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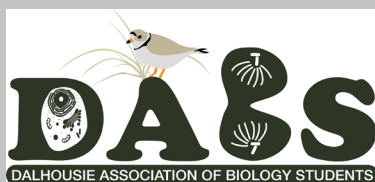
FOR BIOLOGY & MARINE BIOLOGY  
HONOURS STUDENT RESEARCH

Saturday  
12 February 2022  
9:00 am - 12:30 pm

Sponsored by the Department of Biology

&

Dalhousie Association of  
Biology Students



Dalhousie Association of  
Marine Biology Students





## On the Origin of the Cameron Conference

The CAMERON CONFERENCE is named after the late Malcolm Laurence Cameron (1918–2011), always known as Laurence. A native of Cape Breton, Laurence taught at a number of rural schools in Cape Breton before serving with the Canadian Dental Corps during the Second World War II. Dalhousie University followed, where Laurence was awarded the Governor General's medal for his BSc (1949). He then completed his MSc in 1951 before going to England where he completed a Ph.D. (1953) at Cambridge University under the supervision of the world's foremost insect physiologist, Sir Vincent B. Wigglesworth. Two years as a postdoctoral fellow at the University of New Brunswick and ten years on the faculty of the University of Saskatchewan preceded Laurence's position in Dalhousie's Biology Department in the mid 1960s.

Following interests and knowledge fostered at Cambridge, Laurence's scholarly interests turned to the history of medicine in Medieval England, a field requiring a mastery Latin and Old English that few trained scientists possess. In the 1983 Annual Report of the Department, Laurence lists his activity as "*special attention to the uses made of Roman and Byzantine treatises in the compilation of the English medical texts in Anglo-Saxon times*". He is best known for his book *ANGLO-SAXON MEDICINE* (1993) published, appropriately, by Cambridge University Press. His studies also included "*an examination of the pharmacopoeia of these English texts, with a view to determining the use of non-native ingredients and a consequent determination of trade patterns in the medieval world*". These may sound esoteric, but Laurence was in fact the "go-to man" for plant identification whenever a child was admitted to a Halifax hospital having tasted or swallowed a plant thought poisonous. More than one Biology faculty member owes their child's speedy recovery to Laurence's expertise. In 1998, Laurence co-edited *THE OLD ENGLISH ILLUSTRATED PHARMACOPOEIA*, again by Cambridge University Press.

Laurence Cameron devoted all his knowledge, enormous energy, and encyclopaedic knowledge to the teaching of Biology 1000 and to the fourth-year Honours class, roles he continued after formal retirement. The annual event we know as the CAMERON CONFERENCE was started by Laurence as a way for Honours students to showcase their research. It was then, and remains today, the biggest and best Honours conference at Dalhousie.

*Thanks to Professor Brian Hall for this synopsis*



*Programme - Dalhousie University's 36<sup>th</sup> Annual Cameron Conference*



Professor Laurence Cameron at the helm of BIOL 1000 (ca. 1985)



## A Virtual Event

9:00 am

### Conference Welcome

Professor Sophia Stone  
Chair of Biology Department

9:15 – 10:00 am

### Oral Presentations Session 1

**Session Chair - Dr. Patrice Côté**

Calum Blackwood

**Comparing the Physiology and Morphology of Geographically Distinct Sources of Blue Mussels (*Mytilus edulis*)**

Asha Grewal

**Non-Breeding Migratory and Wintering Habits of Herring Gulls (*Larus argentatus*)**

Liam Hagerman

**Exploring the Novel Implications of the TRPML3 Ion Channel Protein Knockdown on the Cancer-Progression Activity of Triple-Negative Breast Cancer Cells**



## 10:00 – 11:30 am ~ Poster Session

- 1 Julia Cantelo Effects Of Elevated Temperature And Light Levels On The Growth And Photophysiology Of *Fragilariopsis Cylindrus*
- 2 Cayle Cross How Overwintering Distance From A Breeding Colony And Latitudinal Variation Impacts Lay-Date In The Rhinoceros Auklet (*Cerorhinca monocerata*)
- 3 Addysen Green Thermodynamic Properties Of Advanced Glycolic End-Products In Diabetic Tendons
- 4 Hannah Griffin Gut Microbiome bcrA Gene Potentially Predictive Of Secondary Antibiotic Outcomes Of Infection And Febrile Neutropenia As Determined By The Pg-Bsm Model
- 5 Annie Grigg Plastic Responses In Zebrafish (*Dania rerio*) Due To Thermal Variability Impact Body Shape And Size
- 6 Rachel Han Relationship Between Daylength And Phytoplankton Diversity In The Bedford Basin
- 7 Nicole Harrington Factors Influencing Movement, Habitat Choice And Breeding Dispersal In Male Grey Seals (*Halichoerus grypus*) On Sable Island, Nova Scotia
- 8 Jazmine Hoffman Traditional vs. Eco-friendly: A Comparison of Polyethylene and Polylactic Acid Plastics During Early Exposure to Coastal Seawater



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- 9 Linda Hutchinson Acoustic Recognizers For Non-Invasive Citizen Science Monitoring Of Leach's Storm-Petrel (*Hydrobates leucorhous*)
- 10 Sokhiba Khayol Muhammad Investigation Of The Phytohormone Auxin (IAA) On Lace Plant (*Aponogeton madagascariensis*) Programmed Cell Death And Perforation Formation
- 11 Sarah Kromberg Analysis Of Predatory Northern Sea Star Distribution And Abundance Suggests A Shift In The Benthic Community Within The Bras d'or Lake, Cape Breton Island
- 12 Shaylyn Lewis Susceptibility Of Existing And Proposed Areas Of Conservation To Climate-Based Change In The Scotian Shelf-Bay Of Fundy Bioregion
- 13 Javon Lo Impacts Of Prey Availability And Tidal Influence On The Behaviour Of White Sharks, *Carcharodon carcharias*, In The Minas Basin
- 14 Jacqueline Lossing Tomorrow's Ocean: Effects Of Ocean Alkalization On Community Composition, Growth, And Grazing Rates In Natural Assemblages Of Phytoplankton
- 15 Kate Love The Madagascar Lace Plant (*Aponogeton madagascariensis*): Investigating Leaf Perforation Formation And Flower Induction In Varied Aquarium Conditions
- 16 Jordan Myles How The Frequency Range Of Noise Affects Response Latency In Tree Swallow (*Tachycineta bicolor*) Nestlings.



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- 17 Sofya Pesternikova      Less Is More: Building A Novel ALGArithm For Real-Time Classification Of Phytoplankton Community Composition
- 18 Jack Quirion              Impact Study Of Sea-Level Rise In The Eastern Shore Islands, Nova Scotia
- 19 Caelin Randall-Scott      Anthropogenic Impacts On Coral And Macroalgal Benthic Cover Among Sites In The Mesoamerican Reef, Northwestern Caribbean Sea
- 20 Kiersten Runte             The Occurrence Of An Unknown Novel Beaked Whale (Cetacea; Ziphiidae) Off West Africa
- 21 Amber Showers            Identification Of Ubiquitin Ligases (E3s) Involved In Plant Tolerance Of Nutrient Stress
- 22 Charlotte Smith            Assessing the Susceptibility of Nova Scotia's Marine Protected Areas to Aquatic Invasive Species in a Changing Climate
- 23 Rebecca Smith            Modeling Associations Between DNA From The Gut Microbiome, And Secondary Clinical Outcomes Of Infection In Pediatric Cancer Patients
- 24 Calisa Staniforth          Spatial and Temporal Variability in Benthic Megafaunal Communities in the Bay of Fundy
- 25 Aleksei Sychterz          Characterizing the Expression of Rhodopsin in *Oxyrrhis marina*
- 26 Rachel Thompson         The Effect Of Synthetic Cannabinoids On The Anti-Inflammatory Response Of Alternatively Activated Cultured Macrophage Cells



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- 27 Sophia Tonks                      Investigating The Role Of Ring-Type E3 Xbat31.1 Overexpression In Iron Uptake
- 28 Marco Turner                      A Comparative Analysis Of Striated Muscles In Non-Bilaterian And Bilaterian Animals
- 29 Liz Weston                          Characterization And Phylogenetic Placement Of A Novel Groove-Bearing Heterotrophic Flagellate
- 30 Alex Wong                          Identification And Characterization Of Novel Aquatic Bacteria With Hydrocarbon Degrading Capabilities Using Minion Nanopore Sequencing Technology
- 31 Susanna Zhang                      An Analytical Investigation And Metabolomics Of Mississauga Food And Medicinal Plant And Fungal Extracts





11:30 am – 12:15 pm  
Oral Presentations Session 2

**Session Chair - Dr. Patrice Côté**

Emily Martens-Oberwelland **Population Trends of Humpback Whales,  
*Megaptera novaeangliae*, Off Brier Island, NS From  
1984-2020**

Mab Speelman **Mushroom For Improvement: Assessing Sequential  
Culture of Algae and Fungi to Remediate Food-  
Grade Wastes**

Molly Wells **Assessing the Impact of Visual Media as an  
Outreach Tool for Marine Conservation: Historical  
and Present Applications**

12:15 pm  
Closing Remarks - Dr. Margi Cooper



Programme - Dalhousie University's 36<sup>th</sup> Annual Cameron Conference



LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME



## **Comparing The Physiology And Morphology Of Geographically Distinct Sources Of Blue Mussels (*Mytilus edulis*).**

**Author:** Calum Blackwood  
**Programme:** Marine Biology & Biochemistry  
**Supervisor(s):** Dr. Ramon Filgueira, Marine Affairs Program, Dalhousie University  
Laura Steeves, PhD Candidate (Biology), Dalhousie University

### **Abstract**

The Blue mussel (*Mytilus edulis*) is a widely distributed marine bivalve that is ecologically and commercially important. To predict mussel growth rates and optimize the production of mussels in spatially limited coastal regions, it is important to understand how physiological traits differ between geographically distinct sources of mussels. Mussel physiology is highly plastic, with feeding and respiration rates often changing significantly with respect to the local environment. This study was designed to compare the morphology and physiology of four groups of mussels initially collected as spat from different bays in Prince Edward Island, Canada and reared together in a common location. A common garden experimental design was used to account for plasticity, allowing for the observation of differences in physiology due to initial mussel settling location. Four mussels from each group were kept in individual flow through chambers. Key physiological traits including active metabolism, pumping rate, and an indication of feeding were measured throughout the study using oximeters, fluorometers and particle counters. Individual gill area and dry weight were used in conjunction with the above physiological measurements to compare the allometric relationships between the four groups of mussels. The experiment was replicated 3 times, twice under laboratory conditions, and once using seawater taken directly from St. Peters Bay, PEI. This study will help determine if settling location has a lasting affect on mussel physiology and morphology. Further, quantifying differences in physiology and morphology between these groups will provide a deeper understanding of the limits of physiological plasticity, and may help to optimize mussel production.



