Schedule

Opening remarks in Biosciences 1010, 2:00pm

Research talks
- 2:05-2:20pm. 12-min. research talk + 3 min. questions
- 2:20-2:35pm, two 5-min. lightning talks

Enjoy light refreshments during Posters in the Atrium (See numbered abstracts below)
- 2:45-3:30pm, Posters, odd-numbered abstracts present
- 3:30-4:15pm, Posters, even-numbered abstracts present

Social time, slideshow in Biosciences 1010
- 4:15-4:30

Awards
- 4:30pm

Title: What role does the cytoskeleton play in maintaining the viability of eggs?

Presenter: Haddad, Christya, N

Co-authors: Schisa, Jennifer

Abstract: Phase transitions of RNA-binding proteins (RBPs) in cells are similar to phase transitions of water; they can exist in a more diffuse, gel-like, or solid state. Each RBP naturally exists in a certain state, and proper regulation between physical states is essential to maintaining cell health. Our lab is investigating the extent to which the dysregulation of phase transitions causes poor quality oocytes and infertility. We identified the CCT chaperonin as a regulator of RBP phase transitions in C. elegans oocytes; however, the mechanism by which CCT acts is unknown. Because actin and tubulin are folded by the CCT chaperonin, I am exploring the relationships among actin, tubulin, and RBP condensation. I used RNA interference to deplete gene expression in worms that have fluorescent reporters tagged to proteins of interest. I depleted actin and detected RBP condensates, consistent with the idea that CCT regulates RBPs via actin. I next asked if CCT regulates the actin cytoskeleton. I did not detect any differences in the actin cytoskeleton between the cct-2-depleted and control worms; however, I had to use a low-resolution microscope for this experiment. We also know that CCT regulates the microtubule cytoskeleton, and decreased levels of tubulin are associated with ectopic RBP condensation. Therefore, I hypothesized that actin regulates RBP condensates via the microtubule cytoskeleton. My preliminary results are that levels of tubulin may be reduced after depleting actin compared to the control group. My current experiments will continue to test the hypothesis that the ectopic granule phenotype seen with CCT or actin depletion may be due to a dysfunctional microtubule cytoskeleton. Ultimately, gaining insight into the regulation of phase transitions of RBPs will provide insight into their function in determining oocyte quality.

Title: Exploring connections between endoplasmic reticulum remodeling and infertility

Presenter: Trombley, Nicholas, J

Co-authors: Schisa, Jennifer

Abstract: Infertility is more common than many people realize, affecting over 10% of couples when a woman is under the age of 30. The causes of infertility are not completely understood; therefore, our lab is investigating a new hypothesis that the dysregulation of RNP granules in eggs may contribute to infertility. RNP granules form when RNA and RNA-binding proteins undergo phase separation in eggs (or oocytes). The dysregulation of phase transitions of RNA-binding proteins is linked to several disease states, supporting the idea that regulation of phase transitions may be critically important to maintain high quality oocytes and fertility. Our lab has identified Extracellular signal-Regulated Kinase (ERK), the CCT chaperonin, and actin as regulators of phase transitions in C. elegans oocytes; however, the mechanism by which they act is not yet known. My study is based on the observation that the endoplasmic reticulum structure undergoes re-modeling at the same time phase transitions of the MEX-3 RNA-binding protein occur in oocytes. We hypothesized that ERK, CCT, and actin may modulate MEX-3 condensation via regulating ER structure. Strikingly, we used RNA interference to deplete ERK, CCT, and actin in GFP::MEX-3 worms and found each depletion resulted in ectopic ER sheets in maturing oocytes. These results are consistent with our hypothesis that ERK, CCT, and actin may form a regulatory network to modulate ER structure and subsequently regulate condensation of RNA-binding proteins in oocytes. Consistent with this model, membrane surfaces such as the ER have gained increasing recognition as one critical means of regulating phase separation by restricting molecular diffusion. My current experiments are aimed to visualize MEX-3 and the ER simultaneously to determine the extent to which MEX-3 granules contact the ER. Ultimately, gaining insight into the regulation of phase transitions will provide insight into their function in determining oocyte quality.

