RETURN REPORT: SABBATICAL LEAVE

Britton Ranson Olson, Biology

Sabbatical Leave: Spring Semester 2025

Title of Sabbatical Leave Proposal: Gaining Expertise in Advanced DNA Methods for New and Exciting Molecular Explorations at LSSU

Project Description

Background

My initial proposal focused on extending my knowledge and skills in advanced genomic applications which I intend to use to evaluate a number of emerging issues. The projects are relevant to our region and they allow LSSU students access to working with the most modern molecular tools. The proposal described various applications such as the effect of environmental contaminants on microbial diversity, bioremediation studies, the detection of invasive species, and the development of a molecular assay for sex determination of sturgeon. The outcomes of the proposal included travel to several institutions to learn from experts on these rapidly advancing methods, with the goal of making them accessible to our LSSU campus community, both for coursework accessibility and senior thesis opportunities, enhancing the on-going and future prospects of molecular based research at LSSU.

Before providing more detail as to meeting the objectives of my leave, I sincerely want to thank the sabbatical committee and the University as a whole for offering me this time and show of support for my research efforts. Though I submitted the proposal for a full academic year, I have met the majority of my objectives, including many summer 2024 and 2025 activities. I look forward to bringing the tools and opportunities gathered here to the classroom and I hope that the students will be as inspired as I have been.

Sabbatical Outcomes

OUTCOMES

The ***first outcome*** of the proposal was directed towards advancing my technical skills and gaining expertise in more advanced DNA methods and genomic analysis. This training began with my travel and participation in the Queens University Environmental eDNA Workshop, in Elgin, Ontario. https://qubs.ca/eDNAWorkshop. This course introduces participants to various methodologies and hands-on training in analysis and interpretation of data, as well as standards to overseeing eDNA studies. Through this, it was my goal was to introduce myself to existing eDNA networks and develop future eDNA research applications. This experience was

very beneficial, particularly to ongoing invasive species detection studies, and resulted in our development of a digital PCR assay for the Rock Snot invasive algae. This assay was included in a presentation of the project at the Society for Freshwater Science, May 2025.

Title: Assessing extent, sensitivity of eDNA detection methods, and potential drivers of the nuisance freshwater diatom, Didymosphenia geminata, in northern Michigan waters, USA.

Authors and Affiliations: Nicole Perigo 1 , Ashley Moerke 1 , Britton Ranson Olson 2 , Robert Pillsbury 3
1 Center for Freshwater Research and Education, Lake Superior State University, Sault Ste. Marie, MI
2 School of Science and Medicine, Lake Superior State University, Sault Ste. Marie, MI
3 School of Biology, University of Wisconsin Oshkosh, Oshkosh, WI

Abstract:

Didymosphenia geminata (Didymo) is a freshwater diatom that is considered a nuisance algae because it produces thick mats of polysaccharide stalks (i.e., blooms) under certain environmental conditions. Didymo blooms may adversely impact aquatic habitat and food webs, especially in regions supporting cold-water fisheries. In 2015, Didymo was first discovered blooming in Michigan waters in the St. Marys River, a Great Lakes connecting channel that supports a major recreational fishery and is nearby numerous small, cold-water streams. Therefore, there is interest in understanding spread, detection, and drivers of blooms in this region. To understand Didymo spread, we completed 50 surveys in Upper Peninsula streams by collecting benthic scrapes for Didymo cell counts and water samples for eDNA analysis. Additionally, we attempted to understand the threshold of eDNA detection using two methods. We sampled downstream of a known Didymo infestation in the St. Marys River, evaluating the effect of distance and volume on eDNA detection, and used artificial streams with varying concentrations of Didymo to assess the effect of density on detection. Finally, we used artificial streams to study how nutrients may contribute to Didymo blooms. We found Didymo spread throughout the 112-km channel of the St. Marys River and reached peak densities (up to 40,000 cells/cm^2) within two years, however, cells and eDNA were not detected in any nearby streams. Concentrations of Didymo eDNA were low and did not differ with distance from the known source and was not detected in the artificial streams with low Didymo densities. Experimental nutrient additions are underway and will provide improved understanding of ecological drivers of Didymo blooms. Due to the spread throughout the St. Marys River and Lower Michigan, continued research of detection methods and drivers of blooms is needed to understand the threat of Didymo to cold-water Michigan rivers.

