for research excellence.

2016 Janet Anderson Lecture Award winner
Maria Burnatowska-Hledin, Chemistry and Biology, Hope College

Hope College Biology and Chemistry professor Dr. Maria Burnatowska-Hledin has been presented one of two 2016 Janet Andersen Lecture Awards by the Midstates Consortium for Math and Science. The award recognizes Dr. Hledin's longstanding success in teaching, research, involving students in research, and innovative curriculum design. Dr. Hledin has directed Hope College's interdisciplinary Biochemistry Molecular Biology (BMB) major since its inception in 2009 and led its accreditation by the American Society of Biochemistry and Molecular Biology (ASBMB) in 2014. Hope College became one of only thirteen institutions in the nation with an ASBMB-accredited major. Her research program has supported an average of 6-8 students per year and has garnered over $1.3 million in external grant funding. It is particularly noteworthy that all of Dr. Hledin's Hope College publications have included students as co-authors. More importantly, students working in Dr. Hledin's lab have enjoyed great success in getting into graduate programs, professional schools, and employed positions in the fields of biology, chemistry, and biochemistry. Last year's Janet Andersen Lecture Award winner, Dr. Laura Listenberger at St. Olaf College, did undergraduate research in Dr. Hledin's lab and has credited Dr. Hledin for her outstanding mentoring of students. Dr. Hledin is the Frederich Garrett and Helen Floor Dekker Professor of Biomedicine and Chemistry at Hope College, and was appointed as an A. Paul Schaap Chemistry Fellow at Hope College in 2013.

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.

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 and 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

Oral Presentations

SESSION A: 9:00 - 10:00 a.m. Room: BSLC 109			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
A.1 (9:00)	Ashleigh Bull	Grinnell College	Assessing indicated and alternative chemotherapeutic approaches to colorectal cancer
A.2 (9:20)	John Beckman	St. Olaf College	Relationships between bone mineral density and coronary calcification in postmenopausal women with history of preeclampsia
A.3 (9:40)	Miles Richardson	University of Chicago	Microbial Forensics in the College Dorm

SESSION B: 9:00 - 10:00 a.m. Room: BSLC 115			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
B.1 (9:00)	Vishok Srikanth	University of Chicago	Analysis of hyperactive MuA transposase variants suggests evolutionary compromises between accuracy and activity
B.2 (9:20)	Argie Claro, Ryan Yont	Carthage College	Comparing Cell Line Propagation Using Three Types of Cell Culture Medium: A Pilot Study
B.3 (9:40)	Olivia Stovicek	University of Chicago	Developing new genetic models for community studies

SESSION C: 10:15 - 11:15 a.m. Room: BSLC 109			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
C.1 (10:15)	Oleksandr Dmytrenko	St. Olaf College	Efficient modulation of gene expression in human hematopoietic stem and progenitor cells by CRISPR interference
C.2 (10:35)	Alex Chen	Washington University in St. Louis	Investigating odor-induced changes in firing activity in the antennal lobe of Schistocerca Americana
C.3 (10:55)	Danielle Rubin	University of Chicago	Differential signature and kinetics of IFN-β-1a vs. PEG-IFN-β-1a in multiple sclerosis treatment

SESSION D: 10:15 - 11:15 a.m. Room: BSLC 115			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
D.1 (10:15)	Rohan Shah	University of Chicago	Denaturative Internally Calibrated Chromatin Immunoprecipitation to Quantify Internal Histone Modifications
D.2 (10:35)	Katherine Zellner	University of Chicago	Wound Healing in Jellyfish
D.3 (10:55)	Remy Lee	University of Chicago	Associations between gut microbiota and neurological disorders in the American Gut data

SESSION E: 2:30 - 3:30 p.m. Room: BSLC 109			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
E.1 (2:30)	Madeline Aberg, Cassidy Coats	Gustavus Adolphus College	American bison cow mate preference
E.2 (2:50)	Annalyn Chia	Knox College	A comparison of bat species diversity in different Illinois habitats
E.3 (3:10)	Alyssa Welle	Gustavus Adolphus College	Oxygen Consumption During the Induction of Rapid Cold-Hardening in Isolated Muscle of Flesh Fly
SESSION F: 2:30 - 3:30 p.m. Room: BSLC 115			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
F.1 (2:30)	Catherine Wingrove	Hope College	Does eating junk-food make it harder to think?
F.2 (2:50)	Madison Kasoff	Washington University in St. Louis	The Beneficial Effects of Directing Attention towards Diagnostic Features in Category Learning

Poster Session 1: 11:15 a.m. - 12:15 p.m. Room: BSLC Mezzanine

Poster #	Presenter Name	Institution	Title of Presentation
1.01	Hansini Krishna	Knox College	The influence of auditory imprinting on music preferences and cortisol levels in chicks
1.02	Kina McCombs	Beloit College	The effects of temperature on enthalpy and entropy in the reaction of NADP+, 6-phosphogluconate, and 6-phosphogluconate dehydrogenase
1.03	Chloe Briney	Grinnell College	Expression and binding analysis of the putative Dictyostelium discoideum mannose 6-phosphate receptor
1.04	Zoe Schmiechen	Grinnell College	Concatenated nicotinic acetylcholine receptor subunits elucidate stoichiometry of modulation
1.05	Jian Zhi Cheong	Beloit College	Investigating the role of Fpgs3 in the Arabidopsis thaliana immune response
1.06	Maureen Lyons	Beloit College	Determining salt tolerance and its effects on the infection response of Arabidopsis thaliana
1.07	Tristan Grams	Carthage College	Isolation and analysis of bacteriophages collected from the International Space Station
1.08	Taylor Tibbs	Carthage College	Growth Deficiencies in Lipoprotein Mutants in Staphylococcus aureus Newman
1.09	Christine Solomon	Grinnell College	Competition and facilitation in neighborhoods of the annual plant, Chamaecrista fasciculata.
1.10	Katherine Aney	Gustavus Adolphus College	Upregulation Of MAD2 And CSE4 In Candida albicans To Investigate Aneuploidy And Cancer Formation
1.11	Daniel Kosiba	Hope College	Wildlife use patterns in a constructed wetland
1.12	Katarina Whittenburg	Knox College	Differential expression of small RNA between vegetative and reproductive tissue in rice
1.13	Rebecca Benner	Knox College	Exploring microRNA Expression in Cuscuta pentagona-Coleus blumei Plant Parasitism
1.14	Brandon Hinrichs	Macalester College	Structural and Biochemical Analysis of the DNA packaging motor of Bacteriophage Lambda
1.15	Penelope Kahn	Macalester College	Microhabitat Preferences of Harvestmen (Arachnida, Opiliones) in a Minnesota Oak Woodland
1.16	Eva Marie Larsen	Macalester College	Seasonal shifts in mating behavior dynamics of an Eastern North American harvestman, Leiobunum ventricosum
1.17	Andrea Studer	St. Olaf College	Improving a technique for visualization of intracellular lipid droplets
1.18	Ruth Blower	St. Olaf College	Investigation of a potential C. elegans perilipin gene: lipid droplet visualization in PLIN-1 RNAi knockdowns
1.19	Brianna Cunniff	St. Olaf College	There's No Place Like Home: Multilevel Selection Favors Viscosity
1.20	Maya Murzello, Elizabeth Casey, Sarah Ciombor	Carthage College	Improving neurite outgrowth in strokes using a cell culture model

Poster Session 2: 1:30 p.m. - 2:30 p.m. Room: BSLC Mezzanine

Poster #	Presenter Name	Institution	Title of Presentation
2.01	Poorva Jain	Washington University in St. Louis	How Ion Channels Maintain Homeostasis in Stressful Environments
2.02	Erica Ryu	Washington University in St. Louis	Factors that Influence Multicellularity in Dictyostelium discoideum
2.03	Snigdha Srivastava	Washington University in St. Louis	Determining How Variation in Brain Size Relates to Species Differences in Mormyrid Social Behavior
2.04	Samuel DeCero, Benjamin Boren	Carthage College	Detection of Mutated Human GNAQ in a Zebrafish Model of Uveal Melanoma
2.05	Tristan Tobias, Adam Krahn	Hope College	Temperature Effects on a Distinct Subset of Mycobacteriophages
2.06	Haley Fischman	Hope College	Host Lipids Associated with Genome Replication in Flock House Virus
2.07	Dylan Stahl	Knox College	A computational psychiatry approach to social valuation in Borderline Personality Disorder
2.08	Allison May Buiser	Knox College	Mycorrhizae in fossilized roots from the Early Cretaceous of Mongolia
2.09	Katherine Johnson	Beloit College	Detecting and quantifying apoptosis-inhibiting proteins activated by IGF-1
2.10	Trinity Gao	Macalester College	Toward Peptidomimetic materials: Optimization of Thiol-ene Coupling Reactions & Testing catalytic peptides
2.11	Amy Pelz	Macalester College	Using Random Mutagenesis to Identify Functional Domains in Trypanosoma brucei Editosome Proteins
2.12	Francisco Sanchez-Conde, Alexandra Schmiechen	Grinnell College	Design, Characterization, and Implementation of a DNA Sensor for HSA-Let-7a miRNA in Breast Cancer Cells
2.13	Isaac Krone	University of Chicago	The shape of 'Theres to come: the evolutionary history of mammalian cranial allometry.
2.14	Natalie Gray	University of Chicago	Probing the phosphoantigen-induced conformational change of the BTN3A1 intracellular domain by site-specific photocrosslinking
2.15	Brett Hahn	Macalester College	Relationship Between Serum Amyloid A & Host Microbiome
2.16	Ellen Iverson	University of Chicago	CRISPR-Cas9 as a novel DNA-Damage Tool for Studying Senescence
2.17	Arielle Hay	Carthage College	Characterizing Receptors for Zika Virus Infection of Retinal Tissue
2.18	Eleanor Mayes	University of Chicago	Characterization of genetically- and geometrically- modified M13 bacteriophage and its recovery via magnetic binding
2.19	Zoe Cohen	Washington University in St. Louis	Automatic Sleep Stage Classification using a Neural Network Algorithm
2.20	Emily Kozik	Grinnell College	Characterization of adult hippocampal progenitor cells on poly (ε-caprolactone) microfibers

Poster Session 3: 3:45 p.m. - 4:45 p.m. Room: BSLC Mezzanine

Poster #	Presenter Name	Institution	Title of Presentation
3.01	Sophie Ramirez	Colorado College	Optimizing the production of FOXA2 to unravel the interaction between Homeodomain and Forkhead Transcription Factors
3.02	Katherine Lane	Macalester College	The 2013 Chikungunya viral outbreak in Grenada: A phylogenetic analysis of introduction and spread
3.03	Carly Merritt	Colorado College	CD40 signaling in germinal center B cells does not change nutrient transporter expression
3.04	Katherine Miller	Colorado College	SUP-26 and Shep are conserved RNA-binding proteins that regulate dendrite development
3.05	John Hartman	Colorado College	BCR and CD40 signaling induce mitochondrial biogenesis in germinal center-like B cells
3.06	Amanda Gibson	Hope College	Effects of mutations on membrane expression and ubiquitination status on System xc- regulation
3.07	Malena Maxwell	Grinnell College	Optimizing FRET spectroscopy for detecting microtubule formation
3.08	Otabek Nazarov	Grinnell College	Surface Plasmon Spectroscopy for Microtubule detection
3.09	Benjamin Reynolds, Kenneth Crossley	Colorado College	Investigating Natural Competence in Acinetobacter baylyi by Atomic Force Microscopy
3.10	Alesia Hunter	Beloit College	The Chemical Properties of Mangrove Leaves from Polluted and Healthy Habitats
3.11	James Eckhardt	Gustavus Adolphus College	Style persistence, pollen limitation and edge effects in fragmented Echinacea angustifolia populations
3.12	Jae Un Yoo	Washington University in St. Louis	Learning Categories of Rocks: Comparing Rock Pictures and Actual Rocks
3.13	William Pan	Washington University in St. Louis	Genetic Variation Linked to Neuroticism is Associated With Amygdala Function
3.14	Lilianne Rothschild	Gustavus Adolphus College	Resting-State Functional Connectivity in Urologic Chronic Pelvic Pain Syndrome (UCPPS): Alterations during Bladder Filling
3.15	Jennifer Santos-Arevalo	Beloit College	Determining IGF-1 Signal Activation and Location in Neurons
3.16	Elliott Johnson	Hope College	Exploring the contribution of oxytocin receptor gene variation upon forgiveness attitudes
3.17	Casey Merkle	Lawrence University	Spiny water flea population dynamics in Green Bay and the lower Fox River.
3.18	Christopher Gager, Santiago Rios	Hope College	Effects of VACM-1/Cul5 Gene Knockout on Cellular Proliferation Using CRISPR-Cas9 Approach
3.19	Lutfe-E-Noor Rahman	Macalester College	The effect of Jasmonic Acid on Arabidopsis stress response to aluminum

Abstracts for all sessions listed in order by presenter's last name

Presenter(s): Madeline Aberg, Cassidy Coats, Gustavus Adolphus College
Session: E.1
Title: A multi-step process to determine the likelihood of inbreeding in an American bison herd
Advisor(s): Jon Grinnell , Biology, Gustavus Adolphus College
Co-Author(s):

Abstract: Female American Bison (Bison bison) tend to mate with more dominant bulls, but it is unclear whether this is due to bull hierarchy or cow preference. During the bison mating season, which occurs from mid-July to mid-August, males compete for access to females and tend a female until she is ready to mate. While being tended, the cows exhibit behaviors such as running, walking directly away from the bull, dodging, and rejecting a chin from the bull. We observed these behaviors during ten minute focal observations of cow-bull tending pairs throughout the mating season. Our observations of these behaviors suggest that female bison do not exhibit a preference toward bulls based on their age, dominance, or condition. This finding does not support our hypothesis that cows have a choice as to which bull they mate with, and instead gives evidence for male dominance hierarchy determining which bull a cow mates with.