Title: Do all regulators of RHO-1 aggregation also regulate MEX-3 granules in oocytes?

Presenter: Thomas, Grace, M

Co-authors: Mohamed Elaswad, Corrin Hays, Jennifer Schisa

Abstract: Declines in oocyte quality are a major contributor to infertility, but the causes are not well understood. RNA-binding proteins (RBPs) undergo many phase transitions during oogenesis in both humans and the model Caenorhabditis elegans. We are using C. elegans to test the hypothesis that oocyte quality is maintained by proper regulation of RBP phase transitions. As a first step, our lab is currently identifying regulators of oocyte RBP phase transitions. Recent results in our lab have identified actin and the CCT chaperonin as key inhibitors of ectopic RBP condensation in maturing oocytes. Actin and the CCT chaperonin were also among dozens of proteins identified as inhibitors of aggregation of the GTP-binding protein RHO-1. The processes of RBP condensation and aggregation are distinct; nonetheless, I investigated the extent to which the two processes are coordinated in maturing oocytes. Using green florescent protein (GFP) tagging MEX-3 and RHO-1 in C. elegans, I tested genes in the following biological processes for roles in inhibiting RBP condensation: protein degradation, vesicle-mediated transport, lysosome acidification, and mitochondrial ATP synthase. After using RNAi to deplete the expression of each gene, I examined RHO-1 aggregation and MEX-3 condensation to determine if the processes are coordinated by the same regulatory network. Ultimately, our results suggest a degree of overlap, but not identical regulation. Our insights into the complex regulation of phase transitions during oogenesis may eventually provide insights to better understand fertility.

1. Title: Effect of macroplastics and land use on microplastic concentrations in Mount Pleasant, MI ponds

Presenter: Sarah Burgoyne

Co-authors: Amanda Suchy and Don Uzarski

Abstract: As plastics have become a more prevalent global pollutant, a better understanding of their concentrations in the freshwater environment is needed. This experiment examined drivers of microplastic concentrations in waterways in and around Mount Pleasant, MI. I hypothesized that macroplastic (trash) concentration could increase microplastic concentrations in local waterways. Nine ponds were sampled with three one-liter samples taken from each pond and filtered to assess the amount of microplastics they contained. The filtered plastics were counted via observation under a dissection scope and sorted by color and shape. For each pond, I quantified macroplastics and divided the land into campus and non-campus areas and analyzed their relationship to microplastic concentrations. There was no significant difference in microplastic concentration between campus and non-campus ponds. However, there was a significant increase in microplastics in ponds with higher levels of macroplastics. Macroplastics compared to microplastics yielded a p-value of 0.01 (R^2 of 0.8265) meaning there was a significant correlation between macroplastic concentrations and microplastic concentrations. By determining a link between microplastic concentrations and macroplastic concentrations, more targeted solutions to the problem can be generated to limit micro plastics from entering the environment