I also traveled to the Great Lakes Institute for Environmental Research, April 21-25, 2025, at the University of Windsor to work with collaborators to enhance my technical skills, train their students on DNA extraction from oil-laden environmental samples, and apply what I have learned from the DNA workshop to the broader metagenomics and metatranscriptomics analyses we are currently performing. As an LSSU faculty member of the 'Biological Impacts of Oil in Our Waters of the North (BIO-OWN) Network', part of the Natural Resources Canada supported MultiPartner Oil Research Initiative (MPRI) awarded to LSSU, I facilitate investigations assessing the impact of oil on the community abundance and diversity of microbes through DNA analysis.

https://www.uwindsor.ca/glier/154/chris-weisener

The following poster was presented at an MPRI event hosted at Algoma University, Oct 6 & 7th 2025:

The ICOR-OWN BIO Project: Understanding Biological Responses to Oil in Freshwater Wetland Ecosystems

C.E. Heuvel[1], A. Moerke[1], M.T. Twiss[2], R.M. McKay[3], B. Liu[1], J. Doubek[1], B. Ranson-Olson[1], C.L. Madliger[2], W.A. Dew[2], C.G. Weisener[3], A. Snider[4], K.L. Kapuscinski[1]

[1]Lake Superior State University, [2]Algoma University, [3]University of Windsor, [4]US Coast Guard

ICOR-OWN

FRESHWATER OIL SPILLS

- Oil behavior in freshwater differs from marine systems. In freshwater, oil sinks faster and disperses differently compared to saltwater. Additionally freshwater organisms have different life histories and sensitivities to oil spills.
- The Laurentian Great Lakes face unique challenges to oil spill preparedness and clean up due to their vast scales, diverse habitats, and seasonal ice cover.
- These ecosystems are likely very vulnerable to oil spills, and their ecological impacts could be high.

Knowledge Gap: Research on the **biological impacts of oil in freshwater** lags behind marine studies — especially in northern systems like the Great Lakes

OBJECTIVES

1. Test multi-trophic level responses to oil under real-world conditions in freshwater wetlands
2. Improve our understanding of oil accumulation in freshwater wetlands in the Great Lakes

CONCEPTUAL DIAGRAM: HYPOTHESES

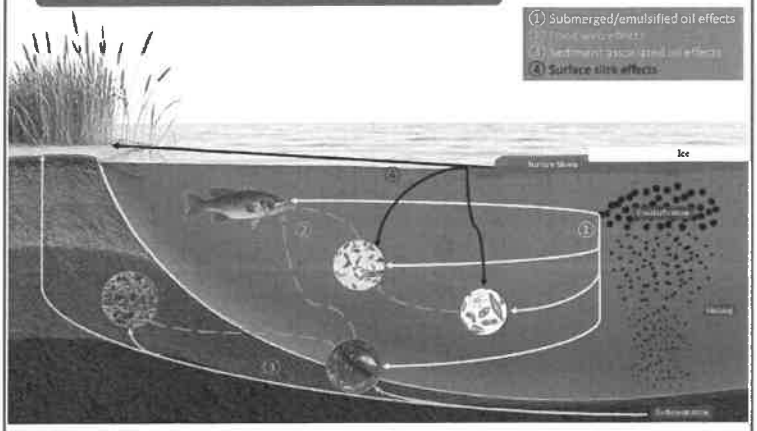


Figure 1: Conceptual model of food web impacts of an oil spill in Great Lakes wetlands. Oil spills can have many direct and indirect effects on food webs. Direct effects include ingestion or inhalation of oil particles, and indirect effects include bioaccumulation and biomagnification through the food web.

