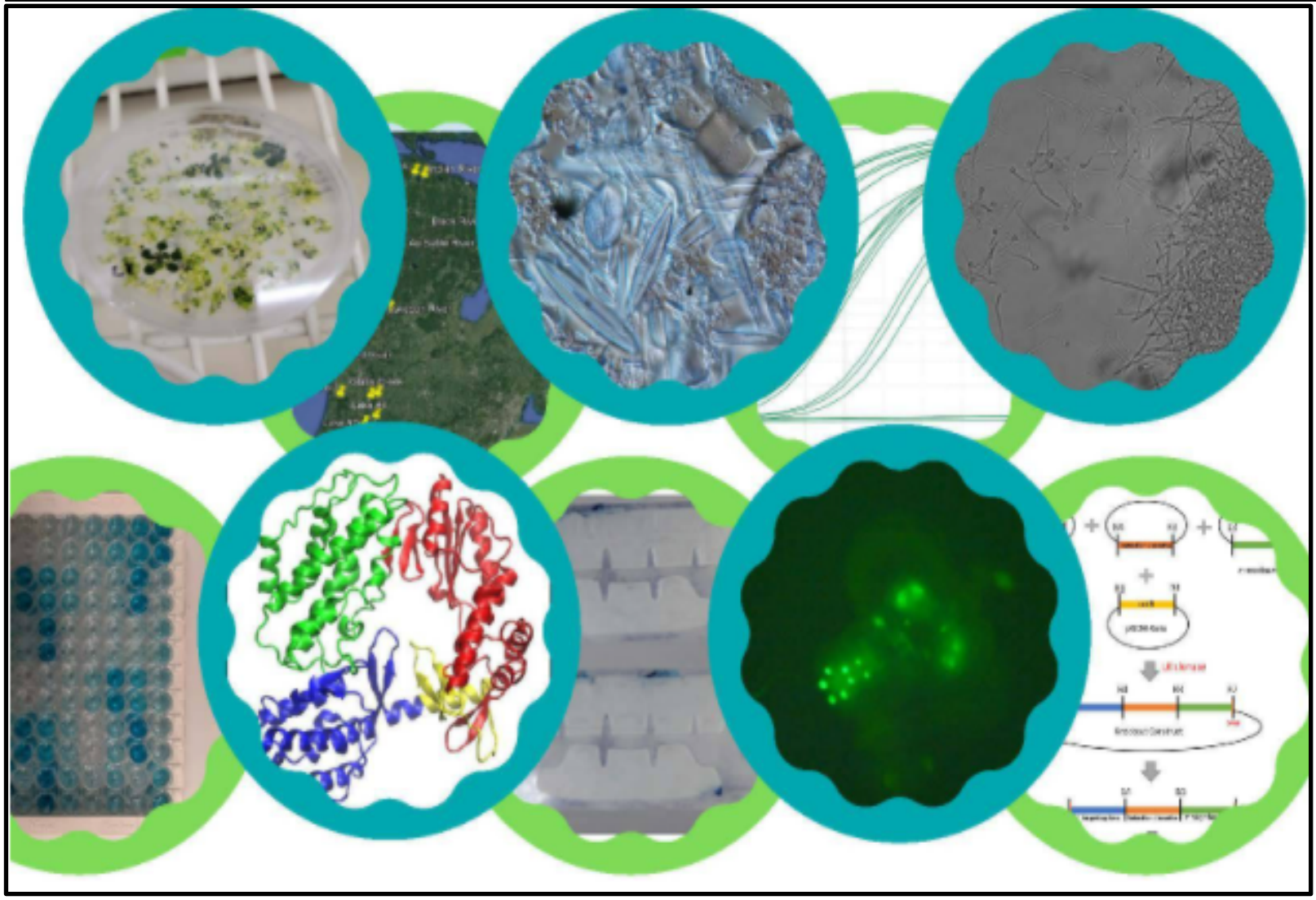
8th Annual CMB Undergraduate Research Symposium

Brought to you by Grand Valley State University
Department of Cell and Molecular Biology

April 8-9th 2022



Schedule

VIII Symposium Schedule

Friday 1101 KHS

2:25	**Opening remarks**	**Chair: Roland Nulph**
2:30-2:50	**Lauren Proctor**	**Planarian Brain Regeneration and Behavior Following RNAi and Injury**
2:50-3:10	**Cameron Coates**	**Does Exercise Change Brain-Derived Neurotrophic Factor Levels in Parkinson's Patients? - a Pilot Study**
3:10-3:30	**Gabrielle Garlicki**	**Over-expression and analysis of genes impacted during spaceflight in *Candida albicans***

Coffee break

Chair: Agnieszka Szarecka

3:45-4:05	**Roland Nulph**	**Effects of Microbial Environment on T-cell Activation and Tumor Suppression in Mice**
4:05-4:25	**Annelise Larson**	**A Noncompetitive Inhibitor's Effect on the Processivity of Telomerase**

5-7pm **CMB Celebration in the Alumni House**

Saturday 1101 KHS

Chair: Garrett O'Dea

10-10:20	**Sean Fleisher**	**Displaying GFP in *Drosophila melanogaster***

10:20-10:40	**Howard Hayward**	**Industry standards for Oral Care Quality Assessment**
10:40-11	**Hanna Pickard**	**Isotopic analysis of the ancient humans from the Black Sea region**

Coffee break

Chair: Agnieszka Szarecka

11:15-11:35	**Garrett O'Dea**	**New quantitative genotyping methods in mixed wastewater sample**
11:35-11:55	**Jack Ruhala**	**PMMoV wastewater monitoring**
11:55-12:15	**Jacob Wolfe**	**Testing the Efficacy of Water Filters and Water Purifier**

Lunch

Chair: Howard Hayward

1-1:20	**Elizabeth Cazallis**	**Disrupted retrotransposons in *Physcomitrella patens* using Gateway Cloning**
1:20-1:40	**Colin Kozar**	**Pathway analysis of mutant strain Physcomitrella patens**
1:40-2	**Shane Vaughn**	**Phylogenetic analysis of CAM evolution in the Bromeliaceae plant family**

Coffee break

Chair: Sean Fleisher

2:15-2:35	**Carlin Moore**	**Assessing the Genetic Relationship of Wild Rice Populations in Michigan**

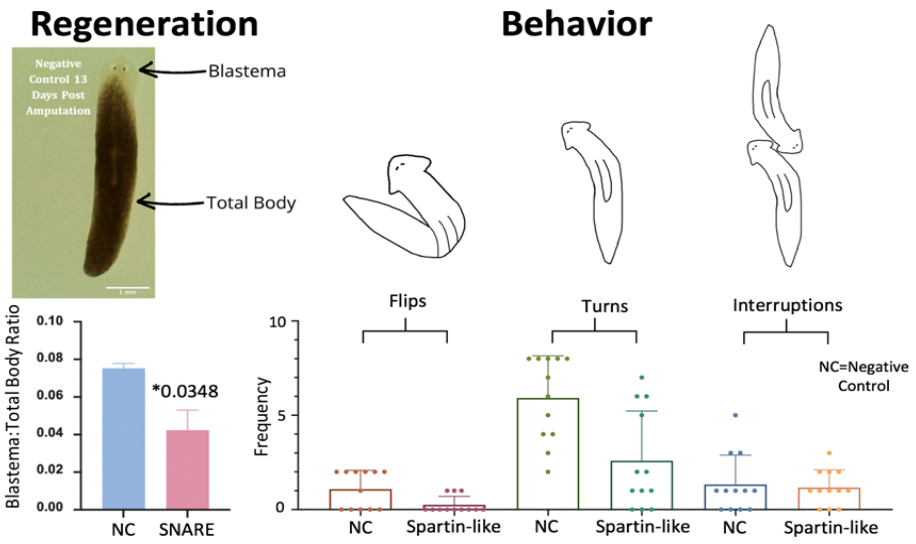
2:35-3:55	**Lyla Dao**	**Studying the gene expression and functions of the GmSLY1a and GmSLY1b genes in soybean plants, as well as their effects on nodule formation**
3:55-3:15	**Tyler Garcia**	**An adventure into diatom biology in two projects: building a local flora and exploring *Nitzschia* evolution**

Photographs/ Best Speaker Award (faculty and popular vote)

Planarian Brain Regeneration and Behavior Following RNAi and Injury

Lauren Proctor[1], Rachel Roberts-Galbraith[2], Dawn Clifford Hart[1]
Mentor: Dr. Dawn Clifford Hart[1]

[1]Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.
[2]Department of Cellular Biology, University of Georgia, Athens GA.