2. Title: RNAi Screening of identified RNAi binding proteins that enhance microRNA activity after dauer in C. elegans.

Presenter: Kopesky, Regan K

Co-authors: Dom Carvounis, Himal Roka, Xantha Karp

Abstract: C. elegans can enter a stress-induced and developmentally arrested stage called dauer. Dauer is a pause in development in response to unfavorable conditions. On the other hand, favorable conditions result in continuous development. Mechanisms behind dauer and subsequent recovery are not fully understood. The C. elegans model system allows for investigation of diapause, utilizing the worm's size, shape, and genetic properties. C. elegans can still reach the same developmental outcome as their continuous counterparts once recovered from dauer. This is likely from modulation of microRNAs (miRNAs), small, non-coding RNA protein that participates in gene expression. These miRNAs recognize the 3,Äô-UTR of messenger RNA (mRNA) before protein production, which then prevents protein production. This gene silencing complex is named the miRNA-induced silencing complex (miRISC). It is established that the genes alg-1 and alg-2 encode Argonaute proteins that are part of binding with miRNA within the miRISC complex. When the alg-1 gene is absent in continuously developing worms, the vulva of the adult worm bursts or protrude. However, when this same worm strain enters dauer and subsequently recovers, no bursting or protrusion occurs. We hypothesize that this phenotypic suppression is the result of increased miRNA activity post-dauer due to the action of RNA-binding proteins. Our experiments aim to compromise the miRISC complex and identify the RNA binding proteins that modulate the complex. We have performed RNAi screens to identify genes that cause bursting or vulval protrusion in post-dauer alg-1(0) adults and evaluate the penetrance. Thus far, we have found that the genes, rpb-8, lars-1, eef-1B.1, mcm-6, and aco-2 are RNA-binding proteins that mediate and subsequently compromise miRISC function in C. elegans. This work is expected to provide insight into mechanisms by which microRNA pathways are modulated as well as the genes and their functions within the miRISC complex.

3. Title: Patterns of shell shape variation in the critically imperiled freshwater mussel genus Epioblasma

Presenter: Haugh, James, P.

Co-authors: Pfeiffer, John, M. and Zanatta, David, T.

Abstract: The freshwater mussel genus Epioblasma comprises 27 species from eastern North America with 2 species being found in southern Canada. Ten species are federally protected under the U.S. Endangered Species Act and both of Canada‚Äôs Epioblasma species are protected under Canada‚Äôs Species at Risk Act. The remaining 17 species are presumed to have gone extinct due to human activity over the past two centuries. Due to their critically imperiled status and extreme rarity, most species have little to no molecular data available for genomic analysis and thus their evolutionary history is poorly understood relative to other North American species. In the absence of molecular data, we set out to better understand aspects of Epioblasma ecology and evolution by quantifying and analyzing shell shape. To quantify and assess shell shape variation within and among species, photographs of Epioblasma specimens (n = 1400) representing all 27 species and 59 different river bodies were sampled from museum collections for geometric morphometric analyses. Each interior shell shape was extracted via Procrustes-transformed landmarks to get a set of coordinates. Linear discriminant analysis was able to correctly identify Epioblasma specimens to subgenus at a rate of 82.7%, and groupings formed by a UPGMA cluster analysis were largely consistent with previous subgeneric classifications. A principal component analysis and examination of thin-plate splines were able to quantify differences in male and female Epioblasma forms and could be used to explain trends in sexual dimorphism among species and subgenera. Correlation analyses showed relationships between waterbody and specific differences in shell shape among subgenera. This supports Ortmann‚Äôs Law of Stream Position, with more elongate and obese (i.e., 2-dimensionally rounder) shell shapes in waters with a lower discharge and velocity. Further explorations of the data examining patterns of shell shape and implications for the ecology and evolution of Epioblasma are ongoing.

4. Title: Exploring the impact of pharmacological calpain inhibition in suppressing the toxicity of tau in photoreceptor neurons

Presenter: Holben, Justus, G

Co-authors: Douglas, Logan, H; Allers, Cooper, C

Abstract: Alzheimer‚Äôs disease (AD) is a neurodegenerative disease that affects more than 6 million Americans. It is characterized by a multitude of symptoms, including memory loss, seizures, and mood swings. There are treatments on the market that are aimed at targeting these symptoms; however, there is no known cure. AD is characterized pathologically by the presence of neurofibrillary tau tangles and beta-amyloid plaques. Because of this, AD belongs to a family of diseases called tauopathies, which are characterized by abnormal phosphorylation of tau proteins in the brain, leading to the characteristic neurofibrillary tangles and ultimately, miscommunication and death of hippocampal neurons. We and other labs have demonstrated that full-length tau (65 kD) is cleaved by the protease calpain, yielding a 17 kD fragment that is intrinsically toxic. In the fruit fly model of tauopathy, expression of wild-type and mutant forms of human tau results in neurodegeneration of photoreceptor neurons in retinal tissue, creating what is known as the tau ‚Äòrough eye phenotype'. For this project, we are using the fly tauopathy model to screen calpain inhibitors for their ability to modify the tau rough eye phenotype. The aim of this study is to determine the viability of calpain inhibition as a potential treatment strategy targeting the pathology associated with tau in AD.