## Effects Of Elevated Temperature And Light Levels On The Growth And Photophysiology Of *Fragilariopsis cylindrus*

**Author:** Julia Cantelo  
**Programme:** Biology  
**Supervisor(s):** Dr. Erin Bertrand, Biology Department, Dalhousie University  
Loay Jabre, PhD candidate, Biology Department, Dalhousie University

### Abstract

Phytoplankton are a diverse group of photosynthetic microbes that form the basis of oceanic food webs, are essential to global biogeochemical and carbon cycles, and are responsible for roughly half of global annual net primary production. The Southern Ocean hosts diverse groups of phytoplankton that play a critical role in absorbing large amounts of atmospheric CO<sub>2</sub> and converting it to oxygen through photosynthesis. Under global climate change, we expect to see shifts in sea surface temperatures, ocean stratification, nutrient availability, and irradiance in the upper layers of the ocean. Phytoplankton growth is highly dependent on environmental conditions such as suitable water temperatures and light availability, however, there has been little research inquiring as to how climate change-induced variation in temperature and light availability will influence phytoplankton physiology, morphology, and photosynthetic efficiency. The primary objective of this study is to investigate the physiological response of the wide-spread polar diatom *Fragilariopsis cylindrus* to fluctuations in temperature and light levels to better understand how environmental changes are impacting Southern Ocean primary productivity. In this study, laboratory cultures of *F. cylindrus* are being grown under a matrix of temperature and light levels representative of ambient and projected surface layer conditions under future warming scenarios in the Southern Ocean. The cultures will be monitored through full growth cycles, and growth rates and cell morphology will be measured. During exponential growth phase, photophysiology measurements including photosynthetic efficiency of PSII ( $F_v/F_m$ ) and the functional absorption cross-section of PSII will be taken, and cells will be harvested to measure cellular chlorophyll-*a*, particulate organic carbon, and particulate organic nitrogen content. We are currently performing these experiments and using these physiological measurements to quantify the effects of increased temperature and light levels on the growth and photosynthetic health of *F. cylindrus*. Ultimately, this research aims to provide insight into the physiological changes phytoplankton undergo in response to temperature and light variation, allowing us to better understand and predict the effects of climate change on Southern Ocean microbial ecosystems.



## How Overwintering Distance From A Breeding Colony And Latitudinal Variation Impacts Lay-Date In The Rhinoceros Auklet (*Cerorhinca monocerata*)

**Author:** Cayle Cross  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Glenn Crossin, Biology Department, Dalhousie University

### Abstract

In seabirds, breeding is the most energetically demanding phase of the annual cycle, the timing of which overlaps extensively with seasonal peaks in prey availability. Because seabirds can migrate thousands of kilometers from natal colonies during the non-breeding period in winter, the distances travelled to and from wintering areas may have some bearing on when individuals return to a breeding colony to initiate breeding. We tested the hypothesis that overwintering centres of distribution affect breeding times at multiple colonies of burrowing, philopatric rhinoceros auklets (*Cerorhinca monocerata*). I investigated if there was an influence of breeding colony latitude on this relationship. Additionally, as there is uncertainty whether rhinoceros auklets exhibit protandry (i.e. males return first), I will also examine sex-specific patterns of pre-breeding arrival times at colonies. A total of 128 birds were analyzed from 12 different colonies distributed throughout the full breeding range in the Northeastern Pacific Ocean. Using geolocation (GLS) data from all individuals, I determined when an auklet initiated breeding by identifying periods of 24 hour darkness (no light detection during the day), which was inferred as first occupancy in the breeding burrow. The start of incubation was identified when an auklet spent at least three alternating days within the burrow. Preliminary results identified a slight positive correlation ( $r = 0.31$ ) between wintering distance from breeding colony and the start of incubation times. Results also show a positive relationship of breeding colony latitude and the start of incubation ( $r = 0.5$ ). Preliminary ANCOVA test suggest a significant relationship between start of incubation and colony latitude ( $P < 0.001$ ); however, there was no significant relationship between start of incubation and wintering distance. Analyses are on-going, but the results of this study will fill basic gaps of our biological knowledge of this important sentinel seabird species.



## **Thermodynamic Properties Of Advanced Glycolic End-Products In Diabetic Tendons**

**Author:** Addysen Green  
**Programme:** Biology & Neuroscience  
**Supervisor(s):** Dr. J. Michael Lee, School of Biomedical Engineering, Dalhousie University

### **Abstract**

Diabetes is a life-changing disease caused by an inability of one's body to create or use insulin, the hormone responsible for eliminating glucose from the bloodstream and therefore regulating blood glucose levels. Without natural regulation, those with diabetes are often in a state of hyperglycemia. This can cause complications in various regions of the body, including tendons. Tendons are a critical component of movement, transmitting muscular forces to the bone. Their ability to transmit these strong forces lies in a unique enzymatically crosslinked design of collagen fibrils. Hyperglycemic conditions can cause the formation of nonenzymatic crosslinks, called advanced glycation end-products (AGEs). AGEs are difficult for cells to break down, preventing denaturation and turnover of collagen and leading to thickened tendons. My study examines how the hyperglycemic conditions caused by diabetes affects the collagen structure of tendons, aiming to view the changes in the thermodynamic properties of the collagen. Diabetic conditions were induced on bovine tail tendons using ribose incubation. The thermodynamic properties of AGEs were investigated using a novel parametric analysis of hydrothermal isometric tension testing (HIT) and differential scanning calorimetry (DSC). The novel approach to analysis is expected to provide a more accurate timeline for collagen denaturation in tendons affected by AGEs. The results of this study will provide functional data on the thermal stability of AGE-affected tendons which can in turn provide insight into future diagnostic measures for diabetes and AGE-related complications.



## Non-Breeding Migratory And Wintering Habits Of Herring Gulls (*Larus argentatus*)

**Author:** Asha Grewal  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Sarah Gutowsky, Biology Department, Dalhousie University  
Dr. Andrew Horn, Biology Department, Dalhousie University

### Abstract

Migration is a key component of the annual cycle of many avian species. It entails cost-benefit trade-offs that reflect spatial and temporal decisions which allow for behavioural flexibility within migration strategies. Herring Gulls (*Larus argentatus*) can be partial migrants, where a breeding colony consists of both resident birds that stay local during the non-breeding period, and migratory birds that travel to overwinter areas. Investigating the relative use of these migratory strategies (resident, and short or long distance) within a population and the consistency in strategies within individuals across years is key to understanding individual variation. I tracked 15 birds over two non-breeding periods from colonies in southwest Nova Scotia using GPS devices to identify individual migratory strategies and to quantify the repeatability of individual behaviour across years measured by phenological and spatial metrics. Individual birds were found to be entirely consistent in their chosen migratory strategies across years. Short and long migrants were highly repeatable in how long they stayed in Nova Scotia each year before a southbound migration ( $R=0.93$ ), with a mean duration of 50 days (range: 0-95 days) for short migrants and 75 days (0-148 days) for long migrants. Migratory individuals were also consistent in the size of the area used and the total distance traveled within Nova Scotia ( $R=0.95$  and  $0.87$  respectively). Birds of all three strategies were consistent in their overwinter regions, based on the 75% contour from kernel density estimation (75% KDE). I found significantly higher proportional overlap in space use between years among the same bird (mean overlap: 95, 94, 67% for resident, short, long, respectively) than among different birds (1, 16 and 29% respectively). There was high repeatability for short migrants in overwintering duration ( $R=0.95$ ; 132-306 days), total distance traveled ( $R=0.88$ ; 1,402-7,244 km), and the area of the 75% KDE ( $R=0.95$ ). This suggests migration decisions vary across individuals but are similar within strategies and highly consistent within individuals over time. These decisions may reflect the trade-offs of individual birds, rather than population-level responses to fluctuating environmental conditions. The remarkable individual consistency I found in location and timing of migratory behaviours can help identify and manage local impacts from Herring Gulls on sensitive coastal ecosystems, communities, and industries.



## **Gut Microbiome bcrA Gene Potentially Predictive Of Secondary Antibiotic Outcomes Of Infection And Febrile Neutropenia As Determined By The Pg-Bsm Model**

**Author:** Hannah Griffin  
**Programme:** Biology  
**Supervisor(s):** Dr. Joesph Bielawski, Biology Department, Dalhousie University

### **Abstract**

When undergoing treatment for diseases such as cancer, significant damage is inflicted on the body in the process. The use of chemotherapy and broad-spectrum antibiotics necessary to treating cancer progression carries the risk of life-threatening secondary antibiotic outcomes for the patient due to a resulting compromised immune system. The focus of this study is on the possibility of early identification of two of the most common and life threatening secondary antibiotic outcomes of pediatric cancer patients, infection and febrile neutropenia through genes in patients gut microbiome. Recently, a connection has been established between the human gut microbiome and phenotypes of diseases. This connection is thought to be due to the vital impact the microbiome has on process such as immune regulation. Human gut microbiome samples were collected from pediatric oncology patients at the IWK Health Centre. For each sample presence and absence of the clinical phenotypes of infection and febrile neutropenia was recorded. Of the bacterial genes extracted using metagenome sequencing techniques, the bcrA gene was selected as a gene known to have a role in bacterial antibiotic resistance, and 73 bcrA sequences were collected. The bcrA protein contributes to an ABC transporter that acts to remove certain antibiotic molecules from the target bacterium, preventing the antibiotic from acting on it. The Phenotype-Genotype-Branch-Site-Model (PG-BSM) combining information on functional phenotypes with evolution of codons to investigate two questions. First, are mutations occurring in the bcrA gene sequence over time. The associated null hypothesis is that no mutations are occurring. Second, is any change occurring associated with a phenotype. The associated null hypothesis assumes that evolution of phenotypes is independent of mutations in the bcrA gene. Rejection of either null can be interpreted as evidence for an association between the process of phenotype evolution and the changes in intensity of selection pressure in the sampled set of gene sequence. If an accurate prediction could be made on when a patient will get an infection or develop febrile neutropenia prior to expressing the classic clinical symptoms, earlier treatment could mitigate the severity of the effect on the patient.





