

Biology Undergraduate Research Symposium

Biosciences Building

Central Michigan University

November 21, 2025



Schedule

- 1:15-2:00 - Poster setup in main atrium
- 2:00-2:15 - Opening Remarks in room 1010
- 2:15-3:00 - Poster Session I (odd numbers)with snacks in main atrium
- 3:00-4:00 – 10-Minute Talks in room 1010
- 4:00-4:45 - Poster Session II (even numbers) with snacks in main atrium
- 4:45 - 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 to vote for your favorite using the ballots provided at the front of the room.



Oral Presentation Abstracts

1. Discovery of Widespread Migrasome Formation During Amoeboid Migration in *Dictyostelium discoideum*

Bridget Plude, Cynthia Damer
Department of Biology, Central Michigan University

Copines are a family of calcium-dependent phospholipid binding proteins that are conserved amongst most eukaryotes. Nine copines (Copine-1-Copine-9) exist in humans and their overexpression is linked to various types of cancer. The correlation between copine expression and cancer pathology highlights the need for further investigation into the unknown cellular mechanisms behind this relationship. We use the model organism *Dictyostelium discoideum*, which has six copines (*cpnA-cpnF*), as a genetically trackable system to study these proteins. This amoeba is an ideal system for studying cancer cells based on a highly motile life cycle that mirrors many processes used by cancer cells, including autophagy, chemotaxis, and collective cell migration. We utilized a GFP-tagged CpnE cell line and confocal microscopy to study this protein's dynamics in live cells under various migratory conditions: crawl under agar while chemotaxing towards folate, migrate randomly, and aggregate together. We identified fluorescent "trails" behind migrating cells and vesicular structures at the ends of these trails that would remain stationary as the associated cell continued moving. Utilizing the literature to identify these structures, we revealed an additional process shared between *Dictyostelium* and cancer cells: migracytosis. Migracytosis is a migration-dependent process where organelles, called migrasomes, form at the ends of membranous strands, called retraction fibers, and eventually release their various inner contents into the environment. Migrasomes are recognized as tools for cell-cell communication and enhanced cell homeostasis. We identified CpnE on retraction fibers and migrasomes during each type of migration. CpnE was most often found on the migrasome membrane, suggesting the protein is performing a specific function at that site. Future studies will investigate the mechanisms in which CpnE contributes to migrasome biogenesis and determine how migrasomes are used by *Dictyostelium* cells. The novel association between copines and migrasomes suggests a potential link between copine function and migracytosis pathways.

2. Coverboard preference of Salamanders at Neithercut Woodland

Jessica Brosky, Elizabeth Martin, Andrew Scott McNaught
Department of Biology, Central Michigan University

Coverboards have been long used for monitoring and examination of amphibians in various locations, especially as they are relatively inexpensive, easy to use, and cause little disturbance of habitat (Heded, 2012). The purpose of this study was to discover salamander's preferences or lack thereof for coverboard type at the Neithercut Woodland. We examined two sites in the Neithercut Woodland: the first site was within close range to the lodge and was more lowland. The second site was about a 10-minute walk from the lodge and was farther upland. There were four board types used at each site: old wood, new wood, metal, and ceramic. At each site, the boards were lifted one by one, and the number of species of salamanders was recorded. Surface temperature and surface humidity were also recorded under each board using handheld meters.

Oral Presentation Abstracts

3. Anthropogenic impacts on birds in a northern temperate riparian corridor

Emily Guiles, Nancy Seefelt
Department of Biology, Central Michigan University

Urbanization is known to degrade habitats, leading to shifts in vegetation assemblages and increased noise pollution. To identify the impacts of these urban factors on resident and migratory birds, this study investigated avian diversity and abundance in relation to vegetation and noise level in a riparian corridor. Bird surveys were conducted using point counts at locations near to and distant from human infrastructure, as defined by distance from paved surfaces. In addition to bird population surveys, ambient noise level (dB) and vegetation surveys were conducted. There were no significant differences in bird diversity and abundance between sites near human infrastructure and distant from human infrastructure, nor were there any correlations between bird diversity and abundance, vegetation populations and noise levels. However, avian community structure and the percentage of non-native plants did differ between sites in relation to human infrastructure. Due to similarities across all locations, this study emphasizes the connectivity within riparian corridors despite anthropogenic factors.

4. Warming waters, growing mussels: understanding temperature effects on freshwater mussel growth

Tadiwanashe Mutasa^{1,2} and Daelyn Woolnough¹
¹Department of Biology and Institute for Great Lakes Research, Central Michigan University
²Honors Program, Central Michigan University

Native freshwater mussels play a vital role in aquatic ecosystems. As filter feeders, they help purify water by removing suspended particles, algae, and pollutants, and they provide food for other species. Their ecological importance is significant; however, freshwater mussels are declining due to environmental stressors. This study investigates the relationship between summer water temperatures and mussel growth in the Kalamazoo River, Michigan, USA, aiming to identify the optimal temperature for their development. We hypothesized that freshwater mussel growth is temperature-dependent and will grow largest in warm waters (above 21°C). To test this hypothesis, we used data from surveys conducted during the summers of 2018 and 2019 across 122 sites in the Kalamazoo River. We analyzed data from over 3,400 mussels, focusing on eight most abundant species in the watershed. Preliminary results indicate that related species (e.g., *Lampsilis* spp.) exhibit similar trends, suggesting that related mussel species have comparable growth patterns. Overall, more live mussels were found in warm waters ($n \approx 2,700$) than in cold waters ($n \approx 300$), and individuals from warmer sites tended to be larger and show greater variation in shell lengths. These results suggest that higher temperatures promote both increased abundance and growth, supporting the hypothesis that temperature influences mussel development. By understanding how temperature variations affect mussel growth, this research provides valuable insights into the ecological needs of freshwater mussels and offers practical recommendations for their conservation.