Presenter(s): Katherine Aney, Gustavus Adolphus College
Session: P1.10
Title: Upregulation Of MAD2 And CSE4 In Candida albicans To Investigate Aneuploidy And Cancer Formation
Advisor(s): Laura Burrack, Biology, Grinnell and Harvard
Co-Author(s):

Abstract: In cancer cells, alterations to the cells chromosome segregation mechanisms are seen, leading to an unstable genome. During the segregation of chromosomes, the kinetochore is the protein complex that facilitates attachment of spindle fibers. One of the main proteins in the complex is centromere protein A (CENPA) and it is seen upregulated in cancer cells. Although the upregulation itself does not cause cancer or aneuploidy (a cancer hallmark), it creates an unstable genome that could lead to its development. MAD2 is a checkpoint gene in dividing cells that protects from rapid division. The goal of the study is to explore if increased expression of MAD2 and CSE4 (gene for CENPA) together induce aneuploidy in Candida albicans, a model for mechanisms that might promote cancer. MET3 and GAL1 were used as promoters to regulate MAD2 and CSE4 expression. Previously constructed strains of URA3-GAL1-GFP and NAT1-MET3 were amplified with PCR and a Lithium Acetate transformation incorporated the plasmids into SC5314 cells. -URA3 and +NAT1 plating as well as PCR selected and confirmed cells with the insertion. RT-qPCR will be used to measure expression levels of RNA and a chromosome loss assay based on resistance to 5-floroorotic acid (poisons cells in the presence of URA3), will be performed. The study hopes to determine whether overexpression of MAD2 and CSE4 in C. albicans will lead to the onset of aneuploidy.

Presenter(s): John Beckman, St. Olaf College
Session: A.2
Title: Relationships between bone mineral density and coronary calcification in postmenopausal women with history of preeclampsia
Advisor(s): Virginia M. Miller, Surgery, Physiology and Biomedical Engineering, Mayo Clinic
Co-Author(s): John P. Beckman, Jon J. Camp, Brian D. Lahr, Ann E. Kearns, Virginia M. Miller, David R. Holmes III

Abstract: Background: Preeclampsia, which is hypertension and proteinuria that occurs during pregnancy and resolves after delivery, may predispose women to cardiovascular disease. Relationships between preeclampsia, bone mineral density (BMD), and coronary artery calcification (CAC) have not been studied. We examined associations between BMD and CAC in postmenopausal women with former preeclampsia.

Method: This was a retrospective cohort study of 40 postmenopausal women with earlier preeclampsia, and 40 age/parity-matched controls with normotensive pregnancies, between 1976 and 1982. Quantitative Computed Tomography was used to assess vertebral BMD and CAC. Statistical analyses included linear regression with GEE to correct for within-subject correlations.

Results: There were no significant differences in BMD between preeclamptic and normotensive cohorts. Preliminary results reveal negative Spearman correlations between central BMD and CAC among normotensive subjects (-.392; P=.017), and positive correlations between cortical BMD and CAC among preeclamptic subjects (.336; P=0.042) and all subjects combined (0.268; P=0.022).

Discussion: We identified no differences in BMD among postmenopausal women with previous preeclamptic and normotensive pregnancies. Associations between cortical BMD and CAC for all subjects raise questions concerning systemic calcium burden and risk for coronary artery disease. Future research should explore relationships between calcium supplementation, BMD, and CAC among postmenopausal women with former preeclampsia.

Presenter(s): Rebecca Benner, Knox College
Session: P1.13
Title: Exploring microRNA Expression in Cuscuta pentagona-Coleus blumei Plant Parasitism
Advisor(s): Michael Axtell, Biology, Pennsylvania State University
Co-Author(s): Nathan Johnson

Abstract: MicroRNAs (miRNAs) are a class of small RNAs processed from hairpin structures, which regulate gene expression in association with Argonaute family proteins. Both plants and animals express miRNAs, and each kingdom's miRNAs have been extensively studied since their discovery in the 90s. To date, Arabidopsis thaliana alone has 325 documents miRNA sequences on miRBase. Although these miRNAs have been well described for cellular events such as heterochronic changes, tissue differentiation, and prolonged tissue identity, little is known about miRNA expression in plant parasitism. Previous studies with Arabidopsis thaliana have pointed to four key miRNAs that play a role in Cuscuta pentagona parasitism. Here, we investigate how host specific this miRNA expression pattern is by searching for the same miRNAs in a new host, Coleus blumei. Although the results of this short project were inconclusive, further research hopes to identify exact miRNA expression patterns in parasitic plant relationships.

Presenter(s): Ruth Blower, St. Olaf College
Session: P1.18
Title: Investigation of a potential C. elegans perilipin gene: lipid droplet visualization in PLIN-1 RNAi knockdowns
Advisor(s): Kimberly Kandl, Biology, St. Olaf College
Co-Author(s): Anna Mattson, Leah Plasek

Abstract: Perilipins are proteins found in the membrane of lipid droplets. In many organisms they determine whether stored fat is maintained or broken down depending on energy needs. Abnormalities in fat storage have been linked to obesity, type II diabetes, heart disease and cancer, so the ability to study perilipin function in an in vivo model is valuable. The somatic cells of Caenorhabditis elegans store and metabolize fat in a manner very similar to mammalian adipocytes, but until recently perilipins were not thought to regulate the process. However, a C. elegans gene with sequences homologous to perilipins was recently identified. Subsequent studies have attempted to demonstrate that this gene, named plin-1, regulates lipid turnover in C. elegans but the results have been inconclusive. To investigate the suggested role of plin-1 in C. elegans, we created plin-1 knockdowns through the use of RNA interference (RNAi). Preliminary results suggest that adult C. elegans with plin-1 knocked down have smaller lipid droplets than wild-type C. elegans, indicating that we may have successfully targeted and knocked down plin-1, and, furthermore, that plin-1 acts as a perilipin in C. elegans.

Presenter(s): Chloe Briney, Grinnell College
Session: P1.03
Title: Expression and binding analysis of the putative Dictyostelium discoideum mannose 6-phosphate receptor
Advisor(s): Richard MacDonald, Biochemistry and Molecular Biology, University of Nebraska Medical Center
Co-Author(s): Megan Zavorka Thomas, Richard MacDonald

Abstract: Dictyostelium discoideum, a social amoeba with a lysosomal system similar to that of humans, has a putative mannose 6-phosphate receptor (MPR). Characterization of this receptor will potentially provide a new model system for the study of lysosomal storage diseases and insight into the evolutionary origin of this family of receptors. This study is a binding analysis of the D. discoideum MPR using mannose 6-phosphate (M6P). The receptor cDNA successfully expressed in both mammalian and bacterial systems, and the expressed receptor did bind in pull-downs from 293-cell conditioned medium (cm) with resin beads bearing immobilized M6P. However, M6P failed to competitively displace the receptors. Future experiments aim to determine the concentration of M6P required to displace the receptor as well as identify other sugars that may act as better ligands.

Presenter(s): Allison May Buiser, Knox College
Session: P2.08
Title: Mycorrhizae in fossilized roots from the Early Cretaceous of Mongolia
Advisor(s): Fabiany Herrera, , Chicago Botanic Gardens
Co-Author(s):

Abstract: Little is known about fossil plants and fungi from Mongolia, especially during the Early Cretaceous Period. The Early Cretaceous (100-120 million years ago) is particularly important for studying the origin of flowering plants (angiosperms) and the diversification of conifer plants. Paleobotanists at the Chicago Botanic Garden have collected abundant lignified fossil plants in central Mongolia dated to the Early Cretaceous, the fossils collected include wood, roots, leaves, seeds and pollen and seed cones. Many of these fossils are related to the spruce and cypress families, and other forms of extinct coniferous and gymnosperm plants. There is evidence that the Mongolian fossil flora was deposited in a swamp-like environment. Spruce and pinus plants today form important symbiotic relationships with soil fungi, this relationship is hosted in the plant roots and it is known as mycorrhizae. The importance of studying fossil mycorrhizae adds further information about when this kind of mutualistic relationship evolved. Is there any evidence of mycorrhizae present in fossilized roots from the early Cretaceous of Mongolia? Given the abundance of fossil roots in the Mongolian flora, this material provides an important and unique opportunity to discover fossil mycorrhizae. The fossilized roots were collected and photographed for analyzing external morphology. The roots were then treated with, hydrogen peroxide, and undergo a root staining process in search of any evidence of mycorrhizae. The stained fossil roots were analyzed under light and fluorescence microscopes. So far, I have found exquisitely preserved forms of endomycorrhizae, mostly arbuscular and vesicular mycorrhizae, based on the presence of hyphae, vesicles, and spores. The fossil hyphae identified show septate and aseptate morphology. Interestingly, evidence of ectomycorrhizae is still lacking from the fossilized roots from Mongolia. The lack of ectomycorrhizae is puzzling given that pine plants today (e.g., spruce genus) form this important symbiotic relationship. Future work on the Mongolian fossil material will continue with the discovery and identification of the mycorrhizal diversity as well as fungal pathogens.

Presenter(s): Ashleigh Bull, Grinnell College
Session: A.1
Title: Assessing indicated and alternative chemotherapeutic approaches to colorectal cancer
Advisor(s): Charles W. Putnam, Cancer Center, University of Arizona
Co-Author(s): Nasrin Ghalyaie, Charles W. Putnam, David M. Mount

Abstract: Sporadic early onset colorectal carcinoma (EOCRC), CRC in patients under 45 years of age and not having a discernible inheritance pattern, is characterized by aggressive clinical behavior and, commonly, resistance to conventional chemotherapy for CRC. We sought to provide physicians with a clinical feature with which they could select a focus chemotherapy treatment. To examine chemotherapeutic options for EOCRC patients, we identified gene expression patterns in colorectal tumors based on clinical features and then queried LINCSCLOUD in order to identify novel drug choices with a greater likelihood of efficacy in EOCRC than conventional regimens. We analyzed the NCBI GEO data set GE39852 and associated clinical information utilizing a receiver operator characteristic curve and ultimately determined that tumor location (proximal or distal) provides the most distinct gene expression profiles. These expression profiles analyzed with LINCSCLOUD then provided chemotherapeutic mechanisms determined by the location: mTOR inhibitors for proximal cancers and tyrosine kinase inhibitors for distal cancers. Additionally, our analyses suggest that the current chemotherapeutic approaches are not suited to reversing the genetic expression.

Presenter(s): Alex Chen, Washington University in St. Louis
Session: C.2
Title: Investigating odor-induced changes in firing activity in the antennal lobe of Schistocerca Americana
Advisor(s): Barani Raman, Biomedical Engineering, Washington University in St. Louis
Co-Author(s):

Abstract: The brain is at every moment confronted with large amounts of sensory data; how it effectively processes this information and orchestrates appropriate responses is an important question in neuroscience. One proposed mechanism for this is predictive coding, whereby the brain uses information from memory and context to predict sensory input. What are the neural substrates underlying predictive coding? We examine the role of spontaneous activity in the locust antennal lobe in context of odor coding. We ask: how do the baseline activities in

projection neurons of the antennal lobe change with repeated presentation of an odor? And how do these changes aid the function of the antennal lobe in odor detection? Based on extracellular PN recordings of responses to regular puffs of a single odor, interlaced with trials of a novel “surprise” odor, we report robust changes in antennal lobe baseline activity with repetitive odor stimulation that function to enhance the salience of odor-evoked activity. We propose that these changes baseline activity in the antennal lobe carry odor-related information and thus may be a correlate of predictive coding.

Presenter(s): Jian Zhi Cheong, Beloit College
Session: P1.05
Title: Investigating the role of Fpgs3 in the Arabidopsis thaliana immune response
Advisor(s): Amy G. Briggs, Biology, Beloit College
Co-Author(s): April A. Apfelbaum, Amy G. Briggs

Abstract: A better understanding of the plant immune system is crucial for advances in fields such as agriculture and conservation. New interactions are constantly being found between the plant immune system and other seemingly unrelated systems. In previous studies probing the role of poly(ADP-ribosyl)ation in the plant immune response, microarray data showed differential expression of the folylpolyglutamate synthase (Fpgs) gene in response to pathogen-associated molecular patterns (PAMPs) in poly(ADP-ribosyl)ation gene knockouts, with further screenings suggesting that Fpgs3, encoding the cytosolic isoform, might be involved in the plant immune system. A gene-knockout approach was used to investigate the role of Fpgs3 in the two main branches of the plant immune system, PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI). Control and Fpgs3 knockout Arabidopsis thaliana plants were measured for downstream effects of immune response activation. Our results showed increased flg22-induced callose deposition and infection scores four days post-inoculation with Botrytis cinerea in Fpgs3 knockouts, while there was no significant difference in flg22-induced seedling growth inhibition and bacterial counts five days post-vacuum-infiltration with virulent and avirulent strains of Pseudomonas syringae. This preliminary study suggests that there might be interactions between the plant immune system and genes involved in folate homeostasis

Presenter(s): Annalyn Chia, Knox College
Session: E.2
Title: A comparison of bat species diversity in different Illinois habitats
Advisor(s): Jennifer Templeton, Jim Mountjoy, Biology, Knox College
Co-Author(s): Jennifer Templeton, Jim Mountjoy

Abstract: There are 12 species of bats that are native to Illinois; previous ecological surveys indicate that most of these species occupy forest habitats. Monitoring bat activity in different habitats provides information on local biodiversity and the effects of land management, wind energy, and disease on the bat communities. Bats utilize echolocation for foraging and navigation so acoustic surveying is one of the most common techniques used to study their occurrence and activity patterns. We surveyed bats in prairie and forest habitats at the Knox College Green Oaks Biological Field Station during mid-summer 2016. Ten species of bat were recorded and identified using the new Wildlife Acoustics EchoMeter and Anabat system. Subsequent data analyses showed that species diversity was similar between the two habitat types but that the species composition of each community differed. Activity levels of each species were also compared between the two habitat types. Most species were more active in forest; however, a few were more active in prairie. In the future, this new research technology will allow us to compare species composition and habitat use in additional habitat types over the course of the season.