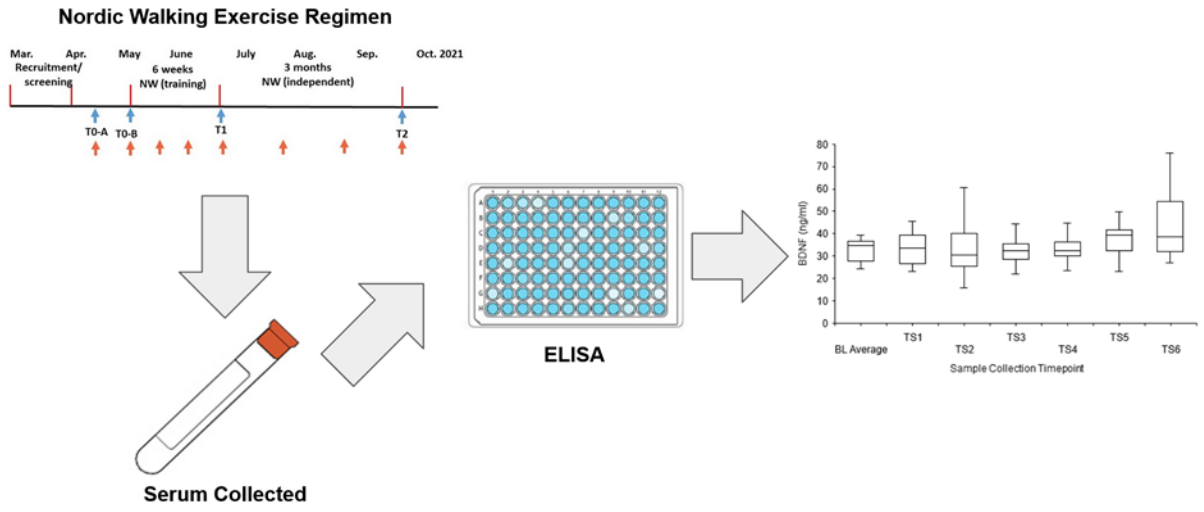
Neurodegenerative diseases are largely associated with neuronal death. Because human brains regenerate poorly, we use an animal model — planarian flatworms — to understand how neurons can be regrown after injury or disease. Planarian flatworms can regenerate their entire central nervous system and replace specific types of neurons. The key question is, how do genes with known roles in mitotic exit alter planarian regeneration and behavior? After establishing behavioral assays that reproducibly measure an output for brain function, I employed RNA interference (RNAi) to systematically knock down 14 different genes. Two genes that are both associated with neurodegenerative diseases will be discussed. The soluble *N*-ethylmaleimide-sensitive factor attachment protein receptor (SNARE) is a membrane fusion protein involved in exocytosis. This protein plays a role in the pathophysiology of many neurodegenerative diseases, such as Alzheimer's and Huntington's Disease, as well as neurodevelopmental diseases such as epilepsy. Spartin-like is a mono-ubiquitinated protein involved in epidermal growth factor receptor trafficking. Mutations in the Spartin-like gene cause Troyer syndrome, a hereditary spastic paraplegia. Results for SNARE RNAi show major phenotypic, regenerative, and behavioral differences in planarian. Importantly, the majority of the animals lysed prior to amputation, suggesting that SNARE is essential for viability. While this is a novel finding, behavioral analysis could not be accurately completed. To demonstrate how the behavioral parameters can be employed, results with Spartin-like will also be discussed. The outcome of this project is identification of genes important for neural regeneration, which could eventually provide insight into therapeutic targets for human disease.

This project was funded by the P. Douglas Kindschi Undergraduate Research Fellowship, Student Summer Scholars program, and the Cell & Molecular Biology Department.

Does Exercise Change Brain-Derived Neurotrophic Factor Levels in Parkinson's Patients? - a Pilot Study

Cameron Coates[1], Zane Walters[1], Julie Hall[2], Dana Vaughan[2], Lilianne Nelson[2], Mattie Brechbiel[2], Cathy Harro[3], Michael Shoemaker[3]
Mentor: Dr. Sok Kean Khoo[1]

[1]Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.
[2]Medical Laboratory Sciences, Grand Valley State University, Allendale MI.
[3]Department of Physical Therapy, Grand Valley State University, Grand Rapids, MI.



Parkinson's disease (PD) is the second most common neurodegenerative disorder in adults affecting 1% of the population above 60 years old. PD is characterized by the loss of dopaminergic neurons and the buildup of α-synuclein proteins in the substantia nigra. With no cure currently available for PD, it is essential to find an intervention to slow or halt its progression. Brain-derived neurotrophic factor (BDNF) is a protein crucial for neuronal health and survival. In people with PD, BDNF levels are lower than in healthy controls. BDNF levels in healthy people are also shown to increase for several days after exercise. Here, we aimed to study the effect of Nordic walking exercise on BDNF levels in people with PD. We hypothesized that BDNF serum concentrations would increase and stay elevated with the exercise regimen. Eight serum samples were collected from 12 subjects over a 4.5-month exercise period. Enzyme-linked immunosorbent assays (ELISA) were performed to assess BDNF concentrations in serum. Friedman test with post hoc Wilcoxon signed-rank pairwise comparisons showed statistically significant time point differences for BDNF levels especially after 4.5 month. This pilot study showed that long-term Nordic walking exercise may increase BDNF levels to improve brain health and benefit people with PD.

This study was funded by the GVSU Office of Undergraduate Research and Scholarships P. Douglass Kindschi Fellowship in the Sciences and CSCE Collaborative Research Grant.

Over-expression and analysis of genes impacted during spaceflight in *Candida albicans*

Gabrielle Garlicki[1]
Mentor: Dr. Ian Cleary[2]

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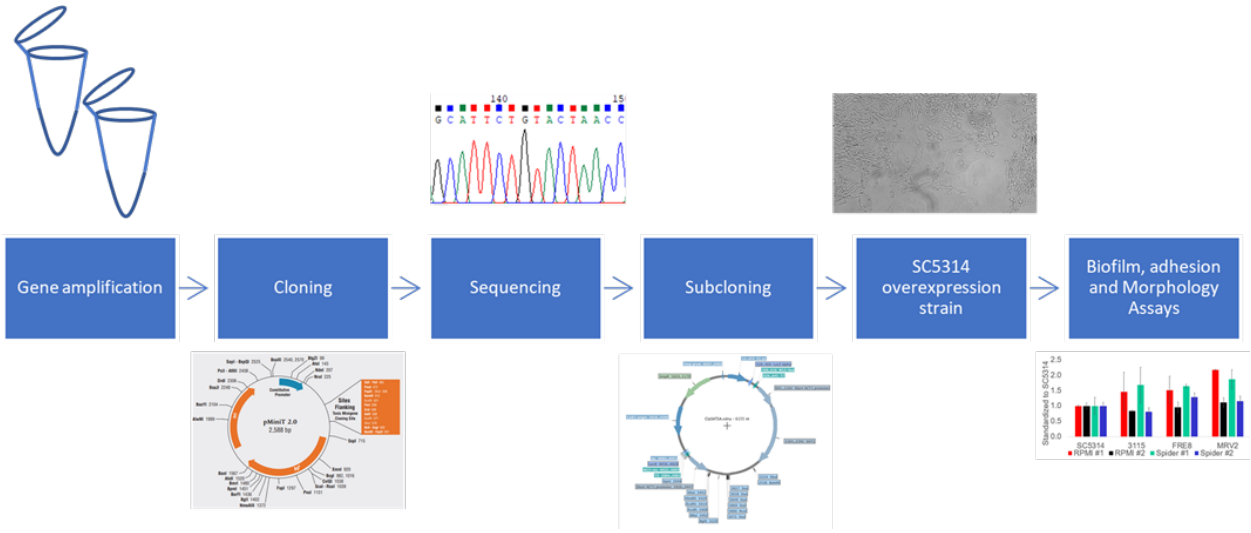
[2]Department of Biomedical Sciences, Grand Valley State University, Allendale MI.

