DALHOUSIE
UNIVERSITY

Cameron 35th Annual Conference

FOR BIOLOGY & MARINE BIOLOGY
HONOURS STUDENT RESEARCH

Saturday
13 February 2021
9:30 am - 4:00 pm

Sponsored by the Department of Biology

&

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Biology Students

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DAMS

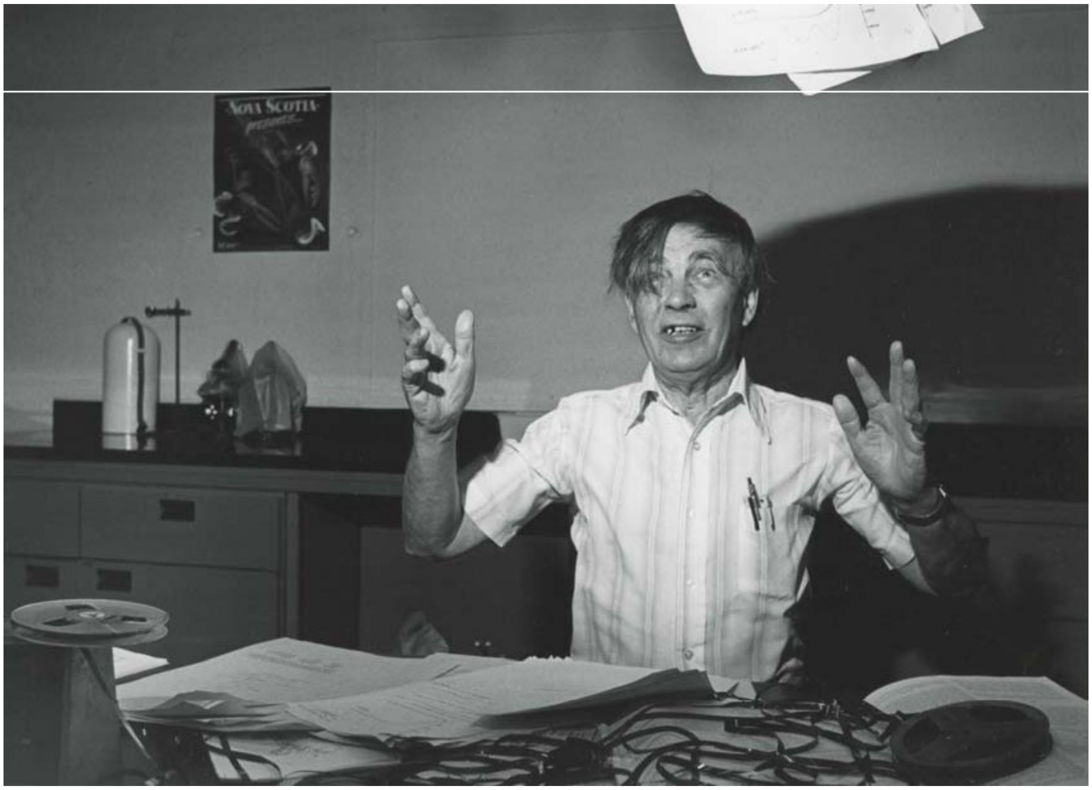
On the Origin of the Cameron Conference

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



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

A Virtual Event

9:30 am

Conference Welcome

Professor Paul Bentzen
Chair of Biology Department

9:45-11:00 ~ Poster Session 1

1	Bashar Alazemi	Effects of Small Molecules on Alpha Synuclein Misfolding
2	Samantha Beal	Detecting Endangered Atlantic Whitefish Presence and Genetic Diversity Using Environmental DNA
3	Chantelle Clermont	Landscape Genetics of the Fish *Basilichthys microlepidotus*, in a Dendritic Freshwater System.
4	Darby Gielewski	Using Gill Surface Area as a Predictor of Metabolic Rate in Teleost Fish
5	Rami Habib	Initial Toxicological Risk Assessment of Germanium nanoGICs
6	Lexi Hall	Molecular Phylogenetic Analysis of Petalomonads Using SSU rDNA Sequence Data