Oral Presentation Abstracts

5. Up Pine River Without a Paddle

Elaine Hamilton, Larae Pulley, Dave Zanatta, Andrew Scott McNaught
Department of Biology, Central Michigan University

Freshwater macroinvertebrates like insects and mussels can be important indicators of stream health. The goal of this study was to determine the quality of the Pine River passing through Lumberjack Park in Gratiot County, Michigan. We hypothesized that a high species richness of macroinvertebrates, particularly ones who are considered sensitive to adverse environmental conditions, means that the river's water quality is also higher. The survey examined biotic and abiotic factors associated with water quality at two sites, each of which consisted of three replicates. Biotic factors were collected via D-nets (benthic macroinvertebrates) and hand-sifting quadrats (freshwater mussels). Abiotic factors (habitat data and water chemistry) were documented and recorded via meters, test strips, and observations. Biotic indices of stream health were calculated from the aquatic insect assemblage data. These indices were rated as excellent at site 1 and somewhat lower quality at site 2. Of the five mussel species found, Spike (*Eurynia dilatata*) was the most abundant. They consisted of about 76.5% of the total mussel assemblage, with a size-class distribution indicating a healthy and stable population that is undergoing recruitment. However, there was not sufficient data to determine the size distribution of other mussel species. The water chemistry data backs that finding, as the readings mirror the quality ratings found via the insect species sensitivity. Some of the water chemistry findings were pH of 7.9 and the oxygen concentration was 511-517ppm. The high water quality of this area may be due to limited human development along this section of shoreline.

Poster Presentation Abstracts – Session 1

1. Developing Green Rivulus as a Model Organism for Functional Genetics

Petra Bora¹, Andrew Kaczmar¹, Michelle LaCross⁴, Andrew W. Thompson^{1,2,3}

¹Department of Biological Sciences, Western Michigan University, Kalamazoo, MI, USA

²Department of Integrative Biology, Michigan State University, East Lansing, MI, USA

³Ecology, Evolution, and Behavior Program, Michigan State University, East Lansing, MI, USA

⁴Comstock High School, Kalamazoo, MI, USA

While there have been many studies focused on traditional laboratory models like zebrafish, mouse, and medaka fish, there remains a lack of in-depth comparative approaches in functional vertebrate genetics. However, some vertebrates, such as killifish, particularly “annual” species that inhabit seasonal pools and live for only about a year or less, have short life cycles and delayed development (dormancy), making them ideal models for studying genetic and developmental changes. Even with the development of the rapidly aging African turquoise killifish as an emergent model for aging and developmental biology research, other related killifish species (>800 species) have been left largely untouched as a potential model species. Thus, we develop the green rivulus *Rivulus cylindraceus* and Rio pearlfish *Nematolebias whitei* as genetically tractable laboratory models. These killifishes have the potential to be valuable experimental model organisms in the field of 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*, successfully creating partial *oca2* knockout embryos. The resulting embryos exhibited reduced pigmentation, demonstrating successful gene disruption. We also generated single nuclei RNA-seq cell atlases of the Rio pearlfish to characterize cell type specific expression shifts between sexes and dormant developmental stages. These findings validate the feasibility of genome editing in *R. Cylindraceus*, provide a foundation for extending “omics” approaches to pearlfish and other related killifish species, and make progress towards understanding the evolutionary genetics of dormancy and aging. Thus, we show that the non-annual *Rivulus cylindraceus* and annual *Nematolebias whitei* killifish pair are valuable, tractable experimental model organisms in the field of functional genetics and genomics.

3. MSI-1, UNK-1 and LIN-41 are RNA binding proteins that promote larval cell fate during dauer diapause in *C. elegans*.

Erin Collier¹, Calub Hicks¹, MyHanh Le¹, Ben Quesada¹, Nehul Tanna^{1,2}, Xantha Karp^{1,2}

¹Central Michigan University, Department of Biology

²Central Michigan University, Biochemistry, Cell & Molecular Biology Program

Genetic mechanisms in stem cells that coordinate quiescence and multipotency are poorly understood. In *C. elegans*, the lateral hypodermal seam cells are stem cell-like cells that are multipotent in larval development and differentiated in adulthood. In favorable conditions, *C. elegans* larvae develop through four larval stages separated by molts before reaching adulthood. In unfavorable conditions, *C. elegans* larvae can enter the stress-resistant and developmentally arrested dauer larva stage after the second larval molt. *C. elegans* contains *daf-16*, a gene which promotes quiescence and multipotency. During dauer, *daf-16* opposes expression of adult-specific collagen encoded by *col-19*, which we can visualize through a *col-19p::gfp* transgene. Wild-type dauer larvae do not express the cell fate marker *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 hypothesize that these RBPs work downstream of *daf-16* and parallel to each other. Thus, we predict that loss of each RBP will have additive effects on *col-19p::gfp* expression. To test this, we created single, double, and triple mutants to assess additive effects on *col-19p::gfp* expression when different proteins are depleted. We have all the strains made and are imaging for levels of *col-19p::gfp* expression. If the RBPs function in parallel, we expect to see increased expression in the mutant larvae as more RBPs are removed. These results will determine the pathway by which *daf-16* regulates RBPs to oppose adult cell fate during dauer.