5. Title: Examining the Impact of Tau Toxicity on Climbing Ability in a Drosophila Tauopathy Model

Presenter: Klan, Noah C

Co-authors: Steinhilb, Michelle L

Abstract: Alzheimer's disease (AD) presents a formidable social and medical challenge, characterized by memory loss, cognitive decline, and behavioral changes. AD belongs to a family of diseases collectively known as tauopathies, whose defining pathological feature is the presence of tau protein tangles in the human brain. Tau, a microtubule-associated protein, typically plays a role in stabilizing microtubules but undergoes post-translational modifications over time, such as hyperphosphorylation, leading to tau aggregation and cognitive impairment. Drosophila melanogaster, the common fruit fly, stands out as an ideal model system to study the role of tau in disease due to the high degree of conservation between humans and flies in the molecular pathways involved in human neurodegenerative disorders. The climbing assay in flies takes advantage of Drosophila‚Äôs natural tendency to climb upwards against gravity, a behavior called negative geotaxis. As such, the climbing assay has been used extensively to study genetic and environmental factors affecting fly behavior. Several labs have successfully utilized the climbing assay to study neurodegenerative disorders; our lab will employ the climbing assay to assess how human tauopathy-associated genes and pharmacological agents affect fly locomotion. To calibrate the climbing assay for use in our lab, we have selected five GAL4 driver lines to direct the expression of wild-type and mutant forms of human tau in specific subsets of fly neurons. We expect to find a positive correlation between tau toxicity and diminished locomotion in the climbing assay. Establishing a robust, reproducible, simple assay using sufficient numbers of flies to do statistical analyses will allow us to use the climbing assay to screen for genetic and pharmacological agents that may modify tau toxicity in vivo. This research represents a crucial step in unraveling the role of tau in neurodegeneration, with potential implications for future treatments of neurodegenerative diseases like Alzheimer's.

6. Title: Reproducibility of microplastic extractions from sediments

Presenters: Shablin, Julia, K and England, Miranda, R

Co-authors: Suchy, Amanda, K and Uzarski, Don, R

Abstract: Microplastics are anthropogenic contaminants (plastic particles <5mm) that have been found in nearly all environments. Microplastics have the potential to negatively impact human and wildlife health via ingestion, carry and transport toxins on their surface, and impact the biogeochemical functioning of ecosystems. The appearance of microplastics in coastal wetlands is concerning as microplastics take a long time to break down and may remain in the sediments for decades. Currently, there is no standard method for microplastic extraction and quantification from sediments due to the heterogeneous nature of sediments and the lack of reliability with extraction methods. This makes it difficult to know the scope of the impact of microplastics on coastal wetlands. One popular method involves wet sieving sediments to include particles between 0.3-5 mm in size, removing organic matter via hydrogen peroxide digestion, and then separating plastics from sediment via density separation. Plastics are then collected on a filter and manually counted using a microscope. Our objective is to examine the reproducibility of this sediment extraction method by duplicating the extraction on 20 sediment samples collected in the summer of 2022 from coastal wetlands in Michigan as part of the long-term Coastal Wetland Monitoring Program. By assessing the reproducibility of extraction and quantification methods from sediments, we will be better informed about the reliability of counts from these extractions therefore better able to move towards more refined and standardized extraction methods moving forward.