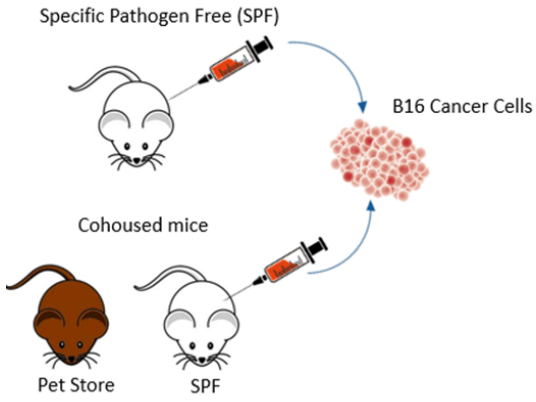


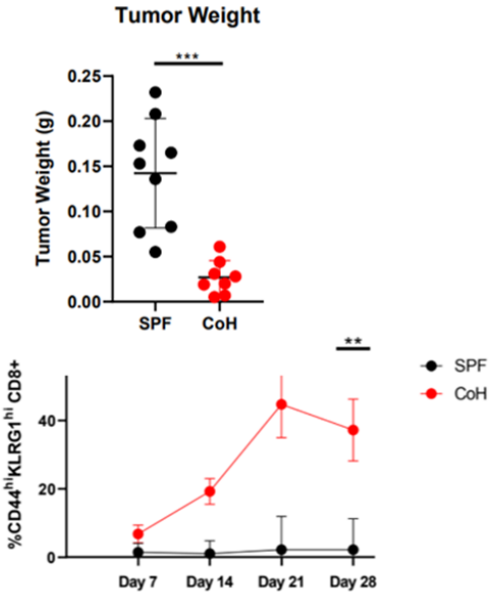
Candida albicans is an opportunistic fungal pathogen that naturally resides on mucosal surfaces and is a part of the natural human microbiota. Commonly found as biofilms on medical devices, such as catheters and IV's, *C. albicans* poses a serious threat to users of those devices, especially the immunocompromised. During space travel, astronauts experience changes in gravity that decrease their immune system function and make them highly susceptible to pathogens such as *C. albicans*. Due to this increased risk, *C. albicans* has been studied in spaceflight conditions and a list of genes that are differentially regulated have been identified. In spaceflight it was observed that *C. albicans* cells were more adhesive, a phenotype relevant to biofilm formation. This study investigates genes whose roles are uncharacterized within biofilm formation and thus there is a need to evaluate their potential as targets for antifungal treatments. Focusing on genes *orf19.3115*, *FRE8* and *MRV2*, we characterized these through differences in morphology, adhesion, and ability to form biofilms, which are related to the virulence of *C. albicans*. We have found that biofilm formation increased in overexpression strains *MRV2* and *FRE8*, whereas the overexpression strain for *orf19.3115* showed a decrease in biofilm formation. Additionally, all three exhibited decreases in glass adhesion, but had similar morphologies to the wildtype. Overall, this research contributes to the characterization of genes that may be responsible for biofilm formation and thus virulence of *C. albicans*.

Effects of Microbial Environment on T-Cell Activation and Tumor Suppression in Mice

Roland Nulph[1], Dr. Kristen Renkema[2], Nick Bunda[1], Marlee Busalacchi[1], Maci Rozich[1]

Grand Valley State University, [1]Department of Cell and Molecular Biology,
[2]Department of Biomedical Science



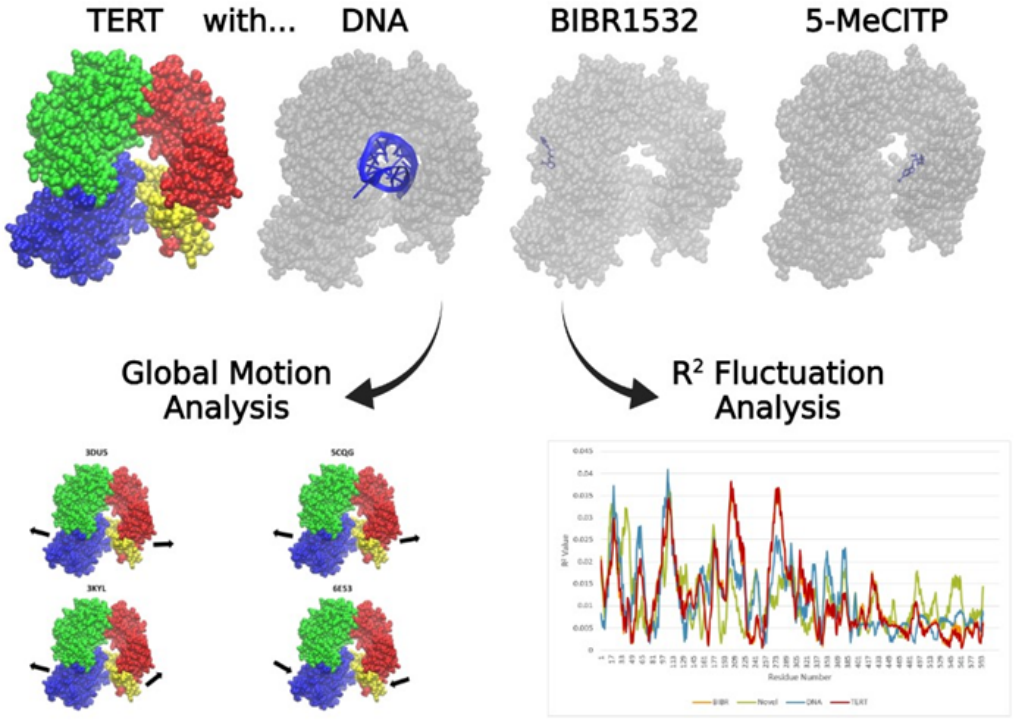


The hygiene hypothesis stipulates that exposure to pathogens during childhood is key to immune system development. It is hypothesized that living within hyper clean environments may hinder this process and contribute to disorders such as asthma, allergies, autoimmune disorders, and even cancer. Previous work has shown that the specific pathogen free (SPF) mouse model resembles that of newborns while mice exposed to microbes more closely reflects the adult human's immune system. In this project, to study how the microbial environment may affect the immune system's ability to fight off cancer we raised mice in a "clean" environment containing only SPF mice and a "dirty" environment containing SPF mice cohoused with pet store mice. The SPF mice were injected subcutaneously with B16 melanoma cells and bled weekly to monitor T-Cell activation. After 10 days the mice were euthanized and their tumors, lymph nodes and spleens were harvested for analysis. Tumor weights were found to be significantly smaller in the cohoused mice. Additionally, CD44 and KLRG1 levels were significantly higher in surrounding tissues, indicating CD8+ T-Cells that are activated and more highly differentiated. These results contribute to our knowledge of anti-tumor immunity and imply that the developmental microbial environment may be a significant factor in the body's ability to fight off cancer later in life.