MESOCOSM SET-UP

- Outdoor facility with 24 fiberglass tanks (1.2 x 1.8m) to create simulated wetlands located at LSSU
  - Filled with water, sediment, aquatic vegetation, invertebrates, and fish from the St. Marys River

EXPERIMENTAL APPROACH

The outdoor mesocosm experiment can help answer many questions about oil behavior in freshwater ecosystems:

- **Oil variables:** types (crude, diluted bitumen, refined), concentrations, and application method (surface slick, dispersed, sediment bound)
- **Temporal and seasonal:** summer vs. winter, ice-covered simulations, short vs. long exposure
- **Ecological context:** habitat type (open water vs. vegetated), food web complexity, resuspension events
- **End-points:** immediate toxicity, sublethal effects, recovery trajectories, and trophic transfer/bioaccumulation

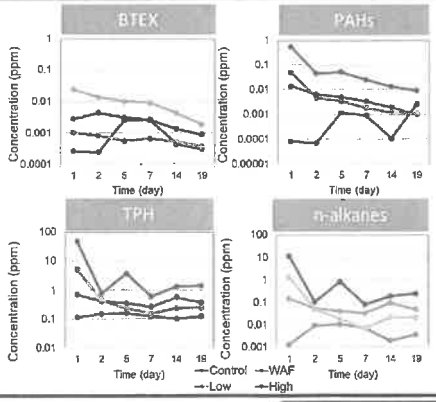
PILOT STUDY: MARINE DIESEL

Fall 2024:

- 4 treatments, 6 replicates
  - Control (no oil)
  - Low (0.098 g/L)
  - High (0.98 g/L)
  - WAF (1% of high energy WAF)
- 20 day exposure

Day 0: November 6, 2024

Day 20: November 27, 2024



Oil Concentrations in Water:

- Most BTEX evaporated in 24 hours
- PAHs ~10x greater in high treatment than others
- Decrease of PAHs in water over time
- WAF was the most stable in the water column compared to bulk oil
- Greatest decrease of saturates (n-alkanes) and total petroleum hydrocarbons on Day 2 was observed in the high treatment

FUTURE DIRECTIONS

- Winter and ice/snow cover experiments
- Water treatment and waste disposal trials
- Increasing food web complexity in experiments
- Testing different oil types (e.g., dilbit)
- Longer-term recovery and resilience studies
- Scaling up findings to improve spill response
- Expanding student training and international collaboration

FUNDING AND PARTNERS

MPRI — Multi-Partner Research Initiative

Canada

Lake Superior State University — Center for Freshwater Research and Education

University of Windsor

Algoma University

U.S. Coast Guard — Great Lakes Oil Spill Center of Expertise

The ***second outcome*** of the proposal was training in methods to perform *in–situ* testing on the effects of oil on indigenous microbial communities, the goal to identify microbes with the potential for bioremediation of oil around the Great Lakes. To achieve this I travelled to the lab of Professor Uta Passow, Canada Research Chair in Ocean Sciences, at Memorial University of Newfoundland, to learn about the preparation, positioning, and collection from on-site samplers described as biodegradation frames. These apparatuses contain the microbial samples from which community effects and biodegradation potential can be examined. This objective aligned with those of the MPRI project and is also a common goal of the U.S. Coast Guard Great Lakes Oil Spill Center, housed at CFRE. During my stay I also attended the PEOPLE 2025 International Conference – *Challenges and Opportunities in Environmental Sustainability under Climate Change*, from July 21–25, 2025, St. John's, Newfoundland and Labrador, Canada..
https://www.mun.ca/research/extraordinary-research/research-chairs/dr-uta-passow/

Student Involvement:
LSSU Chemistry major Elizabeth Angell and Memorial University MS student Shanan Brun, were trained in isolating biofilm from the oil covered mesh, DNA extraction and downstream 16s rRNA analysis of the collective microbial communities. This work produced the following presentations.

The following two abstracts for submission to the upcoming 2026 IAGLR conference:
Project title: When Oil Meets Freshwater: In Situ Biodegradation and Microbial Community Shifts in the Straits of Mackinac

Authors: Shanan Brun-Dabbagh 1 , Verena Kalter 1 , Britton Ranson-Olson 2 , Bo Liu 2 , Ashley Moerke 2 , Uta Passow 1
1 Ocean Sciences Center, Memorial University of Newfoundland, St John's, NL, Canada.
2 Centre for Freshwater Education, Lake Superior State University, Sault-St-Marie, MI, United States of America.