7	Caroline Hill	An Analysis of *Arabidopsis thaliana* RING E3 Gene Expression During Exposure to Abiotic and Biotic Stresses
8	Jenna Liang	Comparative Transcriptome Analysis of Anthocyanin Biosynthesis Genes During Lace Plant *(Aponogeton madagascariensis)* Leaf Development and Programmed Cell Death
9	Ted Lownie	Aerobic Capacity Predicts Breeding Success in Giant Petrels (Macronectes spp.)
10	Tessa Macaulay	Analysis of *Arabidopsis thaliana* RING-type Ubiquitin Ligases Using Protein-Protein Interaction Datasets
11	Hannah Nickel	Developmental Differences and Reproductive Consequences of Submerged and Aerial Floral Morphologies in the Aquatic Plant *Lobelia dortmanna*
12	Oguz Ozgoren	Effects of Nutrient Deficiency and High-Fat Diet Exposure on Maternal and Fetal Hypothalamic Transcriptome
13	Kayla Young-Daigle	Gastropod Buoyancy Behaviour and Regulation using *Biomphalaria alexandrina*
14	Ziyang Zhang	Covalent Probes for Glucocerebrosidase (GBA) and **β**-Glucosidase 2 (GBA2)

11:00 - 12:00
Oral Presentations Session 1

Session Chair - Dr. Patrice Côté

Georgia MacDonald	Molecular Dynamics and Enhanced Pathogenicity in Human Coronaviruses
Zach MacMillan-Kenny	Validating Species Distribution Models for Aquatic Invasive Species
Heidi Tate	Physiological Response of Pacific Auklets to Interannual Variations in Marine Climate
Kristen Tymoshuk	Diversity and Population Structure Among Resident Populations of *Galaxias maculatus* in Patagonia

12:00 - 1:30

Lunch Break
(At the Kitchen Nearest You!)

1:30 - 2:40 ~ Poster Session 2

1	Courtney Baumgartner	Investigating "Motherese" in Eastern Caribbean Sperm Whales (*Physeter macrocephalus*) through Coda Communication
2	Emma Bradshaw	Analyzing the Effects of Sea Surface Temperature and Ocean Acidity on Global Tropical, Shallow-Water Reefs
3	Valentina Ceballos	Comparing Visual and Acoustic Surveys for the Dynamic Management of North Atlantic Right Whales (*Eubalaena glacialis*) in Canada
4	Nan Chen	Coupling Phytoplankton Biomass Production to Remediation of Fish Processing Waste
5	Emma Leitao	Simulating *Calanus finmarchicus* (copepoda) response to environmental variability with a 1-D individual based model in the Northwest Atlantic Ocean
6	Bailey Levesque	Determining the Effect of Hurricane Dorian on the Structure and Composition of the Microbial Community in the Bedford Basin
7	Abbey Lewis	Sperm Whale (*Physeter Macrocephalus*) Social Unit Distribution Around Dominica, Eastern Caribbean
8	Jenny Li	Design, Assessment and Use of Signal Classifiers in Autonomous Recording Unit Data for Five Bird Species at Risk in Nova Scotia

9	Olivia Melville	The Microbial Community in Arctic Waters – A Metagenomic Analysis
10	Victor Papaiz	Using Sportfishing Tournament Data to Determine Factors Influencing Black Bass (*Micropterus* spp.) Catches and Catch Trends
11	Jaime Rae	Elevations of Lobster and Crab Fishery Groundlines and Buoy lines and the Associated Entanglement Risk to North Atlantic Right Whales in the Gulf of St. Lawrence
12	Shannon Myles	Can Biomonitoring the Northwestern Atlantic Scotian Shelf with eDNA Metabarcoding Reveal Interactive Communities and Keystone Species?
13	Hannah Solway	Determining Habitat Use of Baleen Whales in the Northwest Atlantic Ocean That Overlap with Human-Use Patterns
14	Emma Touchie	Comparing Spatial and Temporal Patterns in Trait Diversity Between Fisheries Landings and In-situ Coral Reef Surveys
15	Zachary Wallot-Beale	Localization of North Atlantic Right Whales using a Deformable Array of Passive Acoustic Monitors
16	Taylor Watts	Sediment Grain Size as an Alternative Indicator of Suitable Habitat for *Zostera marina*