A Noncompetitive Inhibitor's Effect on the Processivity of Telomerase

Annelise Larson
Mentor: Dr. Agnieszka Szarecka

Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.

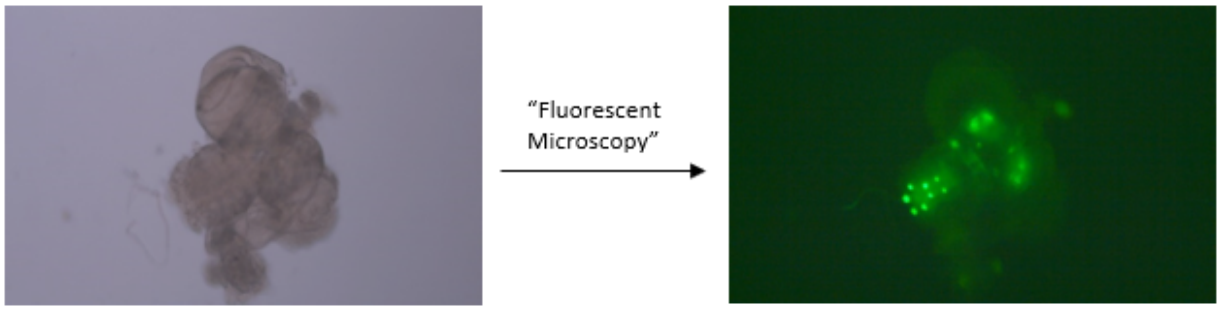


Telomerase Reverse Transcriptase (TERT) is reactivated in ~90% of cancer cells as a means to promote tumorigenesis and evade cell senescence by maintaining chromosomal stability. BIBR1532 is a known allosteric inhibitor of TERT *in vivo*. However, the mechanism of inhibition remains unclear, and research is hindered by poor understanding of TERT's functional dynamics. Here we focus on BIBR1532's mechanism of action. We present structural and Normal Mode Analyses of BIBR1532 binding, based on four crystal structures of TERT (apo, with BIBR1532, with DNA/RNA model, with competitive inhibitor 5-MeCITP). BIBR binds to the TERT thumb domain and appears to have a small modulatory effect on the binding pocket and mode shapes of the first three slowest normal modes. These motions in the slowest modes involve a) concerted outward motion of RNA-binding domain and palm, which "opens" the central catalytic space, and b) thumb and palm/fingers domains moving towards each other, which may be relevant to inhibition of TERT processivity with the motion being reduced in the DNA/RNA structure. Better understanding of functional motions of TERT and their modulations will help in optimizing future drugs.

Specific Expression of Histamine in *Drosophila melanogaster* Brain

Sean Fleisher[1]
Mentor: Dr. Martin Burg[2]

[1]Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.
[2]Department of Biomedical Sciences, Grand Valley State University, Allendale MI.



Drosophila melanogaster is our chosen model organism to study in histamine in the brain as they have short life cycles which allow for selective crossing of transgenic flies. In Drosophila Melanogaster, Histamine functions as a neurotransmitter for photoreceptors, mechanoreceptors, and central brain neurons. Histamine is synthesized by histidine decarboxylase (HDC) and mutations in the *Hdc* gene cause disruption of the histamine synthesis which, in turn, disrupts vision and courtship behaviors. Until now, it was possible to disrupt histamine throughout all cells of the fly, which makes it hard to specifically determine which tissues have altered function without histamine. Our transgenic flies show specific expression of Histamine throughout cells in the brain. Showing that histamine is present in the brain, we can selectively block out this specific region of histamine and move onto optogenetic experiments to show how the lack of histamine in the brain effects the function of the fly. In this project we have amplified genomic DNA from the *Hdc* gene that contains the *Hdc* promoter and cloned into 3 distinct DNA plasmids that enable the *Hdc* promoter region to induce the expression of GAL4, GAL4-DBD, or GAL4-AD proteins in histamine-containing cells. One of these plasmids has been injected into the fly (pHdc-GAL4) and then the fly embryos will be selected for transgenic flies. After this, the pHdc-GAL4 transgene function will be observed through fluorescent microscopy by mating the fly with a UAS-GFP transgenic fly. Histamine expression will be shown by histamine staining. After investigating several crosses, it was determined that only about 80% of fly brains contained GFP. This makes it difficult to move onto histamine staining as we need 100% of the fly brains to display GFP to study the optogenetics of the transgenic flies. 100% of the flies need to display histamine expression so during the time of optogenetic experiments, we can be sure that odd behavior is due to blocking of the histamine gene in the brain and no other reason. Noticing GFP in these brain cells helped show that we were successful in creating transgenic flies. However, GFP was not shown in all the fly crosses that we looked at. One possibility for this is that we do not have a promoter for the *Hdc* gene that covers all the isoforms. This indicates that for future experiments, we must first create a transgenic fly using an *Hdc* promoter that covers the whole gene, so we can move onto histamine staining and optogenetic testing.

Industry Standards for Oral Care Quality Assessments

Howard Hayward-[1,2]
Mentor: Kristy Carey[2]

[1]Department of Cell and Molecular Biology, Grand Valley State University, Allendale, MI,
[2-]Ranir LLC, Grand Rapids, MI

