Biology Undergraduate Research Symposium

Biosciences Building

Central Michigan University

November 20, 2026



SCHEDULE

- 1:15 – 2:00 - Poster setup in main atrium
- 2:00 – 2:10 - Opening Remarks in room 1010
- 2:10 – 3:00 - Oral Presentations Session I in room 1010 (4 talks)
- 3:00 – 3:45 - Poster Session I (odd numbers) with snacks in main atrium
- 3:45 – 4:30 - Poster Session II (even numbers) with snacks in main atrium
- 4:30 – 5:20 - Oral Presentations Session II in room 1010 (4 talks)
- 5:20 – 5:30 - Image Contest Voting room 1010
- 5:30 – Awards in room 1010

The Image Contest slides will be scrolling on the screen in room 1010 during the poster sessions. Please stop in to view the entries and vote for your favorite using the ballots provided at the front of the room.



Overview

Oral Presentation Session I

	Name	Affiliation	Department	Title
1	**Aashka Barot,** Dr. Daelyn Woolnough	CMU	Biology and Institute for Great Lakes Research	Surface surveys underestimate freshwater mussel abundance in the Grand River, Michigan
2	**Calub Hicks**[1], MyHanh Le[1], Kendal Swatosh[1], Nehul Tanna[1,2], Dr. Xantha Karp[1,2]	CMU	[1] Biology [2] Biochemistry, Cellular & Molecular Biology Program	Three RNA-binding proteins that oppose adult cell fate during dauer in (*Caenorhabditis elegans)*
3	**Grace Sobaski**, Dr. Abigail Cahill	Albion College	Biology	Can Genetic Diversity Explain a Lack of Anti-Predator Response in Aquatic Isopods?
4	**Emily Kraenzlein**, Braden Andrejack, Dr. Katie Stumpf	Alma College	Biology	Does Temperature Affect Nesting Success of Cavity Nesting Birds?

Oral Presentation Session II

	Name	Affiliation	Department	Title
5	**Calla Altaani**, Dr. Marcella Cervantes	Albion College	Biology	Identification and Characterization of a Freshwater Ciliate Isolated from Albion Michigan
6	**Shreeya Bhosale**, Ethan Burka, Dr. Peter Dijkstra	CMU	Biology	Environmental Enrichment and Social Status in a Cichlid Fish
7	**Braden Andrejack,** Dr. Katie Stumpf	Alma College	Biology	Changing Avian Population Dynamics and Management Efforts on Isle Royale National Park
8	**Carter Mann**, Dr. Marcella Cervantes	Albion College	Biology	T*etrahymena rostrata*- Identifying Unknown Ciliates

Overview

Poster Presentation Session I

	Name	Affiliation	Department	Title
1	**Claire Buckingham**, Abigail Medler, Dr. Peter Dijkstra	CMU	Biology	Colors and Conflict: Aggression biases in a cichlid fish with reversible body coloration
3	**Anna Drozdov**[1], Ernest Njuguna[2], JP[3], Dr. Neil A. White[2,3]	CMU	Biology, Chemistry & Biochemistry	Characterization of the *algC* RNA Motif as a Regulatory Genetic Switch in *Escherichia coli*
5	**Zachary D. Hager**[1], Clinton Kabutey[1,2], Dr. Benjamin M. Swarts[1,2]	CMU	Chemistry & Biochemistry	Quantitative evaluation of candidate *Mycobacterium tuberculosis* trehalose dimycolate hydrolase inhibitors using a fluorescent-based assay
7	**Chloe Leaman,** Sadey Simpson, Dr. Eliezer Schwarz	Alma College	Biology	Low pH State Transition Effect
9	**Selena M. Macias**, Dr. Cynthia K. Damer	CMU	Biology	Analysis of Gene Expression Changes in *cpnC* Mutants Using RT-qPCR
11	**Riley E. Shiplet,** Bridget K. Plude, and Dr. Cynthia K. Damer	CMU	Biology	*Dictyostelium discoideum* as a Model for Polycystic Kidney Disease
13	**Justin Montgomery**, Dr. Marcella Cervantes,	Albion College	Biology	Manipulating *Tetrahymena* Mating Type Gene Expression via Starvation
15	**Akniyet Alisheva**, Dr. Marcella Cervantes	Albion College	Biology	Identification of an unknown *Tetrahymena* Ciliate
17	**Zhia Martin**, Dr. Marcella Cervantes	Albion College	Biology	Investigating the Identity of an Unknown Cell: D8
19	**Justin Montgomery**, Jay Martinez, Dr. Abigail Cahill	Albion College	Biology	Biodiversity of Invertebrates in the Kalamazoo River
21	**Ava Scott**, Dr. Hunter J. Carrick	CMU	Biology & Institute for Great Lakes Research	Importance of heterotrophic bacterioplankton in northern lake Huron
23	**Luke Snow**, Dr. Todd Barkman	Western Michigan University	Biological Sciences	Evaluation of mechanical removal, herbicide and fire for the control of Autumn Olive, *Elaeagnus umbellata*
25	**Petra Bora**[1], Michelle LaCross[2], Andrew Kaczmar[1], Dr. A. Thompson[1,3,4]	WMU, Comstock, MSU	Biological Sciences High School Integrative Biology	Developing Killifish Models for Function Comparative Genetics
27	**Chloe Lkhamsuren**, Dr. Marcella Cervantes	Albion College	Biology	Identifying Genes Necessary for a Mating Signal in *Tetrahymena thermophila*
29	**Blake Dishaw**, Emily Herron, Lauryl Sullivan, Ty Nelson, Dr. Michelle Steinhilb	CMU	Biology	Evaluating Calpeptin and Calpain Inhibitor III as Potential Suppressors of Tau Toxicity in *Drosophila*,Model of Alzheimer's Disease
31	**Dustin Fields**[1], Brenden Wittenback[1], Ruvarashe Musasiwa[2], Dr. Neil White[3]	CMU	Biology Mathematics Chemistry & Biochemistry	Identifying genes affecting lithium biology in *Escherichia coli*
33	**Pranali Chhapamohan**, Hannah Kennedy, Jasmine Asberry, Dr. Xantha Karp	CMU	Biology	Regulation of adult cell fate via transcription factors in *Caenorhabditis elegans* dauer larvae
35	**Katherine Himmel**, Dr. Michelle Steinhilb	CMU	Biology	Comparative analysis of Tau, TDP-43, and age on locomotive behavior in *Drosophila*

Overview

Poster Presentation Session II

	Name	Affiliation	Department	Title
2	**Akniyet Alisheva**, Sofya Ryisman, Dr. Kenneth Saville	Albion College	Biology	Use of deconvolution to extract single cell information from bulk RNA-seq data using diabetes and multiple sclerosis as examples
4	**Isaac Postema**, Katherine Himmel, Hunter Hitzelberger, Dr. Michelle Steinhilb	CMU	Biology	Evaluating motor neuron vulnerability to tau expression in aging *Drosophila*
6	**Brenden Wittenbach**[1], Dustin Fields[1], Dr. Neil White[2]	CMU	Biology Chemistry & Biochemistry	Environmental factors influencing riboswitch associated gene regulation in *Escherichia coli*
8	**Vi To**[1], Clinton Kabutey[2], Melanie S. Hall[1], Ulysses G. Johnson[2], and Dr. Benjamin Swarts[1,2]	CMU	Chemistry & Biochemistry	Chemoenzymatic synthesis of 2,2-difluorotrehalose, a novel trehalose analogue and possible inhibitor of *Mycobacterium tuberculosis*
10	**Jack Rich**, Dr. Cynthia K. Damer	CMU	Biology	Using RT-qPCR to Investigate the Effects of CpnA Loss on Gene Expression
12	**Allison G. Maillette**, Bridget K. Plude, Cody T. Morrison, and Dr. Cynthia K. Damer	CMU	Biology	Investigating the Role of Copine D in cAMP signaling in *Dictyostelium discoideum*
14	**Neal Singh** and Dr. Marcella Cervantes	Albion College	Biology	Identification of an unknown *Tetrahymena* Ciliate
16	**Victor Olufowote**, **Aldo Martinez**, Dr. Marcella Cervantes	Albion College	Biology	Von Willebrand 17 Gene Knockout in *Tetrahymena*
18	**Elaine Hamilton**, Dr. Daelyn Woolnough	CMU	Biology and Institute for Great Lakes Research	Elders of the river: Ages of common freshwater mussels in the Chippewa River, MI, USA
20	**Elizabeth Martin**, Dr. Kirsten Nicholson, Dr. Scott McNaught	CMU	Biology	Comparative abundance of Eastern Red-Backed Salamanders *Plethodon cinereus* across edge, interior forest, and trail habitats
22	**Emma Haller**, Dr. Lauren Stanley	CMU	Biology	Conservation Genetics in the Michigan Monkeyflower
24	**Trevian Glasper,** Dr. Lauren Stanley	CMU	Biology	The role of Accumulation and Replication of Chlorplasts 6 (ARC6) in carotenoid synthesis and storage
26	**Sarah Gardner**, Dr. Gregory Colores	CMU	Biology	Impact of zinc on antibiotic resistance transfer in *Escherichia coli*
28	**Vusani Ntuli**, Anuja Dahal, and Dr. Xantha Karp	CMU	Biology	The regulation of an adult cell fate marker during dauer by NuRD complex genes
30	**Andrew Park**, Dr. Lauren Stanley	CMU	Biology	Characterizing the pale yellow flower (pyf) carotenoid mutant of *Mimulus guttatus* (yellow monkeyflower)
32	**Xsandrie Guimba**, Jade Smith, Natalie Bales, Dakota Dykhuis, Luke Hanson, Katie Mullin, Lilly Richardson, and Dr. Gary M. Lange	SVSU	Biology	Juvenile exposure to environmentally relevant levels of bisphenols exerts impact on development and behavior in rats (*Rattus norvegicus*)
34	**Emily Herron**, Lauryl Sullivan, Ty Nelson, Dr. Michelle Steinhilb	CMU	Biology	Validation of Flynotyper as a quantitative tool for measuring tau toxicity
36	**Kyleigh Methner**, Dr. Choon Young	CMU	Chemistry & Biochemistry	36.Synthesis of Antioxidant Dendrimers using Hydrophilic and Hydrophobic Gallic Aldehyde-Derivatized Dendrons