Concerns about pipeline breaches and accidental oil spills in the Great Lakes are increasing, yet the persistence and biodegradation dynamics of petroleum in large freshwater systems remain poorly understood. This study assesses crude and marine diesel oil biodegradation in the Straits of Mackinac, where the Enbridge Line 5 pipeline crosses between Lakes Michigan and Huron. It highlights the role of native microbial communities in oil biodegradation processes. Two mooring frames, holding oil and non-oil amended mesh were deployed in the Straits of Mackinac during a 7-week spring period to assess oil biodegradation in situ. Microbial communities were profiled using

16S rRNA sequencing, and oil chemistry changes were analyzed with gas chromatography mass spectrometry (GC-MS). Preliminary community analyses indicate that Betaproteobacteria dominate across all treatments and timepoints, closely followed by Alphaproteobacteria, with both groups increasing in relative abundance over time in the oil treatments and the control. At the genus level, clear selective patterns emerged: Aquabacterium appeared exclusively in the oil-amended treatments and increased in relative abundance over time, whereas Rhodoferax exhibited a stronger affinity for crude oil and remained scarce in the control and marine diesel treatments. These microbial responses will be interpreted in conjunction with the temporal changes in alkanes and polycyclic aromatic hydrocarbons (PAHs) to evaluate petroleum persistence in a freshwater environment alongside microbial responses to a spill.

Title: Oil Biodegradation in the Great Lakes – First Insights from an in-situ Study
Authors: Verena Kalter, Shanan Brun-Dabbagh, Bo Liu, Britton Ranson-Olson, Ashley Moerke, Uta Passow

The Great Lakes, the world's largest group of freshwater lakes, are used extensively for energy generation, drinking water provision, recreation, transport of goods, as well as transport of oil via underwater pipelines. Despite the potential for oil spills into the lakes, the fate of oil spilled into freshwater is still vastly understudied. Some oil spill response options used in the ocean are not appropriate for the Lakes, and natural attenuation of the oil may frequently be the best strategy. Since biodegradation by microbes can be critical for removing oil from the water, we conducted an in-situ experiment to assess the potential of native microbes to biodegrade two types of oil (crude oil and marine diesel), capturing three different seasons and two locations. Preliminary results from the fall show a clear indication of biodegradation from the perspective of alkylated PAH homologs, consistent across both oils. Alkane degradation patterns resembled those previously observed in a laboratory-scale biodegradation experiment, but a more detailed interpretation is outstanding. Microbial community composition, assessed via 16S DNA barcoding, responded noticeably to the oil, with the genus Aquabacterium exhibiting a remarkable increase in abundance in both oil treatments but not the control. Data analysis is ongoing, and we hope to obtain clear insights into the nature and extent of biodegradation in this ecologically and economically crucial freshwater system.

And the following poster which was presented by LSSU Chemistry major Elizabeth Angell at an MPRI event hosted at Algoma University, Oct 6 & 7th 2025:

Assessment of In-situ Biodegradation of Marine Diesel and Mixed Sweet Blend Oil in Freshwaters, Baie de Wasai, Michigan

Ellie Angell[1], Britton Ranson Olson[1], Ashley Moerke[1], Shanan Eleah Brun-Dabbagh[2], Verena Kalter[2], Uta Passow[2]
[1]College of Science and the Environment Lake Superior State University 680 W Easterday Ave Sault Ste. Marie, MI
[2]Memorial University P.O. Box 4200 St. John's, NL A1C 5S7 Canada

Abstract

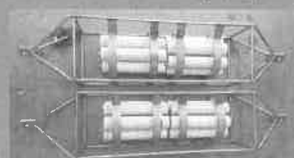
Experimentation surrounding freshwater microbial communities and their ability to degrade oils in this environment is a new and quickly expanding field of study. Offering both proximity to those in the Midwest and probable cause given the looming threat of marine diesel and crude oil spills, Michigan's Great Lakes offer researchers a unique resource to perform metabolic experimentation. In this study, mooring frames containing oil-coated mesh were deployed in Baie de Wasai, Sugar Island Township, to assess microbial degradation of oil. Preliminary results after one round of experimentation showed that *Aquabacterium*, a member of the Betaproteobacteria class, is a key player in breakdown of both marine diesel and crude oil in freshwater environments.