Poster Presentation Abstracts – Session 1

5. Examining the impact of Tau and TDP-43 toxicity on climbing behavior in *Drosophila*

Katherine Himmel, Isaac Postema, Michelle Steinhilb
Department of Biology, Central Michigan University

Alzheimer's disease 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. Tau is a protein predominantly expressed in neurons to stabilize the microtubule network. If Tau becomes hyperphosphorylated, it can dissociate from the microtubules and aggregate, eventually forming neurofibrillary tangles within the neurons. The tangles choke the neuron from the inside, disrupting internal transport, impairing movement, and eventually causing neuronal death. Accumulation of a second neuronal protein, TAR DNA-binding Protein 43 (TDP-43), has also been implicated in AD. TDP-43 mis-localizes from the nucleus to the cytoplasm, where it forms toxic aggregates. The fruit fly, *Drosophila melanogaster*, is a valuable model organism for studying the role of tau and TDP-43 in AD because flies share similar molecular pathways with humans. Behavioral assays are widely applicable for studying the role of genetics on fly behavior. Specifically, climbing assays use negative geotaxis behavior to study neurodegeneration. In our lab, we will measure the climbing ability of aging fruit flies possessing tau and TDP-43 transgenes in all neurons. Ideally, we expect to find a correlation between tau and TDP-43-induced toxicity and impaired climbing ability, with climbing ability decreasing with age. Ultimately, we plan to use our behavioral assay to identify modifiers of neuronal toxicity. This study can help identify tau-related pathways in humans as well as contribute to drug development through an understanding of candidate genes and pathways.

7. Understanding how unk-1 regulates adult cell fate through transcription factors

Evan Linkowski, Pranali Chhapamohan, Jasmine Asberry, Xantha Karp
Department of Biology, Central Michigan University

Adult stem cells have multipotency, or the ability to produce different cell types. These cells are able to go into quiescence, or a state of temporary cell arrest, but how are these cells able to maintain their multipotent potential through quiescent stages? The nematode *Caenorhabditis elegans* is able to enter a quiescent and stress-resistant life stage called dauer under unfavorable conditions. These organisms can exit the dauer stage if conditions return to favorable. Their entrance into dauer is regulated by daf-16, a gene which promotes quiescence. *C. elegans* also contains seam cells, a model for human stem cells. They also contain the adult-specific collagen COL-19, which we are able to visualize through a col-19p::gfp transgene. Wild-type dauer larvae do not express the adult cell fate marker col-19p::gfp, but daf-16 mutants do, indicating that daf-16 blocks adult cell fate during dauer. We hypothesize that daf-16 blocks adult cell fate by promoting expression of an RNA binding protein, UNK-1 that inhibits adult cell fate. Furthermore, we hypothesize that UNK-1 inhibits the expression of an unknown transcription factor that directly regulates col-19. Prior students identified three transcription factors that promote col-19p::gfp downstream from daf-16, dcp-66, ceh-60, and nhr-68. To test whether these transcription factors also regulate col-19p::gfp expression downstream of unk-1, we will use RNA interference to deplete each of these transcription factors in unk-1 mutant dauers and measure expression of col-19p::gfp compared to empty vector controls. These experiments will place these transcription factors in the pathway that regulates adult cell fate during dauer arrest.

Poster Presentation Abstracts – Session 1

9. Investigating cAMP concentrations in Copine mutants of *Dictyostelium discoideum*

Emily Mathewson, Rodney Nichols, Cynthia Damer
Department of Biology, Central Michigan University

Cyclic adenosine monophosphate (cAMP) is a crucial signaling molecule in *Dictyostelium discoideum* (Dicty), orchestrating aggregation and developmental transitions. Copines (Cpns) have been indicated in modulating cAMP levels, particularly in relation to developmental defects observed in various copine mutants. While wild-type Dicty cells exhibit normal cAMP signaling and aggregation, copine mutants display defective streaming patterns and impaired developmental progression. This study aimed to characterize the role of cAMP in copine function using an ELISA-based approach to quantify intracellular cAMP levels in wild-type and mutant strains. Results showed that among the mutants, cpnC- and cpnA- were higher than their parental strain, but not significantly. CpnD50 and cpnD168 mutants were lower than their parental strain AX4, but not significantly. Overall, this study provided evidence that copines may differentially influence cAMP dynamics. These findings enhance our understanding of how calcium-dependent signaling proteins intersect with developmental pathways in *Dictyostelium discoideum* and may inform future research into the molecular regulation of chemotaxis and multicellular organization.

11. Investigating the regulatory region of the col-19 promoter during dauer in *C. elegans*

Vusani Ntuli, Anuja Dahal, Xantha Karp
Department of Biology, Central Michigan University, Mount Pleasant, MI, United States

In *C. elegans*, developmental trajectories are influenced by environmental conditions, with larvae either progressing through continuous development or entering dauer, a stress-resistant and non-feeding larval stage characterized by a temporary exit from the cell cycle. During dauer, progenitor cells such as lateral hypodermal seam cells remain multipotent and quiescent, pausing differentiation until favorable conditions return. Upon dauer exit, seam cells resume development and differentiate into adult cell types. col-19 was selected as our gene of interest because it encodes a collagen expressed specifically in adult hypodermal cells and seam cells but not during larval stages, making it a reliable marker of adult differentiation and seam cell maturation. The col-19 promoter driving GFP expression has been widely used to visualize adult cell fate, but the specific regulatory region responsible for repressing its expression during dauer remains unclear. We are developing a single-copy col-19p::gfp reporter system to identify the promoter sequences that control this regulation. To investigate this, we are generating three single-copy col-19p::gfp reporters using MosTI cloning: one full-length 846 bp promoter and two non-overlapping fragments of 315 bp and 531 bp. All three constructs have been successfully generated and verified by colony PCR and sequencing. Future work will involve injecting these reporter constructs into the *C. elegans* germline to create stable transgenic lines. This will allow us to determine which promoter region mediates col-19 repression during dauer and to test whether specific cis-regulatory elements are responsible for maintaining seam cell quiescence during this stage.