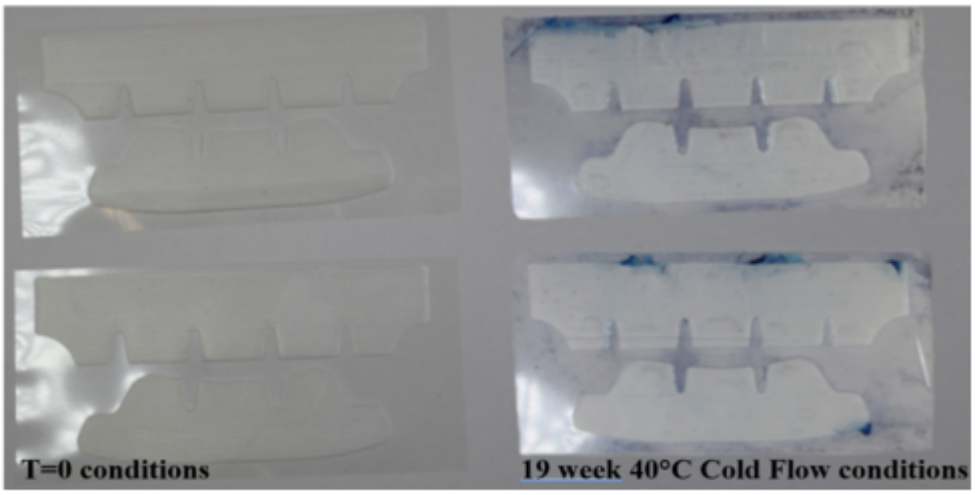


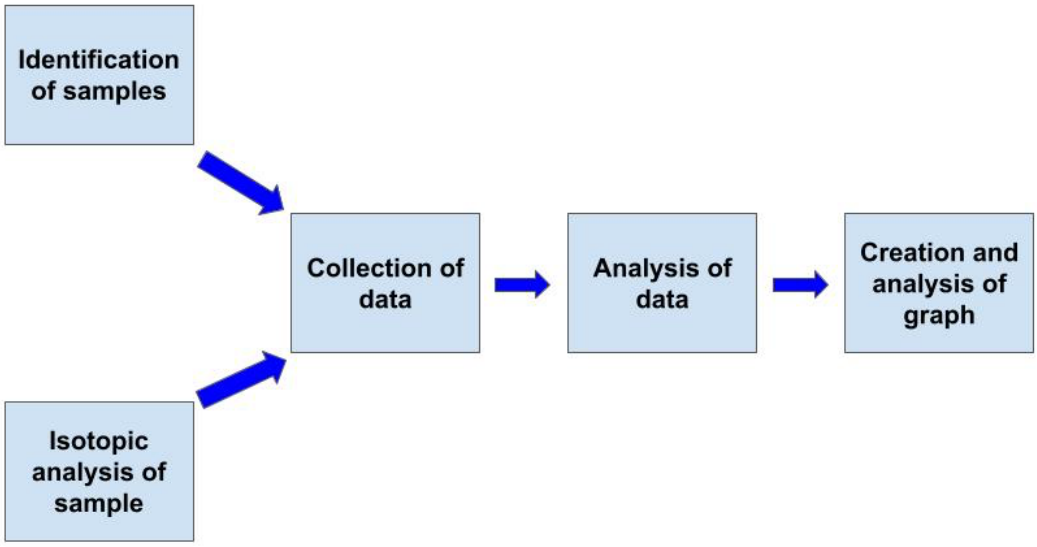
Figure 1. Example of cold flow that occurs as gel layers lose structure over time due to water loss and general degradation. Pictured right

Oral care products, such as teeth whitening strips and toothpaste must meet standards, set by regulatory bodies such as Food and Drug Administration (FDA) or the European Union (EU). These requirements are generally compiled in monograms, specifically commonly used active ingredients such as sodium fluoride or hydrogen peroxide and can be found within associated libraries for either the FDA, EU or the appropriate regulatory. My role within the Formulations lab is between executing various experiments in areas such as new formula development and shelf-life testing of existing products. Products such as tooth whitening strips, undergo several different assays generally over a period of two years. Active ingredient concentration is determined through titrations at various points, with additional assays including adhesion and thickness assays to gauge the effectiveness of the product overtime. Pictured above is an example of an assay determining “cold flow” of the strips. Cold flow involves brushing the strips with dyes that change color in the presence of hydrogen peroxide as a visual method of determining the flow of the gel layer within these strips and general homogeneity of the gel layer. Projects such as these have clearly defined failure states, such as acceptable ranges of active ingredients in addition to other assays that are performed, such as viscosity, pH, flavor. Data collection that falls outside of the project’s defined ranges are directly reported to project leads to determine further action. The resulting data from these projects is then used to inform shelf lives of products or to inform additional changes to formulas to meet desired criteria for the product. This presentation will walk through several of the assays that are performed, in addition to examples of chemicals used within these products and the roles they play.

Isotopic Analysis of the Ancient Humans from the Black Sea Region

Hanna Pickard[1,2],
Mentor: Dr. Alexey Nikitin[3]

[1] Department of Cell & Molecular Biology, Grand Valley State University, Allendale MI.
[2] Department of Anthropology, Grand Valley State University, Allendale MI.
[3] Department of Biology, Grand Valley State University, Allendale MI.



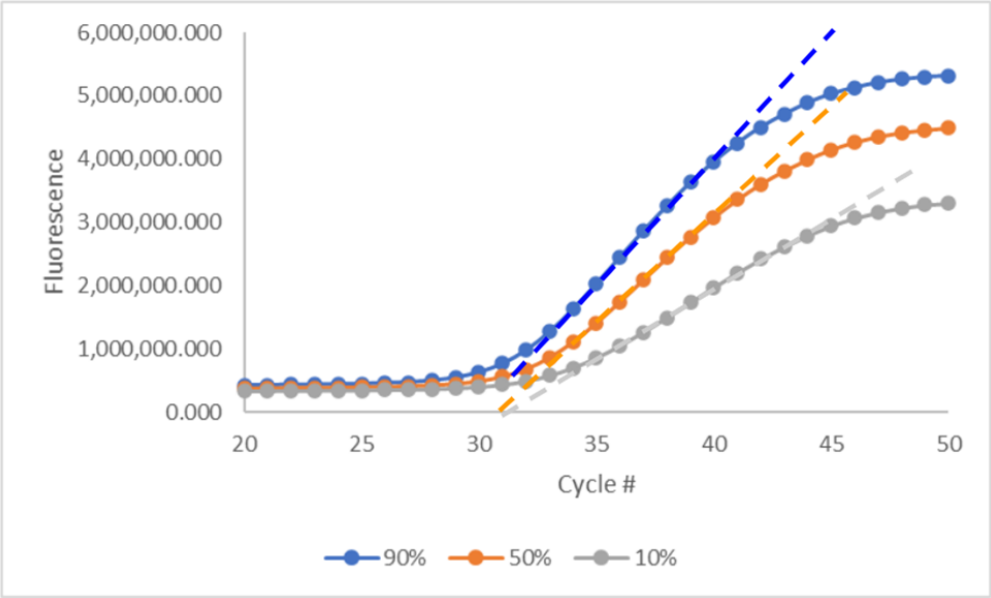
I will be doing a summary of my work from this Fall semester of 2021. This semester I looked at various papers concerning the isotopic analysis of samples from the Black Sea region, with a particular focus on the Northern Black Sea region. This was in preparation for getting isotopic sample results from a sample from the Northwestern Pontic region. From these papers, I was able to gather information regarding the normal ranges of δ13C and δ15N values and build a limited profile of what would be expected from this area at various time points. In this presentation, I will be taking a look at these values and interpreting them so that I can compare our results to this profile and gather more information about the sample.

From Fever to Feces: Tracking the Prevalence of SARS-CoV-2 and its Variants in Wastewater using qPCR