Oral Presentation Session I

1. Surface surveys underestimate freshwater mussel abundance in the Grand River, Michigan

Aashka Barot, Dr. Daelyn Woolnough
Central Michigan University, Biology Department and Institute for Great Lakes Research

Freshwater mussels play an important role in river ecosystems by filtering water, recycling nutrients, and supporting aquatic communities. However, many species are threatened and monitoring them is challenging because they often bury themselves in sediment. This study examined changes in the vertical distribution of freshwater mussels in the Grand River near Lyons, Michigan across two summer sampling periods. During each period, 10 randomly selected 0.25m¬≤ quadrats were surveyed. Each quadrat was divided into four depth categories: sediment surface, <5cm, 5‚Äì10cm, and >10cm below the surface. Mussels (live and shell) were identified, measured, and depth recorded. Based on previous research, it was hypothesized that not all mussels would be found at the surface as mussels burrow. It was also hypothesized that thinner-shelled species would be found closer to the surface, while heavier or thicker-shelled species would burrow deeper. A total of 19 live mussels representing eight species were collected with Threeridge (*Amblema plicata*) being the most common (n=8). No live mussels were found at the sediment surface. In Period 1, 40% of live mussels were buried >10cm compared to 66.7% in Period 2. Shells showed greater species diversity than live mussels in both periods. Asian basket clam (*Corbicula fluminea*), an invasive bivalve, were the most abundant shells found, increasing from 676 to 1,366 between periods, raising the possibility of competition with native mussels for resources and habitat. Average water depth and flow decreased between periods, from 59.1cm and 0.40m/s to 55.7cm and 0.23m/s, but the temperature decreased from 27.0C to 24.8C. These findings highlight the importance of considering burrowing when surveying mussels because in this study 100% of live mussels were found below the sediment even during the summer periods when surveys are normally performed. Understanding vertical distribution can improve sampling methods and support conservation efforts for native freshwater mussels.

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2. Three RNA-binding proteins that oppose adult cell fate during dauer in (*Caenorhabditis elegans)*

Calub Hicks[1], MyHanh Le[1], Kendal Swatosh[1], Nehul Tanna[1,2], Dr. Xantha Karp[1,2]
[1] Central Michigan University, Department of Biology, Mount Pleasant, MI, United States
[2] Central Michigan University, Biochemistry, Cellular & Molecular Biology Program, Mt Pleasant, MI, US

Many stem cell types maintain their multipotency through prolonged cell-cycle arrest, known as quiescence, but the genetic mechanisms that coordinate this are poorly understood. In *C. elegans*, lateral hypodermal seam cells are stem cell-like cells that are multipotent during larval development and terminally differentiate in adulthood. In favorable conditions, *C. elegans* larvae develop through four larval stages separated by molts before reaching adulthood. Under unfavorable conditions, *C. elegans* larvae can enter the stress-resistant, developmentally arrested dauer larva stage after the second larval molt via *daf-16*. During dauer, *daf-16* opposes expression of the adult-specific collagen encoded by *col-19*, which we can visualize through a *col-19p::gfp* transgene. Wild-type dauer larvae do not express *col-19p::gfp*; however, *daf-16* mutants do, indicating that *daf-16* blocks adult cell fate during dauer. We previously used RNAi screens to identify three RNA-binding proteins (RBPs) that inhibit adult cell fate: LIN-41, UNK-1, and MSI-1. We hypothesized that these RBPs work in parallel to each other. Thus, we predicted that loss of each RBP will have additive effects on *col-19p::gfp* expression. To test this, we created single, double, and triple RBP mutants. We quantified *col-19p::gfp* expression in the mutants, but our partial-loss-of-function lin-41 mutant displayed a weaker phenotype than in previous *lin-41* RNAi experiments. To elucidate the additive effects of *lin-41*, we next used RNAi gene silencing to deplete LIN-41 levels in *unk-1*(0) and *msi-1*(0) backgrounds to produce a stronger loss of function for *lin-41* in the genetic pathway. We found that *col-19p::gfp* expression indeed increased additively as each RBP was removed, indicating that *unk-1*, *lin-41*, and *msi-1* work in parallel downstream of *daf-16*. These results provide valuable insight into how *daf-16* regulates RBPs to oppose adult cell fate during dauer.

Oral Presentation Session I

3. Can Genetic Diversity Explain a Lack of Anti-Predator Response in Aquatic Isopods?

Grace Sobaski, Dr. Abigail Cahill
Department of Biology, Albion College

Aquatic isopods are tiny invertebrates found in many freshwater ponds throughout North America working as detritivores. Not only are aquatic isopods crucial detritivores but also a large part of the diets of many predators ranging from fish to other invertebrates. Because of this, many would assume that these aquatic isopods can avoid predators. This led to Iyengar et al. conducting a study on predator recognition in benthic macroinvertebrates at Graver Arboretum in Bath, Pennsylvania across a span of 6 ponds. Unlike other invertebrates, the aquatic isopods did not avoid predators, whether or not they came from a pond with predatory fish. This led Iyengar et al. to question whether or not these Isopods were genetically similar, which might explain a lack of adaptation to predators.
This has now led to my current project asking if the isopods collected from these separate ponds are genetically similar. For this study, I extracted DNA from clusters of individual isopods collected from each of the 6 ponds. I then took this DNA and ran an initial gel electrophoresis on each sample. If the gel was successful, I then repeated this in polymerase chain reaction (PCR) form. This PCR was then sequenced, and I used the DNA sequences for further analysis. I performed population genetic analyses to compare the genetic similarity of isopods from different ponds. From this data it was found that the samples were not seemingly grouped together by each specific pond, but instead widely spread throughout to show that there was genetic mixing between ponds. This genetic similarity between ponds helps us to understand the predator-prey reaction of isopods from different ponds.

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4. Does Temperature Affect Nesting Success of Cavity Nesting Birds?

Emily Kraenzlein, Braden Andrejack, Dr. Katie Stumpf
Department of Biology, Alma College

Increased sensitivity to environmental changes makes birds ideal bioindicators for assessing the impacts of climate change. One of the many negative effects of climate change is the annual rise of global temperatures, which has impacts on the reproduction and nest success of birds. For breeding birds, maintaining an optimal nest temperature is critical for early growth and development, and any deviation from this can result in negative impacts on nesting success. Our research focuses on Eastern Bluebirds and Tree Swallows which are non-threatened secondary cavity nesters who frequently occupy nest boxes, making them a good study species. Our research objective was to understand how temperature extremes during different developmental stages affect clutch size, hatch rate/success, fledging success, and nestling development. We found that clutch size significantly decreases with increasing temperatures during egg laying for both Eastern Bluebirds and Tree Swallows ($p=0.05$), but temperature didn,t affect hatch rate which may be due to the mild temperatures during Michigan summers.To test this, we began experimentally heating nest boxes of Eastern Bluebirds in 2026 and while there is no significant difference yet, more heated nest boxes ($n=5$) did show lower hatch rate than non-heated nest boxes ($n=4$). In 2027, we will begin adding heat to nest boxes of Tree Swallows. Analysis of fledging success and nestling development is ongoing. Understanding how temperature extremes affect the reproduction and nest success of cavity nesters will give us insight into how climate change can impact the breeding biology of all birds.

Oral Presentation Session II

5. Identification and Characterization of a Freshwater Ciliate Isolated from Albion Michigan

Calla Altaani, Dr. Marcella Cervantes
Department of Biology, Albion College

Cilia are important organelles that are vital to sense our environment, to generate force for motility, and to coordinate with other cells for organ development. The ciliated protozoan, *Tetrahymena thermophila*, serves as a model organism for cellular biology due to its robust genetics and high abundance. In this study, the main goal was to identify a ciliate from a pond in Albion, Michigan, using different laboratory techniques, including microscopy, staining, and DNA sequencing. During experimentation, the cell strains tested were grown in different growth media at different temperatures to see under which environment the cells thrived in (by density and motility). Microscopic examination was used to identify cell shape and ciliary movement. Additionally, cellular feeding mechanisms were observed by vacuole formation using India ink as a tracer to detect phagocytosis. Doubling time was calculated to determine the efficiency of cilia to turn nutrients into new cells (reproductive fitness). DAPI staining was used to visualize DNA structures, including the nuclei, within the cell. Using three different genetic loci (cox, mitochondrial, and nuclear) DNA sequencing was used to confirm taxonomic identification by cross-referencing the genomic region. DNA sequencing revealed that the cox gene was 100% identical to the *Tetrahymena americanus* isolate and the mitochondrial ribosomal RNA gene was 98.79% identical to the *Tetrahymena pigmentosa* mitochondrion (note that the nuclear ribosomal RNA gene was unsuccessful during polymerase chain reaction). The highest density and motility for the cilia occurred at 30°C, with a doubling time of 4.65 hours, showing optimal growth and reproductive activity. This experimental work provides deeper insight into the mechanisms and features of eukaryotic cilia and how different biological techniques are used to identify cells.