## Plastic Responses In Zebrafish (*Dania rerio*) Due To Thermal Variability Impact Body Shape And Size

**Author:** Annie Grigg  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Jeffrey Hutchings, Biology Department, Dalhousie University  
Melanie Massey, Biology Department, Dalhousie University

### Abstract

Changing climatic conditions have profound impacts on ectothermic organisms. In particular, human-driven climate change is predicted to increase the amplitude of thermal variation over the coming decades which could vastly alter the thermal landscape for many species. Despite this knowledge, little research has been performed to examine the responses fish may have to thermal variability. In the present study, using zebrafish (*Danio rerio*) as a model organism, we applied morphometric analyses to examine how diel thermal fluctuations impact adult body shape and condition. To explore plastic morphological changes, we exposed zebrafish to diel thermal fluctuations during early ontogeny (days 0-30), late ontogeny (days 31-210), or a combination of both. Thermal fluctuations spanned the species' viable developmental range (22 - 32 °C). We found that body shape, size, and condition were affected, especially by the late ontogenetic fluctuating treatment. Specifically, fish that experienced wider thermal fluctuations in late ontogeny presented shorter body lengths and poorer body condition. Our data suggest that there are non-trivial energetic costs associated with the necessary internal regulation of bodily functions as a result of variable temperatures.

The present study provides insight into the environmentally-driven processes that create morphological consequences in zebrafish. Our findings may be generally illustrative of morphological changes in wild populations of freshwater fish in the coming years.



## Exploring The Novel Implications Of The TRPML3 Ion Channel Protein Knockdown On The Cancer-Progression Activity Of Triple-Negative Breast Cancer Cells

**Author:** Liam-Patrick Hagerman  
**Programme:** Biology  
**Supervisor(s):** Dr. Yassine El Hiani, Department of Physiology & Biophysics

### Abstract

Breast cancer is the most prevalently diagnosed cancer among Canadian women every year, and triple-negative breast cancer (TNBC) is the most aggressive and lethal subtype, affecting 10-20% of this population. TNBC currently lacks effective targeted therapies, constraining patients to the use of vigorous, and relatively ineffective non-specific anticancer treatments. These therapies are harmful to the life quality of TNBC patients, and cumulatively add to the financial strain of hospitals and health authorities, so there is a definite need for novel effective targeted therapies against this disease. Recent research has demonstrated how downstream calcium signaling from the TRPML1 lysosomal ion channel protein contributes to the hyperactive growth and spreading physiology of TNBC, by supporting these activities through the provision of a secondary supply of energy. These studies further demonstrated that genetic knockdown (KD) of TRPML1 inhibits these effects, thus leading to cancer killing. TRPML1 and its close relative, TRPML3, share close functional and structural homology, however the TRPML3 ion channel is understudied in the context of cancer cell physiology. My research aims to explore the impacts of TRPML3 genetic knockdown on the growth and spreading activities of TNBC cells, by monitoring changes in proliferation, migration, and survival compared to control. Due to the apparent trends of cancer-promotion by TRPML1 presented by recent research, I am hypothesizing that TNBC cells without TRPML3 will face significant reductions in each of these activities, compared to control. Sourcing from cell culture of normal (control) and TRPML3-KD TNBC cell lines, I am using MTT and cell counting assays to measure differences in proliferation, gap closure assays for migration, and clonogenic assays for survival. Furthermore, I am performing western blots to observe for changes in expression of key proliferation markers (pAKT and pERK1/2) and migration markers (Vimentin and N-Cadherin), to extrapolate about specific intracellular mechanisms affected by the removal of TRPML3. Current data demonstrates reductions in both proliferation and migration of TRPML3-KD TNBC cells compared to control. Altogether, the findings of this research will come together to answer my central research question, and if my hypothesis is supported, provide an important foundation for the development of targeted anti-cancer drugs for those affected by TNBC.



## **Relationship Between Daylength And Phytoplankton Diversity In The Bedford Basin**

**Author:** Rachel Han  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Julie LaRoche, Biology Department, Dalhousie University

### **Abstract**

Phytoplankton is microscopic organisms that thrive in coastal regions and estuaries. They play a critical role in the marine food chain and global oxygen production. In temperature and high latitude areas, seasonal changes will lead to nutrient cycling in marine systems and cause spring and fall overturning. Nutrients stored in deeper water will be brought up to the surface in spring and fall, triggering phytoplankton blooms each year. Numerous programs were developed internationally to observe phytoplankton species, one of them was The Bedford Basin Monitoring Program (BBMP). Two questions arose to further understand phytoplankton species in The Bedford Basin: the relationship between day length and phytoplankton species and the distribution of phytoplankton species during winter mixing. This study used a 4-year-long time series of weekly flow cytometry and chloroplast 16S rDNA data collected by BBMP. The raw data were converted to ASVs, and the species were identified. I used several R packages to analyze the diversity of phytoplankton in different depths (1, 5, 10, and 60m). Results showed that the diversity of phytoplankton species in the Bedford Basin had a reverse relationship with daylength in depths of 1, 5, and 10 meters. Furthermore, species abundant in 60m during winter were the same species that dominated spring phytoplankton blooms. Phytoplankton species in The Bedford Basin were on a level comparable to that of the Scotian Shelf. Therefore, my results could be applied to the Scotian Shelf, and it could help us protect our coastal marine environments.



## **Factors Influencing Movement, Habitat Choice And Breeding Dispersal In Male Grey Seals (*Halichoerus grypus*) On Sable Island, Nova Scotia**

**Author:** Nicole Harrington  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Damian Lidgard, Department of Fisheries and Oceans Canada  
Dr. Cornelia den Heyer, Department of Fisheries and Oceans Canada

### **Abstract**

Movement behaviours of male grey seals (*Halichoerus grypus*) within the breeding colony are indicative of a polygynous female-defense mating strategy that varies largely according to competitive ability. As such, males exhibit a sex-biased dispersal, with mating tactics broadly characterized by their movement pattern; a tenured (single location defense, low movement) or transient (several locations and females, high movement) tactic, or a combination of both. Male grey seal breeding dispersal and associated movements may be a functional response to environmental (e.g., competition in habitat) and demographic (e.g., age, population density) factors, whose effects on the level of male movement during a breeding season and across years are largely unknown. This study investigates the factors that influence male grey seal movement, habitat choice and breeding dispersal during the breeding season on Sable Island, Nova Scotia, using an established long-term database of repeated sightings of breeding male grey seals. Longitudinal sighting data were collected on 380 known-aged, permanently, and individually marked breeding males. Males used were branded with a three- or four- alpha-numeric character hot-iron brand applied to the lower back shortly after weaning (~ 4 weeks of age), in 1969, 1970, 1973, 1974, 1985–1987, 1989, 1998– 2002. Sighting data of male grey seals were collected during the breeding seasons (December to January) of 2004 to 2021 through weekly censuses of the entire colony. Preliminary analysis described the database with an age range covering the lifespan of the male grey seal, with most sightings of males on the breeding colony between ages 19 and 23. Distance moved by each male between censuses during each breeding season was calculated. An ArcGIS representation of habitat location of male dispersal will be created to illustrate any consistency of male habitat use across breeding seasons. A Generalized linear mixed-effects model (GLMM) will be used to examine the causal factors of male movement (i.e., age, habitat, and population size) with statistical results to be presented. Identifying the factors driving movement will provide an understanding of the causes of variance in male mating success and fitness as it relates to male movement.



## **Traditional vs. Eco-friendly: A comparison of polyethylene and polylactic acid plastics during early exposure to coastal seawater**

**Author:** Jazmine Hoffman  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Alice Ortmann, Bedford Institute of Oceanography

### **Abstract**

Plastics are some of the most abundantly produced materials today due to their durability, convenience, and low cost. An estimated 60% of plastics produced are discarded rather than recycled, resulting in a large environmental impact. Much of this waste makes its way to the oceans. Plastics can exist in the ocean as large debris, but they can also exist as fragments formed by abiotic and biotic processes. Microplastics are created this way, but also can be manufactured as pieces smaller than 5mm. Bacteria interact with plastics, creating a “plastisphere” which results in the eventual removal of the plastic from the environment by biodegradation, suggesting that bacteria could be an important solution to marine plastic pollution. Traditional plastics are made from non-renewable petrochemicals and are highly resistant to biodegradation. Other forms of plastic can be derived from natural, renewable resources, which are more susceptible to biodegradation. This study used polyethylene (PE) as the traditional plastic and polylactic acid (PLA) as the greener alternative to determine how the fragmentation, biodegradation rates, and microbial communities on the plastics and in the seawater differed over time between plastic types. Baffle flasks were filled with Bedford Basin seawater and four plastic pieces of either PLA or PE were added and incubated in the dark. Over 82 days and 8 time points, one PLA and one PE flask were sampled. At each time point, Microtox® assays and flow cytometry were completed, DNA was extracted from the seawater and plastic surfaces, and plastics were imaged with biofilm and after cleaning. Toxicity was not significant in seawater samples. The number of prokaryotes did not differ significantly between PE and PLA exposed seawater. There was no significant difference in mass change between PE and PLA and no trend over time. There was also no trend over time for biofilm mass, but there was more biofilm on the PLA compared to the PE. DNA analysis of seawater and biofilm will be used to identify if the plastics altered the bacterial communities over time. Preliminary analysis suggests minor differences between PLA and PE during early exposure to coastal seawater, suggesting a limited environmental benefit of PLA.