Garrett O'Dea, Puneet Chowdhary,

Mentors: Drs. Sheila Blackman, Pei-Lan Tsou

Grand Valley State University, Department of Cell and Molecular Biology

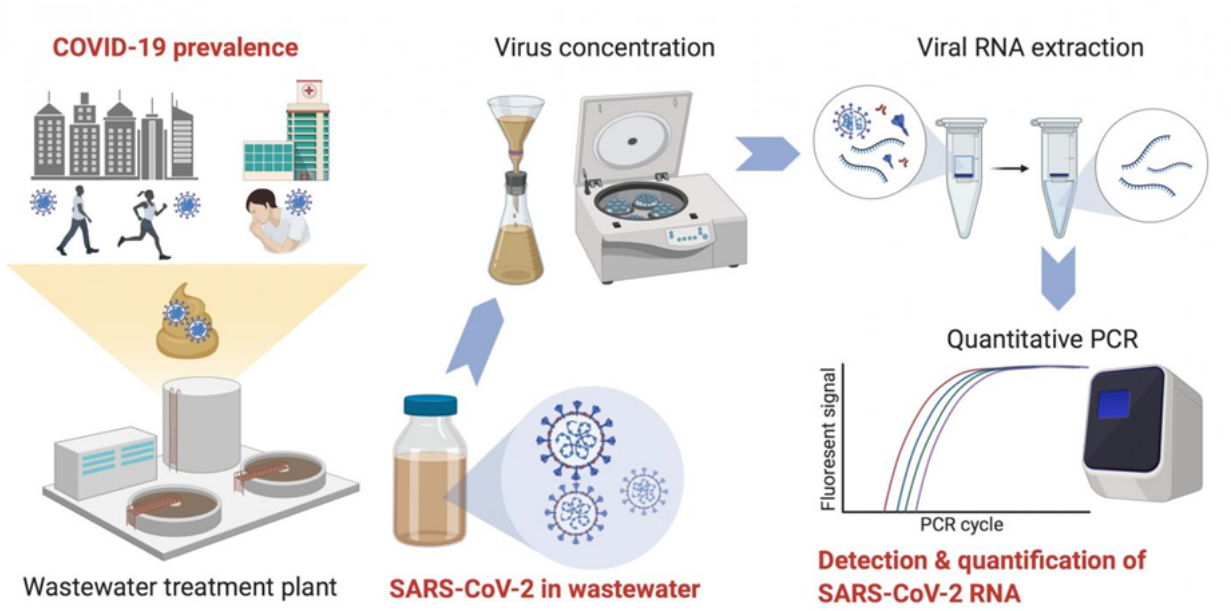


SARS CoV-2 has infected over 50.8 million people in the US, and 1.6 million in Michigan. To inform local health professionals of potential outbreaks, a network of laboratories has been monitoring viral levels in wastewater in a process known as "Wastewater-Based Epidemiology" (WBE), which historically has provided a snapshot of the prevalence of infectious agents in human feces. We extracted viral RNA from wastewater collected from sites throughout Kent County and quantified SARS-CoV-2 RNA using droplet digital PCR. Wastewater viral RNA levels broadly correlated with clinical infection rate and rose throughout the fall with the spread of the Delta variant (B.1.617.2). The aim of this work was to develop a quantitative PCR-based assay for quantifying variants, such as Delta, that vary in only a single nucleotide. Using tools similar to those developed for genotyping (Taqman SNP assays), we found that qPCR can be used to quantify the proportion of variant RNA in a mixed sample. We are also developing an assay to track the Omicron (B.1.1.529) variant in wastewater using conventional qPCR analysis. In conclusion, WBE can accurately, quickly, and cost-effectively track SARS-CoV-2 and its variants with minimal disruption to individuals.

Hot Stuff: Developing a PMMoV Assay to Normalize the Fecal Content in Wastewater to Improve Consistency of SARS CoV-2 Data

Jack Ruhala
Mentors: Drs. Pei-Lan Tsou, Sheila Blackman

Department of cell and molecular biology, Grand Valley State University, Allendale MI

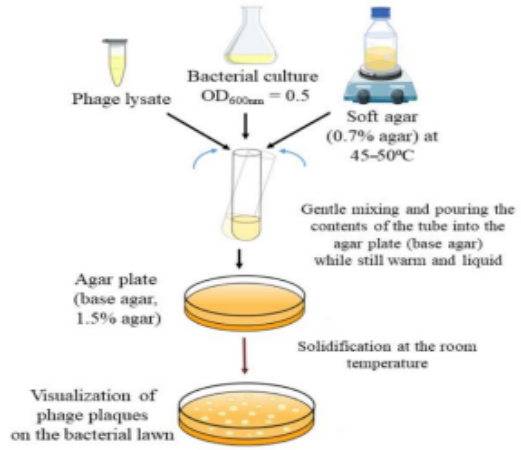


Public health officials around the world have implemented wastewater-based epidemiology as a tool for Covid-19 surveillance. One challenge of wastewater-based epidemiology is normalizing the wastewater signal for human-fecal content with a virus that separates through purification with the target virus. One virus commonly used for human-fecal normalization is PMMoV. PMMoV is ingested by humans ubiquitously through infected peppers and is normally present in wastewater at high concentrations. We designed primers and probes to an evolutionarily conserved region of the PMMoV genome to develop a quantitative PCR assay for normalizing the target genes for SARS-CoV2 with PMMoV. Our PMMoV assay, in a qPCR system, detects between 10^5-10^7 viral gene copies per 100ml of wastewater sample with an efficiency around 92-94%. We conclude PMMoV is present in high concentrations in wastewater and our assay can reliably detect PMMoV. Our lab is currently working on collecting PMMoV gene copy data for all of our reported wastewater samples using qPCR to further improve the consistency of SARS-CoV-2 target gene counts.

Funded by the Michigan Department of Health and Human Services (MDHHS) and the Michigan Department of Environment, Great Lakes, and Energy (EGLE).

Testing the Efficiency of Biosafety Cabinets, Water Filters, and Water Purifiers

Jacob Wolfe[1] ,
Mentor: Dr. Atwain Atwain[2]
Grand Valley State University[1] , Department of Cell and Molecular Biology[1] ,
NSF International[1,2] , Department of Microbiology[1,2]

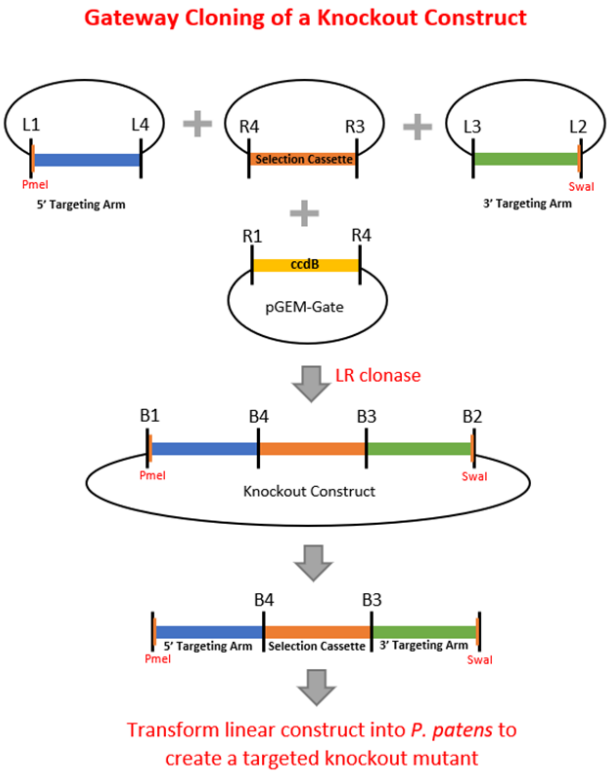


Public health products such as biosafety cabinets, water filters, and water purifiers are tested to determine if these products are safe for consumer use. Biosafety cabinets, used in laboratories, are tested for their effectiveness of preventing cross contamination of samples and protection from airborne bacteria reaching the personnel using the biosafety cabinet. Water purifiers are tested for their effectiveness to remove viruses from drinking water and water filters are tested for their effectiveness to remove cryptosporidium and microspheres from drinking water. In my work, I perform glass funnel filtration and top agar overlay to process samples. Results are read by colony counting, plaque counting, and counting organisms or microspheres by green-fluorescent microscopy. The criteria to deem these products as safe, are there to be less than five of the test organisms or microspheres found in the tested samples. In this presentation, I will show examples of my methods and raw data to present the process of how these products are tested and how our data is read. Typical findings are zero organisms counted from these tests, however reading results from plates or microscope slides with too numerous to count does occur. After results are read, they are reported to clients through different software such as LIMS, DACS, or Beaker.

Retrotransposon Deletion in *Physcomitrium patens* Using Gateway Cloning

Elizabeth Cazallis
Mentor: Dr. Margaret Dietrich

Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.