Presenter(s): Argie Claro,Ryan Yont, Carthage College
Session: B.2
Title: Comparing Cell Line Propagation Using Three Types of Cell Culture Medium: A Pilot Study
Advisor(s): Antle Anderson-Antle, Nursing, Carthage
Co-Author(s): Ryan Yont

Abstract: Priority is wise use of funding resources conducting effective research. Alternative methods may provide cost savings, but studies are lacking. Fetal bovine blood (FBS) prices have increased, mainly to global shortages. A bottle of FBS and donor bovine serum (DBS), are priced at $500, $100, respectively. DBS may be cost advantageous to FBS. We compared two similar mediums: FBS/DBS to serum-free medium. Medium composition,

10% FBS/DBS was added to alpha-minimum essential medium, with 1% Penicillin Streptomycin. Day 0, cells were plated 6 x 104 cells/ml per culture medium. Cell confluence collected days 1-5, medium changed days 2 and 4, and day 6, densities calculated. Results expressed as means and standard deviations, groups compared by one-way ANOVA-HSD Tukey ($p < 0.05$). Cell densities for FBS, DBS, and serum-free ranged from 6.23-12.97 x 106, 7.29-28.31 x 106, and 0.048-4.99 x 106 cells/ml, respectively. FBS vs. DBS had comparable densities; while serum free differed significantly ($p < 0.01$). Cell confluency increased two-fold, stepwise in FBS/DBS. Serum-free grew gradually. We conclude serums, FBS and DBS promote cell propagation comparatively. These data may provide rationale to modify methods providing a cost savings.

Presenter(s): Zoe Cohen, Washington University in St. Louis
Session: P2.19
Title: Automatic Sleep Stage Classification using a Neural Network Algorithm
Advisor(s): Arye Nehorai, Electrical Engineering, WUSTL
Co-Author(s):

Abstract: For this project I developed and tested a neural network algorithm for the purpose of performing automatic sleep stage classification. Sleep is typically classified into five different stages: wake, N1, N2, N3/N4, and REM (rapid eye movement). The classification is based on various standards set by the American Academy of Sleep Medicine (AASM) and requires a trained sleep technician. In this project I wrote a neural network algorithm to perform classification based on these standards, thus making the process automatic. The neural network algorithm was developed by improving and building on previous iterations, the final result being a classifier capable of discriminating between five different classes with 80.82% accuracy.

Presenter(s): Brianna Cunniff, St. Olaf College
Session: P1.19
Title: There's No Place Like Home: Multilevel Selection Favors Viscosity
Advisor(s): Steven Freedberg, Biology, Saint Olaf College
Co-Author(s): Steven Freedberg

Abstract: Dispersal strategies of a species evolve to reduce competition with kin and to increase an individual's chances to produce offspring. While traditional studies focus on selection of dispersal within a species, this study examines the outcome of selection on among-species variation in dispersal tendencies. We created a computer simulation model exploring the population genetics of dispersal strategies. The model contains an autosomal dominant intraspecific aggression allele that presents itself in females and arises via mutation. We measured population sizes over thousands of generations, the distribution of the two species at the end of the simulation, and their rates of origination and extinction. Without the intraspecific aggression allele, dispersal was neutral; there were zero origination or extinction events for both species. Upon introduction of the intraspecific aggression allele, multilevel selection favors the low-dispersal species; the rate of origination exceeded the rate of extinction for the low-dispersal species while the opposite trend occurred in the high-dispersal species. Our results identify multilevel selection as an important force contributing to dispersal rates in natural systems and the distribution of species.

Presenter(s): Samuel DeCero, Benjamin Boren, Carthage College
Session: P2.04
Title: Detection of Mutated Human GNAQ in a Zebrafish Model of Uveal Melanoma
Advisor(s): Angela M. Henle, Biology, Carthage College
Co-Author(s):

Abstract: Uveal melanoma is the most common eye cancer among adults. While it is treatable with modern radiation therapies, approximately 50% of patients experience recurrent metastases to the liver that are often fatal. A novel transgenic line of zebrafish was generated to characterize the complex molecular signaling that causes these metastases and oncogenic growth. These fish possess the transgene mitfa:GNAQQ209L with an internal EE tag that can be used for detection. Our goal was to test antibodies that can recognize the internal EE tag in order to measure levels of mutant human GNAQ protein in transgenic zebrafish during cancer progression and in various tissues. We can then identify proteins involved in signaling pathways downstream of GNAQ, and ultimately determine what role GNAQ has in tumor generation and metastasis. In addition, successful detection of the GNAQ transgene through PCR has allowed for rapid and efficient genotyping of transgenic zebrafish. We have positively

genotyped our transgenic fish and have identified an antibody specific for our internal EE tag. We have therefore been able to detect human GNAQ in our transgenic zebrafish and will now research specific signaling pathways that may be implicated in this disease.

Presenter(s): Oleksandr Dmytrenko, St. Olaf College
Session: C.1
Title: Efficient modulation of gene expression in human hematopoietic stem and progenitor cells by CRISPR interference
Advisor(s): Vijay Sankaran, Hematology/Oncology, Boston Children's Hospital
Co-Author(s): Satish K. Nandakumar, Vijay G. Sankaran

Abstract: The recent development of CRISPR/Cas9 (CRISPRn) genome editing tools have raised substantial promise for targeted mutagenesis or introduction of site-specific modifications. However, several limitations have emerged. One major limitation is the inability to efficiently target genes or regulatory elements for silencing in a homogeneous manner in primary cells that cannot be clonally separated, such as primary human hematopoietic stem and progenitor cells (HSPCs). While progress has been made in using CRISPR in HSPCs, the outcome often results in mosaicism in terms of gene silencing or regulatory element perturbation. This poses challenges for both research and therapeutic applications. In our project, we explore whether CRISPR/dCas9-KRAB (CRISPRi), a transcriptional interference system with deactivated Cas9 nuclease fused to a repressor domain KRAB, can be more effective than CRISPRn for suppression of target genes/ regulatory elements in HSPCs. As a proof-of-principle, we have targeted regulatory elements of the DARC (encoding the Duffy antigen) and BCL11A genes in HSPCs and have characterized the ability of CRISPRi to effectively modulate gene expression and allow robust hematopoietic differentiation, as compared with CRISPRn. We additionally have laid the groundwork for further use of CRISPRi tools for genomic manipulation of HSPCs, particularly in the setting of long-term reconstitution assays.

Presenter(s): James Eckhardt, Gustavus Adolphus College
Session: P3.11
Title: Style persistence, pollen limitation and edge effects in fragmented Echinacea angustifolia populations
Advisor(s): Stuart Wagenius, Plant Biology and Conservation, Northwestern University
Co-Author(s):

Abstract: Echinacea angustifolia is native to the highly fragmented prairies of North America. Fragmented habitats are characterized by small, isolated populations with increased habitat edge to center ratios. Lower reproductive rates in fragmented populations relative to larger, contiguous ones can be a result of decreased pollen quality and quantity, which is termed pollen limitation. Pollen can be limited through nonsynchronous flowering times and isolation, however my research examines the relationships between edge effects and pollen limitation. I quantified the relationship between the distance of an Echinacea plant to the nearest habitat edge and pollen limitation, measured by style persistence, which was recorded every other day on over 800 plants in 25 remnant sites. Plants closer to habitat edges had significantly longer style persistence (ie. lower pollination) than plants further from the edge ($P = 0.02106$ when controlling for site). As plants were further removed from the habitat edge, mean style persistence decreased (ie. pollination increased) demonstrating that edges affect pollen limitation of Echinacea angustifolia. If Echinacea is a model for how edge effects alter reproduction of other similar prairie species, we can postulate that the reproductive fitness of other prairie species may be declining with increasing fragmentation.

Presenter(s): Haley Fischman, Hope College
Session: P2.06
Title: Host Lipids Associated with Genome Replication in Flock House Virus
Advisor(s): Benjamin Kopek , Biology , Hope College
Co-Author(s): Natalie Filipowicz

Abstract: Positive-strand RNA [(+)RNA] viruses are significant human pathogens that replicate their genomes in association with host intracellular membranes. Flock House virus (FHV) is a simple (+)RNA virus that replicates in insect cells. FHV replicates its RNA genome at the outer mitochondrial membrane of infected cells where it forms invaginations creating membrane-bound RNA replication complexes. Previous work by others has shown an increased amount of phosphatidylcholine in FHV infected cells. Additionally, decreasing the amount of phosphatidylcholine in Drosophila cells decreased FHV replication. We hypothesized that increased levels of

phosphatidylcholine were required for the formation and maintenance of the membrane-bound replication complexes .To test this, we synthesized the choline analog, propargylcholine. Propargylcholine is incorporated into phosphatidylcholine and can be “tagged” using copper(I) catalyzed cycloaddition chemistry, and then visualized with confocal fluorescence microscopy in FHV infected cells. Our results suggest an enrichment of phosphatidylcholine at the sites of FHV RNA genome replication. Additionally, two other major classes of cellular lipids, phosphatidylethanolamine and phosphatidylserine, were not enriched at FHV genome replication sites. Ongoing work includes quantitative analysis of the mitochondrial lipid composition of FHV infected cells. Our work provides support for the importance of specific lipids in (+)RNA virus genome replication and the possibility that lipid biosynthetic pathways may be good antiviral targets.

Presenter(s): Christopher Gager, Santiago Rios, Hope College
Session: P3.18
Title: Effects of VACM-1/Cul5 Gene Knockout on Cellular Proliferation Using CRISPR-Cas9 Approach
Advisor(s): Maria Burnatowska-Hledin, ,
Co-Author(s): Santiago Rios

Abstract: The VACM-1 gene codes for the VACM-1/Cul5 protein, which is a part of the ubiquitin E3 ligase system. This system is utilized to degrade cellular proteins. VACM-1/Cul5 expression is shown to decrease cellular proliferation. Lack of regulation in this pathway can lead to cancer. We utilized CRISPR-Cas9 to knockout the VACM-1 gene. The CRISPR system is a bacterial immune system that functions by targeting specific sequences of DNA. It can be programmed to target genes of interest, enabling specific gene editing in eukaryotic cells. We have used this system to knockout VACM-1/Cul5 in a human umbilical vein endothelial cell line (HUVEC). Growth assays indicate that VACM-1/Cul5 knockout allows cells to proliferate at an increased rate. We also explored whether CRISPR-Cas9 knockout of VACM-1/Cul5 comrpomises the antiproliferative effects of resveratrol. Our results indicate that VACM-1/Cul5 knockout cells do not respond to these drugs in the same manner as normal HUVEC cells, and experienced more rapid growth. We also aim to prove gene knockout via genomic analysis, as well as to use microarrays to explore possible pathways impacted by the knockout.

Presenter(s): Trinity Gao, Macalester College
Session: P2.10
Title: Toward Peptidomimetic materials: Optimization of Thiol-ene Coupling Reactions & Testing catalytic peptides
Advisor(s): Leah Witus, Chemistry, Macalester College
Co-Author(s): Demani Shikomba, Xinyu Liu

Abstract: Peptides are short strands of amino acids linked by a carbon backbone chain. They can have similar functions as full size proteins and can catalyze various reactions. Peptidomimetics are molecules that mimic the function of traditional peptides and are slightly more stable when in an unnatural environment. The tradeoff; however, is that peptidomimetics don’t always function as well as traditional peptides. Our goal is to find a novel peptidomimetic that is stable and has high functionality.

Presenter(s): Amanda Gibson, Hope College
Session: P3.06
Title: Effects of mutations on membrane expression and ubiquitination status on System xc- regulation
Advisor(s): Leah A. Chase, Biology and Chemistry, Hope College
Co-Author(s): Emma Hardy, Mackenzie Schmidt, Leah A. Chase

Abstract: System xc- exchanges intracellular glutamate for extracellular cystine, allowing for the synthesis of glutathione, a reducing agent for mitigating oxidative stress. Ubiquitin, a regulatory protein, reversibly attaches at lysine residues, numerous of which are highly conserved on the cytoplasmic side of xCT, a component of System xc-. Decreased ubiquitination is related to increased cell surface expression in other membrane proteins. We hypothesized that mutating lysine residues to arginine, which cannot be ubiquitinated, and mutations of a tyrosine-based motif, 462PAYYLFI468, that may interact with the ubiquitinating enzyme NEDD4-2 would result in increased membrane expression of xCT. We transfected COS-7 cells, which do not endogenously express xCT, with plasmid DNA for wild-type or mutated xCT, and we found that K41R and P462A mutations did not increase membrane expression. Because cells may compensate for the loss of one site, we are investigating additional lysine and tyrosine-motif mutants. Furthermore, we are optimizing a ubiquitination assay to determine if xCT associates with ubiquitin, and if increased membrane expression is related to decreased ubiquitination, providing a better understanding of the regulation of the cell surface expression of xCT.

Presenter(s): Tristan Grams, Carthage College
Session: P1.07
Title: Isolation and analysis of bacteriophages collected from the International Space Station
Advisor(s): Andrea Henle, Biology, Carthage College
Co-Author(s): Andrea Henle, Deb Tobiason, Nitin Singh, Kasthuri Venkateswaran

Abstract: The establishment of a permanent human presence aboard the International Space Station (ISS) in 2000 raised new questions regarding the presence of microorganisms inside the station. High-efficiency particulate filters (HEPA) have been installed inside the ISS as an environmental control system to recirculate and revitalize the air, thus lowering the level of harmful microbes that may affect an astronaut's health. NASA and other space agencies have pronounced interests in detecting and eliminating bacteria. The elimination of microorganisms such as bacteria is key, as it will hinder the ability to definitively conclude the presence of life on another planet. While multiple studies have investigated microorganisms that live inside the ISS, no research has been done on viruses that attack bacteria, bacteriophages. Bacteriophages are the most abundant organism on the planet. They are viruses that specifically infect bacteria and exploit the cell's machinery to replicate and lyse the cell, releasing new progeny. The goal of this interdisciplinary project is to isolate and characterize bacteriophages obtained from ISS HEPA filter samples. The isolated bacteriophage genomes will be sequenced, annotated, and compared to previously identified bacteriophages. Gaining an understanding of bacteriophage populations in space, along with the evolution of bacteriophage genomes in space habitation, allows for the potential application of bacteriophages in therapeutics and control of microbial burden in space.