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6. Environmental Enrichment and Social Status in a Cichlid Fish

Shreeya Bhosale, Ethan Burka, Dr. Peter Dijkstra
Department of Biology, Central Michigan University

Environmental enrichments, such as introducing aquatic plants and habitat modifications, are widely used to promote fish welfare by increasing habitat complexity, providing a more natural environment, and opportunities to avoid social conflict. Previous studies have demonstrated that aquatic plant enrichment can reduce fish mortality, supporting its benefits for fish welfare. However, structural complexity may also create additional opportunities for resource acquisition and territorial defense, potentially altering social hierarchies and the expression of status-dependent traits. This presents a challenge for studies investigating the behavioral and physiological consequences of social status, which often rely on clear distinctions between dominant and subordinate individuals. This study examined how increased habitat complexity shapes social dynamics and status-associated behavioral, reproductive, and hormonal traits in Burton's mouthbrooder, *Astatotilapia burtoni,* a species known for distinct differences in social behavior, gonad development, and endocrine regulation between dominant and subordinate males. Specifically, we examined whether aquatic structural enrichment provides visual barriers that reduce aggression toward subordinate males while influencing behavioral, reproductive, and hormonal indicators of social status. We assigned fish to planted or unplanted treatments and used video observations to quantify social, aggressive, reproductive, and foraging behaviors. We further investigated the effects of aquatic plants on subordinate males by examining whether additional hiding spaces and visual barriers reduced the frequency of aggressive attacks by dominant males on subordinates. Our findings demonstrated that clear differences between dominant and subordinate males in behavioral, reproductive, and endocrine indicators of social dominance persisted despite increased environmental complexity. In conclusion, our findings suggest that the addition of artificial plants does not significantly influence the behavioral or physiological traits of male *A. burtoni.*

Oral Presentation Session II

7. Changing Avian Population Dynamics and Management Efforts on Isle Royale National Park

Braden Andrejack, Dr. Katie Stumpf
Alma College

Successful habitat management requires an understanding of past and present population sizes and trends. Avian species are incredibly useful because they are conspicuous and can serve as bioindicators of ecosystem health. For example, examining the abundance of individual species over time provides information about how the habitat may have changed and can be used to make management decisions in the future. The isolation and limited human interference of Isle Royale National Park, located in Lake Superior, make it an interesting place to investigate such population dynamics. Between 1996 and 2008, researchers worked with the National Park Service to study avian population dynamics on Isle Royale. They concluded that the abundance of 18 species had significantly changed across the 12 years. To ensure conservation actions for these species are working and to determine how they have affected other co-existing species, I traveled to Isle Royale National Park and conducted point count studies in June 2026. Combining these data with data collected from the Great Lakes Landbird Monitoring Network, I am in the process of comparing the trends seen from 1996-2008 with those seen from 2014-2026. I have identified 15 species that have changed in population trajectories; 1 species that was declining is now increasing, 4 species that were decreasing are now increasing, and 10 species that were not changing are now increasing or decreasing. I examine these trends and put them in the context of past, current, and future habitat changes, making recommendations for future management on Isle Royale National Park.

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8. T*etrahymena rostrata*- Identifying Unknown Ciliates

Carter Mann, Dr. Marcella Cervantes
Department of Biology, Albion College

This research investigated an unknown ciliate. The aims of this study were to test the procedure for identifying new ciliates and to identify the unknown organism. This was achieved using a mixed-methods approach involving testing of phenotypic and genotypic elements of the investigatory cells. Phenotypic tests included: A phagocytosis experiment, a look into their doubling time, silver and DAPI staining, and finally observations on mating. From these tests, pictures and observations of cyst formation and the various stages of meiosis and conjugation were made. Genotypic experimentation included sequencing of three barcodes of DNA, including the Cox1 gene, the mitochondrial gene (Mito), and a ribosomal gene (Nuc). Findings revealed the organism of interest to be Tetrahymena rostrata, and the procedure to be effective. This conclusion is based on the percent identity, which was found to be highly similar to *T. rostrata* in the mito barcode (100%) and nuc barcode (99.51%). This research's importance stems from the many unknown species of microorganisms and their possible benefit to humans in medicinal research.

Poster Presentation Session I

1. Colors and Conflict: Aggression biases in a cichlid fish with reversible body coloration

Claire Buckingham, Abigail Medler, Dr. Peter Dijkstra
Department of Biology, Central Michigan University

Competition is a major force in ecology and evolution, shaping the distribution of species and the evolution (or disappearance) of species. Across animal species, aggression is typically directed most at individuals that pose the greatest threat competitively, also known as own-type aggression bias, which could promote the invasion and persistence of new phenotypes. In the cichlid fish *Astatotilapia burtoni* males compete aggressively for mating territories, which are required for spawning. Much is already known about own-type bias in many animal species, however there is very little known about whether these biases extend to species which can change their phenotype based on their environment. In *A. burtoni,* males switch between a blue and yellow color, and we assessed aggression biases using simulated choice tests whereby territorial males were presented with size-matched yellow and blue stimulus males enclosed in clear tubes. We predicted that the male *A. burtoni* would direct a majority of their aggression towards their own color. Additionally, we examined the possible repeatability of these aggression biases to determine if the males consistently displayed similar aggression across the trials. We found that males biased aggression towards their own type. Our findings lend support to the possibility that phenotype-dependent aggression contributes to the maintenance of color variation, even in species where the coloration is reversible.

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3. Characterization of the *algC* RNA Motif as a Regulatory Genetic Switch in *Escherichia coli*

Anna Drozdov[1], Ernest Njuguna[2], JP[3], Dr. Neil A. White[2,3]
[1] Department of Biology, Central Michigan University
[2] Department of Biochemistry, Cell, and Molecular Biology Graduate Programs, Central Michigan University
[3] Department of Chemistry & Biochemistry, Central Michigan University

The *algC* RNA motif represents a regulatory system located within the colanic acid production pathway in bacterial organisms such as *Escherichia coli*. We aim to evaluate the regulatory function of the *algC* RNA in exopolysaccharide (biofilm) formation. We hypothesize that the *algC* RNA functions as a genetic switch that regulates gene expression. To investigate this mechanism, we examined the ON and OFF expression states of the *algC* RNA in *Escherichia coli* using a reporter system. X-gal assays were used to observe differences in beta-galactosidase activity, while o-nitrophenyl-beta-D-galactopyranoside (ONPG) assays quantified beta-galactosidase activity in Miller units. The wild-type construct showed approximately 14,000 Miller units, while the 110C control/mutant showed approximately 5,000 Miller units and the A439, A15C, and A436 mutant constructs showed approximately 3,500 Miller units. These results support the hypothesis that the *algC* RNA functions as a genetic switch and suggest that specific residues are important for its regulatory activity. We are also investigating the biological significance and evolutionary conservation of this RNA motif by aligning *algC* RNA sequences against the Genome Taxonomy Database (GTDB) and constructing a phylogenetic tree to examine its conservation across taxa. In addition, we are using bacterial genetics to investigate the regulatory effects of this RNA in its native organism. Together, these approaches will help clarify the regulatory role of the *algC* RNA and its potential significance in bacterial gene expression and biofilm formation.

Poster Presentation Session I

5. Quantitative evaluation of candidate *Mycobacterium tuberculosis* trehalose dimycolate hydrolase inhibitors using a fluorescent-based assay

Zachary D. Hager[1], Clinton Kabutey[1,2], Dr. Benjamin M. Swarts[1,2]
[1] Department of Chemistry & Biochemistry, Central Michigan University
[2] Biochemistry, Cell, and Molecular Biology Graduate Program, Central Michigan University

Mycobacterium tuberculosis, the bacterium responsible for the respiratory disease tuberculosis, remains one of the most challenging pathogens to treat, largely due to its distinctive cell wall capable of robust protection and adaptability. The outer membrane of the cell wall, known as the mycomembrane, contains an abundance of the cell surface-exposed glycolipid trehalose dimycolate (TDM), which consists of a trehalose sugar core modified with long hydrophobic fatty acid chains. During times of stress or limited nutrient availability, the bacteria can transition into a persister state where the enzyme trehalose dimycolate hydrolase (Tdmh) actively cleaves TDM into free mycolic acids and trehalose, which is fed into central carbon metabolism to maintain energy and antioxidant levels. Prior work from our lab has provided a proof-of-concept that blocking trehalose recycling through inhibition of the intracellular trehalose-isomerizing enzyme, trehalose synthase, disrupts persister formation and increases antibiotic sensitivity. Here, we evaluate a panel of novel synthetic TDM derivatives as candidate inhibitors to block the upstream enzyme in this pathway, Tdmh, which is hypothesized to block persister formation, increase antibiotic sensitivity, and improve the clearance of Mtb. To quantify the activity of Tdmh, a fluorogenic analogue of TDM was previously developed by our group to quantify Tdmh activity in vitro that capitalizes on the phenomenon called fluorescence resonance energy transfer (FRET). Additionally, a planktonic and biofilm growth assay was utilized to monitor the relative growth of closely related *Mycobacterium smegmatis* species when treated with the analogues. We found that a handful of triazole and amine compounds demonstrated promising bacteriostatic properties but were not inhibiting the Tdmh enzyme, suggesting that other cellular targets are likely.

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7. Low pH State Transition Effect

Chloe Leaman, Sadey Simpson, Dr. Eliezer Schwarz
Alma College

Low pH can induce State Transitions in photosynthesis, which affects the way that light is distributed between Photosystem I (PSI) and Photosystem II (PSII). This pH-induced state transition can be observed by 77 K chlorophyl florescence but has not previously been confirmed by biochemical techniques like Clear Native PAGE. State Transitions (ST) occur when the light-harvesting complexes of PSII (LHCII) are redistributed from PSII to PSI, ostensibly to balance the energy absorbance between the photosystems. State Transitions are regulated by the Stn7 kinase, which is in turn activated by reduction of the plastoquinone pool. Phosphorylation of LHCII by Stn7 allows it to move from PSII (state 1) to PSI (state 2), which is observable as an increase in PSI chlorophyll fluorescence. Non-Photochemical Quenching (NPQ) is a photoprotective mechanism that disperses excess light as heat to prevent damage PSII. Although low pH is known to regulate NPQ through protonation of the PsbS protein, the mechanism by which low pH might induce a state transition is not known. We investigated the effects of pH on thylakoid organization by Clear Native PAGE to identify changes in PSI-PSII complexes and PSI-LHCII super complexes. The treated thylakoids and separated bands were then analyzed using 77 K chlorophyll fluorescence to examine changes in energy distribution between PSI and PSII. The results showed that exposure to low pH promoted the formation of PSI-PSII complexes and PSI-LHCII super complexes, which was correlated with State Transitions.