7. Title: Identification of igfbp, lce, and hce Non-Coding Gene Regulatory Regions in N. whitei and O. latipes Using ATAC-seq

Presenter: Kaczmar, Andrew, R

Co-authors: Tan, Shannon; Thompson, Andrew, W

Abstract: Dormancy is an important adaptation for organisms that live in extreme environments. The Rio Pearlfish undergoes a special dormancy known as diapause. Our previous work has identified some gene expression changes during pearlfish diapause, but the underlying developmental gene regulatory mechanisms are relatively unknown.
Non-coding open chromatin regions, or ncOCRs, contain potential cis-regulatory elements such as promoters and enhancers that control expression of nearby genes. Moreover, ATAC-Seq is a technique that uses a Tn5 transposase enzyme that cuts at open chromatin and adds sequencing adapters. When combined with bioinformatic tools, this technique can be used to identify ncOCRs. Therefore, ATAC-Seq can be used to find potential cis-regulatory elements that control gene expression. Recently, we used ATAC-Seq to identify numerous non-coding open chromatin regions in Rio pearlfish (N. whitei) during dormancy and hatching and homologous developmental stages of the related medaka (O. latipes). We identified ncOCRs near low choriolytic (lce) and high choriolytic (hce) hatching enzymes and insulin-like growth factor binding protein (igfbp) genes. These sequences are the first to identify candidate regulatory elements in this species that might be related to dormancy and hatching control as igfbp and hatching enzyme gene expression changes have been identified in pearlfish dormancy.

8. Title: Investigating the role of CCT-6 in regulating condensation in C. elegans oocytes

Presenter: Cichon, Ashley, N

Co-authors: Dr. Schisa, Jennifer, Trombley, Nick

Abstract: Female infertility is a common condition, and reduced egg quality is often the cause. We are interested in identifying the molecular mechanisms that affect egg quality. Several proteins in human eggs undergo regulated condensation during the cell cycle, suggesting that proteins may need to be condensed or decondensed at different times to promote egg quality. In the model organism C. elegans, the CCT chaperonin was identified as a possible regulator of condensation in oocytes (eggs). We have evidence that multiple subunits of the CCT chaperonin inhibit the condensation of MEX-3 in oocytes. C. elegans is useful in studying the regulation of MEX-3 condensation because the worms are transparent, and we can easily monitor protein condensation in living worms that have a green fluorescent protein tagged to MEX-3. My experiment uses the method of RNA interference (RNAi) to determine if the CCT-6 subunit also inhibits condensation of MEX-3 in oocytes. We first synchronize the worms, so they are at the same stage of development, and then expose them to bacteria expressing double-stranded cct-6 RNA. RNAi will deplete levels of cct-6 compared to a negative control, and we can assess effects on MEX-3 condensation. We predict that RNAi of cct-6 will result in ectopic MEX-3 granules. If so, we will conclude CCT-6 is required to prevent MEX-3 condensation, and it‚Äôs likely the entire CCT chaperonin plays a role in the process. By characterizing the CCT chaperonin subunits that regulate MEX-3 condensation, we gain insight into the molecular interactions involved. In the future, we seek to determine the mechanism by which CCT regulates MEX-3 condensation, and better understand the extent to which condensation affects egg quality.

9. Title: Efficacy of clodronate and zymosan on the microglial cells of zebrafish

Presenter: Pasupathy, Nivetha

Co-authors:

Abstract: This paper examines the neuroplasticity of Danio rerio (zebrafish) and how they recover from damage induced by detergent application to their olfactory organs. The zebrafish immune system is heavily involved in their neuroplasticity as disease and injury in the brain require an efficient response. This proposed project aims to establish that we can affect the immune response of zebrafish by using clodronate to see if the number of immune cells can be reduced at various time intervals and zymosan to increase the number of immune cells during immune response at various time intervals. The primary antibody 4C4 is used to label the microglial cells found at the site of damage so that they can be visualized with fluorescence by a secondary antibody (Texas red) under a confocal microscope.