Presenter(s): Natalie Gray, University of Chicago
Session: P2.14
Title: Probing the phosphoantigen-induced conformational change of the BTN3A1 intracellular domain by site-specific photocrosslinking
Advisor(s): Erin Adams, Department of Biochemistry and Molecular Biology, University of chicago
Co-Author(s): May Gu, Erin Adams

Abstract: A major subset of gamma delta T cells, Human Vγ9Vδ2 T cells, respond to both microbial infected and tumor cells which accumulate pyrophosphate containing metabolites called phosphoantigens (pAgs). We have gathered evidence that a cell-surface expressed receptor BTN3A1 mediates this activation via pAgs binding to its intracellular domain. Recent data indicates that BTN3A1 can adopt two distinct dimer conformations, and pAgs could induce a switch between them to signal γδ T cells. I've been exploring the previously unknown process of how pAg binding intracellularly to BTN3A1 triggers signaling to γδ T cells. To test whether the BTN3A1 intracellular domain changes dimer conformation when bound to pAgs, I incorporated a non-natural amino acid at strategic sites in the protein and performed site-specific photocrosslinking in order to probe the dimer conformation in the presence or absence of pAgs. Expression and purification of the mutant proteins was a success, but dimer formation was not observed, possibly due to protein instability or the lack of some key factors. I am attempting to address these issues by shifting the experiment to a mammalian system, which could supply missing factors necessary to facilitate both additional protein stability and the conformational change induced by pAg.

Presenter(s): Brett Hahn, Macalester College
Session: P2.15
Title: Relationship Between Serum Amyloid A & Host Microbiome
Advisor(s): Martin J. Blaser, Department of Medicine, New York University Langone School of Medicine
Co-Author(s):

Abstract: Although the gut microbiome characteristics are determinants of the development of obesity and metabolic disease, as well as immune response, the specific host-microbial interactions to promote these phenotypes are still being defined. In mouse models, we assessed microbial community diversity as determined by Serum Amyloid A genotype, and observed differences relative gene expression of SAA1/2 genes by varied antibiotic treatment. Our hypothesis is that microbiome community composition has an effect on SAA1/2 genotype, and that relative expression of Serum Amyloid A is impacted by perturbations to the microbiome through antibiotic treatment. To test these hypotheses, we assessed microbial communities in SAA1/2 wild type and knockout mice, and measured relative expression of SAA1/2 in ileum tissue from antibiotic-treated mice.

Presenter(s): John Hartman, Colorado College
Session: P3.05
Title: BCR and CD40 signaling induce mitochondrial biogenesis in germinal center-like B cells
Advisor(s): Olivia Hatton , Molecular Biology, Colorado College
Co-Author(s): Kylan Nelson and Olivia Hatton

Abstract: B cell activation is necessary for the response to foreign antigens and the establishment of memory, yet the metabolic changes following activation are not well characterized. T cells, like B cells, are lymphocytes of the adaptive immune system. T cells undergo metabolic reprogramming after activation to support their function and development of a memory response. We hypothesize that B cells undergo a similar metabolic reprogramming following activation. Specifically, we examined whether the two signals required for B cell activation – the B cell receptor (BCR) and CD40 – altered mitochondrial biogenesis. Successful activation was validated by upregulation of intracellular adhesion molecule 1 (ICAM-1). CD40 signaling changed the amount of mitochondria in a cell, measured by flow cytometry, peaking 48 hours post-activation. BCR and CD40 signaling together had a greater increase in mitochondria than signaling by either receptor alone; the combination induced a 2-fold increase in mitochondria over unstimulated cells. Finally, we observed that stimulation through BCR caused a decrease in cell viability after 48 hours, as measured by 7-AAD staining; this was partially rescued by CD40 signaling. Our study reveals that activation by BCR and CD40 ligation simultaneously leads to mitochondrial biogenesis. Additionally, CD40 ligation partially rescues cell viability from BCR-induced apoptosis.

Presenter(s): Arielle Hay, Carthage College
Session: P2.17
Title: Characterizing Receptors for Zika Virus Infection of Retinal Tissue
Advisor(s): Walter Low, Department of Neurosurgery, University of Minnesota
Co-Author(s): Vibha Harindra Savanur

Abstract: Zika virus (ZIKV) has been declared a global health concern. ZIKV is transmitted primarily through mosquitoes, and is able to cross the placental barrier in pregnant women and infect fetuses. There is evidence that the virus causes neural stem cell dysfunction and death in fetal brains, often leading to congenital defects such as microcephaly. ZIKV has been found to attach to host cell surface receptors, initiating endocytosis and allowing replication and increased virulence. The specific receptors and cell types susceptible to ZIKV remain elusive, although neural stem cells appear most vulnerable. Recent studies have identified four membrane receptors, AXL, DC-SIGN, DTK and TIM-1, that bind ZIKV in human skin cells. Clinical studies now demonstrate that the virus additionally can cause ocular malformations. It is hypothesized that these putative receptors allow viral entry into the developing neural retina. Immunohistochemistry demonstrated that AXL and TIM-1 were present in retinal tissue of fetal mice at early gestational stages. These findings indicate a route the virus takes when infecting fetal retinal cells, and give insight into how retinal lesions occur. These receptors may be targets for drug development, as there are currently no treatments available for Zika virus.

Presenter(s): Brandon Hinrichs, Macalester College
Session: P1.14
Title: Structural and Biochemical Analysis of the DNA packaging motor of Bacteriophage Lambda
Advisor(s): Marcos Ortega, Biology, Macalester College
Co-Author(s):

Abstract: The viral DNA packaging system in bacteriophage lambda can be utilized as a model to understand viral replication in the eukaryotic large DNA viruses. The catalytic process of DNA packaging is carried out by a molecular motor called the terminase. We mutated the dynamic ATPase site in order to stabilize the fully assembled lambda terminase structure. We found that the fully assembled mutant terminase was almost completely devoid of ATPase activity and showed increased nuclease and helicase activity, most likely due to increased binding affinity. The gpA subunit showed no differences between the mutant and wild type, showing the importance of assembly for functional activity. These results show that the ATPase inactivation is stabilizing one conformation of the complex. This is likely the processing complex before it transitions to a packaging complex. However, despite the decrease in activity and reduction in its dynamic nature, the proteins proved difficult to crystallize. In order to further increase stabilization of a single conformation for homogenous packing, we produced a 208-mer DNA substrate that would wrap once around the terminase structure. With impaired ATPase activity, the DNA substrate would not be hydrolyzed and instead act as a ligand, locking the terminase into one conformation.

Presenter(s): Alesia Hunter, Beloit College
Session: P3.10
Title: The Chemical Properties of Mangrove Leaves from Polluted and Healthy Habitats
Advisor(s): Angelia Seyfferth, Plant and Soil Sciences, University of Delaware
Co-Author(s): Danielle Dixson, Rohan Brooker

Abstract: Coral reef fish larvae are able to use olfactory cues to select a potential habitat. Recent research has shown that these larvae exhibit preferences for pristine, undeveloped locations and tend to avoid polluted, developed locations, yet the specific mechanism for the preference is unclear. Here, we investigated the metal and nutrient concentrations of Red Mangrove, Rhizophora mangle leaves collected from an undeveloped and developed site off the coast of Belize, for which coral larval fish have shown avoidance of leaves from the developed site. We quantified toxic metal concentrations after microwave-assisted nitric acid digestion using inductively coupled plasma-mass spectrometry (ICP-MS) and nutrients using acetic acid extraction and a technicon analyzer. We found that the developed site has significantly higher amounts of Cu, Zn, As, Sr, Fe, Ti and nutrients N and P in leaves than the undeveloped site. These analyses suggest that coral reef fish larvae are able to detect these chemicals when choosing a habitat.

Presenter(s): Ellen Iverson, University of Chicago
Session: P2.16
Title: CRISPR-Cas9 as a novel DNA-Damage Tool for Studying Senescence
Advisor(s): Stephen Kron, Department of Molecular Genetics and Cell Biology, The University of Chicago
Co-Author(s):

Abstract: Common experimental means of inducing DNA damage, including radiation or drug treatment, are unable to produce pure DNA damage without having other secondary impacts on cells. This limitation has prevented rigorous investigation into the precise role of DNA damage in various cellular processes, including accelerated senescence. Using CRISPR-Cas9, I have developed a means of inducing pure, dose-dependent DNA damage in cells that could help overcome this obstacle. Experiments have shown that the CRISPR-Cas9 construct is capable of inducing extensive DNA damage. I have also demonstrated that the level of stable Cas9 protein present in transfected cells and the degree of DNA damage can easily be modulated using a small molecule. Studies have linked senescence to various age-related pathologies, including serious lung conditions like idiopathic pulmonary fibrosis. Improving understanding of the relationship of DNA damage to accelerated senescence and the mechanism behind this relationship through research facilitated by this novel application of the CRISPR-Cas9 technology may help suggest new treatments for age-related diseases.

Presenter(s): Poorva Jain, Washington University in St. Louis
Session: P2.01
Title: How Ion Channels Maintain Homeostasis in Stressful Environments
Advisor(s): Dr. Yehuda Ben-Shahar, Biology, Washington University in St. Louis
Co-Author(s):

Abstract: Seizure, the Drosophila homolog of the potassium channel hERG, is integral in regulating neuronal excitability. Low expression of seizure or mutations in the gene region increases susceptibility to paralysis and seizure phenotypes in high temperature environments. Past research has shown that the neighboring ppk29 gene encoding for Sodium channel pickpocket 29 regulates seizure expression levels. The 3' UTR of ppk29 overlaps with the 3' UTR of seizure and regulates the mRNA expression levels of seizure by acting as a Natural Antisense Transcript. My research is aimed at understanding the evolutionary significance of this 3' UTR overlap region by testing multiple drosophila species. We want to first see whether the overlap exists in a species and then seeing how that affects both temperature sensitivity and expression levels of both ppk29 and seizure. Additionally, to understand the mechanism of how exactly seizure affects neuronal stress, we are testing flies in cold environments instead of high heat environments. This would be informative in seeing whether seizure works by reducing neuron firing rates, and hence mutations would increase resistance to the cold stress.

Presenter(s): Elliott Johnson, Hope College
Session: P3.16
Title: Exploring the contribution of oxytocin receptor gene variation upon forgiveness attitudes
Advisor(s): Gerald Griffin , Biology , Hope College
Co-Author(s): Trechaun Gonzalez

Abstract: In the context of interpersonal offenses, the level of empathy displayed by the victim for one's offender has been a significant predictor of granting forgiveness. The goal of the present study was to determine how variations in the oxytocin receptor gene at the rs53576 SNP influence attitudes and behaviors related to forgiveness. Participants (n=201) completed a set of surveys to evaluate attitudes towards forgiveness and empathy. Additionally, subjects ruminated on an interpersonal offense committed against them by someone they know. Participants then completed two different positive reappraisal conditions in counterbalanced orders: compassion-focused reappraisal and benefit-focused reappraisal. Next, saliva samples were obtained from each participant in order to extract DNA. The average purity (260/280) of DNA from collected saliva samples was 1.80 (SD: 0.061) and 1.75 (SD: 0.069) for male and female subjects, respectively. While genotyping is still ongoing, preliminary results have determined that 19 participants were homozygous for the A allele, 70 participants were heterozygous (AG), and 68 participants were homozygous for the G allele. Thus far, the study has captured DNA from saliva pure enough to evaluate genotypes at the rs53576 SNP of the human oxytocin receptor, a variation linked to individual differences in behaviors based on empathy.

Presenter(s): Katherine Johnson, Beloit College
Session: P2.09
Title: Detecting and quantifying apoptosis-inhibiting proteins activated by IGF-1
Advisor(s): Rachel Bergstrom, Biology Department , Beloit College
Co-Author(s):

Abstract: Neurons depend on growth factor signaling along the axon for regulation of growth and inhibition of apoptosis. Phosphorylation of intracellular pathways is thought to be caused by the retrograde trafficking of the IGF-1 receptor to the nucleus. The IGF-1 receptor has been found to protect neurons from degeneration as well as maintain neuronal development. This prospective capability of IGF-1 as an apoptosis-inhibiting agent is particularly important in the context of neurodegenerative diseases such as amyotrophic lateral sclerosis. The apoptosis-inhibiting pathways Akt and Erk are likely to be phosphorylated by proteins downstream from the activated IGF-1 receptor. The results of these experiments show that neurons stimulated with IGF-1 caused an activation of the Erk pathway and may play a role in neuron survival. Therefore, the effect of the IGF-1 receptor is important in the study of neuron degeneration.

Presenter(s): Penelope Kahn, Macalester College
Session: P1.15
Title: Microhabitat Preferences of Harvestmen (Arachnida, Opiliones) in a Minnesota Oak Woodland
Advisor(s): Sarah L. Boyer, Biology, Macalester College
Co-Author(s): Eva M. Larsen, Raine Ikagawa, Kasey Fowler-Finn, Sarah L. Boyer

Abstract: Though ecological preferences have been observed for Opiliones (harvestmen or daddy longlegs), few studies have measured those of Midwestern species. We aimed to determine the preferences of Minnesota harvestmen in terms of vegetation cover, canopy cover, plant species, and distance to the nearest tree, by gathering data from 182 quadrats in an oak forest habitat at Macalester's Ordway field station. We found seven species: Leiobunum aldrichi, L. calcar, L. politum, L. ventricosum, L. vittatum, Odiellus pictus, and Odiellus sp. Data we collected were compared with data on the vegetational composition of each quadrat. Significant relationships were found regarding our CVV group, L. calcar, L. ventricosum, and L. vittatum, (similar in their observed ecology), and our OP group, Odiellus species, and L. politum, (similar in their observed ecology), with several vegetation vectors, and between Odiellus species and canopy cover. Low R2 values indicate that though significant relationships exist, many components involved in microhabitat preferences have not yet been observed. The lack of significant relationships between most variables indicates that distribution of Midwestern Opiliones could be influenced by factors we did not measure, and/or that they can withstand habitat variations.