2:45 - 3:45

Oral Presentations Session 2

Session Chair - Dr. Patrice Côté

Kate Arpin	Population Genetics and Dispersal Patterns of *Membranipora membranacea*, an Invasive Bryozoan
Julia Dugandzic	Marine Microbial Interactions and Vitamin-Exchange
Monika Neufeld	Faunal Communities at Inactive Hydrothermal Vents
Megan Shin	Estimating the Current Global Population of Sperm Whales (*Physeter macrocephalus*)

3:45

Closing Remarks - Dr. Margi Cooper

Abstracts

LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME

Effects of Small Molecules on Alpha Synuclein Misfolding

Author: Bashar Alazemi
Programme: BSc Major in Biology (Hons) & Minor in Psychology
Supervisor(s): Dr. Kathryn Vanya Ewart, Department of Biochemistry and Molecular Biology & cross appt. Biology, Dalhousie University

Abstract

Parkinson disease (PD) is the second most prevalent neurodegenerative disorder affecting approximately 1% of the population of 60 years and older (Tysnes & Storstein 2017 J Neural Transm. 124:901–905). In PD, there is decreased dopamine synthesis in the central nervous system, which leads to severe motor symptoms. PD is now considered as a syndrome that encompasses many etiologies (i.e., underlying causes) (Tysnes & Storstein 2017. J Neural Transm. 124:901–905). One etiology is the misfolding of alpha-synuclein (aS) protein, which results in toxic amyloid oligomers and fibril formation (Esposito 2014. Top Med Chem. 18: 43-109). The latter tends to aggregate into structures such as Lewy bodies and neurites, a dense indigestible insoluble core of misfolded proteins (Esposito 2014. Top Med Chem. 18:43-109).

In its native form, aS exists as an unfolded monomer and as an alpha-helical tetramer, in equilibrium (reviewed by Esposito, 2014. Top Med Chem. 18:43-109). Shifting this to favour the alpha-helical tetrameric form may prevent amyloid formation, as it is the monomer that appears to convert to amyloid (Dettmer et al. 2015. Nat Commun. 16:7314). From this perspective, studies have focused on restoring the native form of aS as a potential treatment for PD (Zella et al. 2019. Neurol Ther. 8:29–44). Small molecules may affect protein misfolding in different ways, with some possibly favouring the native structure over amyloid formation. Thus, the hypothesis is that one or more small molecules in a representative selection will affect amyloid formation by aS. Due to the prion-like nature of aS (Zella et al. 2019. Neurol Ther. 8:29–44), rabbit erythrocytes were used as a safer model system to study the protein since erythrocytes contain aS (Barbour et al. 2008. Neurodegenerative Dis. 5:55–59). Osmolyes, antioxidants, natural extracts and a PD drug are being investigated by incubating lysed erythrocytes with these molecules under conditions that favour amyloid formation. Following incubation, western blotting with anti-aS antibody-based binding followed.by a conjugated secondary antibody and chemiluminescent detection allow determination of the amyloid form of the protein. Results and suggestions for next steps will be discussed.

Population Structure and Dispersal Patterns of *Membranipora membranacea*, an Invasive Marine Bryozoan

Author: Kate Arpin
Programme: Biology
Supervisor(s): Dr. Anna Metaxas, Oceanography Department, Dalhousie University
Dr. Paul Bentzen, Biology Department, Dalhousie University

Abstract

The marine bryozoan *Membranipora membranacea* is invasive to the North-West Atlantic Ocean, where it devastates kelp beds and often causes ecosystem phase shifts. It is thought that *Membranipora* colonies spread from the North-East to the North-West Atlantic through ship ballast water, which led to its first observation in the Gulf of Maine in the 1990s. Its range has since appeared to expand northwards; however, the mechanism and pattern of its range expansion along Eastern Canada remain unknown. My research uses microsatellite markers to examine genetic variation and structure among populations of *Membranipora* in the North-West Atlantic. I will investigate the genetic structure of *Membranipora* colonies to assess whether ocean currents could be a potential transport mechanism for larval dispersal. I will also identify potential founder populations to provide evidence for the number of independent invasions. This research will be crucial in predicting future *Membranipora* range expansion and its associated ecological consequences, in addition to acting as a case study for the pattern of spread in an invasive species with a long larval stage.