Poster Presentation Abstracts – Session 1

13. Investigation of COPI and COPII genes as regulators of protein condensation in eggs

Alexis Royer, Helsa Thomas, Jennifer Schisa
Department of Biology, Central Michigan University

Infertility in women can be caused by poor-quality oocytes. Unfortunately, the cause of poor-quality oocytes is not completely understood. During the development of eggs, many RNA-binding proteins (RBPs) undergo phase transitions which are the ability of an RBP to transition between a soluble, diffuse state and a dense, condensed phase. The phase of an RBP can affect its function, including the regulation of target mRNA stability and translation. Our lab's overarching hypothesis is that regulation of phase transitions is required to maintain egg quality. We are investigating this question by first identifying regulators of phase transitions using the model system *Caenorhabditis elegans*. In genetic screens, we identified proteins in the COPI and COPII complexes that are required to inhibit ectopic condensation of the KH-domain, RNA-binding protein MEX-3. We are now determining if these novel regulators are specific to MEX-3 or if they regulate multiple RBPs in oocytes. One protein that is associated with MEX-3 in eggs is OMA-1 which is a Tis11 zinc finger RNA binding protein. I have begun to investigate the role of COPI and COPII genes in regulating phase transitions of OMA-1 using a GFP::OMA-1 strain that allows live-imaging of eggs in worms using the confocal microscope. I am using RNA interference (RNAi) to knock-down the expression of each COPI and COPII, and my control is lacZ, a bacterial gene. In my preliminary results, I detected ectopic condensation of OMA-1 in the proximal oocytes after *copb-2*(RNAi). I am currently conducting RNAi trials for other genes of the COPI and COPII complexes identified as regulators of MEX-3, including *sar-1*. Identifying regulators of RBPs can lead to better understanding of the causes of poor-quality eggs and eventually to improving treatments for infertility.

15. Investigating Age-Related Motor Decline in Fruit Flies Expressing Human Alzheimer's Proteins

Angela Smith, Suhani Thakuri, Michelle Steinhilb
Department of Biology, Central Michigan University

Alzheimer's disease (AD) is an irreversible, progressive brain disease that slowly destroys memory and thinking skills, and eventually the ability to carry out the simplest tasks. As a person ages, their risk of Alzheimer's increases. About one in 13 people aged 65 to 84 and one in three people, 85 and older, live with Alzheimer's. Two proteins found to be abnormally aggregated in patients with AD are the microtubule-associated protein tau and the DNA/RNA-binding protein TDP-43. We use *Drosophila melanogaster* (fruit flies) to learn more about the pathological changes of tau and TDP-43 associated with AD. Fruit flies have a short life cycle (egg to adult is only 10 days), they cost little to maintain, and they are genetically powerful tool to study the molecular mechanisms of disease and test potential treatments. In this project, we are focusing on a behavioral assay, the climbing assay, which focuses on the locomotor function in fruit flies. Climbing behavior requires the use of both motor neurons as well as a complex network of central nervous system (CNS) neurons. Over time, non-transgenic flies show impaired climbing ability; co-expression of disease-related proteins has been shown to further impair climbing relative to controls. This behavior mimics the motor dysfunction seen in humans with neurodegenerative disease. We are testing the hypothesis that expression of human tau or human TDP-43 in specific subsets of neurons will significantly impair climbing ability in flies. Specifically, we will express tau and TDP-43 in motor neurons (D42 driver line) as well as dopaminergic and serotonergic neurons of the CNS (Ddc driver line). We expect to find that expression of both disease-associated proteins, tau and TDP-43, will diminish climbing ability when expressed in either motor or CNS neurons, and that the decline will be most significant in the oldest flies.

Poster Presentation Abstracts – Session 1

17. Evaluating the Effectiveness of Calpeptin in Suppressing Tau Toxicity in a Fly Model of Alzheimer's Disease

Blake Dishaw, Ty Nelson, Josie Staven, Logan Douglas, Cooper Allers, Michelle Steinhilb
Department of Biology, Central Michigan University

Alzheimer's disease (AD) affects about 1 in 10 people over the age of 65. Alzheimer's disease and other neurodegenerative diseases with pathologies that include aggregation and abnormal phosphorylation of the microtubule-associated protein tau are known collectively as tauopathies. Tau promotes assembly and stabilization of microtubules, structures that are essential for transporting nutrients and sending signals within neurons. The Steinhilb lab uses *Drosophila melanogaster*, the common fruit fly, to understand the molecular pathways that contribute to tau dysfunction. In particular, the expression of human tau in fly retinal cells causes extensive neurodegeneration, described as the tau rough eye phenotype. In addition to the photoreceptor neurons, the fly eye also includes support and bristle cells, collectively called ommatidia. Our lab has previously shown that tau-induced toxicity can be suppressed by genetically reducing the expression of calpain, an enzyme that others have shown cleaves full-length 65kD tau into toxic 17kD fragments that are also associated with human AD. This study examines transgenic flies that express human tau in photoreceptor neurons to investigate whether pharmacological calpain inhibition can also suppress tau-induced toxicity, as was found in our genetic studies. Calpeptin is a compound that inhibits the calcium-dependent protease calpain. This project is testing the hypothesis that feeding the calpain inhibitor Calpeptin to flies will suppress tau-induced toxicity in the photoreceptor neurons of the fly eye. Quantification of the ommatidia integrity will allow us to quantitatively assess pharmacological strategies for reducing tau toxicity, which is a crucial step toward effective treatment of Alzheimer's disease.