Presenter(s): Madison Kasoff, Washington University in St. Louis
Session: F.2
Title: The Beneficial Effects of Directing Attention towards Diagnostic Features in Category Learning
Advisor(s): Mark A. McDaniel, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Toshiya Miyatsu, Mark A. McDaniel

Abstract: Identifying conditions that enhance category learning presents an opportunity for improving science education (e.g., teaching rock categories in geology courses). However, research taking this approach is still scarce (e.g., Kornell & Bjork, 2008). We hypothesize that directing the participant's attention toward the diagnostic features of examples of categories will benefit learning of the category. In Experiment 1, participants studied categories of tropical fish at the family-level with small (100 px) and large (1000 px) images. Fish within a family-level category often have similar body shape but differ widely in their color and pattern. We predict categories learned through smaller images to be learned better, because smaller images should discourage attention to features within the image but not attention to the diagnostic shape feature. In Experiment 2, participants studied categories of tropical fish at the species-level, within which color/pattern is also a diagnostic feature. Accordingly, we predict no performance difference based on size manipulation of the pictures. Participants also made Category Learning Judgments (CLJs) to predict expected success of fish classification when presented with new images. We predict similar CLJ's in both experiments, wherein participants believe larger pictures aided learning the most – the opposite of their anticipated actual performance.

Presenter(s): Daniel Kosiba, Hope College **Session:** P1.11
Title: Wildlife use patterns in a constructed wetland
Advisor(s): Kathy Winnett-Murray, K. Greg Murray , Biology, Hope College
Co-Author(s): Amber Bosch, Monica Elliott

Abstract: Wetland habitats fill vital environmental roles because they potentially increase wildlife diversity, and provide important ecosystem services. The Outdoor Discovery Center in Holland began creating a wetland from an agricultural field in 2015, hoping to improve the quality of the environment and restore wildlife populations. However, this site is near a regional airport, which raises concerns for increased aviation collisions with wildlife. Our study investigates the potential wildlife hazard to aviation, and explores ecological questions regarding seasonal changes of wildlife in different habitats. Wildlife activity and abundance, as well as vertical vegetation structure were measured at the wetland and nearby comparison sites. Results thus far suggest no increased hazard to aviation, but wildlife has flourished in the new wetland. Pulses during seasonal migrations dominate changes in abundance, activity, and aviation threat in each habitat. Patterns of species composition and vegetation structure in the new wetland are becoming more similar to the wet meadow habitat it was designed to emulate. Compared to previous agricultural land use, the new wetland has shown an increase in wildlife species diversity and composition.

Presenter(s): Emily Kozik, Grinnell College **Session:** P2.20
Title: Characterization of adult hippocampal progenitor cells on poly (ε-caprolactone) microfibers
Advisor(s): Donald S. Sakaguchi, Genetics, development and cell biology, Iowa State University
Co-Author(s): Bhavika B. Patel, Farrokh Sharifi

Abstract: Cell-based therapies hold considerable promise towards the development of repair strategies for the damaged and diseased brain. Current nervous system regenerative approaches have yielded minimal results. However, advances in biomaterials coupled with neural stem cells provides new platforms for neural tissue engineering. Polymers such as Poly (ε-caprolactone) (PCL) are relatively simple to fabricate and can act as a scaffold to direct alignment of cell processes and may promote cell differentiation. Adult hippocampal progenitor cells (AHPCs) are multipotent neural stem cells that can differentiate into the fundamental cells of the central nervous system (CNS): neurons, astrocytes, and oligodendrocytes. In this study, the proliferation, differentiation, and adhesion of AHPCs on PCL microfibers was investigated. AHPCs were cultured for 7 days in vitro on PCL microfibers of various diameters including 5 μm, 20 μm, and 35 μm. Immunocytochemistry experiments were conducted using antibodies to label specific characteristics of differentiated cells. Ki67 antibody labeled proliferating cells and anti-Nestin labeled neural progenitor cells. Neurons were identified using TuJ1 and MAP2ab antibodies and glial cells were identified using GFAP and RIP antibodies. Preliminary results have shown that cells differentiate, proliferate and adhered to all PCL fiber diameters. This study demonstrates the potential application of PCL microfibers as effective scaffolding that supports the growth and differentiation of neural stem cells. Future studies will provide a detailed characterization of stem cell differentiation and function using additional in vitro and in vivo models.

Presenter(s): Hansini Krishna, Knox College
Session: P1.01
Title: The influence of auditory imprinting on music preferences and cortisol levels in chicks
Advisor(s): Esther Penick and Jennifer Templeton , Biochemistry, Brown University
Co-Author(s): Esther Penick and Jennifer Templeton

Abstract: Previous experimentation has shown that music has a neurochemical impact on the human brain. Young chickens (Gallus gallus domesticus) have been used as a model organism to determine the potential developmental effects that pre-exposure to sound can have on the chick embryo. A recent experiment performed in 2011 suggested that chicks can distinguish between consonant and dissonant music and that chicks have an innate preference for consonant music, possibly due to the similarity to maternal sounds. I hypothesized that prenatal exposure to consonant or dissonant music during incubation would have an impact on the type of music a one-day old chick would prefer and also affect its cortisol levels. After hatching, chicks were tested in a two-choice arena with dissonant and consonant music playing from speakers at either end. The percent time spent in each choice zone did not differ significantly in either the consonant or dissonant pre-exposure chicks, suggesting that pre-exposure altered the innate preference for consonant music, but not in the way we expected. ELISA tests will also be performed; we predict that chicks pre-exposed to dissonant music will exhibit higher cortisol levels than those exposed to consonant music.

Presenter(s): Isaac Krone, University of Chicago
Session: P2.13
Title: The shape of 'Theres to come: the evolutionary history of mammalian cranial allometry.
Advisor(s): Kenneth Angielczyk, Committee on Evolutionary Biology, University of Chicago
Co-Author(s): Kenneth Angelczyk, Christian Kammerer

Abstract: Within clades of both placental and marsupial mammals, there is a strong tendency for larger members of the group to have proportionally longer snouts compared to their braincase length and overall size. This same pattern has been documented in fossil temnospondyls, the likely ancestors of all extant tetrapods. This allometric pattern is theoretically enticing, but without a more comprehensive view of tetrapod cranial morphometrics it is impossible to distinguish whether the trait is derived independently in mammals and temnospondyls, or is a key feature of the tetrapod bauplan. Our study aims to discover when this pattern first appears in the synapsid lineage using a geometric morphometric analysis of ~270 non-mammalian synapsid taxa.

Presenter(s): Katherine Lane, Macalester College
Session: P3.02
Title: The 2013 Chikungunya viral outbreak in Grenada: A phylogenetic analysis of introduction and spread
Advisor(s): Shannon Bennett, Microbiology, California Academy of Sciences
Co-Author(s):

Abstract: Chikungunya virus (CHIKV) is a rapidly re-emerging global pathogen causing both acute and chronic disabling illness. There is currently no vaccine. CHIKV is transmitted to human by the mosquito vector Aedes aegypti and related species. CHIKV's rapid spread at the end of the 20th century has been driven by a) expanding mosquito vector populations as a result of urbanization and climate change and b) increased human global travel. CHIKV was introduced to Grenada in 2013 and collaborating scientists collected 143 CHIKV positive patient sera samples during the outbreak. At the California Academy of Sciences, RNA was extracted, RNASeq libraries were prepared, and Illumina Miseq sequencing was performed on 12 initial samples. Sequencing reads were parsed, cleaned, and assembled into viral consensus genomes. Phylogenetic analyses were performed using maximum likelihood methods. All of the Grenada samples except for one form a monophyletic group, suggesting a single main introduction of CHIKV into Grenada, as well as a rare importation from Brazil. This reflects human travel among Grenada and other islands in the Caribbean as well as South America. Because viral mutations facilitate emergence and determine disease dynamics, phylogenetic analyses of CHIKV provide a deeper understanding of this pathogen and public health challenges.

Presenter(s): Eva Marie Larsen, Macalester College
Session: P1.16
Title: Seasonal shifts in mating behavior dynamics of an Eastern North American harvestman, Leiobunum ventricosum
Advisor(s): Sarah Boyer, Biology, Macalester College
Co-Author(s): Sarah Boyer, Penelope Kahn, Raine Ikagawa

Abstract: Reproductive behavior in animals can vary seasonally, potentially in part because of seasonal changes in selection pressures on males and/or females. We examined seasonality in mating behavior in a North American species of Opiliones (commonly known as daddy longlegs or harvestmen), for which little is know about behavior or ecology. We provide the first formal description of mating behavior in Leiobunum ventricosum, and test for seasonality in behavior. We collected individuals from Inver Grove Heights, MN in mid-June, the middle of their mating season, and ran mating trials the following day. We ran a second set of mating trials 15 days later, and compared the precise timing, frequency, and sequence of mating behaviors between the mid- and late-June trials (e.g., mating attempt, eversion, insertion, and withdrawal of penis, etc.). We found significant increases in male mating attempts, the duration of male mate guarding, and female resistance to male mating attempts. Seasonal shifts in mating behavior may reflect changes in selection due to decreased mate availability later in the season, when we have observed decreased population density in the field. Notably, male attempts and female resistance suggest increased conflict in mating interests in the sexes as the season progresses.

Presenter(s): Remy Lee, University of Chicago
Session: D.3
Title: Associations between gut microbiota and neurological disorders in the American Gut data
Advisor(s): Dan Nicolae, Departments of Statistics and Human Genetics, University of Chicago
Co-Author(s):

Abstract: There is growing interest in gut microbial influences on brain functions in humans. Here we investigated associations between gut microbial composition and seven neurological disorders. Data were drawn from the American Gut Project, which collects fecal samples through a crowdsourcing model and detects the abundance of bacterial strains, termed operational taxonomic units (OTUs). The dataset includes abundance counts of each OTU in each sample and a compilation of participant responses to a questionnaire on health and demographics. Statistical analyses showed that for three of the seven disorders, cases contain significantly more diverse microbial compositions than controls. A regression-based test for association between the abundance of individual OTUs and disorder status showed few significant signals across the board, especially when the regression accounted for confounding variables strongly correlated with each disorder. Without the additional covariates, however, 48 of 142 genera were significantly associated with migraine. This finding calls for a focus on confounders that mediate the microbial influence of neurological disorders. One genus Brevibacterium was strongly associated with epilepsy; a different genus in the same order has previously been linked with seizure. The study demonstrates that while difference in microbial composition may influence neurological disorders, individual microbial effects are rarely significant.

Presenter(s): Maureen Lyons, Beloit College **Session:** P1.06
Title: Determining salt tolerance and its effects on the infection response of Arabidopsis thaliana
Advisor(s): Amy Briggs, Biology,
Co-Author(s):

Abstract: Crops are vulnerable to both environmental and biotic stresses. Environmental stressors can take many forms, drought, light, extreme temperatures, heavy metals, or salt. Because farming soil is slowly becoming more saline, understanding plant reactions to salt in combination with biotic infections is important. Abiotic and biotic stress signaling is started by many of the same phytohormones. Preliminary work was undertaken to determine a viable range of salt (NaCl) concentrations to use as stressors. These concentrations were then used in combination with flg22 to elicit an immune response during the early growth of Arabidopsis thaliana (Colombia) seedlings to determine if there was a visible effect on the growth rate. It was determined that 10 and 100mM concentrations of NaCl showed sufficiently different reactions to act as a viable assay. Plants when exposed to the higher concentration of salt did not grow normally. This implies that in early growth salt can significantly change the growth of Arabidopsis seedlings. There was not sufficient data to determine if flg22 in combination with NaCl changed growth significantly. Future studies to be conducted include an increase in data for NaCl in combination with flg22, assays with adult plants, salt assays with bacterial infiltration of adult plants.

Presenter(s): Malena Maxwell, Grinnell College
Session: P3.07
Title: Optimizing FRET spectroscopy for detecting microtubule formation
Advisor(s): Keisuke Hasegawa, Physics, Grinnell College
Co-Author(s): Francesca Varias

Abstract: Mitosis is the main mechanism through which cells proliferate. A major piece of molecular machinery used to perform mitosis is the mitotic spindle. This spindle is self-assembled by cytoskeletal protein filaments called microtubules. Tubulin heterodimers, the building blocks of microtubules, cannot be resolved using standard microscopy. A two-color Förster Resonance Energy Transfer (FRET) assay was developed in vitro to gain a better understanding of microtubule formation. We initially tested the efficiency of FRET between tubulin labeled with HiLyte-488 and Rhodamine. By calculating the Förster distance and spectral overlap between various fluorescent dyes, we discovered other optimal FRET pairs. To verify our calculations, we purified our own tubulin from porcine brains and fluorescently labeled them. We found FRET to be more efficient between an orange-red and near-infrared (NIR) pair as it had a two-fold increase in the sensitivity of microtubule formation.

Presenter(s): Eleanor Mayes, University of Chicago
Session: P2.18
Title: Characterization of genetically- and geometrically- modified M13 bacteriophage and its recovery via magnetic binding
Advisor(s): Elaine D. Haberer, Electrical and Computer Engineering, University of California Riverside
Co-Author(s): Joshua M. Plank, Tam-Triet Ngo-Duc, Elaine D. Haberer

Abstract: Phage display has been developed over the past 30 years as a method that allows for the creation of specialized multifunctional bacteriophage. These phage act as biotemplates, which have been used in the synthesis of bioimaging or photocatalyic devices, as their versatility allows binding of many materials. M13 is a filamentous bacteriophage that has groups of modifiable pIII and pVIII proteins, which have 5 and 2700 copies, distributed on the end of the filament and forming the viral protein coat, respectively. Genetic modification of these proteins results in peptide fusions, which can bind molecules such as streptavidin, or metal ions such as gold and zinc, to the phage. We transform the filamentous phage into a spheroid of 60 +/- 15 nm in diameter by exposing it to chloroform. The spheroid then has the potential to be converted into a janus particle of gold and zinc sulfide surfaces, to be used as a photocatalytic material for water decontamination. The transformation process from filament to spheroid was optimized and analyzed using circular dichroism, dynamic light scattering, UV-vis spectroscopy, and transmission electron microscopy. In addition, removal of phage from solution was investigated by binding to streptavidin-coated magnetic microbeads under an applied magnetic field.