Poster Presentation Session I

9. Analysis of Gene Expression Changes in *cpnC* Mutants Using RT-qPCR

Selena M. Macias, Dr. Cynthia K. Damer
Department of Biology, Central Michigan University

Copines are calcium-dependent phospholipid-binding proteins found in many eukaryotic organisms. Altered copine expression has been reported in human cancers, but their molecular functions remain poorly understood. We are studying copine function in the amoeba *Dictyostelium discoideum*, which has six copine genes (*cpnA*, *cpnF*). During starvation, individual cells aggregate to form multicellular fruiting bodies. Cells lacking the *cpnC* (*cpnC*-) gene show defects in early development, aggregating by clumping rather than forming streams. To better understand the role of *cpnC* in early development, we examined the expression of four genes: *sibA*, which encodes an adhesion protein; *carA*, which encodes a cAMP receptor; *regA*, which encodes a cAMP phosphodiesterase; and *gtaC*, which encodes a transcription factor. RNA was isolated from parental cells and *cpnC*- mutant cells during vegetative growth and after six hours of starvation. RNA was converted into cDNA, and relative mRNA levels were measured using qPCR. During vegetative growth, *sibA*, *carA*, and *regA* expression was lower in mutants than in parental cells, while *gtaC* expression was unchanged. Starvation increased *carA*, *regA*, and *gtaC* expression and decreased *sibA* expression in both strains. After starvation, expression levels of *carA*, *regA*, and *sibA* were similar in parental and mutant cells, whereas *regA* expression was a little lower in the *cpnC*- cells. These findings suggest that disruption of *cpnC* affects basal expression of several developmentally important genes during vegetative growth, whereas the transcriptional response to starvation remains largely intact.

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11. *Dictyostelium discoideum* as a Model for Polycystic Kidney Disease

Riley E. Shiplet, Bridget K. Plude, and Dr. Cynthia K. Damer
Department of Biology, Central Michigan University

Polycystic kidney disease (PKD) is a genetic disease that is characterized by fluid-filled cysts in the kidneys and is caused by mutations in either polycystin-1 *pkd1* or -2 *pkd2* genes in humans. We are using the model organism *Dictyostelium discoideum* to study these genes, which allows us to study the fundamental functions of these genes in a simple and genetically tractable organism. In humans, polycystin-1 and polycystin-2 form a complex with a third protein called fibrocystin. We discovered four related genes to these three human proteins in the *Dictyostelium* genome and obtained insertional mutants for all four genes: *pkd1* (a fibrocystin homolog), *pkd2* (polycystin-2 homolog), *rliB* (a fibrocystin homolog), and *pgtD* (polycystin-1 homolog). First, the mutants were clonally isolated and the site of insertion was verified by PCR. The *pgtD* mutant was not able to grow in media and has not been studied yet. Next, we looked at phenotypic characteristics of the other three mutants and compared them to wild-type cells. These characteristics included growth, development, contractile vacuole function under hypoosmotic stress, cytokinesis, and mitochondrial function. We found that all three mutants grew normally in media and developed into fruiting bodies that were smaller than wildtype. Contractile vacuole function and cytokinesis appeared to be normal in all three mutants. To assess mitochondrial function, we treated cells with MitoTracker, which labels active mitochondria. Compared to wild-type cells, mutant cells exhibited markedly reduced MitoTracker fluorescence, suggesting a decrease in mitochondrial membrane potential and/or altered mitochondrial morphology. This finding suggests that mitochondrial dysfunction may be a shared mechanistic consequence of mutations among the genes associated with polycystic kidney disease. Future studies will further characterize mitochondrial structure and function using transmission electron microscopy and additional fluorescence-based techniques to better understand the roles of these genes in polycystic kidney disease.

Poster Presentation Session I

13. Manipulating *Tetrahymena* Mating Type Gene Expression via Starvation

Justin Montgomery, Dr. Marcella D. Cervantes,
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Tetrahymena thermophila is an aquatic ciliate with seven different mating types. They are reproductively compatible with each mating type other than their own. Prior research has shown *T. thermophila* doesn't mate when starved in Tris-Cl at 60 mM concentration. At lower concentrations such as 10 mM, the cells starve, but they still mate. More in-depth molecular techniques are available today than when this was first established. The goal of this experiment is to determine what the relationship is, if any, between the metabolic and mating pathways or if they are the same at the genetic level. This can be done by measuring the gene expression of cells starved in different concentrations of Tris-Cl. Starving the cells for at least 30 minutes triggers the expression of the mating type genes. By using qPCR, I can determine if there is a decrease in expression between 10 mM and 60mM Tris. If so, then the next step in this ongoing experiment is to find the exact threshold where the decrease in mating type gene expression occurs. If mating type gene expression remains constant at 60 mM, then the next step is to determine where else, or why, mating is failing to occur.

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15. Identification of an unknown *Tetrahymena* Ciliate

Akniyet Alisheva, Dr. Marcella Cervantes
Biology Department, Albion College

The goal of this project was to identify an unknown *Tetrahymena* isolate, RRP-7, using cell observations, growth characteristics, and DNA barcode comparisons.The sample was collected near Newburg Road in Albion, Michigan. Under the microscope, RRP-7 cells appeared small and active, with circular and irregular movement patterns. Cell density and activity differed across growth media, with Neff medium supporting particularly dense and active cultures. The estimated doubling time in Neff medium was approximately 4.8 hours, pending verification of the initial concentration correction.
We used polymerase chain reaction (PCR) to amplify DNA barcode regions. Nuclear small-subunit ribosomal RNA (rRNA), mitochondrial small-subunit rRNA, and cytochrome c oxidase subunit I (cox1) gene sequences were compared with reference sequences using the Basic Local Alignment Search Tool (BLAST). The nuclear sequence was identical to reference sequences from both *T. americanis* and *T. hegewischi*, so this marker alone could not distinguish between them. The strongest cox1 match was *T. americanis*, while the mitochondrial rRNA sequence matched *T. pigmentosa* most closely.
Overall, the nuclear and cox1 results support *T. americanis* as a possible identification for RRP-7, although the conflicting mitochondrial result leaves some uncertainty. Further work will include examining nuclear structure to determine whether a germline micronucleus is present. If present, we plan to conduct mating experiments with known Tetrahymena strains to help identify RRP-7 and test whether mating results support the DNA sequence comparisons.

Poster Presentation Session I

17. Investigating the Identity of an Unknown Cell: D8

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Cilia are tiny, hair-like structures found on the surface of some cells. They help move cells move through their environment and move substances around the cell. This study investigated and sought to identify a possibly unknown ciliate, D8. It was collected from a downspout located on Albion College's campus in Michigan. The goal was to identify its possible species and examine its growth characteristics and biological properties. D8 was cultured in six different growth media: PPY, PPYE, Neff, 10% Neff, 10% PPY, and PPYE trich, to compare its growth under different conditions. More methods included calculating its doubling time, extracting genomic DNA, doing barcode PCR using Mito, Cox, and Nuclear primers, and analyzing its mitochondrial DNA sequence using BLAST. Results showed that D8 grew best in PPY medium and had a doubling time of 11.09 hours. BLAST analysis identified *Tetrahymena rostrata* as its closest relative, with a 94.10% sequence similarity. These findings provide information about D8's growth, physical aspects and suggest a possible connection with *T. rostrata*, although its exact species identification remains undetermined. Further research is needed to better establish the specific identity and classification of D8.

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19. Biodiversity of Invertebrates in the Kalamazoo River

Justin Montgomery, Jay Martinez, Dr. Abigail Cahill
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Understanding the relationship between the Mnomen (wild rice) beds and invertebrate biodiversity within the Kalamazoo River provides possible insight into the ways humans can increase invertebrate biodiversity and overall system health. Between the months of May and June, 3-D printed containers (wigwasmkok), developed by other students, were placed in both natural and artificial Mnomen beds. In July, the containers were collected, and the contents were preserved in alcohol for sorting. We identified macroinvertebrates, sorting based on taxa to determine community composition, species richness, and diversity in the river. The organisms found among the leaves and detritus inside the containers were then referenced against a list of known species to occupy the river. The data was placed in the program R so that the relationships within the data could be understood. In addition to what was expected to be found, there were also a couple reoccurring organisms in both the real and the fake Mnomen beds that are introduced species of interest in Michigan. Additionally, the diversity of the artificial Mnomen beds was determined to be greater than the real Mnomen beds, possibly because of differences in water level. Understanding these interconnected aspects of a water system could reveal things about its overall health, and the native wild Mnomen that grows in the Kalamazoo River may directly relate to its biodiversity.