Investigating "Motherese" in Eastern Caribbean Sperm Whales (*Physeter macrocephalus*) Through Coda Communication

Author: Courtney Baumgartner
Programme: Marine Biology
Supervisor(s): Dr. Hal Whitehead, Biology Department, Dalhousie University
Taylor Hersh, Biology Department, Dalhousie University

Abstract

Sperm whales use stereotyped patterns of clicks, called codas, for social communication. Calves acquire the coda repertoire of their cultural clan, but how exactly they do so is unknown. One possible assistive mechanism for the acquisition of complex communicative repertoires is 'motherese', where mothers change some aspect of their vocal communication when directed at their infant. The present study set out to determine if codas made in mom-calf clusters differ from codas made in mom-adult clusters, a trend which could indicate that motherese is being used by sperm whales. Behavioural, photographic and acoustic data were collected off the coast of Dominica between 2005–2020. Audio recordings from clusters of two animals (mom-calf and mom-adult) were marked for codas and metrics (number of clicks, duration, inter-click intervals) were extracted for analysis. Codas were classified into discrete types using contaminated mixture models. Analyses were conducted at two levels: all moms combined (n=13 moms) and individual moms with at least 25 codas recorded from both mom-calf and mom-adult clusters (n=6). Codas were compared using three metrics: click length, type, and duration. General Linear Models were used to assess significance of any differences in coda production. For all moms combined, 672 codas were extracted from mom-calf recordings and 651 codas from mom-adult recordings. For both types of clusters, 5-click codas were most abundant (72.8% of mom-calf codas, 76.2% of mom-adult codas) and subsequent analyses were restricted to 5-click codas. The most common types followed the 1+1+3 pattern (89.5% for mom-calf, 85.2% for mom-adult). For the six individual moms investigated in more detail, there was some variation in coda types made in mom-calf compared to mom-adult clusters, but these patterns varied across moms. The average duration of each type did not significantly differ between mom-calf and mom-adult clusters at the combined level but were mostly significant at an individual level. These results suggest that preferences for specific coda types can significantly differ in mom-calf vs. mom-adult clusters, but moms do not modulate their vocal repertoires in the same way. If motherese is at play in sperm whales, it is likely highly influenced by mom identity.

Detecting Endangered Atlantic Whitefish Presence and Genetic Diversity Using Environmental DNA

Author: Samantha Beal
Programme: Marine Biology Co-op
Supervisor(s): Dr. Paul Bentzen, Biology Department, Dalhousie University
Dr. Ian Bradbury, Department of Fisheries and Oceans Canada

Abstract

Endemic to three small, interconnected lakes in Nova Scotia's Petite Riviere drainage, the Atlantic Whitefish is a critically endangered salmonid fish. The most serious threat to the species survival is the spread of invasive predators, Smallmouth Bass and Chain Pickerel, into the remaining Atlantic Whitefish habitat. The number of individuals remaining in the wild is unknown, but genetic estimates of the effective population size are below 100 individuals. Sequencing whole Atlantic Whitefish mitochondrial genomes has revealed 13 haplotypes within the population, providing evidence that the species retains some genetic variation. Current recovery efforts are focused on removing the invasive predators as well as relocating juvenile Atlantic Whitefish to Dalhousie University, where they are captively reared in the Aquatron Laboratory. The goal is to breed Atlantic Whitefish in captivity, and then reintroduce them into their present and former habitats, as well as new habitats. The analysis of DNA shed from organisms, called environmental DNA (eDNA), is a promising tool for detecting species in the wild without the need for visual observation or direct sampling of the target species. Presently, eDNA analysis is being developed as a tool to assess the presence (and potentially the abundance) of Atlantic Whitefish in natural habitats, as well as the presence of predators and other fishes to aid species recovery efforts. This study aims to create an eDNA protocol which can detect Atlantic Whitefish presence in the Petite Riviere, as well as each of the 13 known haplotypes. The relative abundance of the haplotypes will be assessed, providing insights to the genetic variation of the population. Assessing the relative abundance of mitochondrial genotypes is a novel application of eDNA. This work can help conservation efforts for the endangered Atlantic Whitefish by establishing new tools for detection which are non-invasive and do not rely on visual observation. As such, critical habitats for further protection can be identified and conservation efforts targeted to maximize benefits.