Presenter(s): Kina McCombs , Beloit College
Session: P1.02
Title: The effects of temperature on enthalpy and entropy in the reaction of NADP+, 6-phosphogluconate, and 6-phosphogluconate dehydrogenase
Advisor(s): Theodore Gries , Biochemistry , Beloit College
Co-Author(s): Theodore Gries

Abstract: The enzyme 6-phosphogluconate dehydrogenase is a catalyst of the decarboxylation reaction of 6-phophoglucontae (6-PG) in the pentose phosphate pathway. A greater knowledge of the enzyme's mechanism can lead to drug treatments for African trypanosomiasis, cancer, and Alzheimer's disease because these cells also undergo this reaction. Velocity studies were conducted of the reaction at varying temperatures to calculate the thermodynamic contributions to each mechanistic step. Based on the velocity studies it was concluded that temperature, [6-PG], and [NADP+] are directly related. Conformational changes during the reaction were determined based on the equilibrium constants (Km, 6-PG, Km, NADP+, Ki, 6-PG, Ki, NADP+, Vmax) calculated at each temperature. It was found that the Km, 6-PG and Km, NADP+ steps had conformational changes. However, during the Ki, 6-PG, Ki, NADP+, and Vmax stages, no conformational changes were detected. In addition the enthalpy, entropy, Gibbs energy, and heat capacity of each step were calculated. All steps of the reaction were found to be enthalpically favorable and entropically unfavorable.

Presenter(s): Casey Merkle, Lawrence University
Session: P3.17
Title: Spiny water flea population dynamics in Green Bay and the lower Fox River.
Advisor(s): Bart De Stasio, ,
Co-Author(s): Cherise John, Jori Warwick, Rachel Wilson

Abstract: The spiny water flea, Bythotrephes longimanus, is an invertebrate aquatic invasive species in the Great Lakes that competes with native fish species for smaller prey. Bythotrephes makes two types of eggs, immediately hatching vs. resting eggs that tolerate harsh conditions and allow rapid dispersal. We determined spiny water flea population dynamics in Lake Winnebago, the Lower Fox River, and Green Bay in 2015 and 2016. Spiny water fleas were not observed in Lake Winnebago. They were not found in the Fox River in 2015 and only on a single date at one site in 2016. In Green Bay juveniles occurred as early as the third week of June in both 2015 and 2016. Adult females were observed by late June in both 2015 and 2016. Population dynamics were similar at both sites in each year, with peak population abundances in September of 2015 and late July in 2016. Resting eggs were produced by July 8 in 2015, and by June 17 in 2016, with continued production into at least early October in both years, after which sampling ceased. The results are being used by state authorities to guide management decisions related to boat use throughout the Fox River system.

Presenter(s): Carly Merritt, Colorado College **Session:** P3.03
Title: CD40 signaling in germinal center B cells does not change nutrient transporter expression
Advisor(s): Oliva Hatton , Molecular Biology, Colorado College
Co-Author(s): Carly Merritt and Olivia Hatton

Abstract: Metabolic reprogramming plays an important role in an immune response. For example, T cells shift their metabolism towards aerobic glycolysis after activation, supporting rapid proliferation. Nutrient transporters, like GLUT1, GLUT5, LAT1, and ASCT2, assist in metabolic reprogramming of T cells by providing substrates for ATP generation and macromolecular biosynthesis. In contrast, B cells increase oxidative phosphorylation and glycolysis equally upon activation through the B cell receptor (BCR) and CD40. CD40 signaling is also required for the generation of memory B cells from germinal center B cells; however, less is known about metabolic reprogramming in memory B cells. We examined if CD40 signaling changes nutrient transporter expression in germinal center B cells, using Ramos cells as a model. Stimulation of CD40 signaling by MEGACD40L was confirmed by examining ICAM upregulation by flow cytometry and quantitative real-time PCR (qRT-PCR). There were no significant differences in GLUT1, GLUT5, ASCT2, or LAT1 transcription after MEGACD40L stimulation, as determined by qRT-PCR. Our data suggests that CD40 signaling does not change transcription of GLUT1, GLUT5, ASCT2, or LAT1 in the germinal center like-line. Future studies may involve examining if CD40 or BCR signaling alters nutrient transporter expression in B cells at different stages of differentiation.

Presenter(s): Katherine Miller, Colorado College
Session: P3.04
Title: SUP-26 and Shep are conserved RNA-binding proteins that regulate dendrite development
Advisor(s): Darrell Killian, Molecular Biology, Colorado College
Co-Author(s): Amber Marean, Kiersten Kelly, Simona Antonacci, Logan Schachtner, Meghan Lybecker, Eugenia Olesnicky, Darrell Killian

Abstract: Dendrites are cellular processes of neurons that receive information from other cells or the environment. Proper branching of dendrites is important for making connections with other cells that dictate learning, memory, and behavior. Defects in dendrite branching are associated with neurological disorders such as autism and schizophrenia. Therefore, an understanding of how dendrite development is controlled at the molecular level is important. Recently, RNA-binding proteins (RBPs) have been implicated in neuron development in several species such as Drosophila, C. elegans, and mouse. However, the specific roles that RBPs play in neurons is still under investigation. RBPs can regulate RNA at many levels such as transcription, splicing, localization, translation, and degradation. The Drosophila RBP Shep and its' C. elegans homolog SUP-26 are important for dendrite development, suggesting they play an evolutionarily conserved role in dendrite development. However, their molecular functions are unknown. To investigate the molecular mechanism of SUP-26/Shep in dendrite development, we sought to identify (1) the molecular machinery that these RBPs physically interact with and (2) the RNAs they bind and regulate. To this end we immunoprecipitated SUP-26::GFP and Shep from worm and fly neurons respectively, and identified interacting proteins with mass spectrometry and interacting RNAs with deep sequencing.

Presenter(s): Maya Murzello, Elizabeth Casey, Sarah Ciombor, Carthage College
Session: P1.20
Title: Improving neurite outgrowth in strokes using a cell culture model
Advisor(s): Denise Cook-Snyder, Neuroscience,
Co-Author(s): Denise Cook-Snyder, Elizabeth Casey, Sarah Ciombor

Abstract: Stroke, the fifth leading cause of death in America, results in astrocytes becoming reactive and forming a glial scar surrounding the area of dead neurons. While the glial scar acts to protect the healthy part of the brain, it also prevents healthy neurons from repairing the dead tissue by inhibiting neurite regeneration.The focus of the research was to further understand neurite outgrowth using a neuroblastoma cell culture model. To induce differentiation, N2a neuroblastoma cells were exposed to either different concentrations of retinoic acid added at various time points in the cell's life cycle, serum starvation, or a combination of both. The retinoic acid was added over a period of two days. The results suggest that serum starvation and the addition of retinoic acid increases neurite length and outgrowth. Specifically, serum starved N2a cells in Fetal Bovine Serum exposed to high concentrations of retinoic acid at plating showed the highest percentage of differentiated cells. The conditions found to best differentiate N2a cells can aid future research in developing treatments in which the brain will repair connections lost through neurite regeneration. The long term goal of the project is to improve patient recovery after stroke by improving neurite outgrowth.

Presenter(s): Otabek Nazarov, Grinnell College
Session: P3.08
Title: Surface Plasmon Spectroscopy for Microtubule detection
Advisor(s): Keisuke Hasegawa, Physics, Grinnell College
Co-Author(s): Evan Porter

Abstract: Microtubule is an important protein for cell mitosis but a little known about it. This study uses gold nanoparticles (AuNPs) to discover whether surface plasmon resonance (SPR) can detect the microtubule. Gold nanoparticle solution and microtubule were mixed and their extinction spectrums were analyzed. The results suggest that SPR can be used for studies of microtubule and further research in this area can be continued.

Presenter(s): William Pan, Washington University in St. Louis
Session: P3.13
Title: Genetic Variation Linked to Neuroticism is Associated With Amygdala Function
Advisor(s): Ryan Bogdan, Psychological Brain Sciences, Washington University In St. Louis
Co-Author(s): Nadia Corral-Frias, Ryan Bogdan

Abstract: Neuroticism is a heritable personality trait characterized by emotional instability that places individuals at risk for psychopathology. The amygdala is a brain region that plays a critical role in assigning emotional significance to stimuli that may contribute to neuroticism. A recent GWAS (n=180,911) identified eleven genetic variations associated with neuroticism. Here, we explored whether single nucleotide polymorphisms (SNPs) that were associated with neuroticism at genomewide levels of significance are associated with neuroticism and threat-related amygdala function.

Genomic, neuroimaging, and self-report data were available for 448 non-Hispanic European-Americans who completed the ongoing Duke Neurogenetics Study. Threat-related amygdala reactivity was assayed using an emotional face-matching task while fMRI data were acquired. Neuroticism was assessed with self-report. Covariates included sex and ancestrally-informative principal components.

The risk alleles of three (TYRP1 rs10809559, SBF2 rs13923776, PAFAH1B1 rs12938775) SNPs were associated with elevated amygdala reactivity (all $\beta>0.032$, all $p<0.04$). The PAFAH1B1 rs12938775 allele associated with neuroticism in the GWAS was also associated with neuroticism in our dataset ($\beta=3.31$, $p<0.016$), however, neither TYRP1 rs10809559 nor SBF2 rs13923776 were (both $p>0.68$).

Genetic risk for neuroticism is associated with elevated threat-related amygdala reactivity. Increased amygdala response may be a genetically influenced neural mechanism conferring neuroticism and risk for psychopathology.

Presenter(s): Amy Pelz, Macalester College
Session: P2.11
Title: Using Random Mutagenesis to Identify Functional Domains in Trypanosoma brucei Editosome Proteins
Advisor(s): Susan Green, Chemistry, Macalester College
Co-Author(s): Suzanne McDermott, Ken Stuart

Abstract: African Sleeping Sickness (Human African Trypanosomiasis) is a disease caused when a eukaryotic organism called Trypanosoma brucei overwhelms the body. This protozoa is transmitted by tsetse flies, and affects humans and livestock in sub-Saharan Africa. Unlike virtually every other eukaryotic cell, trypanosomes post-transcriptionally edit their mitochondrial RNA to allow them to change methods of energy metabolism in the highly diverse environmental switch between the fly and the mammalian bloodstream. This RNA editing is carried out by protein complexes called editosomes. Research has isolated several endonuclease partner proteins on these complexes, which correspond with genes KREPB6 to KREPB8. In our project, we created a library of randomly mutated KREPB6, KREPB7, and KREPB8 genes to be used for testing in trypanosomes to see if the mutations they contain inhibit the cell from performing mitochondrial RNA editing. These mutations can then be specified as target loci for drug treatments.

Presenter(s): Lutfe-E-Noor Rahman, Macalester College
Session: P3.19
Title: The effect of Jasmonic Acid on Arabidopsis stress response to aluminum
Advisor(s): Susan Bush, Biology, Macalester College
Co-Author(s):

Abstract: Aluminum in acidic soil can inhibit plant root growth.1 Tomato plants with wild species ALS1 gene (a half-type ABC transporter on vacuolar membrane) show increased Al tolerance and higher expression of Jasmonic Acid (JA), a hormone involved in stress and wounding related response. Arabidopsis carrying domestic alleles of ALS1 gene as well as JA mutants can be tested for their sensitivity to different concentration of AlCl3 in agar growth media. Based on the results, we
concluded that JA alerts the plants to initiate stress response leading to less aluminum damage to the roots.

Presenter(s): Sophie Ramirez, Colorado College
Session: P3.01
Title: Optimizing the production of FOXA2 to unravel the interaction between Homeodomain and Forkhead Transcription Factors
Advisor(s): Olivier Lequin, Laboratory of Biomolecules, Universite Pierre et Marie Curie Paris 6
Co-Author(s): Olivier Lequin, Ludovik Carlier, Damien Samson, Sophie Ramirez

Abstract: Homeoproteins form a broad class of transcription factors with key roles in the embryonic development of animals, linked to many physiological and pathological processes [1]. In this family, Engrailed has an important role in the establishment of the nervous system and in the dopaminergic neurons physiology. Administrating Engrailed in animal models of Parkinson's disease has an antiapoptotic effect, which increases the survival of dopaminergic neurons, making it a potential pharmaceutical protein [2]. Engrailed holds interactions with manifold partners (DNA, proteins, membranes) and is essential for the regulation of both transcription and translation. It also engages in cell signaling pathways implying direct translocation through biological membranes [3]. The regulation of transcription of specific target genes by Engrailed involves the interaction with other protein partners. The project's goal is to characterize the structure-dynamics-function relationships of the homeoprotein Engrailed interacting with DNA sequences with/without partners[4,5]. One of the identified protein partners is FOXA2, a Forkhead transcription factor co-expressed with Engrailed. The interaction of FOXA2 with Engrailed has been demonstrated and is likely to play a key regulating role. The present research project aims to optimize a protocol for the isolation and purification of FOXA2 so the interaction with Engrailed can be further studied.

Presenter(s): Benjamin Reynolds, Kenneth Crossley, Colorado College
Session: P3.09
Title: Investigating Natural Competence in Acinetobacter baylyi by Atomic Force Microscopy
Advisor(s): Kristine Lang & Phoebe Lostroh, Physics & Molecular Biology, Colorado College
Co-Author(s): Kenneth Crossley, Caroline Boyd, Kristine Lang, Phoebe Lostroh

Abstract: Acinetobacter baylyi is a soil-dwelling bacterium which has the unique ability to take in DNA from its surrounding environment and incorporate it into its genome, a phenomenon known as natural competence. The mechanism by which natural competence occurs is largely unknown. One proposed model predicts that cells produce appendages which extrude from the membrane, attach to extracellular DNA, and reel the DNA back inside the cell- much like a fishing pole. It is hypothesized that the competence appendages are structurally homologous to the Type IV pilus, another appendage responsible for cell twitching. Here we present data from an experiment looking at the effects of varying DNA concentrations on appendage production. We used atomic force microscopy (AFM) to generate three-dimensional nanoscale images, enabling visualization and computerized quantification of appendages. Initial results show two peaks in appendage production at two specific DNA concentrations, suggesting two different functional thresholds. In an ongoing investigation, we seek to identify the proteins involved in the competence system and determine their specific functions. This study utilizes knockout mutants to analyze five proteins associated with competence and/or Type IV pili. We are using AFM, twitching and transformation efficiency assays, and protein modeling to examine these mutant strains.