## Acoustic Recognizers For Non-Invasive Citizen Science Monitoring Of Leach's Storm-Petrel (*Hydrobates leucorhous*)

**Author:** Linda Hutchinson  
**Programme:** Marine Biology Co-op  
**Supervisor(s):** Dr. Cindy Staicer, Biology Department, Dalhousie University  
Dr. John Kearney, lead partner for the Listening Together Project, John F. Kearney and Associates

### Abstract

Passive acoustic monitoring (PAM) is a promising non-invasive monitoring technique that has been utilized for the conservation of many Species at Risk and incorporates valuable citizen scientist data in bioacoustics monitoring projects. The Leach's storm-petrel, (*Hydrobates leucorhous*), has not benefitted from PAM, and current population monitoring techniques are highly invasive. An endangered species of seabird with two distinct main calls, one of which is indicative of a breeding pair, they were the perfect candidate for exploitation of PAM and acoustic recognizers for target species vocalisation extraction. Using two sets of recordings taken on Bon Portage Island, NS (distance and density focused respectively), I created classification computer algorithms on two bioacoustics software platforms (KaleidoscopePro and Rfcx-Arbimon). I also utilized specific vocal parameters to create detectors on another two (KaleidoscopeLite and RavenPro). Metrics compared were recognizer performance, user friendliness of the platforms, and net cost. The most accurate classifier was used to determine call rates, which I graphed in relation to time, date, and distance to burrow or burrow density. Using generalized linear models, I determined whether variation in call rates could be explained by variation in those factors. Model fit was evaluated using the  $\Delta AIC$ . If distance from occupied burrow was the most-supported predictor in the models generated from the distance transect recordings, then it was clear that the distance to the recorder was important. Preliminary results indicated the Audiomoth recorders picked up an abundance of "chatter" calls along the distance transect and "purr" calls from 2 m away from the burrow entrance. If burrow density was found to be the most-supported predictor variable in the models generated from the burrow density recordings, then it was concluded that recordings provide some information on occupied burrow density. In this case, colony size may be roughly extrapolated from recordings. Although this may not be sufficient to replace current monitoring techniques completely, this is useful for mobilising citizen scientists in storm-petrel conservation.



## **Investigation Of The Phytohormone Auxin (IAA) On Lace Plant (*Aponogeten madagascariensis*) Programmed Cell Death And Perforation Formation**

**Author:** Sokhiba Khayol Muhammad

**Programme:** Biology

**Supervisor(s):** Dr. Arunika Gunawardena, Biology Department, Dalhousie University

### **Abstract**

Programmed cell death (PCD) is an intracellular mechanism wherein cells undergo death in a controlled manner. The lace plant (*Aponogeten madagascariensis*) is an aquatic monocot that forms perforations across its leaf lamina via developmentally regulated PCD. Perforation formation begins in the window stage and is highly controlled by a few key regulators.

Anthocyanin, a potent antioxidant is abundant in early stages leaves. Its loss from certain cells cues the beginning of cell death and allows for the accumulation of reactive oxygen species (ROS). The leaf continues to lose anthocyanin pigment until perforations are fully formed leading to the final mature stage. Auxin in its most common form, indole acetic acid (IAA), is a naturally occurring phytohormone that has an important role in plant growth and development. Auxin is distributed throughout the plant in a polar manner where PIN1 efflux proteins direct its flow. Previous literature has implicated auxin plays a role in the PCD mechanism of lace plant, however, its exact role and direction of flow remains unknown.

This study aims to determine whether an increased amount of auxin hormone can alter perforation formation or if there is an effect on key regulators of PCD by quantifying anthocyanin and detecting ROS. In addition, one of the objectives is to detect the direction of auxin flow via immunolocalization of PIN1 proteins using confocal microscopy.

Pharmacological experiments were conducted on lace plants with six different IAA concentrations 0 (control), 1, 5, 15, 50 and 100  $\mu\text{M}$ . Two independent experiments have been conducted with a minimum of five replicates per treatment. Leaves were harvested, and data collected such as leaf length, leaf width, number of perforations, microscopy analysis and anthocyanin extraction.

Results indicate that plants treated with high auxin concentrations (50, 100  $\mu\text{M}$ ) demonstrated a significant decrease in perforation number per  $\text{cm}^2$ . Likewise, all treatments with auxin concentrations greater than one micromolar demonstrated significant decrease in anthocyanin concentration. This further indicates the importance of auxin in perforation formation and suggests an optimal auxin concentration is crucial for the occurrence of the PCD mechanism. ROS levels in addition to immunolocalization of PIN1 proteins using confocal microscopy are still currently under investigation.



## **Analysis Of Predatory Northern Sea Star Distribution And Abundance Suggests A Shift In The Benthic Community Within The Bras d'or Lake, Cape Breton Island**

**Author:** Sarah Kromberg  
**Programme:** Marine Biology, minor in Ocean Sciences & Co-op  
**Supervisor(s):** Dr. Frederick Whoriskey, Biology Department, Dalhousie University  
Caelin Murray, Msc and Shannon Landovskis, Msc

### **Abstract**

Sea stars (Asteroidea) and urchins (Echinoidea) are important but frequently neglected ecosystem components which can structure the communities in which they live either by exerting top-down pressures as predators or bottom-up controls as grazers (Schultz et al., 2016). Many sea stars are keystone species that control overall biodiversity within an ecosystem and can significantly disrupt the commercially valuable shellfish populations on which they prey (Bucci et al., 2017). The Northern Sea Star, *Asterias vulgaris*, is a primary subtidal predator within the western North Atlantic Ocean, however, there is currently little research on asteroids in subtidal regions (>15m depth) (Gaymer et al., 2001; Gale et al., 2015). My honours project aimed to categorize the epibenthic macrofaunal invertebrate community in the Bras d'Or Lake/Pitu'paq on Cape Breton Island/Unama'ki.

Sea stars and Green Sea Urchins dominate the benthic echinoderm fauna at the study site and are often associated and compete for space (Tremblay et al., 2005; Schultz et al., 2016). I examined the Northern Sea Star's subtidal distribution, selected behaviour patterns and co-occurrences with Green Sea Urchins in the Bras d'Or Lake by analyzing ROV footage from 16 study transects (16-43m depth) within the East Bay region of the Bras d'Or Lake. The study tested for whether asteroids were equally likely to occur on all bottom substrate types encountered. I also examined aggregation behaviour by determining whether sea star aggregations were more often present on soft bottom substrate and, if aggregations were assembled according to size class. Finally, I compared present abundances of sea stars and urchins to historic reports of their abundances in order to estimate changes in ecosystem structure and function. I found no evidence of sea star habitat preferences, although low habitat diversity may account for this. There was evidence to suggest adult sea stars were capable of competing with Green Sea Urchins while juvenile asteroids were not. Finally, urchin numbers were much reduced compared to historic values. The results suggest there has been a shift in benthic community structure and function in the Bras d'Or system. Changes to the benthic community structure can affect the health and resiliency of an ecosystem and sequentially, impact commercially valuable species.





## **Susceptibility Of Existing And Proposed Areas Of Conservation To Climate-Based Change In The Scotian Shelf-Bay Of Fundy Bioregion**

**Author:** Shaylyn Lewis  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Ryan Stanley, DFO, Bedford Institute of Oceanography  
Dr. Christine Stortini, DFO, Bedford Institute of Oceanography

### **Abstract**

The effects of climate change can be seen across the world especially within the warming Ocean. Marine Protected Areas (MPAs) are one tool that help mitigate the impacts of climate change through the protection of marine ecosystems and biodiversity, but climate change can also impact the ability of MPAs to achieve their conservation objectives, as species' distributions shift. This study predicts the Time of Emergence (ToE) of 30 important marine species found within the draft network of conservation areas (37 sites) for the Scotian Shelf-Bay of Fundy bioregion, in order to forecast when thermal habitat conditions are likely to become uninhabitable for these species. The site-specific ToE is described as the first year in which the average temperature during the warmest month exceeds a species' upper thermal tolerance limit, and this exceedance continues for a period of at least two consecutive years. For each species, the regional network was constrained to sites with at least one record in the Ocean Biological Information System within a 25km range and cropped based on the preferred depth range. These 'niche-informed' networks were then analysed under the Coupled Model Intercomparison Project (CMIP) projections using two emission scenarios - SSP1 RCP2.6 (best-case scenario, global emissions reductions) and SSP5 RCP8.5 ('business as usual', emissions continue to rise) - and four climate models (AWI, GFDL, HAD, IPSL). This process generated ToE results for each CMIP 0.25° grid cell that overlapped a niche-adjusted site, for each emission scenario, model, and species. In total, ~42,000 estimates of ToE were generated. Preliminary results indicate that, under both emission scenarios, southern sites and species with restricted, generally colder-biased thermal niches had earlier ToEs, suggesting that design interventions may be required in the southern portion of the bioregion. Results also indicate that average site-level ToEs under the SSP1 RCP2.6 emission scenario, while still indicating emergence within the next 80 years, tend to be later than under the SSP5 RCP8.5 emission scenario. In conclusion, the mitigation of climate change through emission reductions is of the utmost importance to ensure the long-term protection of marine biodiversity, and global action must be taken.



## Impacts Of Prey Availability And Tidal Influence On The Behaviour Of White Sharks, *Carcharodon carcharias*, In The Minas Basin

**Author:** Javon Lo  
**Programme:** Marine Biology, Co-op; Animal Behaviour Certificate  
**Supervisor(s):** Dr. Charles Bangley, Department of Biology, Dalhousie University  
Dr. Fred Whoriskey, Department of Biology, Ocean Tracking Network

### Abstract

In recent years, the Minas Basin has been a site of interest for the implementation of tidal turbines. To determine their optimal placement, a risk assessment is being done to determine their encounter probability with wildlife. This project focuses on the white shark, *Carcharodon carcharias*, and their movement in and out of the basin to aid in this risk assessment. With the help of acoustic telemetry, tidal influence and striped bass availability were studied to help predict trends and patterns of shark movement. It is hypothesized that shark movements will strongly correspond with striped bass abundance and be influenced by the incoming and outgoing tides. The Minas Basin was divided into three distinct study areas: the main basin, the mouth of the Avon River, and the passage to the Bay of Fundy. Twelve white sharks were monitored using acoustic telemetry between the months of July to October from 2017 to 2020. Striped bass abundance and movement was also recorded using acoustic telemetry between 2017 to 2020, all year round. The life history stage of the sharks was calculated from total length measurements to mitigate variance in behavioural findings within the population. To determine the influence prey availability has on white shark movement, it was assumed that predation occurred when aggregations of white sharks and striped bass spatially overlapped. A generalized linear mixed model was used to determine significance between white shark presence, tidal height, and striped bass abundance. White sharks in the Minas Basin were all juveniles to subadults between the ages of 12 to 24 years old. Statistical significance of tidal influence and prey availability has not been calculated as of right now, but further findings will be presented during the conference. Studying these behaviours will help to determine factors that influence site fidelity or importance of the Minas Basin to less studied life history stage of juvenile white sharks, as well as unlocking the importance of striped bass as a main prey item. Understanding and therefore predicting the movement of white sharks are pertinent to shark conservation and management for the endangered western North Atlantic population.