Poster Presentation Session I

21. Importance of heterotrophic bacterioplankton in northern lake Huron

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Limited information exists about the heterotrophic bacterioplankton assemblages in the Great Lakes, and particularly Lake Huron, despite considerable declines in phytoplankton populations following the establishment of invasive mussels. Because these organisms are vital in organic material decomposition and recycling of nutrients, we hypothesize significant changes in their numbers may further limit ecological productivity, particularly. Therefore, we measured the abundance and morphological composition of bacterioplankton along a key near to offshore habitat in northern Lake Huron (Thunder Bay). A total of 18 samples were taken in June, August, and September from surface (1-2 m) and near bottom (10-44 m) depths along an established near to offshore. Abundance was estimated using epifluorescence microscopy direct counting methods (syber-green staining). Overall, bacterioplankton abundance varied over an order of magnitude, ranging from 125 to 1,407 x 10^3 cells/ml (average ¬± one Std; 407 ¬± 306 x10^3 cells/ml). Bacterioplankton abundance varied significantly among dates (one-way ANOVA, F=5.52, p=0.016), whereby numbers were higher during early thermal stratification (June) compared with mid to late thermal stratification (August and September). Bacterioplankton had higher numbers at the most nearshore station (TB10) compared with the other more offshore sampling stations TB18 and TB46 (one-way ANOVA; F=3.595, p=0.053). These results suggest variation in the abundance of bacteria is likely regulated by factors that vary along spatiotemporal condition in the lake. In terms of morphological diversity, the assemblage relatively consistent among sites and dates; it was dominated by coccoid cells (80%), with rod and crescent shaped cells being subdominant (~20%). Future work will evaluate the potential importance of bacterioplankton, through direct comparisons of it biomass with other components of the planktonic food web.

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23. Evaluation of mechanical removal, herbicide and fire for the control of Autumn Olive, *Elaeagnus umbellata*

Luke Snow, Dr. Todd Barkman
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The aim of this project was to investigate the use of prescribed fire to complement standard approaches to Autumn olive management. Specifically, we intended to determine if the application of fire to uncut plants is effective in comparison to burning after cutting, with or without herbicide treatment. We investigated the effects of burning on stump resprouting using 8 x 8 ft burn boxes on 64 plots with both a high and low fuel load. Analyses of mechanical removal indicated that stump regrowth is significantly lower if herbicide is applied to stumps after cutting. After burning, cut + untreated plants had a significant reduction in regrowth as compared to controls and. Additionally, plants that were not cut had significantly less regrowth after burning than plants that were burned after cutting but were not treated with herbicide. This suggests that it may not be worthwhile cutting Autumn Olive prior to burning. Furthermore, plants that were cut and treated with herbicide and subsequently burned at high temperatures did not differ in regrowth compared to uncut plants that were burned under high fuel loads. Plants treated with herbicide responded similarly in all burn conditions.

Poster Presentation Session I

25. Developing Killifish Models for Functional and Comparative Genetics

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While traditional laboratory models such as zebrafish, mouse, and medaka have advanced vertebrate genetics, comparative approaches in functional genetics remain limited across vertebrate diversity. However, some vertebrates, such as killifishes, particularly “annual” species that inhabit seasonal pools and live for about a year or less, offer valuable models because of their short life cycles and delayed development (dormancy), making them ideal models for studying genetic, developmental, and age-related changes. Although the rapidly aging African turquoise killifish has emerged as a model for aging and developmental biology, most of the >800 other killifish species remain largely unexplored. Thus, we develop the green rivulus, *Rivulus cylindraceus*, and Rio pearlfish, *Nematolebias whitei*, as genetically tractable laboratory models for evolutionary and functional genetics. As a proof of concept, we used CRISPR-Cas9-mediated targeting of the pigmentation gene *Oculocutaneous albinism 2* (*oca2*) in *R. cylindraceus*, generating partial *oca2* knockout embryos. These embryos exhibited reduced pigmentation, demonstrating successful gene disruption. We also generated single-nuclei RNA-seq cell atlases of Rio pearlfish to characterize cell type-specific expression differences between sexes in the adult liver. Together, these findings validate genome editing in *R. cylindraceus*, establish a foundation for applying omics approaches to pearlfish and related killifish species to advance our understanding of the evolutionary genetics of dormancy and aging. Thus, the non-annual *R. cylindraceus* and annual *N. whitei* represent valuable, tractable models for functional genetics and genomics.

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27. Identifying Genes Necessary for a Mating Signal in *Tetrahymena thermophila*

Chloe Lkhamsuren, Dr. Marcella Cervantes
Department of Biology, Albion College

This project will focus on understanding how cells communicate and find the right partner. *Tetrahymena thermophila*, a single-celled pond organism with seven biological sexes. When two compatible cells meet, a visible signal appears on their surface within minutes. While we know this signal is essential for mating, we do not yet know which genes create it. My goal is to build knockout strains to test whether two specific genes, MTA and MTB, are required for this signal. I designed constructs intended to delete the MTA gene, the MTB gene, or both. The process involved amplifying specific DNA pieces and assembling them. I have successfully amplified, verified, and assembled all DNA fragments for the constructs. These are now ready to be sent to the Tetrahymena stock center for insertion into living cells. Once complete, these "knockout" strains will allow me to test whether the mating signal still appears without these genes, helping us understand how cells communicate and choose partners.

Poster Presentation Session I

29. Evaluating Calpeptin and Calpain Inhibitor III as Potential Suppressors of Tau Toxicity in *Drosophila*,Model of Alzheimer's Disease

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Department of Biology, Central Michigan University

Alzheimer's disease (AD) affects about 1 in 10 people over the age of 65. AD and other similar neurodegenerative diseases are known collectively as tauopathies, characterized by the abnormal accumulation of tau protein due to increased phosphorylation. Tau plays a critical role in stabilizing microtubules, a process essential for proper neuronal function. Our lab has previously shown that tau-induced toxicity can be suppressed by reducing calpain expression genetically in a fruit fly model of tauopathy. Calpain is a calcium-dependent protease that has been implicated in the generation of toxic tau fragments and the progression of neurodegeneration. This study builds upon the genetic experiments to investigate whether pharmacological calpain inhibition suppresses tau-induced toxicity. In AD, intracellular calcium levels can become dysregulated, leading to increased calpain activation. Activated calpain cleaves full-length tau into smaller fragments, including a 17-kDa tau fragment that our lab has shown to be particularly neurotoxic. We hypothesized that the calpain inhibitors Calpeptin and Calpain Inhibitor III would suppress tau-induced toxicity in the photoreceptor neurons of the fly eye. Quantification of the change of ommatidia integrity in fly eyes was used to assess the efficacy of our pharmacological strategy for reducing tau toxicity. After comparing the retinas of flies that have been treated with our calpain inhibitors, we found that drug treatment did not suppress the tau rough eye phenotype compared to controls. Although we have found that tau kinase inhibitors significantly reduce tau-induce toxicity in the past, our studies here, as well as with six other calpain inhibitors, have not yielded similar suppression of the tau rough eye phenotype. Future work will focus on promising results with calpain inhibitor drug feeding using a different neurodegenerative fly model focused on polyglutamine disorders.

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31. Identifying genes affecting lithium biology in *Escherichia coli*

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Elemental ions play a crucial role in biochemistry in ways which are not fully understood. There exists species of bacteria which contain genes controlled by aptamers that are selective for lithium ions exclusively. One pathway regulated by a lithium aptamer controls the production of an antiporter protein capable of ejecting one sodium or lithium ion and intaking two protons. This proton intake can allow the cell to survive in otherwise lethal basic conditions. Despite being able to function with sodium ions, gene regulators exist which selectively favor lithium ions to control their expression. The mutation of genes producing lithium regulated antiporter systems inhibited bacteria,Äôs ability to grow in a media containing lithium salts. The role lithium plays within the cell and the mechanisms which bring lithium into the cell remain to be explored.
The goal of this study is to identify genes which affect lithium uptake in *Escherichia coli* (*E. coli*) and to gain a wider understanding of lithium biology. Having such a high rate of reproduction, high rate of mutation, and having one of the most sequenced genomes of any species makes *E. coli* an ideal model organism for this study. When *E. coli* is grown in high enough concentrations of lithium chloride to prevent growth of the wildtype population, it is expected that surviving replicating cells will contain mutations of genes involved in lithium biology. Once a mutant strain better suited to growing in a lithium solution is identified and verified, the genome can be sequenced and compared to known *E. coli* genomes to locate genes associated with lithium biology. This applies not only to microbiology but also to human health. Human gut microbiomes are differentially affected by lithium, a treatment for bipolar disorder, yet the understanding of lithium biology is poorly understood in this context as well.

33. Regulation of adult cell fate via transcription factors in *Caenorhabditis elegans* dauer larvae

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Adult stem cells retain multipotency, or the ability to produce different cell types, during periods of cellular quiescence, but the mechanisms by which stem cells maintain their multipotent potential during quiescence are poorly understood. Under unfavorable conditions, the nematode *Caenorhabditis elegans* can enter the quiescent and stress-resistant dauer diapause stage after the second larval molt. These organisms can exit dauer diapause if conditions become favorable. We use lateral hypodermal seam cells as a model for human stem cells. Larval seam cells are multipotent and undergo a stereotyped pattern of divisions, whereas adult cells differentiate and express adult-specific genes, including *col-19*, encoding an adult-specific collagen. *daf-16* promotes dauer formation and blocks adult cell fate during dauer, coordinating developmental arrest and dauer formation. Specifically, *daf-16*(0) dauer larvae aberrantly express the adult cell fate marker *col-19p::gfp*. We previously identified an RNA binding protein, UNK-1, that opposes *col-19p::gfp* expression during dauer downstream of *daf-16*. Because *col-19p::gfp* is a transcriptional reporter, we hypothesize that UNK-1 inhibits the expression of a transcription factor that directly regulates *col-19p:gfp*. We have identified CEH-60 and NHR-68 as transcription factors that may promote *col-19p::gfp* expression downstream of *daf-16*. To test whether these transcription factors also regulate *col-19p::gfp* downstream of *unk-1*, we have used RNAi to deplete these genes in unk-1 mutant dauers and measured expression of *col-19p::gfp*. Thus far, we have found that *ceh-60* RNAi produces little to no effect on *col-19p::gfp* expression in *unk-1*(0) dauer larvae. To confirm that *ceh-60* RNAi reduces *col-19p::gfp* expression in *daf-16*(0) dauer larvae, we repeated these experiments in that background and quantified expression levels. Surprisingly, we found that *ceh-60* RNAi did not reduce *col-19p::gfp* expression. We are currently performing similar experiments using *nhr-68*. Taken together, these experiments aim to elucidate the pathways regulating adult cell fate.