Analyzing the Effects of Sea Surface Temperature and Ocean Acidity on Global Tropical, Shallow-Water Reefs

Author: Emma Bradshaw
Programme: Marine Biology
Supervisor(s): Dr. Derek Tittensor, Biology Department, Dalhousie University

Abstract

A rise in atmospheric carbon dioxide concentrations is threatening the survival of calcifying marine species worldwide, including corals. Anthropogenic emissions of CO_2 absorbed by the oceans leads to increases in ocean acidity and decreases in the carbonate ions used by corals for skeletal growth. In addition, increases in greenhouse gas emissions are leading to more frequent bleaching events. In conjunction, these climate change impacts are significantly altering the environment of these sensitive ecosystems. Moreover, given that corals are ecosystem engineers that provide habitat for numerous other species, appropriate management is critical in order to minimize other threats such as overfishing or pollution, and help build resilience over the coming century. Here, I compare and analyze projections of sea surface temperature and surface ocean pH for 2100 from earth-system models with the current global distribution of tropical, shallow-water reefs and coral-containing marine protected areas (MPAs). I then examine whether the effectiveness of these MPA networks will suffice given changes in habitat suitability for these species, with the ultimate goal of understanding how climate change, marine conservation and management will interact to affect the global persistence of coral reefs and their associated biodiversity.

Comparing Visual and Acoustic Surveys for the Dynamic Management of North Atlantic Right Whales (*Eubalaena glacialis*) in Canada

Author: Valentina Ceballos
Programme: Marine Biology Honours
Supervisor(s): Dr. Christopher Taggart, Oceanography Department, Dalhousie University
Hansen Johnson, Oceanography Department, Dalhousie University

Abstract

Until recently, dynamic management of critically endangered North Atlantic right whales in Canadian waters was solely based on visual observations, mainly from aircrafts. This changed in early 2020, as the Government of Canada began using near real-time acoustic detections of right whale calls interchangeably with visual observations to trigger risk-mitigation measures. Comparing visual and acoustic survey methods has become critical for the correct interpretation and combination of survey data, as well as for the development of optimal monitoring strategies. This comparison is impossible to measure empirically due to our inability to observe the true number of whale surfacings and calls that are available for detection. The goals of this study were to develop a simulation-based method to quantitatively compare acoustic and visual surveys, and to use the simulation to inform future right whale management. We first expanded upon an established whale movement model by adding calling and diving behaviors based on previous observations. We then applied this model to generate a realistic distribution of surfacings and calls available for visual or acoustic detection, respectively, for various numbers of whales constrained within dynamic management zones established by Fisheries and Ocean's Canada and Transport Canada in the Gulf of Saint Lawrence. The next step was to model acoustic surveys from ocean gliders and visual surveys from planes and vessels of the simulated whales using realistic survey designs, platform movement characteristics, and detection functions. A Monte Carlo approach was used to estimate the probability of detecting a single call or surfacing from each platform as a function of the number of whales within and transits through each management area. Preliminary results suggest that there are substantial differences between acoustic and visual survey performance, as a single ocean glider transit always correctly identified right whale presence, while the visual surveys required multiple transits and large numbers of whales to detect whale presence. Our results can potentially inform the optimal use of acoustic and visual surveys for right whale monitoring and risk mitigation efforts, and also show that certain limitations must be considered by decision-makers when reviewing survey data.