## Tomorrow's Ocean: Effects Of Ocean Alkalization On Community Composition, Growth, And Grazing Rates In Natural Assemblages Of Phytoplankton

**Author:** Jacqueline Lossing

**Programme:** Biology

**Supervisor(s):** Dr. Hugh MacIntyre, Oceanography Department, Dalhousie University

### Abstract

Behind the omnipotent curtain of climate change lurks an increase in the uptake of carbon dioxide into the world's oceans. Artificial ocean alkalization (AOA) is a novel and underexplored carbon capture technology that holds promise in reversing ocean acidification. Isolated effects of alkalization on individual phytoplankton species have been explored, but research gaps are present in community wide responses to artificial ocean alkalization. Little research has been found with respect to the effects of sodium hydroxide – a by-product of the industrial process of hydrogen production – as an alkalizing agent. This study quantifies the impact of sodium hydroxide and elevated bicarbonate levels on phytoplankton using growth and grazing rates of native phytoplankton assemblages on the East Coast of the North Atlantic. Samples were collected in the Atlantic Ocean off the coast of Nova Scotia, the Laurentian Channel, and Placentia Bay in Newfoundland, Canada at 2m, 41m, and 15m depth, respectively, using a CTD-Rosette Sampler during August 2022. Mesocosm experiments were performed via bottle-incubations with flow-through seawater at ambient temperature on-deck between two 150 Qt coolers, screened with 50% neutral density filters. Bottles were amended with nitrate (16  $\mu\text{M}$ ) and phosphate (1  $\mu\text{M}$ ), and incubated for 48 hours. Treatments included 1mM NaOH-, 1mM NaH<sub>2</sub>CO<sub>3</sub> and an otherwise unaltered control. Growth and grazing rates were measured using Landry and Hassett's dilution method (1982). Samples for bulk growth was measured via fluorometric chlorophyll analysis and were collected every 24 hours to estimate growth curves. Community analysis and isolations were analyzed via genetic analysis of 16S amplicon sequencing techniques. The findings will include comparison of growth rates between treatments of sodium hydroxide and sodium bicarbonate to determine effects of treatments on growth rates. Composition of phytoplankton communities via genetic analyses will provide general insight into how abundances change over time and treatments. Insight into the potential ecological consequences of alkalization on native phytoplankton assemblages will inform discussions of using sodium hydroxide as a safe and viable carbon capture technology.



## **The Madagascar Lace Plant (*Aponogeton madagascariensis*): Investigating Leaf Perforation Formation And Flower Induction In Varied Aquarium Conditions**

**Author:** Kate Love  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Arunika Gunawardena, Biology Department, Dalhousie University

### **Abstract**

The Madagascar lace plant is an aquatic monocot endemic to the Comoros Islands and Madagascar, and is currently used extensively in laboratories to study the process of programmed cell death. During development, plant leaves form a predictable pattern of perforation throughout the leaf lamina, and leaves are ideal for various forms of laboratory study. Thus, the lace plant is currently under development as a model organism. Despite being extensively researched in terms of programmed cell death, little is known about the ecology of this plant or why the leaves form holes. Past research suggests the lace plant has been found growing in a wide variety of environmental conditions, however this plant is difficult to keep in aquaria and there is virtually no literature concerning its growth in an aquarium setting. For use in laboratory study, lace plants are grown in sterile culture and are propagated asexually, but to increase genetic diversity and plant vigour, plants need to undergo sexual reproduction via inflorescence, which can be done in an aquarium setting. Lace plant leaves form in heteroblastic series, and the first three to four leaves are unperforated, after which subsequent leaves exhibit the characteristic perforation. Several hypotheses exist explaining the reason for perforation, but all remain untested. The objectives of this study are twofold: to determine if water velocity impacts leaf perforation structure, and to investigate if varying seasonality in aquarium conditions results in the production of inflorescences. Preliminary results suggest greater anthocyanin production in leaves grown under high flow, meaning the leaves undergo greater stress, however significant difference in leaf perforation has not been found. Lace plants thrive in winter conditions (20 °C and 8-hour photoperiod), and may undergo dormancy in summer conditions (26°C and 12-hour photoperiod), however inflorescence production has yet to occur as a result of seasonal switch. Ongoing work focuses on increasing the number of replicates to analyse leaf perforation between high and low flow environments, and continuing to monitor plant growth upon switching seasonality. This study provides insight into the ideal conditions in which to grow the Madagascar lace within aquaria, and contributes to an ongoing effort to establish a reliable protocol for inflorescence induction.



## **Population Trends Of Humpback Whales, *Megaptera novaeangliae*, Off Brier Island, NS From 1984-2020**

**Author:** Emily Martens-Oberwelland  
**Programme:** Marine Biology & History, Minor in Musicology  
**Supervisor(s):** Dr. Hal Whitehead, Biology Department, Dalhousie University

### **Abstract**

Humpback whales, *Megaptera novaeangliae*, take part in an annual migration from tropical waters (calving and breeding grounds) to higher latitudes in the summer (feeding grounds). The North Atlantic humpback whale population is made up of five separate feeding stocks, among them, the Gulf of Maine stock to which the humpback whales off Brier Island, NS belong. Using whale watch data from 1984 to 2020, the overall population trends and variation of humpback whales that frequented the Brier Island feeding grounds were studied over an impressive 36-year span. Four possible factors were analyzed that could explain these overall trends and variation seen from year to year in individual humpback whale sightings: (1) the overall North Atlantic humpback whale population trends, (2) the level of effort, (3) whale residency, and (4) prey availability. To determine the levels of increase and mortality in the overall North Atlantic and Gulf of Maine humpback whale stocks, a literature analysis was conducted. The level of effort was determined by calculating the number of trips and number of days data was collected in a year and comparing them over the study period. The impact of whale residency was calculated by assessing the average number of days each individual whale was seen in a season across the study period. And lastly, the effect of prey availability was calculated by analyzing two different measures of herring abundances in the study area using DFO data. Using a general linear model (multiple regression analysis), the proportion of variance that is accounted for by each factor was calculated. A stepwise linear regression analysis was used to simplify the model to the factors which accounted for the most variance and thus were most important. Understanding the population dynamics of this specific group of humpback whales is not only beneficial for Gulf of Maine humpback conservation efforts but assessing the relationship between prey availability and humpback whale population trends can help inform fisheries management decisions in the Upper Bay of Fundy to better protect this species.



## How The Frequency Range Of Noise Affects Response Latency In Tree Swallow (*Tachycineta bicolor*) Nestlings.

**Author:** Jordan Myles  
**Programme:** Biology  
**Supervisor(s):** Dr. Andrew Horn , Biology Department, Dalhousie University

### Abstract

In recent years, anthropogenic noise pollution has increased in intensity and extent on a global scale, escalating concern over its impacts on wildlife populations. Studies indicate that the constant hum of our activities disrupts several animal behaviours essential for survival, including reproduction, foraging and acoustic communication. In particular, white noise has been found to disrupt parent-offspring communication in Tree Swallows (*Tachycineta bicolor*), in that nestlings are less likely to respond to parental calls in noisy environments. However, the mechanisms by which the disruption occurs are unknown. Background noise can interrupt communication by masking auditory signals in two ways: by interfering with perceptual processing (informational masking), or by blocking the signal at the auditory periphery (energetic masking). Therefore, the aim of this field study was to determine which type of signal masking is responsible for interfering with acoustic communication in Tree Swallows. This was achieved by studying how readily Tree Swallow nestlings respond to playback recordings of parental calls combined with white noise filtered so its frequencies either overlapped and or did not overlap parental calls. If energetic masking was occurring, I predicted that nestlings exposed to ambient noise exclusively within the range of parental calls (1-6 kHz) would exhibit an increase in response latency. Alternatively, if informational masking was occurring, I anticipated no difference in response latency between when nestlings are exposed to noise within versus outside the frequency range of parental calls. I found that nestlings were much slower to respond to noise within the frequency range of parental calls, suggesting that energetic masking is responsible for the disruption of parent-offspring communication. To further validate response latency as a measure of signal detection by Tree Swallow nestlings, I also explored its correlation with factors that are likely to influence it. These findings contribute to a better understanding of the effects of anthropogenic noise pollution on wildlife and provide evidence for how conservation efforts might reduce the particular noises that disrupt acoustic communication.



## Less Is More: Building A Novel ALGArithm For Real-Time Classification Of Phytoplankton Community Composition

**Author:** Sofya Pesternikova  
**Programme:** Marine Biology Co-op; French Language Minor  
**Supervisor(s):** Dr. Hugh MacIntyre, Oceanography Department, Dalhousie University

### Abstract

Monitoring phytoplankton communities is essential for understanding their responses to global climate change and for detecting the increasing occurrence of harmful algal blooms (HABs). Optical remote sensing of reflectance via satellites offers unparalleled spatial coverage but has limited resolution of depth distributions, temporal variability, and community composition. In-water monitoring of chlorophyll fluorescence is a technology that can complement remote by addressing these limits. Spectral fluorescence excitation and/or emission signatures have the potential to provide real-time classification of community composition. Instruments are available commercially (e.g. from bbe Moldaenke or JFE) but, to my knowledge, no objective means of optimizing the classificatory wavelengths has been published.

I have used machine learning methods with a library of full spectra from 40+ phytoplankton species to identify and optimize the wavelengths used to classify 4 pigment-based groups (chlorophytes, chromophytes, phycoerythrin-rich cryptophytes, and phycocyanin-rich cyanobacteria). Full fluorescence excitation spectra contain important differences in only a few parts of the spectrum. I used machine learning to optimize the discriminatory ability of a signature-based classification by using LASSO to identify a greatly reduced number of wavelengths (7 vs 460). I used the same approach to optimize the accuracy of an existing instrument with multiple optical channels, the Multi-Exciter (JFE Advantech, Nishomiya, Japan). Optimal classification of the 4 main pigment groups is achieved using only 4-5 of the 9 Multi-Exciter's channels. This reduced the error estimate by [e.g 10-fold] compared to use of all 9 channels.

This machine learning approach can be used in a forward model, such as designing a next-generation battery-powered spectrofluorometer to be used in autonomous monitoring (e.g., moorings, Argo floats, or wave gliders). Equally, it can be used in reverse to optimize the classificatory power of an existing instrument with multiple optical channels. In this case, less is more.