Presenter(s): Miles Richardson, University of Chicago **Session:** A.3
Title: Microbial Forensics in the College Dorm
Advisor(s): Jack Gilbert, Department of Surgery, University of Chicago
Co-Author(s): Simon Lax

Abstract: Numerous recent studies have uncovered the extent to which humans influence the microbial ecology of the spaces they occupy through microbial exchange between skin and the built environment. Some have focused on the microbial ecology of public spaces, such as classrooms. Although they have been able demonstrate that most of the taxa colonizing those spaces are skin-associated, they are unable to link individual human microbial signatures to their data.
Dorm buildings, which have a standardized architectural design, common building materials and furnishings between rooms, and even a common ventilation system, represent an intriguing model system in which to characterize the direct effects of an individual's skin microbiota on their surroundings, and to further elucidate the forensic potential skin microbial signatures.
They are a "metacommunity" in which it is possible to record a network of interaction by logging visits between rooms and the use of common spaces. The divide between private rooms and common spaces such as hallways, lounges, and restrooms further enables us to tease apart individual microbial signatures in shared spaces. We sample one dorm at the University of Chicago in depth, including its rooms, common areas, and occupants.

Presenter(s): Lilianne Rothschild, Gustavus Adolphus College **Session:** P3.14
Title: Resting-State Functional Connectivity in Urologic Chronic Pelvic Pain Syndrome (UCPPS): Alterations during Bladder Filling
Advisor(s): Vincent Magnotta, Radiology, The University of Iowa
Co-Author(s): Joseph Shaffer, Vincent Magnotta

Abstract: Urological chronic pelvic pain syndrome (UCPPS) is a set of chronic pain disorders comprised of interstitial cystitis/bladder pain syndrome and chronic prostatitis/chronic pelvic pain syndrome. Although the cause of UCPPS is unknown, aberrant pain processing in the central nervous system has been identified as a prominent component of the disorder. To determine if functional connectivity (FC) differences related to pain are present in UCPPS patients, we conducted preliminary analysis of resting-state functional magnetic resonance (fMR) images from 36 UCPPS patients that were scanned both when their bladder was full and after bladder emptying. Conducting FC analysis and utilizing the Louvain method to identify neural networks resulted in the emergence of sensory, limbic, and motor-related networks of increased FC when the bladder was empty compared to full. Additionally, when the bladder was empty compared to full, a decrease in FC between the prefrontal areas and several regions of interest thought to be involve in pain processing was observed. Alterations in FC may reflect participant focus on bladder sensation or pain when the bladder was full. Future analysis will examine pain severity and urinary urgency ratings as covariates and explore FC alterations associated with UCPPS progression over time.

Presenter(s): Danielle Rubin, University of Chicago
Session: C.3
Title: Differential signature and kinetics of IFN-β-1a vs. PEG-IFN-β-1a in multiple sclerosis treatment
Advisor(s): Anthony Reder, Neurology, University of Chicago
Co-Author(s):

Abstract: The relative efficacies of IFN-β-1a (Avonex) and PEG-IFN-β-1a (Plegridy) in relapsing-remitting multiple sclerosis (RRMS) treatment have been well-documented in clinical trials. However, the effects of PEGylated IFN on STAT1 activation and interferon-stimulated gene (ISG) induction kinetics are unknown. This study aimed to determine a unique signature for PEG-IFN-β-1a, predicting that PEG-IFN-β-1a would remain on its receptor and in circulation longer than IFN-β-1a and therefore prolong ISG expression. MNCs were isolated from washed-out, IFN-treated MS blood and stimulated in vitro with IFN for 0, 30', 2h, 4h, 24h, and 48h. MNCs were also isolated from in vivo-treated MS blood at 6h, 24h, and 48h post-injection. 8 RRMS patients newly started on IFN-β-1a and 8 RRMS patients newly started on PEG-IFN-β-1a had blood drawn at baseline and 6 months later. 8 RRMS patients chronically on IFN-β-1a had blood drawn before switching to PEG-IFN-β-1a and then again 6 months later. IFN induction of phospho-tyrosine-STAT1, phospho-serine-STAT1, and MxA was measured via flow cytometry and western blot. Data will be gathered for chemokine and cytokine regulation with the ProcartaPlex Multiplex Immunoassay, for serum IFN activity with a serum type-1 IFN assay, and for global gene expression with the Affymetrix GeneChip Human Transcriptome Array (HTA). Preliminary data shows peak in vitro MxA induction at 24 hours and p-Y-STAT1 induction at 30' for PEG-IFN-β-1a-treated patients.

Presenter(s): Erica Ryu, Washington University in St. Louis
Session: P2.02
Title: Factors that Influence Multicellularity in Dictyostelium discoideum
Advisor(s): Joan Strassmann, Biology, Washington University
Co-Author(s): Fredrik Inglis, Odion Asikhia, Dave Queller

Abstract: The appearance of multicellular life is one the major evolutionary events; however, the conditions leading to its appearance are poorly understood. We know that cooperation between cells is important for multicellularity, but cheaters, mutant selfish individuals, harm the cooperative associations and cause the system to break down. Previous studies have shown that sexual reproduction through single-celled bottlenecks can resist cheaters, but numerous organisms, such as potatoes and green onions, produce through multicellular propagules. How these organisms are able to resist cheaters and maintain a multicellular system is unclear. The goal is to investigate whether two factors, growth and dispersal, are sufficient for resisting non-multicellular cheaters. Dictyostelium discoideum, a social amoeba that undergoes unicellular and multicellular stages, was used to create pseudoorganisms undergoing synthetic life cycles. Pseudoorganisms were subjected to four different systems: structured growth and dispersal, structured growth only, structured dispersal only, and both unstructured. Results show that the number of cheaters for the structured growth condition is high, suggesting that structured growth is not sufficient to resist cheaters. This may have occurred because cheaters have increased growth rate, so they spread faster and outcompete the cooperator strain. These findings have implications in better understanding how multicellularity evolved and how to prevent the breakdown of multicellularity in disease such as cancer.

Presenter(s): Francisco Sanchez-Conde, Alexandra Schmiechen, Grinnell College
Session: P2.12
Title: Design, Characterization, and Implementation of a DNA Sensor for HSA-Let-7a miRNA in Breast Cancer Cells
Advisor(s): Cooper Battle, Chemistry, Grinnell College
Co-Author(s): Alexandra Schmiechen

Abstract: HSA-let-7a is an oncogenic miRNA, known to up regulate caspase expression and down regulate RAS expression, with differential expression in two human breast cancer cell lines, MDA-MB-231 and MCF-7. Previous studies have found that let-7a has a higher expression in the less aggressive and less metastatic MCF-7 line. In order to test for the expression of miRNA HSA-let-7a in the MCF-7 and MDA-MB-231 cell lines an oligonucleotide sensor was designed based on strand exchange mechanisms and ability to yield a fluorescent response in the presence of HSA-let-7a. Stability of the sensor system was studied by thermal denaturation, and fluorescence titrations were used to determine the efficacy of sensor response. Additionally, the effects of Mg2+ on the kinetics of duplex formation and strand switching were investigated, as magnesium has been shown to play a role in the

stabilization of DNA duplexes and Holliday junctions. Preliminary in vivo testing of the sensor in MCF-7 and MDA-MB-231 cells was effected by chemical transfection, with let-7a expression quantified by live cell fluorescence microscopy methods. Future work will be done on these samples ex vivo via RNA extraction and fluorescence quantification.

Presenter(s): Jennifer Santos-Arevalo, Beloit College
Session: P3.15
Title: Determining IGF-1 Signal Activation and Location in Neurons
Advisor(s): Rachel Bergstrom, ,
Co-Author(s): Rachel Bergstrom

Abstract: Studies have shown a possible linkage between IGF-1 (Insulin-like Growth factor-1) and neurodegenerative diseases affecting the elderly. IGF-1 is needed in neuronal maintenance and survival, excitatory and inhibitory neurotransmission, maintaining normal free fatty acid levels, cognition improvement, and protection against cellular injury. The IGF-1 growth hormone activates the IGF-1 receptor at the distal axon, through dimerization and autophosphorylation. This activation then causes a chain of intracellular reactions which include the activation of other signaling pathways needed for cell maintenance like PI3K and MAPK. Nerve Growth Factor (NGF) is the canonical signaling pathway for neurotrophic factors that are activated by receptor phosphorylation, TrkA receptor, and go on to activate PI3K and MAPK pathways. Using Immunofluorescence, we anticipate to prove that the IGF-1 receptor has been activated causing a chain of reactions that also activate Erk 1/2 and Akt, based on relative similarities between the activation process of other neurotrophins. Embryonic mice brain samples were used to extract neurons, and a timed breeding strategy was used to induce estrus in female mice prior to introduction of males and improve pregnancy rates, providing a more reliable strategy than pairing males with females without knowing the female's cycle.

Presenter(s): Zoe Schmiechen, Grinnell College
Session: P1.04
Title: Concatenated nicotinic acetylcholine receptor subunits elucidate stoichiometry of modulation
Advisor(s): Mark M. Levandoski, Biological Chemistry, Grinnell College
Co-Author(s):

Abstract: Nicotinic acetylcholine receptors (nAChRs) are implicated in the pathology of Alzheimer's and Parkinson's diseases, and are used in signaling throughout the central nervous system. I investigated the stoichiometry of these pentameric receptors and the associated pharmacological differences, and used concatemers to restrict the order and stoichiometry of α3β2 nAChRs. In order to study nAChRs, I expressed cRNA of the receptor subunits in Xenopus laevis oocytes, and recorded responses to drugs using the two-electrode voltage clamp method. I found that the free subunit and concatemer models of the (α3)2(β2)3 isoform behaved in the same way to acetylcholine and oxantel. Moreover, with both models, I found that oxantel caused inhibition, which was found in reduced potency, but no significant change in efficacy. Additionally, when studying just the concatemer of (α3)2(β2)3, I found that morantel co-application with acetylcholine leads to potentiation, as evidenced by a large increase in efficacy. Overall, concatemers are valid models for studying nAChRs, and oxantel and morantel require further study on how they acts as modulators to various isoforms.

***two greek letters are used, aplha α, and beta β

Presenter(s): Rohan Shah, University of Chicago
Session: D.1
Title: Denaturative Internally Calibrated Chromatin Immunoprecipitation to Quantify Internal Histone Modifications
Advisor(s): Alexander Ruthenburg, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s): Adrian Grzybowski; Alexander Ruthenburg

Abstract: On a fundamental level, the accessibility of metazoan genomic DNA is controlled by nucleosomes, or protein-DNA complexes made of histone octamers and DNA wrapped around the histone octamers. The activity of these nucleosomes is modulated through various histone post-translational modifications (PTMs). The locations of these modifications in the genome can be discovered by chromatin immunoprecipitation, whereby an antibody is used to purify nucleosomes bearing the modification of interest, and the associated DNA is mapped to the genome

and quantified. Recently, a quantitative version of ChIP, Internally Calibrated Chromatin Immunoprecipitation (ICeChIP) was developed. Despite being highly accurate for modifications on the histone tail, one of the drawbacks of ICeChIP was its inability to measure accurately PTMs residing on the globular domain of the histone. This project aims to develop a denaturative form of ICeChIP to assess nucleosome modifications on the globular domain of the histone, specifically the clinically-relevant dimethylation of histone H3 lysine 79 (H3K79me2), and to use that information to better understand and diagnose the MLL-rearranged leukemias associated with the modification.

Presenter(s): Christine Solomon, Grinnell College
Session: P1.09
Title: Competition and facilitation in neighborhoods of the annual plant, Chamaecrista fasciculata.
Advisor(s): Vince Eckhart, Biology, Grinnell College
Co-Author(s): Vince Eckhart

Abstract: In plant communities, interactions between neighbors are expected to be competitive, but recent studies find facilitation in some circumstances. To investigate those circumstances and to complement ongoing studies of genetic effects on performance, I carried out experimental and observational studies of the annual plant Chamaecrista fasciculata. Repeating an experiment performed the previous year, I found that seedlings had higher survival and lower herbivory when their neighbors of other species were left intact (rather than clipped) and when seedlings had higher densities of C. fasciculata neighbors. These effects declined with time, becoming negligible by mid-season. To determine if early-life facilitation arises from protection from severe weather, I asked whether an index of neighborhood cover (leaf area index, LAI) predicts seedling establishment in an experimental population. LAI did not affect establishment, but the presence of an exotic invasive species (crown vetch, Coronilla varia) delayed it. A growth-chamber experiment revealed that germination probability of the offspring of C. fasciculata plants declined with the density of their intraspecific neighbors, suggesting higher inbreeding in dense patches. Facilitation occurs, partly via reducing herbivory risk and partly by uncertain mechanisms. Variation in neighborhood effects are likely important sources of environmental variation in plant performance.

Presenter(s): Vishok Srikanth, University of Chicago
Session: B.1
Title: Analysis of hyperactive MuA transposase variants suggests evolutionary compromises between accuracy and activity
Advisor(s): Phoebe Rice, Biochemistry & Molecular Biology, University of Chicago
Co-Author(s): James Fuller, Phoebe Rice

Abstract: MuA, the transposase encoded by bacteriophage Mu, shares its “DDE” catalytic domain with many DNA transposases and retroviral integrases, making Mu an informative model system for understanding a variety of mobile DNA elements. In vivo screens identified multiple single nucleotide substitutions that greatly increase the rate of transposition, raising the question of why natural selection has not favored the incorporation of these changes into the wild type MuA sequence. We have purified several of these mutant transposases and analyzed several aspects of their reaction kinetics in vitro. Our results demonstrate that the mutants’ increased activity over the wild type transposase results from faster assembly of the MuA homotetramer that catalyzes transposition (transpososome) rather than a faster chemical reaction. These findings corroborate the structure-based hypothesis that the hyperactivating mutations we studied improve protein-protein contacts between the MuA monomers assembled in the active tetramer. The omission of these evolutionarily accessible mutations from the wild type MuA sequence intimates that improved rates of transpososome assembly deleteriously affect propagation of the phage. This may reflect a decreased ability of MuA to selectively incorporate correct phage DNA ends into a more rapidly assembled transpososome.