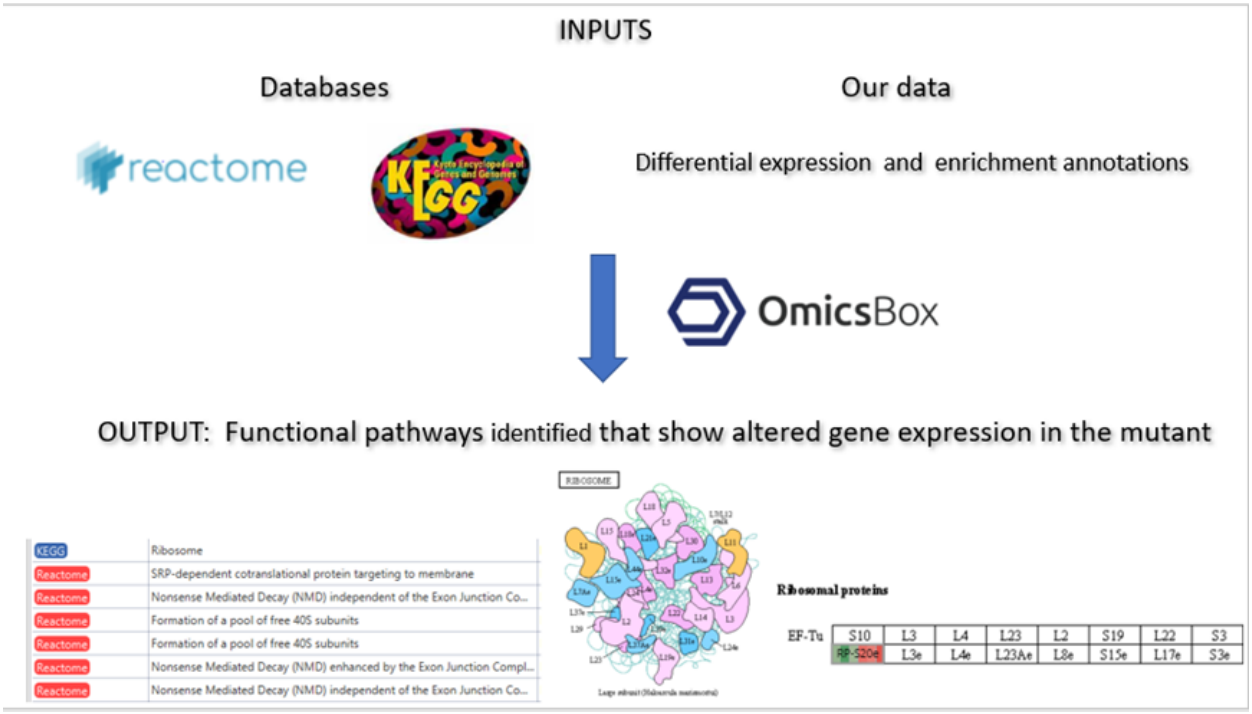
Polar growth is ubiquitous across kingdoms; tip growth is an extreme version in which, for example, a filament tip cell elongates dramatically before cell division. In plants, a similar process is responsible for root hair and pollen tube growth via polarized exocytosis of vesicles. *P. patens* is being used as a model to study tip growth due to its critical role in moss filament development. In a previous study, random insertional mutagenesis produced an insertion/deletion in the middle of a retrotransposon (RT) island yielding a variety of phenotypes in the filamentous stage due to abnormal tip growth. Here, we investigate how deletion of this entire RT island in the wild type will affect the phenotype compared to that of the original mutant. Three-fragment recombination Gateway Cloning, which is based on lambda phage recombination, is being used to create the linear targeting construct which will be used to make the deletion allele to elucidate the role of RTs in *P. patens* tip growth.

Funding for this project comes from the Department of Cell and Molecular Biology at Grand Valley State University.

Pathway Analysis of Mutant Strain *Physcomitrium patens*

Collin Kozar
Mentor: Dr. Margaret Dietrich

Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI

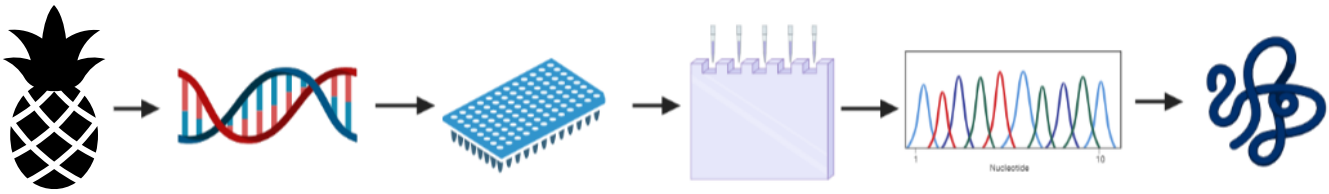


Polar growth, in which cells elongate in one direction, is important across all kingdoms. Tip growth, an extreme type of polar growth, is important in the seed plant life cycle due to a role in pollen tube and root hair development. In *Physcomitrium patens*, a moss, tip growth is critical in the filamentous stage, making it an ideal model for the study of tip growth. In a previous study, a random insertional mutant was created that displays abnormal growth patterns due to tip cell defects involving growth and differentiation. Subsequently a transcriptome project was initiated to determine the gene expression profiles of the mutant and wildtype. In this project, the Combined Pathway Analysis in OmicsBox is employed, in which the differential gene expression and gene set enrichment data from the transcriptome study and the KEGG and Reactome pathway/function databases are inputs. Our data reveal several pathways involving select ribosomal proteins as well as several photosynthetic and stress functions that are underrepresented in the mutant. Through this work, a greater understanding of the mechanisms underlying tip growth will be achieved.

Phylogenetic Analysis of CAM Evolution in the Bromeliaceae Plant Family

Shane Vaughn[1]
Mentor: Dr. Timothy Evans[2]

[1]Department of Cell and Molecular Biology, Grand Valley State University, Allendale MI.
[2]Department of Biology, Grand Valley State University, Allendale MI.



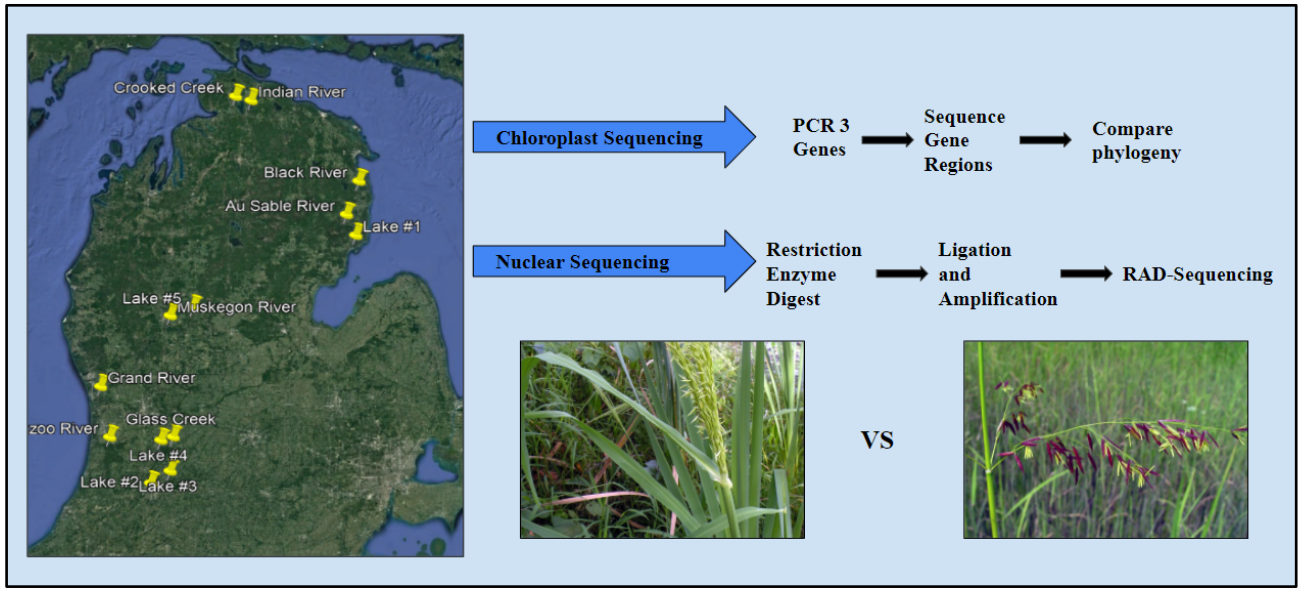
CAM photosynthesis is a unique pathway used in certain plant families that uses the enzyme PEP carboxylase (PEPC) to allow the capture of CO_2 at night rather than during the day like typical plants. The evolution of CAM photosynthesis has been essential to the increasing range of habitats that plants can thrive and therefore is seen as an evolutionary novelty. In the plant family Bromeliaceae, there has been several times where CAM photosynthesis has been derived independently, providing an ideal model to study the factors of CAM photosynthesis evolution. Here, we investigate the evolution of the 3-dimensional structure of one of three enzymes involved in CAM photosynthesis, PEPCK. In order to analyze the evolution of this protein, primers were designed and PCR was conducted to obtain sequences for analysis.