## **Impact Study Of Sea-Level Rise In The Eastern Shore Islands, Nova Scotia**

**Author:** Jack Quirion  
**Programme:** Biology; Sustainability  
**Supervisor(s):** Dr. Patricia Lane, Biology Department, Dalhousie University

### **Abstract**

Sea-level rise (SLR) is an increasingly well-documented threat, such that Governments are now taking preventative action in places particularly vulnerable to associated impacts like floods and storm surges. Low-lying coastal areas are among the most vulnerable to SLR. Much of Nova Scotia's coastlines fall under this definition, but outstanding for their vulnerability are the Eastern Shore Islands. This area includes over 100 ecologically preserved islands. Home to many animals, including spawning fish, nesting birds, and photo-respiring kelp, the islands are in need of protection. The recently proposed Eastern Shore Island Marine Protected Area promises protection against SLR for both marine and terrestrial wildlife, but has been criticized for its shortsighted protection proposals that are locally disfavored.

To guide conservation efforts, and to hopefully provide a clear common goal between the federal Government and local fishers, I am undergoing a research project aiming to present the impacts of SLR in the Eastern Shore Islands. Three experimental scenarios were analyzed: 1-meter, 2-meter, and 3-meter SLR above the current sea-level. Additionally, a control scenario, or 0-meter SLR, was assessed for comparative results. The total terrestrial area that is to become submerged in each experimental scenario was quantified, then more specifically quantified by ecoregion to determine which ecological and geophysical zones are more or less at risk to SLR. These analyses were executed using GIS. Their results, supplemented by information and data from ongoing literature reviews, will be compiled into Leopold Matrices along with the five most relevant and plausible SLR mitigation strategies. This will yield a score that measures the overall effectiveness of each potential solution, but also the way that each ecological component responds to certain solutions. Purposefully, this research will facilitate and encourage a multi-pronged, targeted approach to protecting vulnerable parts of the Eastern Shore Islands from SLR.





## **Anthropogenic Impacts On Coral And Macroalgal Benthic Cover Among Sites In The Mesoamerican Reef, Northwestern Caribbean Sea**

**Author:** Caelin Randall-Scott  
**Programme:** Marine Biology; Minor in Ocean Sciences  
**Supervisor(s):** Dr. Heike Lotze, Biology Department, Dalhousie University

### **Abstract**

Coral reefs are diverse ecosystems that support a multitude of ecosystem services, providing social and economic benefits to human societies. A healthy reef ecosystem is characterized by its structure (diversity, coral cover, indicator species) and function (coral recruitment, growth, mortality). Reef health can be measured by the ratio of coral:macroalgal cover, with greater coral cover indicating a healthier reef. Human activities have been a major factor in the loss of over 50% of the world's reefs since 1980, with a 70-90% loss predicted by mid-century. The Bay Islands National Marine Park (BINMP) of Honduras in the Mesoamerican reef ecosystem is experiencing intense human pressures, specifically from fishing, tourism, agricultural runoff, sewage outfalls, and coastal development. The purpose of my research is to (i) determine the coral:macroalgae ratio and species composition among 23 study sites in the BINMP, (ii) quantify the level of human impacts at each site, and (iii) link the coral:macroalgae ratio and species composition to the level of human impacts among study sites. Underwater photographs were taken using SCUBA diving along six 30-meter transects at each study site in Roatan (n=21) and Cayos Cochinos (n=2). Presence/absence of coral and macroalgae on each photograph was used to determine the coral:macroalgae ratios for each site. Nested analysis of variance (ANOVA) was performed to test whether coral cover or coral:macroalgae ratio differed across the 23 study sites within 5 regions (North, South, East, West, Offshore). A cumulative impacts model was created to quantify the level of anthropogenic disturbance at each site. Regression analyses were used to determine the relationship between the cumulative and individual anthropogenic impacts, respectively, and each of the coral:macroalgae ratio, coral cover, species richness, diversity, and evenness, across study sites. Preliminary results suggest that human impacts are indicative of reef health, with lower the reef health (i.e., more macroalgae, less coral cover) at sites with greater level of impact. Further analyses will reveal which individual or cumulative human uses have the most influence on the coral:macroalgae trade-off and species composition in the studied area, which can inform management and conservation.



## The Occurrence Of An Unknown Novel Beaked Whale (Cetacea; Ziphiidae) Off West Africa

**Author:** Kiersten Runte  
**Programme:** Marine Biology; Indigenous Studies Minor  
**Supervisor(s):** Dr. Katie Kowarski, PhD, JASCO Applied Sciences Ltd.  
Dr. Bruce Martin, PhD, JASCO Applied Sciences Ltd.

### Abstract

Out of the 23 described species of beaked whales (Cetacea; Ziphiidae), only 13 have been acoustically characterized by their species-specific, frequency modulated echolocation signals. Acoustic monitoring relies on signal characterizations to measure species presence or absence and spatial-temporal occurrence. A novel echolocation click type belonging to an unknown beaked whale species was identified off West Africa, off São Tomé and Príncipe. This signal was identified within data from a passive acoustic monitoring study carried out by JASCO Applied Sciences Ltd. A bottom-mounted autonomous acoustic recorder with a sampling rate of 375 kHz, was deployed off São Tomé from Oct 2018 to Aug 2019 (294 recording days). An automated detector-classifier was run through the data set to identify possible detections of the click. To characterize the novel unknown beaked whale click and assess the performance of the automated detector-classifier, manual analysis was carried out in two phases; 100% manual annotation of clicks within selected files and partial annotation of clicks within all files to measure temporal occurrence. In addition, a subset of files with no automated detections (142 files) were analyzed to confirm that the click was truly absent. The automated detector-classifier was excellent at identifying 2 min files containing clicks with a per file Precision of 1.00 and Recall of 1.00, but missed many individual clicks (per click automated detector Precision=1.00 and Recall=0.01). The novel click had a median centroid frequency of 45.4 kHz, median peak frequency of 42.1 kHz, median duration of 2333  $\mu$ s, and a median -10 dB bandwidth of 1.4 kHz. The median inter-pulse interval was 88.4 ms. The click was present in all recording months with no mean change in the number of files containing clicks across months ( $H = 9.30$ ;  $p$ -value = 0.50;  $df = 293$ ). This click was only present at night, indicating a prominent diel cycle and suggesting nocturnal foraging. When compared to signals of described beaked whale species, this click appears to be unique and therefore, species identification remains unsolved. This study provides a detailed acoustic characterization of the unknown click, which improves the diagnostic criteria for future studies.



## Identification Of Ubiquitin Ligases (E3s) Involved In Plant Tolerance Of Nutrient Stress

**Author:** Amber Showers

**Programme:** Biology Co-op

**Supervisor(s):** Dr. Sophia Stone, Biology Department, Dalhousie University

### Abstract

The ubiquitin-proteasome system (UPS) is what cells use to degrade proteins that are no longer needed to maintain homeostasis. Ubiquitin ligases (E3s) are what give the UPS its specificity to target proteins by binding to them attaching a chain of ubiquitin (a signalling molecule) to the proteins, which signal the UPS to degrade that protein. Each E3 will only target a couple of different types of proteins. There are many different types of E3s which allows for the UPS to have a wide range of proteins that it regulates. Plants such as *Arabidopsis thaliana* use the UPS to regulate pathways that are involved in the plant's response to Iron and Nitrogen stress by controlling the abundance of activators and inhibitors of these pathways. Iron is a micronutrient that can be toxic to the cells if in too high quantities leading to chlorosis. Low iron conditions can be detrimental to the plant's health as it is needed for photosynthesis and chlorophyll synthesis. Nitrogen is a macronutrient that is used in DNA replication and protein synthesis. Excess nitrogen can lead to over vegetative growth that can reduce the plants' overall health while an inadequate amount of nitrogen can cause chlorosis or even death of the plant. The plants' ability to tolerate nutrient stress is a highly regulated process and to better understand this, I am using *Arabidopsis thaliana* to learn how iron and nitrogen stress are regulated by different E3s. I have used *Arabidopsis thaliana* seeds that contain knockdown mutations of different E3 genes At2g38920, At5g58580, and At5g37910 to compared them to wild-type seedlings that were grown on the same MS media plates. The plates contained different concentrations of iron or nitrogen with there being low, high and control treatments for each nutrient. It is suspected that loss of expression of the genes of interest will alter the plants' tolerance to iron and/or nitrogen stress. To determine if this is the case, I have been measuring the number of lateral roots, length of primary roots, the biomass of the plants and the chlorophyll content.



## **Assessing the Susceptibility of Nova Scotia's Marine Protected Areas to Aquatic Invasive Species in a Changing Climate**

**Author:** Charlotte Smith  
**Programme:** Marine Biology with a minor in French  
**Supervisor(s):** Dr. Derek Tittensor, Biology Department, Dalhousie University  
Dr. Nick Jeffery, Bedford Institute of Oceanography

### **Abstract**

Expanding aquatic invasive species (AIS) distributions are a rising concern, as invasive species are one of the five principal drivers affecting global biodiversity and are a significant economic challenge. AIS and climate change are critical ecosystem stressors that can impact Marine Protected Areas (MPAs), designed to preserve and restore ecosystems and achieve long-term conservation. Incorporating climate-driven AIS into MPA planning is therefore increasingly necessary to ensure their effectiveness and to mitigate invasion impacts. This research focuses on assessing the risks of invasion in Nova Scotia's three MPAs and two Areas of Interest (AOIs) under current and future climate change scenarios. It analyzes how invasion patterns may differ under moderate and high climate change projections and highlights the impacts of climate mitigation strategies. I used a combination of two tools to assess the invasion risk of six AIS prevalent in Nova Scotia: (1) a set of current and future species distribution models (SDMs) to predict areas suitable for establishment and (2) a screening level risk assessment tool (The Canadian Marine Invasive Screening Tool (CMIST)) to generate risk scores, based on likelihood and impact of invasion, for each species. SDMs were developed by combining AIS presence data, provided by Fisheries and Oceans Canada (DFO), and the environmental variables temperature and salinity, to project distributions and predict the spread across MPAs. SDMs were run for each species in the present day and for the year 2075 under the RCP4.5 and RCP8.5 climate scenarios. Under a changing climate, I identify high risk MPAs and AOIs that are vulnerable to future expansion of invaders. Predicting and understanding the current and future spatial distributions of AIS is a powerful tool to help inform optimum MPA network design, management and monitoring.