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35. Comparative analysis of Tau, TDP-43, and age on locomotive behavior in *Drosophila*

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Department of Biology, Central Michigan University

Alzheimer's disease (AD) is a progressive neurodegenerative disorder associated with memory loss, spatial disorientation, and deterioration of complex thinking. The primary pathological markers for AD are extracellular amyloid plaques and intracellular neurofibrillary tau tangles. In addition, the accumulation of a second neuronal protein, TAR DNA-binding Protein 43 (TDP-43), has shown to be present in 46% of the cases for pathologically diagnosed AD, highlighting its role in neurodegenerative disease. Past studies have shown a linkage between tau and TDP-43, where TDP-43 may downregulate tau expression by destabilizing its mRNA transcripts. Under physiological conditions, tau organizes microtubules for efficient cellular trafficking, and TDP-43 regulates gene expression, RNA processing, and the cellular stress response. In diseased states, tau becomes hyperphosphorylated and misfolds into toxic neurofibrillary tangles, causing the breakdown of microtubule transport. Mutations in TDP-43 result in its mislocalization to the cytoplasm where its absence from the nucleus causes a buildup of abnormal exons in mRNA. To assess the impact of hyperphosphorylated tau and mutant TDP-43 on neuronal networks, the fruit fly, *Drosophila melanogaster*, is an effective model organism with gene analysis studies revealing 77% of human disease-associated genes sharing homology with genes in *Drosophila*. Using a standard negative geotaxis assay, this study assessed the locomotor performance in *Drosophila* models expressing human tau and a high-expression form of TDP-43 (TDP-43hi). We hypothesized that the separate, pan-neuronal expression of these proteins would produce age-dependent impairments in locomotor function when compared to controls. While age-dependent locomotor impairments were observed overall, only TDP-43hi-expressing flies exhibited diminished climbing ability, and this deficit was evident only at day 24, the final and oldest age examined. Although the observed effects differed from our predictions, they reveal previously unrecognized aspects of tau pathology that warrant further investigation and may guide the development of future interventions for AD.

Poster Presentation Session II

2. Use of deconvolution to extract single cell information from bulk RNA-seq data using diabetes and multiple sclerosis as examples.

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Gene expression studies are important resources to explain how cells function and how they adapt to different conditions, like stress, changes in environment and diseases. Proper gene regulation makes it possible to function properly to these different conditions, while dysregulation leads to various diseases. RNA sequencing (RNA-seq) provides a complex genetic picture of the organism, revealing information about differential gene expression and splicing variants. Bulk RNA-seq methods are used to study global gene expression within a tissue sample. On the other hand, Single cell RNA-seq (scRNA-seq) provides investigation of up to 20,000 individual cells at once, revealing distinctions between distinct cell populations as well as identification of rare cell types. However scRNA analysis is experimentally complex, requiring expensive equipment. Deconvolution is a method to extract cell population information directly from bulk RNA sequence data without the need for experimentally isolating individual cells. With the public availability of vast amounts of RNAseq data, deconvolution can be used to gain more in-depth insights from previous bulk RNA seq experiments. Deconvolution has different methods to measure this proportion and of them is called MuSiC. Galaxy is an online platform that gives possibilities to complete bioinformatics tools, including MuSiC to complete the analysis. Using Galaxy, we used the MuSiC method of deconvolution to complete an example analysis using data from type II diabetic patients. And as a result graphs were made that showed the estimated proportion of cells in each of the cell types in normal and diabetic patients. We are in the process of repeating this analysis focusing on multiple sclerosis.

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4. Evaluating motor neuron vulnerability to tau expression in aging *Drosophila*

Isaac Postema, Katherine Himmel, Hunter Hitzelberger, Dr. Michelle Steinhilb
Department of Biology, Central Michigan University

Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by memory loss, impaired spatial awareness, and declining cognitive function. Two major pathological features of AD include extracellular amyloid plaques and intracellular neurofibrillary tangles composed of tau protein. Normally, tau plays an important role in stabilizing microtubules within neurons, allowing for proper cellular structure and intracellular transport. However, when tau becomes hyperphosphorylated, it can detach from microtubules and accumulate into aggregates that disrupt neuronal function and may eventually lead to cell death. Another protein associated with AD is TAR DNA-binding protein 43 (TDP-43), which can become mislocalized from the nucleus to the cytoplasm and form potentially toxic aggregates. The fruit fly, *Drosophila melanogaster*, provides a useful model for investigating neurodegenerative diseases because many cellular pathways are conserved between flies and humans. Behavioral assays, particularly those utilizing negative geotaxis, allow researchers to examine changes in locomotor function associated with neuronal damage. In this study, we evaluated the climbing ability of aging *Drosophila* expressing human tau using the D42-GAL4 driver to target protein expression in motor neurons. We hypothesized that expression of tau would negatively affect climbing performance, with locomotor impairment becoming more pronounced as the flies aged. Our findings revealed significant age-related declines in climbing performance, although the overall effect of tau expression was generally not statistically significant. By examining these behavioral changes, this research aims to improve our understanding of tau-associated neurotoxicity, potentially contributing to the identification of genetic modifiers and future therapeutic targets.

Poster Presentation Session II

6. Environmental factors influencing riboswitch associated gene regulation in *Escherichia coli*

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Riboswitches are segments of RNA with regulatory roles that can alter gene expression in response to specific metabolites and signals in their environment. The specific riboswitches used were recently characterized and respond to monovalent cations, Na+and Li+, which are associated with genes involved in cellular homeostasis and the transport of ions. Here, we are investigating two of these specific systems, DUF1646, which is a Na+ responsive riboswitch and the riboswitch, nhaA-I which is responsive to Li+. We are studying these riboswitches to gain a better understanding of their roles in regulation and the potential physiological roles they have. A DUF1646 associated lacZ reporter was used to examine the effects of sodium and glucose availability on gene expression in *E. coli*. Galactosidase activity was quantified using ONPG assays using varying conditions of NaCl and glucose availability. Preliminary data indicate that the reporter activity is influenced by these environmental conditions, with an increase in activity found when sodium and glucose are present together compared to no-salt growth conditions. Bacterial responses to lithium are being characterized using growth-based lithium toxicity assays. In isolates, distinct lithium response phenotypes have been observed which include, minimal, intermediate, and typical responses to increasing lithium concentrations. We plan to gather genomic analysis of the isolates that represent the phenotypes that are adapting to the lithium conditions and comparing them to the unmutated genomes. Together, these attempt to further characterize the Na+ and Li+ responsive riboswitch systems and their roles in bacteria adapting to the changing ionic and metabolic environments.

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8. Chemoenzymatic synthesis of 2,2-difluorotrehalose, a novel trehalose analogue and possible inhibitor of *Mycobacterium tuberculosis*

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The disaccharide trehalose plays an essential role in the pathogenicity of *Mycobacterium tuberculosis*, the causative agent of tuberculosis in humans. Recent studies have found that interfering with trehalose metabolism can inhibit the growth of *M. tuberculosis*. Our group previously demonstrated that monosubstituted trehalose analogues, such as azido- and amino-trehaloses, have inhibitory activity against various mycobacterial species and can sensitize these organisms to existing antitubercular drugs. Separately, studies have shown that 2,2-difluorosugars may possess inhibitory activity against cognate glycosyltransferase and glycoside hydrolase enzymes. Therefore, we aimed to synthesize the novel trehalose analogue 2,2-difluorotrehalose (2,2-DFT) and test the hypothesis that this compound could act as an inhibitor of enzymes involved in mycobacterial trehalose metabolism. Here, we report progress toward chemoenzymatic synthesis of 2,2-DFT starting from 2,2-difluoroglucose, a route which utilizes a trehalose-synthesizing glycosyltransferase enzyme (TreT) in the key glycosidic bond-forming step. Purified 2,2-DFT was successfully synthesized through a TreT-catalyzed chemoenzymatic approach and characterized by NMR and mass spectrometry. These results establish a foundation for further investigation of 2,2-DFT as a potential inhibitor of trehalose metabolism in mycobacteria. Future work will focus on repeating the TreT-catalyzed synthesis to confirm reproducibility, and evaluating the biological activity of 2,2-DFT in *Mycobacterium smegmatis*, including its effects on planktonic growth and biofilm formation.

Poster Presentation Session II

10. Using RT-qPCR to Investigate the Effects of CpnA Loss on Gene Expression

Jack Rich, Dr. Cynthia K. Damer
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Copines are calcium-dependent phospholipid-binding proteins found in most eukaryotes. Copines are thought to connect calcium signaling to membrane processes, but it is still unclear whether they play a role in gene regulation. *Dictyostelium discoideum* is a good model for studying this because it is easy to grow and switches from single cells to a multicellular organism during development, which requires large changes in gene expression. *Dictyostelium* has six copine genes (cpnA-cpnF) that have different functions. Cells lacking copine A (cpnA-) have defects in cytokinesis, contractile vacuole function, calcium homeostasis, and development. Earlier RNASeq transcriptome data comparing wild-type and cpnA- cells showed that *p62* and *pyk3* genes were significantly downregulated and *fslM-1* and *fscG* genes were significantly upregulated in cpnA- cells. To validate the RNASeq data, RT-qPCR was used to confirm the differential expression of these four genes in wild-type and cpnA- cells. RNA was isolated from both vegetative and starved wild-type and cpnA- cells, converted to cDNA, and then amplified with gene-specific primers using qPCR. Relative expression was then analyzed using the Ct method. The results matched the transcriptome data, confirming that the loss of cpnA produces major changes in the expression of these genes. Downregulation of the autophagy-associated gene *p62* and the kinase *pyk3*, together with the upregulation of the frizzled-like receptor genes *fslM-1* and *fscG*, suggests that CpnA influences genes involved in multiple signaling pathways.