Introduction

- From the years 2013 to 2019, approximately 1300 oil spills occurred in the Laurentian Great Lakes[1]. While most of them were small, less than 10 gallons, they leave an impact on the environment.
- There have been larger spills, such as the 2010 Kalamazoo oil spill, which spanned 30 miles of river and released up to a million gallons of crude oil[2].
- Enbridge's Line 5 presence in the Straits of Mackinac poses a threat for a massive oil spill that could be catastrophic for the freshwater Great Lakes
- Prior research shows that abundant amounts of Betaproteobacteria is present in sediment in the Great Lakes, as well as large amounts of Alphaproteobacteria[3]
- There has been little investigation into freshwater spills, while marine systems are well-researched[4,5]

Methodology

- Two frames containing a synthetic mesh were deployed in Baie de Wasai and secured for 18 and 35 days, respectively.



- Treatments consisted of mixed sweet blend oil and marine diesel-coated nylon mesh, along with non-oil control mesh
- Frames were retrieved after 18 and 35 days, and processed to assess changes in microbial composition
- Biofilms were collected from the mesh and DNA was extracted using a PowerSoil extraction kit
- 16S DNA sequencing revealed the bacterial composition on the treated and untreated mesh.

Results

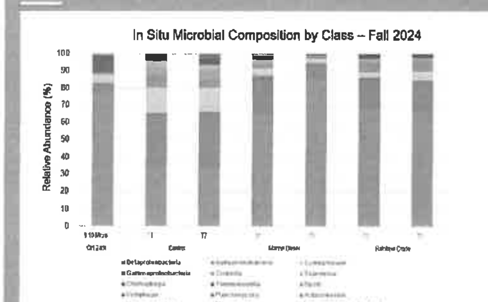


Figure 1. Relative abundance of various classes of bacteria shown for control, marine diesel, and mixed sweet blend (crude) oil samples at two different time points.

- Marine diesel had a higher affinity rate for Betaproteobacteria by approximately 45%
- Mixed sweet blend oil had a higher affinity rate for Betaproteobacteria by approximately 35%
- *Aquabacterium*, a member of the Betaproteobacteria, was found to be the outstanding genus
- Betaproteobacteria totaled 65% of the microbial composition for marine diesel and of mixed sweet blend oil composition
- Relative abundance of *Aquabacterium* in marine diesel averaged 65% and 45% in mixed sweet blend oil

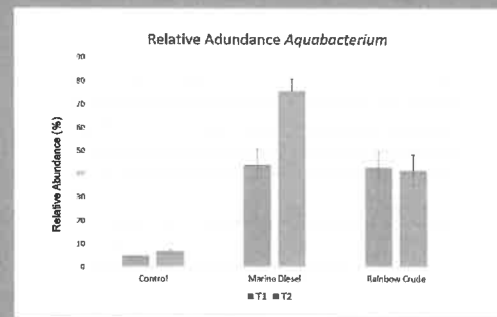


Figure 2. Relative abundance of *Aquabacterium* present in all treatments.

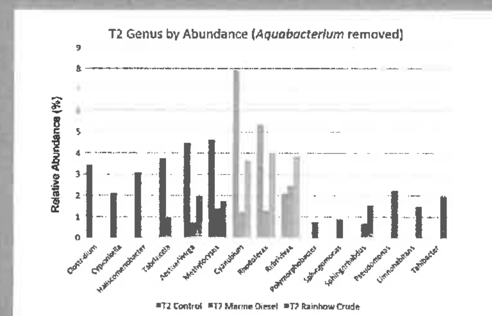


Figure 3. Relative abundance of genera in the treatments, excluding *Aquabacterium*.

- If *Aquabacterium* is excluded, a trend can still be observed across the genera displayed
- Even though the abundances of the above genera are relatively low, there are clearly different members present that are known biodegraders, including members of the *Pseudomonas* genus, within the treatments[4]

Discussion

- The microbial composition changed in the case of both oil treatments with a significant increase in the prevalence of the genus *Aquabacterium*.
- *Aquabacterium* strain was not among the genera detected in prior Great Lake oil studies, though it has been described as nitrate reducer and has been found in freshwater prior to this study[3,4,5]
- It has also been found in areas contaminated with aliphatic hydrocarbons, where it was not detected prior to hydrocarbon presence[3]
- Previous experimentation on freshwater bacteria bioremediation demonstrated that *Aquabacterium* became the dominant genus when mixed sweet blend oil was added[6]

Conclusion

- This research allows for many avenues of future research into Betaproteobacteria and *Aquabacterium* regarding the remediation of freshwater oil spills.
- In our experimentation, Betaproteobacteria, and in particular, the genus *Aquabacterium*, was found to be predominant in both oil treatments, warranting future research to assess its ability to metabolize mixed sweet blend oil and marine diesel.