Coupling Phytoplankton Biomass Production to Remediation of Fish Processing Waste

Author: Nan Chen
Programme: Marine Biology
Supervisor(s): Dr. Hugh MacIntyre, Oceanography Department, Dalhousie University

Abstract

Phytoplankton, prokaryotic cyanobacteria and eukaryotic microalgae, are widely used for bioremediation projects and to produce aquaculture feeds. Some phytoplankton are mixotrophic, utilizing both photosynthesis and heterotrophy to support growth. This can enhance their growth rates and reduce production costs compared to photosynthetic growth alone. This makes phytoplankton good potential candidates for bioremediation of high-nutrient food-grade waste products. Growth of the phytoplankton would reduce concentrations of organic carbon, phosphorous, and nitrogen present in the target waste. The phytoplankton biomass produced could then be used for products such as pharmaceuticals, health supplements, or aquaculture feeds.

Aquaculture is a growing industry that constitutes over 30% of Canadian fisheries. Fish processing in Canada results in more than 50,000 tons of fish biomass annually that must be disposed of. This waste can be digested using hydrothermal liquefaction (HTL) to produce a mixture of char, lipid phase, aqueous phase (AP), and carbon dioxide. Char and the lipid phase are used in fertilizers and biofuels while the ammonium- and organic-rich aqueous phase is considered a waste product.

The aim of the study is to determine was to optimize production of phytoplankton protein using HTL-AP as an amendment in the growth medium. In the first phase, several strains of phytoplankton used in aquaculture feeds were screened to identify candidates, growth light intensity, and amendment concentrations suitable for larger-scale testing. This showed that light intensity had only a minor effect on the concentration-dependence of growth on HTL-AP. The eustigmatophyte *Nannochloropsis oculata* and the green alga *Tetraselmis suecica* had the highest growth rates in the presence of HTL-AP. These are being grown in larger-volume cultures to test for any change in cellular protein content when grown on HTL-AP-amended media.

Landscape Genetics of the Fish *Basilichthys microlepidotus*, in a Dendritic Freshwater System.

Author: Chantelle Clermont
Programme: Marine Biology
Supervisor(s): Dr. Daniel Ruzzante, Biology Department, Dalhousie University

Abstract

This study examined the effect of anthropogenic impact through hydroelectric dams on gene flow and genetic structure on a silverside fish (*Basilichthys microlepidotus*) in 2 dendritic freshwater systems. It was hypothesized that there would be relatively high differentiation between and within river systems, as well as among locations seperated by natural or anthropogenic barriers. Basilichthys microlepidotus is a freshwater pelagic species of silverside fish that is endemic to Chile. Silversides have high dispersal abilities, which may be inhibited or altered by hydroelectric dams in the Biobío and Itata river systems in Chile. A set of 29 microsatellites were analyzed for a total of 1222 individuals collected from 19 locations. Hierarchical STRUCTURE analysis identified 8 population groups with some connectivity between systems, likely arising from the existence of irrigation canals connecting these systems. One population group exhibited high homozygosity, potentially due to its geographic location above a natural waterfall and high elevation. No individuals were found in a number of upstream locations in both river systems, likely as a result of a decline in gene flow resulting from anthropogenic habitat fragmentation and changes in water flow regime.

Marine Microbial Interactions and Vitamin-Exchange

Author: Julia Dugandzic
Programme: Biology
Supervisor(s): Dr. Erin Bertrand, Department of Biology, Dalhousie University