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12. Investigating the Role of Copine D in cAMP signaling in *Dictyostelium discoideum*

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Copines are a family of calcium-dependent phospholipid-binding proteins found in most eukaryotic organisms. Abnormal expression of several copine genes has been observed in various types of human cancer. However, the specific molecular roles of these proteins remain unclear. We are studying copines in the organism *Dictyostelium discoideum*, which has 6 copines (*cpnA*-*cpnF*) and is a good model organism for studying cell signaling pathways. Previous research showed that the loss of *cpnD* leads to increased Ras activation, suggesting that CpnD has a role in the regulation of cell signaling. In this study, we expressed GFP-tagged CpnD in Dictyostelium cells to examine the intracellular localization of CpnD and to identify the lipids it binds. GFP-CpnD localized to the cytosol and nucleus and translocated from the cytosol to the plasma membrane and back in response to cAMP stimulation. In addition, GFP-CpnD was found to transiently localize with small intracellular vesicular structures. Using lipid dot blots containing 24 different lipids, we found that GFP-CpnD bound to a single type of lipid, lysobisphosphatidic acid (LBPA), found mainly in late endosomes. We also examined GFP-tagged CRAC localization following cAMP stimulation in both wild-type and *cpnD* mutant cells. CRAC, which stands for cytosolic regulator of adenylyl cyclase, binds to the lipid PIP3 and translocates to the membrane in response to cAMP stimulation. We found that *cpnD* mutant cells exhibited a more robust CRAC plasma membrane association compared to the wild-type cells. CRAC translocation to the plasma membrane is downstream of Ras activation, so these results corroborate our previous finding that *cpnD* mutants exhibit increased Ras activation, suggesting CpnD may be involved in the attenuation of cAMP signaling. The binding of GFP-CpnD to LBPA suggests that CpnD may regulate endosomal trafficking of cAMP signaling components.

Poster Presentation Session II

14. Identification of an unknown *Tetrahymena* Ciliate

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Department of Biology, Albion College

This study aimed to identify and characterize an unknown organism isolated from a downspout on the Albion College campus. Mitochondrial rRNA, nuclear rRNA, and mitochondrial cytochrome oxidase (COX) gene sequences from an unknown *Tetrahymena* organism was used determine its closest genetic match. The unknown organism was tested in different medias to see what worked best for cell growth for the organism. PPYE was determined to be the best because it had the most living cells. The cells started to encyst after a while because they stopped moving, and they developed a protective wall around them. The mitochondrial and COX reactions produced detectable DNA bands. However, the initial nuclear and mitochondrial amplifications were unsuccessful because, even though the mitochondrial amplification worked, there were too many bands, which made it unreliable and required more barcode PCR optimization, so we didn't get the barcodes for them and just got the barcode sequence for the nuclear rRNA sequence. The nuclear rRNA sequence was analyzed, which identified *Tetrahymena allegheniensis* as its closest sequence match. These results showed how molecular techniques can be combined to investigate genetic similarities and assist in the identification of unknown microorganisms. Further analysis and successful nuclear DNA amplification would help strengthen the molecular identification. DNA was initially made using a quick-lysis technique. PCR amplification with specific primers targeting COX, mitochondrial, and nuclear rRNA genes.

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16. Von Willebrand 17 Gene Knockout in *Tetrahymena*

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Tetrahymena thermophila is a single-celled organism widely studied in cellular biology to understand the fundamentals of eukaryotic biology. Despite *Tetrahymena* being a unicellular organism, *Tetrahymena* shares many core cellular processes with human cells. *Tetrahymena's* defining feature is nuclear dimorphism which allows *Tetrahymena* to house both a silent germline nucleus for reproduction and an active somatic nucleus for daily function. Due to these nuclei functioning differently, this study aims to identify which somatic genes are necessary for *Tetrahymena* reproduction by knocking out selected genes. The gene that is being knocked out is von Willebrand 17. Researchers hypothesized that the VW17 (Von Willebrand 17) protein may be required for *Tetrahymena* conjugation, which means that mating pairs that lack this gene may fail to successfully have a nuclear exchange. To test if the VW17 gene is essential for reproduction make the knockout in two different mating types. Then mate them with each other and a wild-type cell to determine if VW17 is required for mating. Ultimately, this research aims to provide insight into the mechanisms controlling *Tetrahymena* reproduction. By establishing the functional necessity of VW17 in conjugation, this work promises to offer a foundation for understanding broader eukaryotic conjugation and cellular growth dynamics.

Poster Presentation Session II

18. Elders of the river: Ages of common freshwater mussels in the Chippewa River, MI, USA

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Freshwater mussels, known as unionids, hold ecological value as habitat providers and biofilters. Unionid age can be used to infer population fecundity and recruitment, which are factors of ecosystem health. Unionids exhibit a wide variation in age; most species average about 15-40 years old, however there is variation from ~5 years to as long as 100 years. Unionid age is closely linked to their growth, which is highly plastic in response to environmental variables. External growth lines can be used to estimate a unionid‚Äôs age; however, those measurements can be river dependent. Dunlap (2025) developed an ellipsoid model representing the relationship between unionid shell length and age of common species found in the Chippewa River, Michigan. The aim of this study was to create a baseline age measurement of five common unionid species (*Amblema plicata*, *Eurynia dilatata*, *Lampsilis cardium*, *Lasmigona costata*, and *Ortmanniana ligamentina*) found throughout the entire river. In this current study, live unionids gathered from three past studies (Chambers 2016; Springer 2024; Dunlap 2025), were used to estimate the minimum age of 3,586 individuals. A 9-year span of unionids across all sites and species yielded an average age of 8.01 ± 3.14 years (min=0.82, max=27.72). In species groups comparisons, *E. dilatata* most frequently had the oldest age average (n=888, 8.36 ± 1.37 years, min=4.67, max=13.64). All species' average age estimates measured within a normal distribution, indicating the population is experiencing recruitment, which is desirable for the conservation of imperiled species. Knowing the ages among these mussel populations is imperative to determining how populations respond to changes in habitat or management practices. This study can be used as a baseline population assessment for the Chippewa River and potentially used to compare unionid populations within other regions.

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20. Comparative abundance of Eastern Red-Backed Salamanders *Plethodon cinereus* across edge, interior forest, and trail habitats

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Human activity and habitat fragmentation can alter wildlife habitat quality and behavior. Forest edges and areas adjacent to hiking trails may experience increased disturbance and altered microclimates, but their effects on terrestrial salamanders remain unclear. I investigated the comparative abundance of Eastern red-backed salamanders *Plethodon cinereus* across forest interior, forest edge, and hiking trail-adjacent habitats. I hypothesized that abundance would be greatest in forest interior habitat, and lowest near hiking trails due to increased human disturbance. Two study sites were selected, each containing all three habitat types. Five coverboards of varying materials were placed within each habitat and checked weekly over a four-week sampling period. Salamander counts, soil temperature, air temperature, and soil relative humidity were recorded. I observed 108 salamanders in total. I modeled peak abundance using full and reduced generalized linear mixed-effects models. I found that habitat type ($p=0.0002$) and coverboard material ($p=0.016$) were significant predictors of salamander counts. Mean maximum counts of salamanders were highest in forest interior habitats (3.5), followed by forest edges (1.375), and hiking trail-adjacent habitats (1.0). Old plywood coverboards had the highest observed salamander counts, potentially because weathering increases moisture retention, and time allows the board to become better integrated with the ground. Measured environmental variables did not significantly affect salamander counts. These findings suggest areas that are relatively undisturbed may support greater salamander abundance, and habitat change and human disturbance may lower it. Understanding these relationships can help inform forest management and recreational trail planning to support terrestrial salamander populations.

Poster Presentation Session II

22. Conservation Genetics in the Michigan Monkeyflower

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Michigan monkeyflower (*Mimulus michiganensis*, syn. *Erythranthe michiganensis*) is a yellow-flowered perennial plant endemic to the Mackinac Straits of Lake Michigan. The species is currently listed as endangered and is at risk of extinction due to habitat loss and sterility in most populations. This could potentially lead to a loss of genetic diversity and accumulation of mutations. It has been twenty years since genetic data for the Michigan monkeyflower has been analyzed, and methods for sequencing have greatly advanced in that time. My project aims to analyze the genetic diversity of the Michigan monkeyflower and construct a phylogenetic tree to describe relationships between populations for use in conserving the species. We extracted DNA from individuals from each population, amplified various single copy genes, and Sanger sequenced them in search of informative SNPs and indels. Because no reference genome currently exists for Michigan monkeyflower, we also extracted high molecular weight genomic DNA for whole genome Illumina sequencing, which could help to pinpoint the unknown origin of the species. Determining the relationships between populations of the Michigan monkeyflower will further aid in efforts to conserve the species by guiding potential hybridization or relocation efforts.