19. Investigating the Regulation of RNA Binding Protein Phase Transitions by ERK and MEK-2 Kinases in the *Caenorhabditis* Germline

Leah Themel, Jennifer Schisa
Department of Biology, Central Michigan University

Infertility affects 13% of couples when the woman is under 30 years old, and poor-quality oocytes are a contributing factor. However, the causes of poor-quality oocytes are incompletely understood. Evidence suggests that the regulation of RNA-binding protein (RBP) phase transitions plays a role in maintaining oocyte quality across species. Protein phase transitions are dynamic changes between diffuse and condensed states. One candidate regulator of RBP phase transitions in *C. elegans* oocytes is the Extracellular signal-Regulated Kinase (ERK). Based on results showing ERK depletion induces ectopically condensed MEX-3 protein, we hypothesize that ERK inhibits ectopic MEX-3 condensation. Past research suggests ERK broadly regulates RBP phase transitions. In this study, my first aim was to determine if ERK and its upstream activating kinase MEK-2 inhibit ectopic condensation of the OMA-1 RBP. I depleted ERK and MEK-2 in GFP::OMA-1 worms using RNA interference (RNAi), followed by confocal imaging to characterize the phase of OMA-1 compared to controls. Preliminary results show ectopically condensed OMA-1 after MEK-2 depletion; ERK depletion experiments are ongoing. My second aim was to determine if the regulation of RBP phase transitions by ERK is conserved in another *Caenorhabditis* species, *C. remanei*. I first asked if ERK is differentially activated in *C. remanei* oocytes. Using immunostaining, I found that activated ERK is detected only in maturing *C. remanei* oocytes. Second, I asked if ERK is required to prevent ectopic condensation of the CAR-1 RBP in *C. remanei*. I determined that the *C. elegans* CAR-1 antibody cross-reacts with the *C. remanei* CAR-1 using immunostaining, and ERK RNAi experiments are in progress. This study provides insight into the role of the ERK signaling pathway in regulating oocyte RBP phase transitions and may lead to new conserved mechanisms of oocyte quality.

Poster Presentation Abstracts – Session 1

21. Exploring the role of protein regulation in maintaining fertility and oocyte quality

Helsa Thomas, Victoria Tice, Alexis Royer, Leah Themel, Ethan Harris, Christya Haddad, Grace Thomas, Ashley Cichon and Jennifer Schisa
Department of Biology, Central Michigan University, Mount Pleasant, Michigan, USA

Female infertility is common among women of all ages, affecting 13% of couples when women are under age 30. One cause of infertility is poor quality oocytes (eggs); however, the reasons oocyte quality decreases are not well understood. Our lab hypothesizes that the dysregulation of RNA binding protein (RBP) phase transitions contributes to poor quality oocytes. RNA binding proteins undergo phase transitions between diffuse and condensed states, and dysregulation can compromise protein function. MEX-3 is an RNA binding protein that is normally diffuse in oocytes but can form condensates under certain conditions. In a genetic screen to find regulators of MEX-3 phase transitions, we identified one COPI gene (*copb-2*) and two COPII genes (*sar-1* and *sec-24*). The COPI complex mediates retrograde transport of proteins from the Golgi apparatus to the endoplasmic reticulum and is comprised of seven proteins. The COPII complex transports cargo from the endoplasmic reticulum to the Golgi apparatus and is comprised of eight proteins. Our current hypothesis is that all proteins in the COPI and COPII complexes are required to inhibit ectopic condensation of MEX-3. To test our hypothesis, we conducted a blinded screen by depleting target genes using RNA interference (RNAi) in GFP::MEX-3 worms. In the primary screen, we used epifluorescence, a rapid, low-resolution imaging method. Our primary results suggested that five of seven COPI and three of eight COPII proteins are required to regulate MEX-3 phase transitions. Independent students validated the positive hits, and we are currently collecting high-resolution images with confocal microscopy. Our confocal results have confirmed depletion of five of seven COPI genes result in significantly increased MEX-3 condensation. The confocal results of COPII depletions are currently in progress. Ultimately, understanding the regulation of RNA-binding protein phase transitions will provide a foundation to determine their function in maintaining oocyte quality and fertility.

23. Harvesting photosynthetic electrons with exotic cytochromes

Ashton Trnka, Eliezer Schwarz
Department of Biology, Alma College

In plants, photosystem I (PSI) is responsible for transferring electrons to ferredoxin in order to power the molecular machinery of metabolism. If ferredoxin is replaced with a controllable electron acceptor, then it is possible to harness the electrons from PSI. This has the potential for us to harvest electricity from photosynthetic organisms. *Schwannella Oneidensis* is a gram-negative electrogenic bacterium that contains Small Tetraheme Cytochrome (STC). These bacteria use STC to transfer electrons from inside the cell to the outside. This leads STC to be a good candidate for replacing ferredoxin, as it serves as an electron acceptor and donor. STC was cloned into an expression vector with an arabinose-inducible promoter. The STC sequence was fused with a MalE leader sequence for expression into the periplasm, which is necessary for the assembly of cytochromes in *E. coli*. In addition, a Strep II tag was added for later affinity column purification of the expressed protein using streptavidin resin. The purified protein will now be characterized by monitoring the electron transfer kinetics from thylakoid membranes to the purified cytochrome via spectroscopic techniques.

Poster Presentation Abstracts – Session 2

2. Social behaviors of Greater Flamingos and Chilean Flamingos at the Detroit Zoo

Jessica Witkowski, Nancy Seefelt
Department of Biology, Central Michigan University

As social species, the wild Greater Flamingo *Phoenicopterus roseus* and Chilean Flamingo *Phoenicopterus chilensis* are often seen in large flocks, creating the mutual benefit of reducing vulnerability while preening, resting, and other distracting activities. In captivity, the lower risk of predation is exchanged for greater longevity, emphasizing the importance of long-term social welfare in artificially formed flocks. Some species of flamingo have been found to form non-reproductive social bonds in captivity, but the factors that encourage such bonds remain in speculation, and these “friendships” have not yet been identified in Greater Flamingos. This study explores social interactions within a mixed flock of Greater and Chilean Flamingos at the Detroit Zoo, measured by proximity between individuals and their behavior in social groups. My results support the existence of specific social groups in Greater Flamingos and Chilean Flamingos, with implications for captive flamingo welfare.