Abstract

Cobalamin (vitamin B_{12}) is widely required by organisms across taxa, for metabolic purposes. Over half of all cultured marine eukaryotic phytoplankton have an obligate requirement for cobalamin, as it is a cofactor in the synthesis of the amino acid methionine. Despite widespread metabolic requirements for cobalamin, no known eukaryotes have been shown to produce it, and the only identified cobalamin producers are select species from bacterial and archaeal domains. Marine cobalamin producers are of particular significance, given that the vitamin has been shown to limit marine primary productivity. This is of note, because phytoplankton play a key role in global biogeochemical cycles, and can have harmful ecological impacts when proliferating in the form of algal blooms. Here, we isolated and cultured marine bacteria from phytoplankton cultures originating from the Northwest Atlantic Ocean, and subsequently classified them according to their role in the cobalamin cycle. We measured bacterial cell density in cobalamin-replete and cobalamin-deplete media to identify bacteria with a metabolic requirement for cobalamin and those without the ability to synthesize it. We then used liquid-chromatography mass spectrometry to measure cobalamin concentrations in bacterial cells, to resolve cobalamin-producing bacteria and cobalamin-blind bacteria (those that do not produce or consume cobalamin). After classifying these bacterial isolates, we re-introduced them to the algae they were isolated from, through the use of co-cultivation experiments. We are currently using these experiments to quantify these microbial interactions as they relate to cobalamin, through measurements of cell density, chlorophyll fluorescence and photosynthetic health. This will allow for the categorization of these interactions as mutualistic, parasitic, or commensal for cobalamin. Through this research, we aim to better understand the roles of cobalamin producers, and the nature of their interactions regarding nutrient availability and cobalamin exchange in marine microbial environments.

Using Gill Surface Area as a Predictor of Metabolic Rates in Teleost Fish

Author: Darby Gielewski
Programme: Marine Biology
Supervisor(s): Dr. Jeff Hutchings, Department of Biology, Dalhousie University
Dr. Anna Kuparinen, Department of Biological and Environmental Science University of Jyväskylä

Abstract

The gill-oxygen limitation theory (GOLT) suggests that the metabolism of aquatic species is limited by the ability of the gills to supply oxygen to body tissues. Keeping GOLT in mind it would then make greater sense to use the area of the gill to estimate metabolism in fish rather than the established method using body mass. Relying on GOLT, we aim to see if using gill surface area is a better predictor of the metabolic rates in teleost fish than total body mass. Using existing experimental data amassed from Fishbase, these three parameters, gill surface area, mass and metabolism, were plotted against each other. Using R, linear models were created, fitting fish gill surface area to metabolism as well as mass to metabolism. A regression will be created for both models and used to see which variable is a better predictor of metabolism. If GOLT holds true, we expect to see gill surface area be a better indication of a fish's metabolic rate over mass. Completion of this research will lead to a more accurate method of calculating fish metabolic rates and could be used to predict how fish's allocation of energy may differ with increased ocean acidification and lower oxygen levels due to climate change.

Initial Toxicological Risk Assessment of Germanium nanoGICs

Author: Rami Habib
Program: Biology
Supervisor(s): Dr. Daniel Boyd, Department of Applied Oral Sciences, Dalhousie University

Abstract

Glass Ionomer Cements (GIC) are esthetic composite dental materials that chemically bond to dentine and enamel. They are a promising treatment for many dental restorations and are inexpensive, minimally invasive, require minimal equipment, and contain a bioactive component that provides antibacterial effects. However, limitations in strength, resistance to abrasion and susceptibility to bulk fractures have prevented their broader adoption in dentistry. NanoGICs offer the potential to address these limitations; however, the glass chemistry required to produce a nanoGIC means deviating from conventional chemistries and exploring new formulations of glass. Consequently, these new formulations raise questions of safety and efficacy that must be systematically examined, in particular toxicological risk. Thus, the objective of this study was to determine the initial biological safety of a promising nanoGIC based on unique aluminum free glass comprising germanium (Ge) and other elemental constituents. The elemental composition designated for this toxicology risk assessment comes from in vitro evaluations of varying Si:Ge ratios of Al-free GICs. This assessment was completed using guidance from ISO-10993-17 and included extensive research from available literature and governmental databases on each elemental component to gain the *no observed adverse effect level* (NOAEL) for statistical analysis. In our most conservative scenario in which the lowest NOAEL, a *concomitant exposure factor* (CEF) value of 0.2 and under the assumption of a full mouth restorations (40 teeth), all the proposed elements are deemed biologically safe (MOS>1). These findings are encouraging for future development of nanoGICs and suggests that biological safety would not be a concern at any composition of the studied elements.