10. Title: Reassessment and Assemblage Evaluation of Unionids in the Upper Tittabawassee River Watershed 40 Years After Historical Study

Presenter: Vlasak, Aaron, L

Co-authors: Woolnough, Daelyn, A

Abstract: Unionids (native freshwater mussels; family Unionidae) provide many ecosystem services such as, filtering and storing nutrients, providing habitat for invertebrates, and indicating water quality, and fish diversity. However, unionids are understudied especially in smaller head waters, tributaries, and in inland lakes and reservoirs. Our objectives were to determine the current diversity and density of unionids in numerous tributaries and reservoirs of the Tittabawassee River and to compare our data to the limited historical data (40 years ago; Hoeh and Trdan (1984)) of the watershed. We also wanted to identify changes to the habitat that could help explain changes in the unionid assemblages over time by recording presence of invasive species, river alterations, and land use changes. We surveyed a total of 39 sites using standard snorkel and SCUBA time search methods; sites included 28 historical sites, 5 new tributary sites, and two reservoirs (3 sites in each reservoir). We will present unionid community composition, abundances, changes from historical data as well as risk to these communities found during the surveys. In total we found > 1000 live unionids represented by 16 species. This study found multiple species that were not found in the study 40 years ago as well as loss of species at numerous sites. The density of the mussels changed at every site except three where only shells were previously found. Every species also underwent a change in density at least one site, with the most variation from the past study per species being 16 sites with density changes (Pyganodon grandis). We will address how these data can be used as a new baseline to monitor and conserve the unionids of the Upper Tittabawassee River Watershed. We will discuss how the infrequent timeline of mussel surveys can make it difficult to explain why changes have occurred.

11. Title: Length classes among unionids in different stream class categories from the Kalamazoo River watershed

Presenter: Heinz, Megan E.

Co-authors: Woolnough, Daelyn A.

Abstract: Native freshwater mussels (family Unionidae; unionids) are declining worldwide but currently are represented by over 300 species in North America. North American unionids can live over 50 years and are documented to grow larger throughout their lives and grow less, or cease growth, during cold periods. Fisheries research often develop categories of rivers, based on fish habitats, that are reflective of river size classes, temperature, and stream order; however, little is known about how unionids grow relative to river size and temperature. This study considered length classes of the 10 most common species of unionid in the Kalamazoo River watershed and how lengths related to classic stream class categories used by fisheries managers. Lengths of 2317 unionids were used in this study all of which were collected during a 2018 and 2019 survey by the Woolnough Lab. We considered stream class categories of: 1) river type (large river, small river, tributary), 2) temperature (warm or cold) and, 3) whether streams were transitional and not. Finally, we used a combined class of all 3 categories. We considered distributions of lengths of unionids at every site the species was found at relative to the stream class categories. ANOVAs and, when significant, post-hoc Tukey tests were performed to see if there were any significant relationships between categories and length classes. This poster will present our findings which did find many novel and unique relationships that have never been documented for unionids before. In fact, three species of unionid: Lasmigona costata (Flutedshell), Pyganodon grandis (Giant Floater), and Strophitus undulatus (Creeper) were never found to occur in any cold-water portions of the Kalamazoo River watershed which was unknown before this study. These data will be important when considering restoration, including propagation and augmentation, during the conservation of unionids in Michigan and across North America.