4. Freshwater mussel assemblages in the Grand River Michigan: Assessing community stability over time post dam-removal

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

Freshwater mussel populations serve as valuable bioindicators of aquatic ecosystem health due to their sensitivity to environmental change. This study examines temporal shifts in mussel assemblages in the Grand River (Lyons, Michigan) by comparing data collected during a 2025 survey downstream of a dam removal site to historical surveys conducted, at the same site, up to 11 years ago using data from 2014 to 2025. Species abundance ratios, from the recent short survey using standardized methods, were analyzed relative to previous datasets to evaluate whether the current assemblage accurately represents long-term community structure or whether there has been a shift in mussel assemblage since the dam-removal. Preliminary results suggest that species dominance patterns, such as the continued prevalence of *Amblema plicata* (Threeridge) and *Lampsilis cardium* (Plain Pocketbook), have remained generally stable over time by consistently representing $\geq 50\%$ of the mussel assemblage. However, subtle variations in less common species may indicate changes in recruitment, habitat conditions, or post-dam-removal substrate shifts that could influence species distribution. Observed differences may also reflect changes in waterflow, sediment transport, or habitat connectivity following the dam-removal, potentially affecting mussel colonization and survival. It is important to note that several factors may influence comparisons across years, including differences in total search time, the number and expertise of searchers, and seasonal timing of the surveys. These variables may introduce sampling bias or affect detection probability and will be discussed further in relation to the observed assemblage trends. For example, over the 11-year period 19 species of native freshwater mussel have been found at this site but in any one year 13 or fewer species were found. These findings contribute to understanding the stability and resilience of Michigan's Grand River mussel community and provide insights for ongoing conservation and monitoring efforts.

Poster Presentation Abstracts – Session 2

6. Flying Through Microsatellite Primer Redesign of Southwestern Willow Flycatcher

Michael Fox, Dr. Eliezer Schwarz, Katie Stumpf
Department of Biology, Alma College

The Southwestern Willow Flycatcher (*Empidonax traillii extimus*) is an endangered sub-species of Willow Flycatcher that breeds in riparian habitats within isolated subpopulations of the southwestern United States. Southwestern Willow Flycatchers are neotropical migratory species, which makes it difficult to track population structure through demographic analysis alone; however, genetic monitoring has been employed successfully in previous studies. Specifically, DNA microsatellites are used to determine population structure, how migration impacts gene flow across subpopulations, and overall breeding success of returning groups. Microsatellite analysis of Southwestern Willow Flycatchers last occurred during 2009, and both microsatellite loci mutation and technology improvements have made older primers outdated for future work. The objective of this study was to redesign primers by comparing existing primer sequences to catalogued genomes of the Southwestern Willow Flycatcher. We modified existing forward and reverse primer sequences in accordance with paired melting temperature, similar base-pair length, and location in comparison to the targeted tandem repeats of (AAAG), (CTT), (ACG), and (GATA). Our next steps are to evaluate the compatibility of these primers with the targeted repeated sequences used for microsatellites. These new primers will be tested on DNA collected from 315 individuals sampled throughout Arizona and Nevada between 2019 and 2023. We will use housekeeping genes like mitochondrial alleles to determine the quality of the DNA sample library and conduct further PCR trials of both new and existing primer sets upon PCR quality template DNA. Updating older primer sets will allow for the reevaluation of population structure of recently sampled individuals, which would reinforce prior knowledge and potentially offer new information towards the genetic flow of returning breeding migrant populations.

8. Emergent Insect Family Richness and Biomass Across Ludington State Park's Interdunal Wetland Successional Stages

Erica MacQueen, Tiffany Schriever
Department of Biological Sciences, Western Michigan University

Interdunal wetlands are understudied habitats due to their relatively limited global presence. Nonetheless, their ability to support local wildlife makes understanding their ecosystem dynamics valuable. Emergent insects are key members of the interdunal wetland food web due to their existence in both aquatic and terrestrial environments and their ability to provide nutrients and energy to consumers at higher trophic levels. Knowledge of emergent insect patterns and preferences can improve local conservation efforts and resource management practices for the improvement or maintenance of interdunal wetland health. To compare emergent insect community composition across interdunal wetland successional stages, emergent insects were collected at 12 wetland ponds in Ludington State Park from May through July 2024 and 2025. A total of 3,074 adult emergent insects were collected. The specimens were identified to family. Length measurements and dry mass data were collected for biomass analysis. It was hypothesized that forest interdunal wetlands supported the greatest taxa richness and contained the largest quantity of emergent insect biomass as increased foliage has the potential to stabilize wetland temperatures as well as provide protection from predators. Increasing emergent insect family richness was found across the interdunal wetland successional stages supporting the claim that forest wetlands would have greater family richness, however, dry mass collected over the study's two-year span did not produce significant differences between successional stages. Additional data will be required to produce more substantial conclusions relating to emergent insect biomass across the open, intermediate and forest interdunal wetland habitats.