## **Modeling Associations Between DNA From The Gut Microbiome, And Secondary Clinical Outcomes Of Infection In Pediatric Cancer Patients**

**Author:** Rebecca Smith  
**Programme:** Biology Co-op  
**Supervisor(s):** Dr. Joseph Bielawski, Biology Department, Dalhousie University

### **Abstract**

Despite improvements to cancer treatments leading to increased overall survival rates, infections remain a major cause of morbidity in pediatric cancer patients. Emerging research has linked the gut microbiome to immune function, and more specifically the prevalence and outcomes of infection in pediatric cancer patients. This research examines whether the bacterial PER-1 gene, collected from the gut microbiome of pediatric cancer patients, is causally related to the secondary clinical outcomes of 'infection' and 'febrile neutropenia', a condition characterized by a high fever and low neutrophil count. Genetic samples of the gut microbiome were collected through stool samples, and a shotgun metagenomic approach was taken to isolate the PER-1 gene. To determine if a causal relationship is present between the various collected genotypes of the PER-1 gene and the clinical phenotypes of infection and febrile neutropenia, the Phenotype-Genotype Branch-Site Model (PG-BSM) is used. This framework is a unique statistical approach developed to formally test whether an association exists between the evolutionary dynamics of gene sequences and any discrete phenotype. Using PG-BSM, the evolutionary dynamics of selection intensity and rate of change in selective intensity over time of the PER-1 gene can be estimated. PG-BSM will also test for statistical evidence of association and causation between the genotypes of the PER-1 gene and the clinical phenotypes of 'infection', 'febrile neutropenia', and 'no infectious symptoms'. If an association is found, this will provide evidence of a possible causal relationship between the PER-1 gene and clinical outcomes of infection in pediatric cancer patients. These findings will act as a guide for future research into the impacts of the gut microbiome on infectious outcomes. As well, these findings may provide clinicians with a general tool to better predict the probability of a patient developing secondary infectious outcomes based on a metagenomic analysis of their gut microbiome. This would allow treatment of pediatric cancer patients to be individualized by informing clinical approaches that can be streamlined to each patient's risk of infection. Overall, these findings could help to improve quality of life in pediatric cancer patients.



## Mushroom For Improvement: Assessing Sequential Culture Of Algae And Fungi To Remediate Food-Grade Wastes

**Author:** Mab Speelman  
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**Supervisor(s):** Dr. Hugh MacIntyre, Oceanography Department, Dalhousie University

### Abstract

Microalgae are produced commercially for aquaculture, human consumption, and building materials. However, large-scale production of algae requires nutrients and energy, which can be costly. Organic- and nutrient-rich liquid by-products of food industries may be used to reduce these costs. Their use provides nutrients to the algal cultures and reduces nutrient loading in aquatic environments. Excess nutrient loading contributes to near-shore hypoxia, harmful algal blooms, and loss of critical habitat such as seagrass beds. I have tested food-grade wastes as substrates for growth of several marine phytoplankton. Mixotrophic algae can use the wastes as alternative nutrient sources, but after harvest, the media remains high in inaccessible residual nutrients (notably dissolved organic nitrogen). Fungi are able to digest and consume a wide variety of organic substrates, making them a prime candidate for further remediation. Subsequent culture of fungi, following the growth of algae on waste-amended media, would be a source of additional high-value biomass.

While there are marine fungi, many are pathogenic and unsuitable for cultivation. However, one study has demonstrated growth of terrestrial oyster mushrooms in seawater (Lalitha et al., 2019, J. Coast. Res. 86: 138-141). I have tested growth of five species of edible fungi, gradually acclimated to increasingly saline media, to assess their growth rates and biomass production in saltwater media. Four of them now grow in full-strength seawater. These will be tested in media amended with three food-grade wastes—vinasse (from distillation), whey permeate (from cheesemaking), and the aqueous phase from hydrothermal liquefaction (HTL-AP) of fish processing waste. Those that can grow with these organic substrates will be tested for growth on the residual nutrients from culture of the diatom *Phaeodactylum tricornutum* grown on the food-grade wastes. The efficiency of remediation will be assessed by nutrient analysis following harvest of the fungal biomass. This will determine whether the sequential culturing of algae and fungi is more cost-effective and more efficient at remediation than culture of either organism alone. The sequential culturing under testing in this project has the potential to produce both marine algal and fungal biomass, valorize food-grade liquid wastes, and remediate nutrients before they enter aquatic environments.



## **Spatial and Temporal Variability in Benthic Megafaunal Communities in the Bay of Fundy**

**Author:** Calisa Staniforth  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Ellen Kenchington, Bedford Institute of Oceanography

### **Abstract**

The Bay of Fundy hosts extensive sea scallop (*Placopecten magellanicus*) beds that are fished yearly within six management areas known as scallop production areas (SPAs). Bottom trawling operating in these SPAs has created a cause for concern as these fishing activities spatially overlap with important benthic habitats. This study aims to investigate the impacts of bottom-contact fishing on the associated benthic communities of these commercial scallop grounds. Multivariate community analyses of presence/absence data from three survey sites, or SPAs, were used to quantify and describe spatial and temporal differences in the composition and structure of the benthic communities between 1997 and 2007-08. Environmental and anthropogenic (fishing activity) drivers of community change were further analyzed. Preliminary results indicate that community composition and structure has changed over the ten-year period. There has also been a community-wide shift in the biological traits of the benthic species. Considering the persisting trawling activities, it is likely that large, attached, and filter-feeding epibenthic species were replaced with small, motile scavenging and opportunistic species. The primary cause of the temporal change is unknown, however the literature suggests that the physical impacts from the fishing gear largely contributed to this shift. This may have also been driven by secondary factors such as post-fishing mortality events, and environmental stressors.



## Characterizing the Expression of Rhodopsin in *Oxyrrhis marina*

**Author:** Aleksei Sychterz  
**Programme:** Biology  
**Supervisor(s):** Dr. Claudio Slamovits, Biochemistry Department, Dalhousie University

### Abstract

*Oxyrrhis marina* is a marine unicellular protist found all over the world in warm ocean conditions. They are the closest living relative to modern dinoflagellates and their position as a basal dinoflagellate provides a unique ability to study the evolutionary basis for unique dinoflagellate genomic features. One such feature is the absence of transcriptional and translational regulatory factors for some dinoflagellate genes, instead relying on post-translational modifications. It is unknown which genes have evolved this unique reliance on post-translational modifications or even the evolutionary origin of an emphasis on post-translational modifications. This experiment hopes to provide insight into this question by analyzing the genetic expression of rhodopsin genes in *Oxyrrhis marina*. Since rhodopsin genes are present in the eukaryotic common ancestor, I hypothesized that rhodopsin genes in *Oxyrrhis marina* would not rely on post-translational modifications. To analyze rhodopsin expression, *Oxyrrhis marina* was cultured in three light levels: 24 hours of light a day, 24 hours of darkness a day and, 12 hours of light and 12 hours of darkness a day. This was done to facilitate differential expression of rhodopsin proteins. If the mRNA expression did not match this differential expression, then it would show that rhodopsin genes rely more on post-transcriptional regulation. RNA was then extracted from each condition every 24, 48 and 72 hours before being converted into cDNA. Finally, a qPCR test was performed on each sample and CQ values were compared using a student's t-test. I intend to express these results at a later time.





## **The Effect Of Synthetic Cannabinoids On The Anti-Inflammatory Response Of Alternatively Activated Cultured Macrophage Cells**

**Author:** Rachel Thompson  
**Programme:** Biology  
**Supervisor(s):** Dr. Eileen-Denovan Wright, Pharmacology Department, Dalhousie University

### **Abstract**

The endocannabinoid system (ECS) impacts many physiological functions in the human body as cannabinoid receptors are distributed across various systems and cell types. There is a potential to use synthetic cannabinoids to modulate the ECS for therapeutic effects but this opportunity is limited by the lack of understanding of how the activation of either cannabinoid type 1 (CB1), cannabinoid type 2 (CB2), or both CB1 and CB2 receptors can impact cell function where these receptors are present. Both CB1 and CB2 receptors are abundant in immune cells, such as macrophages; these innate immune cells are responsible for defense and repair after infection or injury to the body. Macrophages release pro-inflammatory mediators as they phagocytize and clear cellular debris while also having the plasticity to transition to an anti-inflammatory phenotype involved in tissue repair and the resolution phase of healing; a balanced immune response by macrophages is critical for proper immune function. This project determined whether synthetic cannabinoids selective for either CB1, CB2, or both CB1 and CB2 receptors enhance or inhibit the anti-inflammatory phenotype of macrophages. To determine how cannabinoids impact the plasticity of macrophages, cultured RAW 264.7 cells were treated with 20 ng/mL of interleukin-4 to induce an anti-inflammatory phenotype and 10 ng/mL of synthetic cannabinoids selective for either CB1, CB2, or both CB1 and CB2 receptors. Changes in mRNA expression for genes associated with the pro-inflammatory and anti-inflammatory phenotypes were observed using polymerase chain reactions. Results for how synthetic cannabinoids with varying selectivities for CB1 and CB2 receptors affect the anti-inflammatory phenotype of macrophages will be presented. These findings will help guide the development of novel cannabinoid-based therapies as they will further the understanding of how cannabinoids impact immune function.



## Investigating The Role Of Ring-Type E3 Xbat31.1 Overexpression In Iron Uptake

**Author:** Sophia Tonks  
**Programme:** Biology Co-op  
**Supervisor(s):** Dr. Sophia Stone, Biology Department, Dalhousie University

### Abstract

The ubiquitin proteasome system (UPS) is a critical part of iron uptake, as it can control the abundance of iron-uptake-related-genes by ubiquitin ligases, or E3s. E3s are responsible for recruiting substrates through the attachment of ubiquitin molecules to selected proteins, ultimately regulating the presence of selected substrates within a cell. Of interest is the *Arabidopsis* RING-type E3, XBAT31, which has previously been shown to have a role in iron uptake in plants. Alternative splicing produces two isoforms, XBAT31.1 and XBAT31.2, of which only XBAT31.1 transcript levels are upregulated under low iron conditions. When XBAT31.1 function is disrupted in mutant plant lines, *xbat31-1*, they grow similarly to wild type under iron deficient growth conditions, but are more tolerant of excess iron. These findings suggest a role for XBAT31.1 in regulating iron uptake and added tolerance to excess levels.

In order to further characterize XBAT31.1, an overexpressing version, XBAT31.1OE, was generated. Rhizosphere acidification and stress assays were then used to assess growth and iron uptake under excess and low iron conditions. XBAT31.1OE displayed the same growth patterns as wild type and *xbat31-1* in low iron conditions, and grew less effectively than wild type and *xbat31-1* on excess iron. These results further display the presence of XBAT31.1 in iron uptake. Studies of this E3 as a regulator of iron-uptake are important for understanding growth and development in plants, thus, enhancing plant productivity.