GVSU Phoenix high performance cluster, supported by the (NSF) Grant No. CNS-122829.

Assessing the Genetic Relationship of Wild Rice Populations in Michigan

Carlin Moore[1], Elliot Fair[2], Alex Wieten[2]
Mentor: Dr. Charlyn Partridge[1,2]

[1]Robert B. Annis Water Resources Institute, Grand Valley State University, Muskegon, Mi
[2]Pierce Cedar Creek Institute, Hastings, Mi



Wild rice native to Michigan is both culturally important to the Anishinabe people of the Great Lakes region and ecologically beneficial to aquatic habitats. In recent years, the population of wild rice has consistently declined as a result of poor water quality, pollution, and habitat loss. The two main species of wild rice in Michigan include northern wild rice (*Zizania palustris*) and southern wild rice (*Z. aquatica*), with *Z. palustris* also used as a cultivated crop and *Z. aquatica* listed as a threatened species. These two species normally have distinguishable phenotypic traits that make it easy to differentiate between them, but recently this has not been the case. Observational work has indicated that some populations may be the result of hybridization by the two species, and this could have implications in terms of population health and management. In this project, we are using nuclear and chloroplast genetic markers to evaluate the genetic relationships among *Z. aquatica* and *Z. palustris* populations around Michigan and to identify potential hybrid populations. This approach starts with the use of PCR on three genes to sequence and analyze the chloroplast phylogeny followed by a series of steps to prepare the DNA for RAD sequencing where the entirety of the genome can be observed. These data will be used to improve current management practices for this important species.

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Studying GmSLY1a and GmSLY1b Gene Expression in Soybean Nodules

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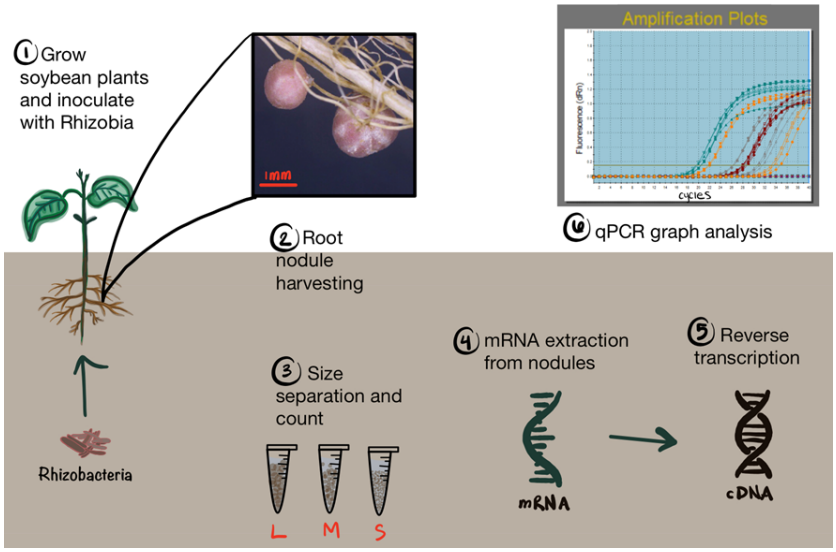

Due to extreme climate change, food security becomes a crisis due to less cultivable land worldwide. Learning about hormone signaling pathways involved in plant development and growth can potentially help improve crop yield in the future. Soybean is one of the most important crops worldwide. Like all legumes, it is a nitrogen fixating plant—meaning they can convert atmospheric nitrogen into ammonia with the nodules of the roots mediated by N-fixing Rhizobia bacteria. Gibberellic acids (GA's) are important plant hormones that regulate growth, cell division, seed germination, and even nodule formation in the root. In Arabidopsis, the SLEEPY1 (SLY1) gene functions as a positive regulator of GA signaling. There have been two orthologs identified in soybean: GmSLY1a and GmSLY1b. Here, we investigate the gene expression of the GmSLY1a and GmSLY1b genes in soybean nodules. In order to study the expression of these genes, soybean plants were grown and inoculated with Rhizobia, the specific nodular root tissue was harvested, mRNA was isolated from the various tissue samples and then converted to cDNA, and then gene expression was measured through qPCR. The results showed that GmSLY1a and GmSLY1b were both expressed in nodules, and there is also more GmSLY1b expressed in the medium nodules than GmSLY1a. These results help advance research in the area of Gibberellic acid signaling in plant physiology by studying the role of the two SLY1 genes in root nodule formation.

An Adventure into Diatom Biology in Two Projects: Building a Local Flora and Exploring *Nitzschia* Evolution

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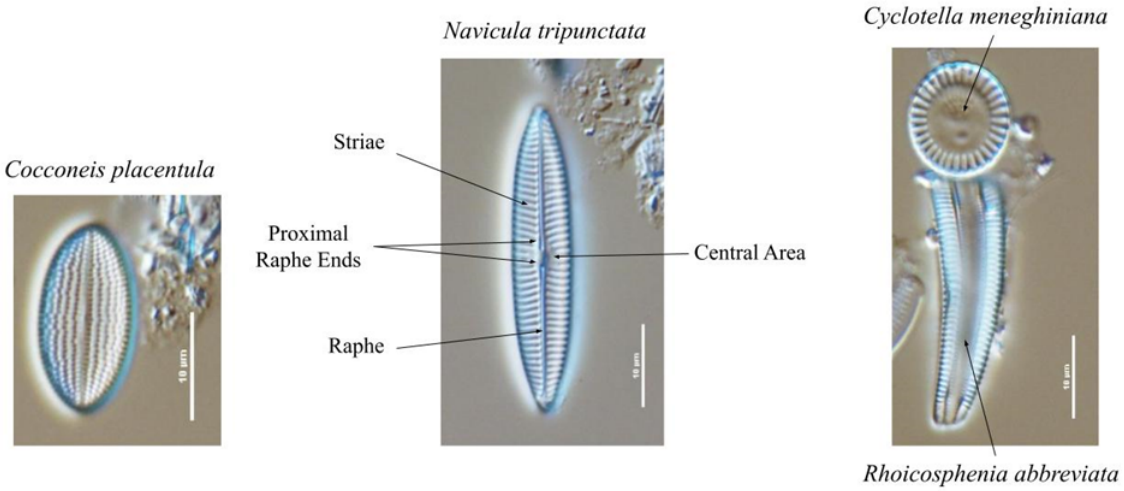

Diatoms are photosynthetic protists responsible for 20% of the world's oxygen production and often used as ecological indicators. Difficulty in species identification and their poorly understood evolution are barriers to understanding their ecology. To these ends, we are working on two projects. 1- Compiling a species-level flora of the Grand River to use as a baseline for water quality monitoring. Preliminary data reveal *Navicula cryptotenella*, *Cocconeis placentula*, and *Staurosira construens* as dominant species. 2- A study of diversity and evolution of members of the diverse genus *Nitzschia* (known to be indicators of poor water quality) because their evolution is not well understood. These data will contribute to a larger dataset to eventually produce a robust phylogeny of the genus. Both projects have increased our understanding of the local diatom flora and further resolved the phylogeny of *Nitzschia*, assisting in future studies that use diatoms for biomonitoring.

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