Poster Presentation Abstracts – Session 2

10. Understanding the life history of coaster brook trout in the Lake Superior watershed

Sara Gillette, Kevin Pangle
Department of Biology, Central Michigan University

Coasters, a migratory form of brook trout, are native to the waters of Lake Superior. They are born in streams and then migrate out to Lake Superior, returning to streams for spawning. The goal of this research is to understand their life history by using elemental concentrations of the maxilla. Currently, the method for researching and understanding life histories of fish is to use their otolith, which is lethal to extract, whereas the use of maxilla is non-lethal. The objective of this research is to test efficacy of this non-lethal method in its ability to compare the life histories of coaster brook trout that live in Lake Superior to those in streams with direct access and to those in streams in the watershed that do not have direct access to the lake. The Michigan Department of Natural Resources (MDNR) and the U.S. Fish and Wildlife Service (USFWS) collected maxilla from brook trout across the Lake Superior watershed. These samples were then processed down to a simple cross-section of the bone and taken to Michigan State University, where they underwent laser ablation (LA-ICP-MS) to gather data on the chemical signature across the layers of bone for seven elements (magnesium, manganese, zinc, rubidium, strontium, barium, and lead). We then compared the patterns of each element across the three groups of samples. Our findings allowed us to draw conclusions on the similarities and differences between coasters that live within the lake versus those that live in connected and non-connected streams in the watershed.

12. Microplastics in the Tittabawassee-Saginaw River: an analysis of freshwater river microplastic pollution based in varying landscapes

Rachel Rasette, Amanda Suchy
Department of Biology, Central Michigan University

This study investigated how landscape composition and land use influence the abundance and types of microplastics in freshwater ecosystems. The research focused on the Tittabawassee–Saginaw River system as it flows through Midland, Saginaw, and Bay City. Three primary land use categories were identified: developed, agricultural, open water, and woody wetland. Water samples were collected at 12 sites along the river, with each location including upstream and downstream sampling points relative to the focal land use type. Samples were filtered onto microscopic slides and analyzed for microplastic abundance, type, and color. Across all land use types, the dominant microplastic was clear fibers. In two of the three developed sites, microplastic concentrations (particles/L) increased from upstream to downstream. Overall, developed areas contained the highest concentrations of microplastics, followed by agricultural areas, while undeveloped areas showed the lowest concentrations. No clear trend was observed in microplastic color among the different landscape types. These results suggest that urbanization and human activity are key drivers of microplastic contamination in freshwater systems. The higher concentrations observed in developed regions and agricultural regions indicate that runoff and surface discharge may serve as major pathways for microplastic input.

Poster Presentation Abstracts – Session 2

14. Temperature-based nest selection in tree swallows and eastern bluebird

Jack Yodzevicius, Katie Stumpf
Department of Biology, Alma College

Growing climatic instability as a result of climate change has affected the biology and behavior of countless species. Tree swallows (*Tachycineta bicolor*) and eastern bluebirds (*Sialia sialis*) are obligate cavity nesters that co-exist in some habitats, including open fields and forest edges. Cavity nesting species are ideal for monitoring changing temperature effects on nest outcomes because their nest boxes are a controlled and stable environment. Our research objective was to determine whether nest box temperature affects nest box choice and/or outcomes. Specifically, we examined 1) whether tree swallows and eastern bluebirds nest box use was thermally partitioned, and 2) whether nest success was correlated with temperature. We used 50 nest boxes at 4 sites in the Alma and Mount Pleasant area. The boxes were equipped with iButton temperature loggers on the inside wall, which recorded temperature every hour. We checked nest boxes 3–4 times a week, monitoring number of eggs and fledglings as well as when the birds began laying, duration of each stage of development (egg laying, incubation, and nestling), and overall successful fledging. For each nest, we calculated overall average, average daily high, and average daily low, during each stage. There is no significant difference in nest success between the species ($X^2=2.9$, $p=0.09$) nor is there a significant difference in the temperature during egg-laying between species ($t=-1.39$, $p=0.18$). Currently, we are performing linear and logistic regression analyses to determine whether any of the temperature metrics are associated with nest success. The next stage of our study will involve artificially manipulating temperatures in boxes to determine if higher or lower temperatures than those that occur naturally impact the success rate and thermal partitioning of the test species. These results will be important to demonstrate the biological and behavioral response of cavity nesters in the face of rising global temperatures.

16. Modeling Tau and TDP-43 Neurotoxicity in Drosophila: Effects on Age-Dependent Climbing Behavior

Hunter Hitzelberger, Michelle Steinhilb
Department of Biology, Central Michigan University

Alzheimer's disease (AD) is a neurodegenerative condition characterized by memory loss, cognitive impairment, and behavioral changes. It belongs to a group of disorders called tauopathies that involve abnormal aggregation of highly phosphorylated tau protein deposits in neuronal cells. Tau is normally responsible for regulating the assembly and maintaining the structural stability of microtubules, but in AD patients, tau becomes hyperphosphorylated causing it to form insoluble neurofibrillary tangles, disrupting synaptic transmission, resulting in neuronal cell death. Tau DNA-binding protein 43 (TDP-43), like tau, is implicated in neurodegenerative diseases. Abnormal TDP-43 misfolds and aggregates, mis-localizing from the nucleus into the cytoplasm, causing damage to neuronal integrity. *Drosophila melanogaster* is an excellent model organism to study neurodegenerative diseases due to the structural and functional similarities of fly neurons with humans, allowing both behavioral and molecular testing. The RING (rapid iterative negative geotaxis) assay uses fly negative geotaxis to assess and quantify a fly's climbing ability. By creating a high-throughput system that involves tapping multiple groups of flies to the bottom of a vertical tube and digitally photographing their ascent, RING assays allow for the simultaneous collection of data on a large scale. By measuring the distance that flies climb over a set time, this assay is a powerful tool for studying aging, neurodegeneration, and the effects of genetic or pharmaceutical interventions on locomotion. This project tests the hypothesis that expression of tau and TDP-43 transgenes will impair overall climbing ability in an age-dependent manner. Since age reduces climbing ability in flies, we expect flies expressing tau or TDP-43 in all neurons to show an age-dependent decline in climbing performance, with significantly lower ability than age-matched controls.