References

1. [illegible]

2. [illegible]

3. [illegible]

4. [illegible]

5. [illegible]

6. [illegible]

Acknowledgements

- This work funded by Natural Resources Canada Multi-Partner Research Initiative.

The ***third outcome*** of this proposal was the development of a DNA assay (multiplex qPCR technique) for the sex identification of sturgeon. This required qPCR primer and probe design based on the female-DNA specific sequences, as well as species-specific sequences, thus providing a critical control and male indicator for the method. There were many aspects I learned from the Queen's University eDNA workshop that I applied to the approach and the design of this assay, which we have successfully optimized and are currently running. We have thus far processed ~90 samples with the new detection method and are receiving requests for several hundred additional samples to be analyzed. A modernized, molecular-based test for sex determination does reasonably substantiate a manuscript, and that is near the final stages of preparation, as well as future funds for the processing of samples collected from around the Great Lakes basin.

A figure from the manuscript illustrating results of the sex determining assay:

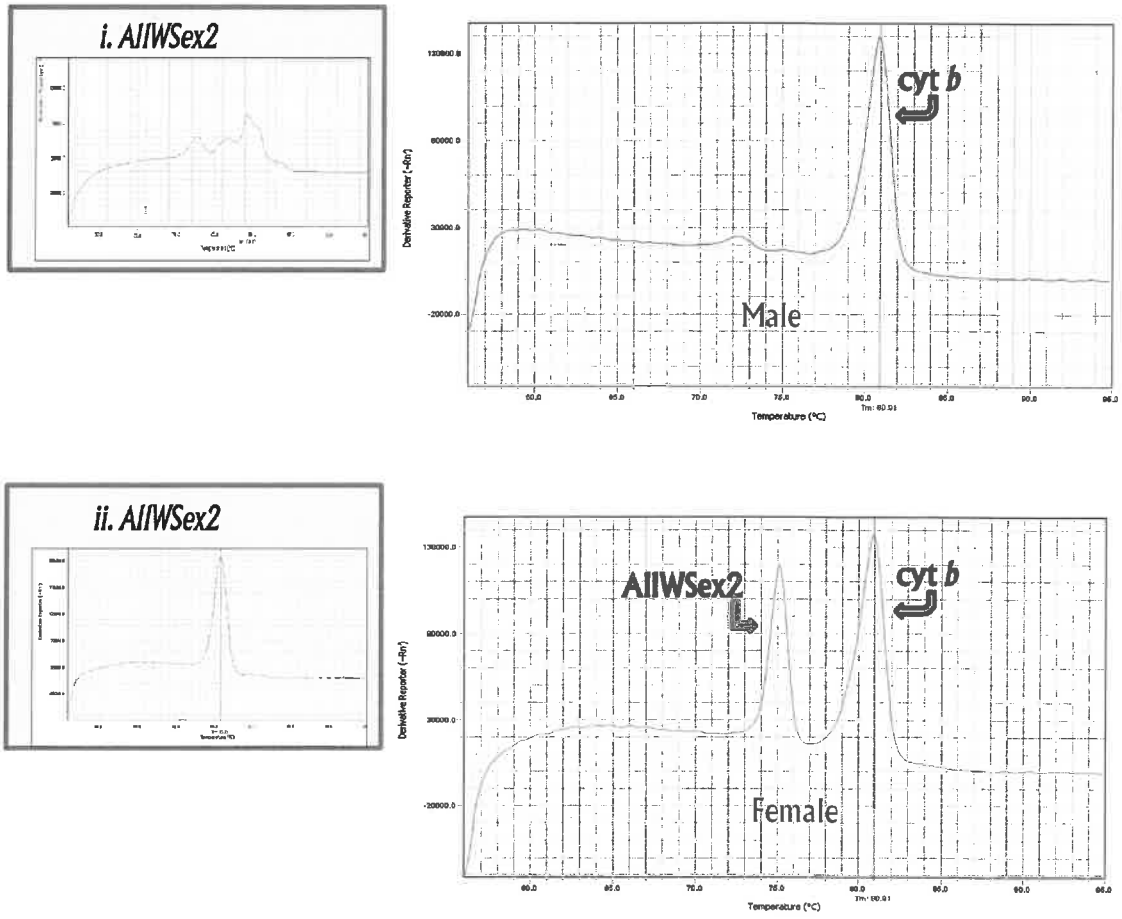


Figure I Melt curve profiles with AllWSex2 and cyt *b* duplex qPCR. Insets comparing i) male with AllWSex2 primers only plot and ii) female with AllWSex2 primers only plot.