## A Comparative Analysis Of Striated Muscles In Non-Bilaterian And Bilaterian Animals

**Author:** Marco Turner  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Nicanor González-Morales, Biology Department, Dalhousie University  
Dr. Roger Croll, Physiology Department, Dalhousie University

### Abstract

Evidence of striated muscles has been documented in both bilaterian and non-bilaterian animals. Striated muscles have been documented within both ctenophores and cnidarians, which are the two phyla of non-bilaterian animals with defined muscle systems. Prior work has found that ctenophores and cnidarians lack relevant orthologs for some of the key proteins that make up striated muscles. Considering that these proteins are conserved throughout the rest of the animal kingdom, this observed phenomenon brings forth the potential for striated muscles to have evolved separately, once in Bilateria and once in ctenophores and cnidarians. The broader goal of this study is to support this theory and contribute to the ongoing discussion pertaining to the evolution of striated muscles. To achieve this, there are two major methodologies that were employed. The first is to perform dissections and document the presence of striated muscles within ctenophores available off the coast of Nova Scotia (*Pleurobrachia pileus*). This was done by staining the samples with phalloidin, which binds to actin and allows for a clear view of the striations under fluorescence microscopy. The second methodology is to repeat the bioinformatics work surrounding the relevant orthologs across more species of ctenophores, as the preliminary work was only done for a single species of ctenophore. This was done using the available genomic data across 29 species of ctenophores, along with several bilaterian and cnidarian controls. The preliminary results of this work indicated that *P. pileus* does not have striated muscles, although the work has provided a foundational understanding of the muscle systems within the animal. It has also been determined that ctenophores and cnidarians are missing several orthologs related to Z-disc proteins, some of which are documented to be crucial to muscle structure and function within Bilateria. Future work for this project involves sampling other species of ctenophores or cnidarians and following similar dissection and staining techniques, with the goal of identifying striated muscles within other species. Overall, the results of this study were unable to definitively support the prior theory of convergent evolution, however, this work adds to the ongoing discussion.



## **Assessing The Impact Of Visual Media As An Outreach Tool For Marine Conservation: Historical And Present Applications**

**Author:** Molly Wells  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Heike Lotze, Biology Department, Dalhousie University  
Dr. Jennifer Stamp, Psychology & Neuroscience Department, Dalhousie University

### **Abstract**

There is often a disconnect between the academic and public spheres in terms of knowledge and understanding of ocean issues, which limits conservation action. Throughout history, visuals have bridged this gap by facilitating ocean education and exploration by proxy. More recently, art-science collaborations have been promoted as a way to engage with the public and elicit emotional responses and changes in behaviour or action. Still, many scientists hesitate to use art in outreach as it is considered unconventional and difficult to evaluate. The purpose of this study was to evaluate the usage of different types of visual media in marine science outreach over time, using historical and modern survey methods. First, a historical review was conducted to investigate changes and trends in marine zoological illustration through time. European illustrations from 350 BC up to the 21st century were analyzed with respect to their purpose, execution, scientific and social impact, and trends were compared qualitatively between and within time periods. Overall, visuals were used to investigate, communicate, and popularize marine science. The coevolution of marine zoological illustration and public interest in marine life provides insight into the potential of contemporary marine art-science collaborations. Second, an online survey was created to assess the impact of different visual media types on university student responses to marine conservation topics. Participants read three articles and responded to 19 questions including Likert scales, multiple choice, and open answer formats, designed to evaluate attributes that contribute to a person's likelihood to take action regarding conservation issues. Each article was accompanied by either an art piece, a scientific illustration, or a photograph. Responses were analyzed using Analysis of Variance and Chi-Square tests to measure the effect of media type on responses. Results can inform marine science outreach strategies as to how the visual presentation of topics may affect public opinion and action. Overall, this research can help overcome concerns regarding art-science collaborations and encourage their use in ocean education and marine conservation.



## Characterization And Phylogenetic Placement Of A Novel Groove-Bearing Heterotrophic Flagellate

**Author:** Elizabeth Weston  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Alastair Simpson, Biology Department, Dalhousie University

### Abstract

The overwhelming majority of described eukaryotic species are macroscopic organisms in the kingdoms Plantae, Animalia, and Fungi; however, single celled protists make up the bulk of eukaryotic diversity. To improve the resolution and utility of the Eukaryotic Tree of Life, more cell morphological and molecular data for undescribed, deep-branching protists is needed. Soap-colp is an undescribed heterotrophic flagellate extracted from sediments of Soap Lake, WA. Soap-colp bears a conspicuous ventral groove, a trait also observed in distantly related lineages across the breadth of eukaryote diversity. Preliminary analyses of 18S rDNA suggest that Soap-colp may be a deep branching stramenopile, though with weak statistical support. Together this implies that Soap-colp may be of outsize importance for understanding the early evolution of eukaryotes, including the cellular characteristics of the Last Eukaryotic Ancestor (LECA).

The initial culture of Soap-colp also contained *Isochrysis* sp. provided as prey and an uncharacterized eukaryotic contaminant. In this study, a dieukaryotic culture containing Soap-colp and *Isochrysis* sp. was established using single cell isolation. Then, the prey range of Soap-colp was tested using six species of marine algae in triplicate cultures with Soap-colp abundance measured at 10-day intervals. After 20 days Soap-colp abundance plateaued in cultures feeding on five out of six algal prey species. By contrast, cultures feeding on *Phaeodactylum tricorutum* grew to an abundance similar to that observed in controls with the original prey ( $2 \times 10^4$  cells/mL after 30 days).

Preliminary Transmission Electron Microscopy indicates that Soap-colp has tubular mitochondrial cristae (a trait consistent with, but not proving stramenopile affinity) and eukaryotic prey were observed within food vacuoles. Additional 18s rDNA analyses will be reported focused on alternate taxon sampling and limiting long branch attraction to improve statistical support for the placement of Soap-colp. Nuclear genome sequence data are available for *Phaeodactylum tricorutum*. Therefore, efficient cultivation of Soap-colp on this prey will facilitate future work involving transcriptome or genome sequencing. This will make it possible to better infer the phylogenetic placement of Soap-colp using multigene phylogenetic analyses.



## Identification And Characterization Of Novel Aquatic Bacteria With Hydrocarbon Degrading Capabilities Using MinION Nanopore Sequencing Technology

**Author:** Alexander CWC Wong  
**Programme:** Marine Biology  
**Supervisor(s):** Dr. Joerg Behnke & Dr. Caroline Chénard  
NRCC Halifax: Algal Genomics and Synthetic Biology Lab

### Abstract

While anthropogenic spills cause costly, extensive damage to aquatic ecosystems, nearly half of hydrocarbon released into the ocean each year originates from natural sources called oil seeps. As a result of this, many aquatic microbial communities have acquired a natural metabolic response to environmental hydrocarbon contamination. In these communities the presence of hydrocarbons triggers a cascading shift in community composition where bacteria with specialized metabolisms degrade specific hydrocarbons within the complex mixture, leaving behind more simple substrates for subsequent strains to metabolize. Following the Deepwater Horizon spill in 2010, researchers noticed these compositional shifts and began research to understand the hydrocarbon degrading capabilities of the microbial communities for the development of new bioremediation methods. In our research, we worked with two strains of hydrocarbon degrading bacteria isolated from freshwater samples collected in the Gulf of Saint Lawrence on a research cruise conducted in 2020 by the Center for Offshore Oil and Gas Energy Research. Using MinION nanopore sequencing technology we sequenced the genomes of both strains. The 16s ribosomal RNA retrieved from genomes revealed that both strains belong to the genus *Pseudomonas*, which are known to have a wide metabolic diversity and to metabolize many different forms of volatile pollutants. We conducted growth experiments to determine a suitable single carbon source growth medium for subsequent incubation experiments. Growth mediums DY-V, M9 minimal medium, and mineral salts medium in combination with acetate, glucose, and pyruvate as candidate carbon sources were examined. Growth curves generated from OD600 readings showed that after a 72-hour incubation strain MD05 yielded the most growth when cultured in M9 minimal medium with glucose and strain MD04 did not appear to yield significant growth in any of the tested media/carbon combination. We are now developing a protocol to test the effects of marine diesel as a hydrocarbon source and as a contaminant on the bacteria's transcriptome using MinION nanopore sequencing. By comparing the transcriptomes of contaminated cultures against control cultures we hope to identify differentially expressed genes to better understand and characterize the response towards hydrocarbon contamination.



## **An Analytical Investigation And Metabolomics Of Mississauga Food And Medicinal Plant And Fungal Extracts**

**Author:** Susanna Zhang  
**Programme:** Biology  
**Supervisor(s):** Dr. Jonathan Ferrier, Biology Department, Dalhousie University

### **Abstract**

Canada exhibits a structural system that affects the health and healthcare of Indigenous populations. This system prioritizes Western medicine, and other approaches to medicine have thus been limited in order to enforce assimilation. The potential for discovery of useful metabolites and natural products have also been limited as indigenous medicine has been largely uninvestigated. The Mississaugas of the Credit First Nation (MCFN) is part of the Anishinaabe (Ojibwe) Nation, one of the largest Indigenous nations in Canada. Traditional Anishinaabe territory extends across southern Ontario. This land is the habitat for numerous boreal, continental and Carolinian plants.

A catalog developed previously by the Ferrier lab focused on identifying, categorizing and indexing plants from the Anishinaabe nation. A Bayesian analysis was used to create a ranking of plant priority based on frequency of citation in the Ferrier library. This method of listing will then dictate which plant families should be investigated. In order to determine which plants are most pharmacologically significant, plant extracts were analyzed using NMR, creating a fingerprint spectra.

The statistical analysis of NMR spectra created by NMR bucketation allows for outliers to be easily identified. Outliers are created through searching for spectra that showed unusual compositional characteristics; either unusually high levels of secondary metabolites, or atypical secondary metabolites. An S plot created through PCA of NMR spectra indicates that certain members of plant families are more bioactive than others. These plant families should be further investigated in medicinal usefulness, or toxicity. Some plant families ranked highly did not appear as outliers, while other plant families with low predicted bioactivity appeared more bioactive than predicted. This is attributed to differences in traditional preparation methods.

In continuation, bioassays will be performed on significant plant species to further examine the mechanisms behind a plant's medicinal significance in relation to its chemical profile, as well as potential as a method of treatment. By investigating these plants, we can provide an idea of why certain plants have been utilized effectively as medicine, discover useful natural products, and provide insight to anyone seeking to better use and understand Anishinabe ethnobotany through Western science.