Presenter(s): Snigdha Srivastava, Washington University in St. Louis
Session: P2.03
Title: Determining How Variation in Brain Size Relates to Species Differences in Mormyrid Social Behavior
Advisor(s): Bruce Carlson, Biology, Washington University in St. Louis
Co-Author(s): Erika Schumacher

Abstract: Mormyrids, or fish of the family Mormyridae, are freshwater weakly electric fish native to Africa. These fish are known for their large range in brain size and their unique ability to use electric organ discharges (EODs) in

social communication. In previous studies, these EODs have been shown to be highly stereotyped for each individual and within species. The inter-pulse intervals (IPIs) of these EODs, however, are context-dependent and associated with specific behaviors. To offset the metabolic costs of encephalization, we hypothesize that a larger brain size affords a greater complexity of social communication, characterized by a greater repertoire size of signals and a higher dependence on social communications in establishing dominance relationships. Conversely, we hypothesize that individuals with smaller brain size depend more heavily on physical attributes when establishing dominance relationships. To test our hypothesis, we used a custom MATLAB script and MATLAB-based unsupervised algorithm called Wave_clus, which relies on wavelet transformation and superparamagnetic clustering for spike sorting. Preliminary recordings between two individuals of Brienomyrus niger reveal a proportion of our data that do not match the EOD signal likely due to background electrical noise and EODs from both fish at nearly the same time. Thus, we propose to add a component to the program that will automatically set upper and lower thresholds to filter out abnormal waveforms while still allowing the most EODs to be retained for higher accuracy.

Presenter(s): Dylan Stahl, Knox College
Session: P2.07
Title: A computational psychiatry approach to social valuation in Borderline Personality Disorder
Advisor(s): Judith Thorn, Neuroscience, Knox
Co-Author(s): Jacob Leavitt, Andreea Diaconescu, Sarah K Fineberg, Phil Corlett

Abstract: Background: People with Borderline Personality Disorder (BPD) suffer tumultuous relationships. Computational approaches have recently gained ground in psychiatry as a way to ground psychological theory and behavioral experiments in quantitative models. This approach holds promise for improving understanding of the complex behaviors involved in social interaction.

Hypothesis: In an interactive social task, subjects with BPD will demonstrate higher sensitivity to betrayal.

Method: We used a computer-based task with social and non-social cues to test for differences in expectation and weighting of social data in BPD versus control subjects. The task varies reward probability and volatility for each cue. We developed a multi-level model (MLM) to test group-wise differences in the weights subjects assigned to reward predictors.

Results: BPD subjects were significantly more sensitive to betrayal than were non-psychiatric control subjects ($p < 0.05$).

Conclusions and Future Directions: Our computational model allowed quantitative confirmation of the psychological theory. In future work, we will analyse further behavioral predictors with the MLM and with another modelling method, the Hierarchical Gaussian Filter. Ultimately, these approaches will allow us to test the effects of social exclusion, and differences by subject gender.

Presenter(s): Olivia Stovicek, University of Chicago
Session: B.3
Title: Developing new genetic models for community studies
Advisor(s): Sean Crosson, Department of Biochemistry and Molecular Biology, University of Chicago
Co-Author(s): Kristy L. Hentchel

Abstract: Studies in multiple organisms have demonstrated that only 7-15% of the genome is required for growth in standard laboratory conditions. We hypothesize that many “non-essential genes” are actually vital to interspecies interactions and growth and survival in natural environmental conditions. To explore the relationship between community complexity and gene function, we propose to identify the essential genome of Gram-negative freshwater bacterium Caulobacter crescentus in its natural environment individually (i.e. filtered lake water) and reconstructed microbial communities (i.e. filtered lake water with additional freshwater species). To identify candidate species for these reconstructed communities, we isolated over 70 bacteria from Lake Michigan. Characterization by 16S rRNA gene sequencing, microscopy, antibiotic screening, and growth studies identified candidate species to be used for essentiality experiments. Through these experiments, we hope to gain insight into the genes required for growth in these conditions and how they differ, improving understanding of their role in the natural environment and eventually enabling us to connect interspecies interactions to specific genes and gene functions.

Presenter(s): Andrea Studer, St. Olaf College
Session: P1.17
Title: Improving a technique for visualization of intracellular lipid droplets
Advisor(s): Laura Listenberger, Biology, St. Olaf
Co-Author(s): Laura Listenberger

Abstract: Lipid droplets are compartments that store excess fat in cells. Visualization of these structures facilitates study of fat storage in healthy and diseased tissues. Published procedures for visualization of lipid droplets vary, but all have two main steps: fixation of cellular proteins and staining of lipid droplets. We streamlined the fixation and staining steps for the most efficient visualization of lipid droplets. Fixation with 3% paraformaldehyde or formaldehyde for 10 minutes followed by three rinses was optimal. We also compared three different lipid droplet stains. Nile Red specifically stained lipid droplets bright green, but its wide emission spectrum overlaps many of the fluorescent labels used for visualization of lipid droplet proteins. LipidTox Deep Red dimly stained lipid droplets and was overpowered by the lipid droplet protein fluorescent labels. BODIPY 493/503 exhibited specific lipid droplet staining, produced the clearest pictures with minimal background fluorescence, and is suitable for experiments with co-staining of other cellular structures.

Presenter(s): Taylor Tibbs, Carthage College
Session: P1.08
Title: Growth Deficiencies in Lipoprotein Mutants in Staphylococcus aureus Newman
Advisor(s): Deborah Tobiason, Biology, Carthage College
Co-Author(s): Anica Beyer, Jan Pané-Farré

Abstract: The bacterium, Staphylococcus aureus, is a human pathogen which can cause chronic and acute infections. It is responsible for mild infections such as pimples and abscesses as well as potentially life-threatening illnesses like endocarditis and sepsis. Over time, multiple strains have become resistant to antibiotics and have become an increasing problem in hospitals worldwide. The proteins at the surface of this bacterium are of particular interest as they directly interact with the infected individual's body. The aim of this study to is illuminate the role of lipoproteins which associate with the outer bacterial membrane. Some lipoproteins have been indicated to have important roles in cell adhesion, inflammatory response, and virulence. Various mutations were made in uncharacterized lipoproteins of S. aureus Newman. Twenty mutants were screened under various conditions including: different growth media, temperature, and antibiotic supplementation. From theses screening experiments, mutants L14 and L16 appeared to have several deficiencies in growth compared to the wild type. Phase contrast and fluorescence microscopy show that these mutants form large cellular aggregates in liquid media. Electron microscopy reveals that the mutants also form multiple, disordered septa resulting in irregularly sized and shaped cells.

Presenter(s): Tristan Tobias, Adam Krahn, Hope College
Session: P2.05
Title: Temperature Effects on a Distinct Subset of Mycobacteriophages
Advisor(s): Joseph Stukey, Biology, Hope College
Co-Author(s):

Abstract: Mycobacteriophages are bacterial viruses that infect mycobacterial hosts. Over 1180 mycobacteriophages have been organized into at least 33 distinct clusters based on genomic sequence similarity. Some Cluster A and K mycobacteriophages can also infect Mycobacterium tuberculosis, a distinction of potential medical importance. Recently, Hope College SEA-PHAGES students discovered a disproportionate number of putative Cluster K phages after changing the isolation temperature from 37°C to 32°C. Additionally, these phages were unable to propagate at 42°C, suggesting that Cluster K phages may have a growth advantage at lower temperatures. We investigated these temperature-dependent growth properties with known and presumptive Cluster K phages, Bella96, Krueger, and Polymorphads. We examined phage adsorption rate, thermostability, latent period and burst size. At ≥ 37°C, the stability of Bella96 and Krueger decreased, however, D29 (Cluster A control), as well as Polymorphads, were largely thermostable at 42°C. Also, the adsorption rate of Bella96 and Krueger decreased at ≥ 37°C compared to D29. These results suggest the Cluster K phages may have a growth disadvantage at 37°C compared to D29. Our findings provide insight into the growth behavior and temperature sensitivity of Cluster K phages and may lead to discoveries about M. smegmatis and M. tuberculosis infection by mycobacteriophages.

Presenter(s): Alyssa Welle, Gustavus Adolphus College
Session: E.3
Title: Oxygen Consumption During the Induction of Rapid Cold-Hardening in Isolated Muscle of Flesh Fly
Advisor(s): Yuta Kawarasaki, Biology, Gustavus Adolphus College
Co-Author(s): Yuta Kawarasaki

Abstract: Rapid cold-hardening (RCH) describes an extremely swift response of insects to enhance their cold tolerance. A brief exposure to a moderately low temperature dramatically increases insect survival to a subsequent cold exposure. In the flesh fly, Sarcophaga bullata, as little as 15 min at 5°C significantly improved organismal survival at -7°C from 0 to 66.7±11.1%. Previous studies have demonstrated that the induction of RCH occurs at the cellular level through calcium signaling. In this project, we examined the changes in the oxygen consumption during the RCH induction, using isolated flight muscles of S. bullata. Compared to tissues that had been maintained at 5°C for 2 h, those at 5°C for 10 min, therefore during the early phase of RCH induction, exhibited significantly higher rates of oxygen consumption (1.18±0.09 vs. 2.82±0.29 µl O2 mg-1 DM h-1). When these tissues were exposed to LaCl3, blocker of calcium channels that inhibits the RCH response, their oxygen consumption rate were reduced significantly to a level similar to those that had been maintained at 5°C for 2 h. Our initial results suggest that the high rate of oxygen consumption is associated with the RCH induction, likely to meet the energetic demand of eliciting this response.

Presenter(s): Katarina Whittenburg, Knox College
Session: P1.12
Title: Differential expression of small RNA between vegetative and reproductive tissue in rice
Advisor(s): Michael Axtell, Biology, Penn State University
Co-Author(s):

Abstract: Plants undergo phase change, where they transition from producing vegetative tissue to producing inflorescences. There is evidence to suggest that small RNAs are regulators of some of the changes in gene expression associated with phase change. Our goal was to broadly compare small RNA expression between vegetative and reproductive tissues. In this experiment, we analyzed previously published small RNA libraries from rice. We created a list of small RNA loci by aligning the processed libraries to the complete rice genome. We found that approximately one third of rice small RNA loci were expressed more highly in reproductive tissue. Focusing specifically on the subset of small RNAs called microRNAs, we found that approximately one-third of microRNAs were upregulated in reproductive tissue, which is consistent with the heightened need for gene regulation in the differentiating tissue of inflorescences. Several potential novel microRNAs were found in the rice libraries and analyzed to determine their validity.

Presenter(s): Catherine Wingrove, Hope College
Session: F.1
Title: Does eating junk-food make it harder to think?
Advisor(s): Peter Vollbrecht, Biology, Hope College
Co-Author(s): Peter Vollbrecht

Abstract: Obesity is a worldwide concern as consumption of processed foods and global obesity rates continue to rise. Obesity increases the risk of developing numerous health problems including cardiovascular disease and type II diabetes. MRI studies have demonstrated that human obesity is associated with alterations in the prefrontal cortex (PFC). The PFC mediates executive functions including inhibitory control, working memory, and decision-making. Few studies have explored whether observed changes in the PFC are a result of diet, obesity development, or a genetic predisposition. Our studies utilized a rat model to explore the effects of a typical Western “junk-food” diet on PFC mediated behaviors. Following 4 weeks of “junk-food” or chow diet exposure, rats underwent cognitive behavioral tests, including Egocentric Morris Water Maze, Spontaneous Alternation, Novel Object Recognition and Attentional Set Shift. Junk-food fed rats did not demonstrate significant weight gain. Similarly, junk-food fed rats failed to display cognitive deficits. Therefore, our data suggest that a “junk-food” diet, independent of obesity development, is not enough to cause cognitive deficits observed in obese individuals. Further studies are needed to explore the role of genetic predisposition and obesity in the development of cognitive deficits.

Presenter(s): Jae Un Yoo, Washington University in St. Louis
Session: P3.12
Title: Learning Categories of Rocks: Comparing Rock Pictures and Actual Rocks
Advisor(s): Mark A. McDaniel, Psychological & Brain Sciences, Washington University in St.Louis
Co-Author(s): Toshiya Miyatsu, Mark A. McDaniel

Abstract: Learning Categories of Rocks: Comparing Rock Pictures and Actual Rocks

Jae UnYoo, Toshiya Miyatsu, & Mark A. McDaniel
Washington University in St Louis

Category Learning is a process of establishing knowledge of categories that enable learners to identify novel items from the learned categories. While it is a widely studied subject in psychology, research in category learning almost always used pictures to learn categories, and very few studies used actual samples. In order to examine how using actual samples affect category learning, we looked at the learning of rock categories as often taught in college level geology courses. To compare learning with rock images and learning with actual rocks, participants were given a set of rock items from different categories, either in pictures or actual samples, and were later tested on their ability to classify novel items into their corresponding categories. By including both rock images and actual rocks in the classification task, we also examined transfer appropriate processing (Lockhart, 2002) which suggests that learning and memory performance is best when the type of item used in the encoding process match the type of item used at test. The generalization task had two conditions: immediate test and a 48 hour delay. A cue-dependent theory of memory (Tulving & Pearlstone, 1966) predicts the actual sample condition to be better at delay because of the greater number of cues (e.g., tactile cues). By contrast, a prototype theory of category learning (Posner & Keele, 1970) predicts the picture condition to be better at delay because memory for specific items fades as time passes, but the prototypical representation endures delay. Our results may not only be of theoretical interests but also can have implications in how we may optimize category-learning instruction.

Presenter(s): Katherine Zellner, University of Chicago
Session: D.2
Title: Wound Healing in Jellyfish
Advisor(s): Jocelyn Malamy, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s):

Abstract: A critical feature of any organism is its ability to self repair its wounds. Clytia hemisphaerica provides an excellent system for wound healing as the transparent animal heals quickly and allows live imaging providing insights unable to be found in a tissue culture. Instead of regenerating new cells, sheets of pre-existing cells protrude and migrate to the site of injury from other areas to heal the wound. Healing mechanisms can generally be separated into two categories: lamellipodial driven healing and non lamellipodial driven healing. The non-lamellipodial driven mechanism generally attributed to small circular wounds in the epithelial layer is an actomyosin contractile cable commonly referred to as a 'purse string.' Existing literature points to the imaging of a ring surrounding the wound through actin staining as evidence for a purse string, however, it is difficult to determine whether the stain indicates an actin cable or lamellipodia. A series of Rho GTPases (Rac1, CDC42, and RhoA) have an integral role in activating downstream pathways for many cellular functions including cellular migration. Through inhibiting Rho GTPases in wounded animals, we can determine the roles of the GTPases in healing mechanisms and gain insight about when and how different healing mechanisms are used.

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