12. Title: Characterizing Regulators of Egg Quality

Presenter: Themel, Leah, M

Co-authors: Elaswad, Mohamed; Schisa, Jennifer

Abstract: The likelihood of infertility increases as women age; however, women of all ages can experience infertility. Although we do not fully understand the mechanisms behind infertility, we know that maintaining oocyte (egg) quality is critical. Many proteins in oocytes undergo regulated phase transitions, and their condensed and diffuse states may be important in determining oocyte quality. We used C. elegans as a model system to study protein condensation in oocytes. In C. elegans oocytes, ERK kinase activity is correlated with the phase of MEX-3 protein, which makes ERK a potential regulator of protein condensation. Data from our lab shows that depletion of ERK results in MEX-3 condensation; however, we know that ERK depletion can inhibit the progression of meiosis. Therefore, the purpose of this experiment was to assess worms after ERK-depletion and determine the stage of meiosis for the cells where we detect MEX-3 condensation. To visualize MEX-3, we used a worm strain with a green fluorescent protein (GFP) tag fused to MEX-3. To examine the effects of ERK depletion, we used RNA interference (RNAi) to knockdown the expression of the ERK-encoding gene (mpk-1). Our negative control was RNAi of lacZ. To visualize chromosomal DNA and assess the stage of meiosis, we used blue fluorescent Hoechst dye. We dissected the worms and quickly imaged using confocal microscopy. We predicted that the cells with MEX-3 condensates would be in the diakinesis stage like control worms. The results showed chromosomes in the typical diakinesis formation in the cells; therefore, we conclude MEX-3 condensates form in differentiated oocytes. This finding supports the idea that ERK may directly regulate the MEX-3 condensation process. Future directions include determining if ERK/MPK-1 regulates condensation of another protein, CGH-1. We hope these studies will eventually help us determine if ERK and MEX-3 condensates affect oocyte quality.

13. Title: Phenotypic Characterization of Copine D Mutants in Dictyostelium

Presenter: Ruiz, Sonya, M

Co-authors: Morrison Cody T, Damer-Daigle Sela K, Anklam Jordyn E, and Damer Cynthia K

Abstract: Copines are a family of calcium-dependent membrane-binding proteins found in most eukaryotes. The Damer lab utilizes Dictyostelium discoideum as a model organism to investigate the function copines in the regulation on cellular processes. Dictyostelium is an amoeba that has six copines genes, cpnA to cpnF. Our lab observed that each of the copine genes has distinct developmental expression patterns and phospholipid binding properties. We obtained insertional mutants from the Dictyostelium REMI mutant experiment to investigate the function(s) of cpnD. The REMI cpnD mutants were created from the parental strain, AX4. We first verified the site of the large insertion within the cpnD gene using PCR and then explored the role of cpnD in growth, development, adhesion, and contractile vacuole using phenotypic assays. We discovered that the cpnD mutants grew faster in suspension culture than the parental AX4 cells. When cells were developed, the cpnD mutants made smaller fruiting bodies than AX4 cells. cpnD mutants were also significantly less adhesive than AX4 cells. The mutants showed no significant difference in contractile vacuole size compared AX4 cells. Our objective is to determine the biological functions of each copine gene. This knowledge is potentially valuable in understanding the function of evolutionarily conserved copine genes in humans.

14. Title: Identifying transcriptional activators that regulate adult cell fate downstream of ztf-16

Presenter: LeRoux, Madeleine, S

Co-authors: Karp, Xantha

Abstract: Organisms develop in long processes and stages. Continuous development is when organisms develop without stopping their development. In unfavorable environmental conditions, some animal species can undergo diapause, a reversable state of developmental arrest. In favorable conditions, C. elegans larvae develop through four larval stages separated by molts before reaching adulthood. In unfavorable conditions, C. elegans can enter a stress-resistant diapause stage called dauer. Once favorable conditions return, C. elegans can continue to develop as post-dauer worms. To determine the effects of dauer on developmental outcomes, we study epidermal seam cells. Larval seam cells are multipotent and divide during larval development but terminally differentiate at adulthood. The transition from larval fate to adult fate is regulated by heterochronic genes that control stage specific gene expression. In adults, the adult cell fate marker, col-19p::gfp, is expressed in seam cells, and in larvae it is repressed. Seam cell fate is regulated differently during post-dauer development since many heterochronic genes post-dauer are dispensable after dauer, suggesting a modulated post-dauer pathway which is mostly unknown. Our lab identified two genes that control col-19p::gfp in the dauer developmental trajectory: ztf-16 blocks col-19p::gfp expression after dauer, and daf-16 blocks col-19p::gfp expression during dauer. Prior lab members found that dcp-66 suppressed precocious col-19p::gfp expression in ztf-16 mutants. dcp-66 encodes a part of the Nucleosome Remodeling and Deacetylase (NuRD) complex. We hypothesized that dcp-66 and three other genes encoding of the NuRD complex proteins would also regulate col-19p::gfp expression in daf-16(0) mutants. To test this hypothesis, I performed RNAi to knock down dcp-66 and the other NuRD complex genes in daf-16(0) dauer larvae. My preliminary data showed that col-19p::gfp expression was dramatically reduced. This is the first time the NuRD complex has been implicated in the regulation of adult cell fate.