Poster Presentation Abstracts – Session 2

18. Expression and Activation of Synaptic Plasticity Related Proteins in GluN2B Haploinsufficiency

Morgan Mussehl, Shasta Sabo
Department of Biology, Central Michigan University

GRIN2B-related neurodevelopmental disorder results in mutations in the GRIN2B gene encoding GluN2B proteins that are associated with autism spectrum disorder. Symptoms of this disease are intellectual disability, seizures, muscle tone abnormalities, and many other behavioral and physical conditions. It is unknown how the mutations are related to the symptoms. GluN2B signaling induces synaptic plasticity and activates a transcription factor, cAMP-response element binding protein (CREB) involved in plasticity. This study investigated the impact of GluN2B haploinsufficiency on the expression and activation of CREB. Western blot analysis was performed on brain tissue samples from rats aged P18-P24. The hypothesis of this study was that GluN2B heterozygous knockout rats would have decreased expression and activation of pCREB and CREB compared to the wild type model.

20. Investigating the impact of pharmacological inhibition of calpain in Machado-Joseph disease

Jadelena Truong^{1,2}, Blake Dishaw¹, Logan Douglas¹, Michelle L Steinhilb¹

¹ Department of Biology, Central Michigan University

² The Honors Program, Central Michigan University

Machado-Joseph disease (MJD), also known as spinocerebellar ataxia type 3 (SCA3), is a neurodegenerative disorder, and it is the most common dominant ataxia disease. MJD mainly impacts the cerebellum, affecting speech, motor skills, and coordination. On a worldwide scale, MJD has an average prevalence rate of 1-5 per 100,000 people. The neuropathological symptoms in MJD derive from the abnormal expansion of cytosine-adenine-guanine (CAG) repeats, which code for the amino acid glutamine (one letter abbreviation is Q) forming a polyglutamine (polyQ) tract that impairs key cellular functions leading to neurodegeneration. Human neurodegenerative diseases, including MJD, can be effectively modeled in the common fruit fly, *Drosophila melanogaster* since flies have disease-relevant orthologs and the critical enzymes necessary to execute the putative posttranslational modifications involved in disease pathogenesis. In particular, we are utilizing two relevant fly strains from the *Drosophila* stock center to study MJD: Transgenic line 8149 that expresses a HA-tagged C-terminal fragment of the human Machado-Joseph Disease/Spinocerebellar Ataxia 3 protein with a normal 27 repeat polyglutamine tract that causes no toxicity; and line 8150 that expresses the same protein but with a 78 repeat polyglutamine tract that causes a severe degeneration phenotype. This project focuses on the cysteine protease calpain, as many labs have emphasized the importance of the role of calpain in numerous neurodegenerative disorders. In flies expressing MJD8150 in photoreceptor neurons, we observe loss of pigment and the appearance of necrotic spots. My project is testing the hypothesis that pharmacological calpain inhibition will suppress MJD-induced toxicity in transgenic flies that express MJD in photoreceptor neurons. Demonstrating successful reduction of the pathological effects of MJD toxicity in a model organism is a key first step to pave the way for clinical trials yielding effective therapies for human patients.

Poster Presentation Abstracts – Session 2

22. Impact of heterozygous knockout of *GRIN2B* on the prevalence of synaptic plasticity proteins

Evan VanDriessche, Melanie Kwierant, Madelyn Offer, Sophia Staricha, Shasta Sabo
Department of Biology, Central Michigan University

Neurodevelopmental disorders pose a challenge in neuroscience because they involve disruptions to the complex and poorly understood mechanisms that govern the formation and maintenance of functional neural circuits. In healthy brains, neural circuits rely on precise patterns of synaptic communication to influence perception, cognition, behavior, and movement. Disease-causing genetic mutations can disrupt development or synaptic communication. Here, we focus on mutations that cause *GRIN2B*-related neurodevelopmental disorder.

GRIN2B-related neurodevelopmental disorder is a rare disease caused by mutations in the *GRIN2B* gene, which encodes the GluN2B subunit of NMDA receptors [NMDARs]. Symptoms include intellectual disability and developmental delay, autism spectrum disorder, epilepsy, and motor dysfunction. We model disease-associated deficits in GluN2B using heterozygous knock-out rats. These rats lose half of the amount of GluN2B-containing NMDARs normally present in wild-type rats. This reduction in functional NMDARs is predicted to affect synaptic communication and the prevalence of synaptic proteins. Here, we focus on Arc and AMPA receptors [AMPARs] since these proteins are important for synaptic plasticity downstream of NMDARs.

NMDARs, AMPARs, and Arc interact dynamically to control activity-dependent synaptic strength. NMDARs act as coincidence detectors that bi-directionally regulate synaptic plasticity through processes such as long-term potentiation [LTP] and long-term depression [LTD], which strengthen or weaken synaptic connections by altering AMPAR number and function. NMDAR-mediated calcium entry during LTD triggers Arc expression, which facilitates AMPAR endocytosis, weakening local synapses. Therefore, changes in NMDAR activity are likely to trigger compensatory or maladaptive shifts in both Arc expression and AMPAR prevalence at synapses. We examine this relationship by using immunoblotting of synaptosomes to determine how synaptic AMPAR and Arc prevalence are affected at synapses. This work aims to clarify how disrupted glutamatergic signaling contributes to the pathophysiology of *GRIN2B*-related neurodevelopmental disorder and may point toward specific therapeutic strategies. The outcome of our experiments is difficult to predict, considering the complex role of NMDARs in synaptic plasticity.