Student Involvement:

LSSU Fisheries and Wildlife Management student Alana Schofield, has been trained and is currently processing samples with the new method. Her senior thesis project also includes the 'Molecular Sex Determination of Sturgeon' method and she plans on presenting her work at the Midwest Fish and Wildlife Conference in 2026.

Other scholarly activities during this time that I hosted, presented or participated in:

February 2025, hosted the Early Assurance interviews with LSSU student applicants to the Michigan State University College of Human Medicine program

Maintained communications with professional programs around the state

July 2025, attended the Michigan Advisors for the Health Professions Financial Aid meeting

Queen's UNIVERSITY

CERTIFICATE OF ACHIEVEMENT

Britton Ranson Olson

has successfully completed the

Queen's University Short Course in Environmental DNA

offered by

QUEEN'S UNIVERSITY BIOLOGICAL STATION

Dr. Stephen Lougheed

Dr. Dilini Abeyrama

Allen Tian

Dr. Bo-Jian Chen

Stafford Maracle

May 17th, 2024

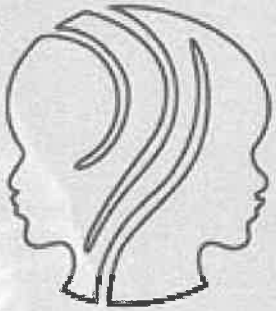
Queen's University, Department of Biology and
Queen's University Biological Station

LSSU Library Scholar Series

presents

Twins:

An illustration of epigenetics



Identical twins have the same DNA and are, in fact, genetic clones of one another. Yet, they can have different traits, physical features, and health conditions, despite being genetic carbon copies.

Epigenetics - the influence of environment and chemicals that attach to our genes and modify the way that we express them - may be accountable for some of these differences.

LSSU Biology Professor Dr. Britton Ranson Olson will explore the impact that these outside factors can exert on human biological development.

Thursday, January 23, 2025 @ 1pm

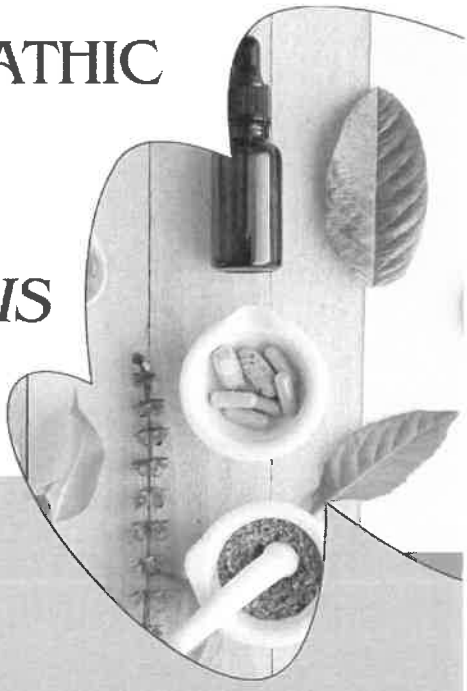
in the Library Learning Commons

Lake Superior State University LIBRARY

906 Ryan Ave., Sault Ste. Marie, MI
906.635.2815 — www.lssu.edu/library
This event is free and open to the public.

ROOTED IN NATURE, GROUNDED IN SCIENCE

TRAINING AS A NATUROPATHIC MEDICAL STUDENT TO ADDRESS *AMERICA'S HEALTH CRISIS*



WHAT WE WILL DISCUSS:

- My Naturopathic Journey
- Education & Training in Holistic Health
- Root-Cause Health Solutions
- Holistic & Evidence-Based Care
- Transforming Patient Care

MARCH 14TH

3 PM - 3:50 PM

CRW 205

GUEST SPEAKER

KATHRYN LEVITAN

Naturopathic Medical Student Year 3