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24. The role of Accumulation and Replication of Chlorplasts 6 (ARC6) in carotenoid synthesis and storage

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Carotenoids are yellow, orange, and red pigments in photosynthetic organisms. In plants, carotenoids have essential functions in photosynthesis and stress responses and non-essential functions in flowers and fruits, where their colors attract pollinators and seed dispersers. Carotenoids are not only important in plants, but are also required for vitamin A production in animals, including humans. For these reasons, it is important to know more about how these pigments are made and stored. In this study, we use the crimson monkeyflower (*Mimulus verbenaceus*) as our model. This species normally has red flowers due to the layering of two pigment types: pink anthocyanins and yellow carotenoids, but our lab has generated a pink-flowered mutant that makes reduced carotenoids. We have mapped the mutation to the Accumulation and Replication of Chloroplasts 6 (ARC6) gene, which is known to be involved in chloroplast division in the model plant Arabidopsis. Because *Arabidopsis* does not produce storage structures for carotenoids in its flowers or fruits, our arc6 Mimulus mutant provides a unique opportunity to study this gene's function in non-photosynthetic tissues. The three goals of this study are to 1) understand how the arc6 mutation alters protein function; 2) check for successful knockdown of ARC6 in RNAi plants, and 3) build an over-expression plasmid to express a the functional ARC6 gene in the mutant background. This will allow us to learn how ARC6 affects pigmentation in flowers, which is important for pollination in *M. verbenaceus*, and also improve our basic knowledge of carotenoid production and storage in plants. In the future, this work could be applied to the genetic engineering of carotenoid production in crop plants to increase their nutritional value.

Poster Presentation Session II

26. Impact of zinc on antibiotic resistance transfer in *Escherichia coli*

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Antibiotic resistance is an ongoing public health concern that leads to ineffective treatment options for bacterial infections. Bacteria can acquire this resistance through conjugation, a process in which two bacteria make direct contact and transfer plasmid DNA containing antibiotic resistance genes. Supplemental zinc has been investigated as a potential method for reducing the transfer of antibiotic resistance. However, findings to date have been inconsistent, possibly due to differences in bacterial strain, bacterial species, and form of zinc used. My project investigates the effect of zinc form and concentration on antibiotic resistance plasmid transfer in *Escherichia coli*. I mixed a donor strain resistant to kanamycin and a recipient strain resistant to nalidixic acid at a 1:2 ratio. I supplemented the cultures with zinc gluconate, zinc picolinate, and zinc bisglycinate at concentrations of 0.1 mg/mL and 0.25 mg/mL. Results show that with increasing zinc concentration across all three forms, there is a decrease in the transfer rate of antibiotic resistance genes. Kruskal-Wallis tests indicated statistically significant differences in groups treated with zinc bisglycinate ($p = 0.0349$) and zinc gluconate ($p = 0.0347$) but not zinc picolinate ($p = 0.2$). These findings suggest that zinc supplementation may influence antibiotic resistance transfer in *E. coli*. Targeted use of zinc compounds may offer a promising strategy for mitigating the spread of antibiotic resistance in bacterial populations.

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28. The regulation of an adult cell fate marker during dauer by NuRD complex genes

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In *Caenorhabditis elegans*, environmental conditions determine whether larvae proceed through continuous development or enter dauer. This dauer stage is initiated after the second larval molt in response to unfavorable environments. During dauer, progenitor cells such as lateral hypodermal seam cells remain both multipotent and quiescent. If environmental conditions become favorable again, larvae exit dauer and seam cells complete their normal developmental process. COL-19 is an adult-specific collagen expressed in seam cells and other hypodermal cells. We previously showed that daf-16 opposes col-19 expression during dauer. Furthermore, we found that daf-16 does not directly repress col-19 but instead appears to regulate unidentified downstream factors that in turn regulate col-19 expression. We found that RNAi of dcp-66 strongly suppresses col-19p::gfp expression in daf-16(0) dauer larvae, suggesting that daf-16 may oppose col-19p::gfp via regulation of dcp-66. dcp-66 encodes a Zinc finger protein and a component of the nucleosome remodeling and deacetylase (NuRD) complex. Surprisingly, depletion of other NuRD complex genes in daf-16 mutants did not alter col-19 expression, suggesting that dcp-66 may function independently of the NuRD complex. To further define this regulatory network, we are currently depleting NuRD complex genes in wild-type dauer larvae and analyzing col-19p::gfp expression. Thus far, we have interestingly found that chd-3 RNAi induces col-19::gfp expression in the wild-type dauer larva while let-418 and dcp-66 do not. These studies aim to clarify how chromatin regulation and dauer signaling pathways coordinate adult seam cell differentiation.

Poster Presentation Session II

30. Characterizing the pale yellow flower (pyf) carotenoid mutant of *Mimulus guttatus* (yellow monkeyflower).

Andrew Park, Dr. Lauren Stanley
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Carotenoids are isoprenoid compounds that serve crucial functions in plants. They function as accessory pigments for photosynthesis, protect against photooxidative damage, and are precursors for hormones and volatiles. They also contribute to the red, orange, and yellow pigmentation in flowers and fruits, which attract pollinators and seed dispersers. Carotenoids are an essential component of the human diet, required for the synthesis of Vitamin A, and increasing the amount of these pigments in crops is a major goal of plant biology. In this study, we use a lab-induced mutant of yellow monkeyflower (*Mimulus guttatus*) called pale yellow flower (pyf) to understand the production of carotenoid pigments in floral tissues. The goals of our study are to (1) extract and pool DNA from mutant plants from an F2 cross, (2) whole genome sequence the pooled sample to map the mutated gene underlying this phenotype, and (3) characterize the mutant plant through pigment extractions and microscopy of carotenoid storage organelles. By identifying and characterizing the PYF gene, we will better understand how carotenoids are synthesized and stored, which could be applied to improving the carotenoid content of crops to increase both plant and human health

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32. Juvenile exposure to environmentally relevant levels of bisphenols exerts impact on development and behavior in rats (*Rattus norvegicus*)

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Bisphenols are a group of synthetic organic chemicals used globally in manufacturing of plastics. There are several different bisphenols used in plastic manufacturing, but Bisphenol-A was the original form that gained widespread use. Bisphenol-S and/or Bisphenol-F are newer bisphenols that are now found in many types of plastic used in everyday life. Both Bisphenol-S and Bisphenol-F are now common replacements for the original, widely used bisphenol, Bisphenol-A. Changes in types of bisphenols used in the manufacture of plastics have occurred as Bisphenol-A has become recognized as a pollutant of concern by the general public. While Bisphenol-S and Bisphenol-F are technically NOT Bisphenol-A, both are recognized as endocrine disrupting chemicals due to the cyclic ring morphology they share with Bisphenol-A. All bisphenols have been associated with exogenous mimicry of estrogen; however, we do not have as detailed an understanding of how Bisphenol-S and/or Bisphenol-F may exert their endocrine disrupting effects compared to Bisphenol-A. Bisphenols leach from plastics and are inadvertently ingested by organisms. Research into the developmental, behavioral and physiological impacts of Bisphenol-S and/or Bisphenol-F ingestion are limited. We theorize that juvenile exposure to Bisphenol-S or Bisphenol-F may specifically influence behavior by reshaping organization and physiology during puberty, resulting in potential changes affecting various behaviors. In our research, exposure to either Bisphenol-A, Bisphenol-S or Bisphenol- F occurred post-weaning at environmentally relevant levels. At maturity, weight and neuromuscular development were assessed. Behaviorally, measures related to stress responses and exploratory behavior were measured. These data are compared across each bisphenol type. Results indicate that juvenile exposure to each of these different bisphenols affects neuromuscular strength, anxiety, and exploratory behavior in rats, but that each bisphenol type does so in different ways.

Poster Presentation Session II

34. Validation of Flynotyper as a quantitative tool for measuring tau toxicity

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Alzheimer's disease is a neurodegenerative disorder caused by several factors, including the toxic accumulation of hyperphosphorylated tau protein. The Steinhilb lab expresses human tau proteins in the photoreceptor neurons of the fruit fly, *Drosophila melanogaster*, to model human disease pathologies. Typically, the adult fly eye consists of ~800 ommatidia containing photoreceptor and support cells, arranged in a highly ordered hexagonal lattice; retinal neurodegeneration disrupts the eye, resulting in the loss of structure that is commonly referred to as the tau rough eye phenotype. Our lab routinely uses drug feeding to identify whether kinase- or calpain-inhibiting compounds can reduce the severity of the rough eye phenotype, indicating a suppression of tau toxicity. However, quantifying the rough eye phenotype is difficult. The Flynotyper software was developed to address this challenge by producing a phenotypic score, determined by identifying each ommatidium and measuring the distance and angles between them. Flynotyper was originally developed as both a standalone program and a plugin that can be run through ImageJ or FIJI. These programs have become outdated, users report difficulty downloading and running the software, and developers have indicated that the software will become unsupported soon. More recently, Flynotyper 2.0 was developed to address these issues, as well as eliminate bugs and speed up analysis time. This project examined the results produced by the different software versions to understand why each was producing different phenotypic scores, indicating that images are being processed differently. During testing of image-editing strategies, we found that cropping regions near the eye frequently led to ommatidia misidentification, whereas blacking out or removing the background often prevented the images from being processed altogether. Overall, we found that removing the background in Photoshop and using Flynotyper 2.0 was the most reliable method for quantifying *Drosophila* eye roughness.

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36. Synthesis of Antioxidant Dendrimers using Hydrophilic and Hydrophobic Gallic Aldehyde-Derivatized Dendrons

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Highly reactive free radicals are generated through endogenous and exogenous processes. The free radicals cause oxidative stress on cells, which is a contributing factor to many human diseases, including cancer, cardiovascular damage, and neurodegenerative disease (Lee et al., 2010). To neutralize the free radicals, antioxidants are used by donating an electron. Some antioxidants are available naturally and can be obtained through diet and supplements. However, the majority of these antioxidants are not water-soluble, severely limiting their bioavailability. Due to this, this study aims to create antioxidant dendrimers that have both hydrophilic and hydrophobic regions to be soluble in water and organic media in our body. The amphiphilic dendrimers are synthesized by attaching a hydrophilic dendron to a hydrophobic dendron. The hydrophilic dendron has 6 D-mannose units on the surface, and the hydrophobic dendrons have 12 syringaldehyde units or 6 syringaldehyde units with 6 pyridoxal units on the surface.