15. Title: The effects of vegetation on soil organic matter and nitrogen retention in the Great Lakes coastal wetlands

Presenter: Huber, Viktoria, J

Co-authors:

Abstract: The Great Lakes coastal wetlands provide many ecosystem services, which include but are not limited to improving water quality, crucial habitat, and recreation. However, as shoreline development increases, pollution and loss of habitat are becoming more prevalent. Invasive species, such as Phragmites australis, and changes to vegetation cover due to variable water levels can also contribute to changes in ecosystem services provided by coastal wetlands. The purpose of this research is to gain a better understanding of how vegetation communities and other environmental factors can influence nutrient cycling in barrier, lacustrine, and riverine coastal wetland systems. Sediments were collected in summer 2023 as part of the Coastal Wetland Monitoring Program (CWMP). Soil samples will be analyzed for organic matter content, moisture, and extractable nitrogen in different vegetation zones of each wetland. Soil moisture will be determined gravimetrically. Soil organic matter will be determined by loss on ignition or mass lost after 4 hours in a muffle furnace at 550 ¬∞C. Soil extractable nitrogen will be determined by extracting N from soil using 2M KCl. The extracts are then filtered and analyzed with an autoanalyzer. We expect that vegetation zones with high biomass species, such as Typha sp. or Phragmites sp., will have higher amounts of organic matter and thus greater nitrogen retention in soils. Overall, a wider perspective and knowledge of the current conditions in the Great Lakes coastal wetlands and the impact of vegetation on nutrient retention will help shed more light on the changes occurring in our wetlands that perform many crucial ecosystem services and serve as homes for migrating birds, invertebrates, and fish.

16. Title: Background, Progress, and Future of Native Mussel Propagation in Michigan; Central Michigan University Assists with Advances

Presenter: Judge, Aiden F

Co-authors: Woolnough, Daelyn A

Abstract: Native freshwater mussels (family Unionidae) is an incredibly diverse group with many species being endemic to North America. Mussel populations worldwide are declining and efforts to conserve these populations requires more research and investment into mussel propagation. Propagation techniques for conservation are already in use in the US and internationally but not in Michigan. The Central Michigan University (CMU) Native Mussel Labs are in a unique position to help further research needs in Michigan. Through their partnership with the DNR Saline Fisheries Research Station (SFRS) CMU is helping to build the first propagation facility for mussels in Michigan. This poster will highlight how CMU has advanced mussel research for successful propagation as well as how the SFRS could be successful with propagation efforts, in the near future, thanks to advances aided by CMU. Located on the Saline River, SFRS hosts outdoor ponds as well as six raceways and an indoor research facility. The Woolnough lab has worked to equip the indoor facility with many rearing systems (e.g., dog pans, adapted Barnhart buckets) and has worked with the DNR to replicate CMU vivarium facilities with Aquatic Habitat Units. The SFRS ponds have historically been stocked with bluegill, perch, and largemouth bass populations, and are capable of supporting other host fish species in tandem propagation with juvenile mussels; CMU has shown that these outdoor facilities could support mussels for quarantine if needed (e.g., oil spill). Current CMU state-wide survey data, research on host fish, genetics, and developing knowledge on mussels and water quality can help inform decisions on stocking techniques and biosecurity concerns. Further research into techniques and biosecurity must be conducted to ensure successful propagation efforts in Michigan in the future. The SFRS facilities have a great potential to become an indispensable location for future freshwater propagation efforts in Michigan.