Molecular Phylogenetic Analysis of Petalomonads Using SSU rDNA Sequence Data

Author: Lexi Hall
Programme: Marine Biology
Supervisor(s): Dr. Alastair Simpson, Biology Department, Dalhousie University

Abstract

Most of the breadth of eukaryote diversity occurs not in the well-known kingdoms of animals, plants, and fungi, but rather within the microbial protists. Included amongst these are the euglenids: an ecologically and evolutionarily important group of free-living phototrophic, osmotrophic, or phagotrophic cells that are abundant in marine and freshwater sediments. One major subgroup of phagotrophic euglenids are the petalomonads: small, rigid cells, distinguished by having fewer pellicle strips (usually 4-8) than other euglenids. The four most prominent petalomonad genera, *Petalomonas*, *Notosolenus*, *Scytomonas*, and *Sphenomonas*, have been studied using molecular sequencing to examine their phylogenetic placement. Previous analyses, both single and multigene, indicate that neither *Petalomonas* nor *Notosolenus* are monophyletic groups within the petalomonad clade, and the placement of petalomonads has variously been inferred as within ploeotids (another assemblage of rigid phagotrophs), or as the deepest branch amongst euglenids. Limited taxon sampling within petalomonads, however, has hindered prior phylogenetic analyses. In order to better understand how phylogenetically intermingled the major petalomonad genera are, and the branching location of petalomonads within euglenids, SSU rDNA sequence data from nine new strains of *Petalomonas* and *Notosolenus* were added to a refined dataset of previously available euglenid sequences. Phylogenetic trees inferred using maximum likelihood methods show a poorly resolved placement of petalomonads among euglenids. Within petalomonads, six of the new strains branch within one of the three known major clades, however a potential new fourth clade has been inferred, consisting of one novel *Petalomonas* strain and two novel *Notosolenus* strains. Consequently, both *Petalomonas* and *Notosolenus* remain non-monophyletic across the new and the previously recognized clades. Because the inferred new clade represents an additional conflict between genus-level taxonomy and phylogeny, it becomes increasingly important to examine the accuracy of the morphology-based genus-level assignments. Petalomonad phylogeny will continue to be investigated through further refinement of the existing alignment and analyses using maximum likelihood and Bayesian methods.

An Analysis of *Arabidopsis thaliana* RING E3 Gene Expression During Exposure to Abiotic and Biotic Stresses

Author: Caroline Hill
Programme: Biology
Supervisor(s): Dr. Sophia Stone, Department of Biology, Dalhousie University

Abstract

Plants are constantly faced with environmental stresses, both abiotic and biotic, which affect their overall growth, development, and yield. The Ubiquitin Proteasome system (UPS) composed of ubiquitin molecules, 3 ubiquitination enzymes and the 26S proteasome, allows plants to alter their proteome by selectively removing and destroying proteins in response to external stresses and ultimately helps promote survival. One step of UPS is facilitated by E3 ubiquitin ligases, which attach ubiquitin molecules to the target proteins and mark them for degradation by the proteasome. E3 ligases are categorized into 4 groups based on their substrate binding domain structure: one of which is the RING group. This study aims to understand the roles of RING E3 ligases in response to abiotic and biotic stresses. Through the creation of a searchable database of differential gene expression of 459 known RING encoding genes in the *Arabidopsis thaliana* genome, the genes' responses in the context of different stresses were analyzed. Data used was collected from opensource databases including BAR uToronto and Expression Atlas. Just under half of all RING E3 genes were found to show differential expression toward both abiotic and biotic stresses, and many were shown to respond to abiotic stress alone. Few showed differential expression solely to biotic stresses. Other interesting findings include a noticeably large groups of genes which responded to all 3 stresses of ozone, bacteria and fungi, as well as a group which showed positive expression toward nitrogen limitation while also showing negative expression toward iron deprivation. Four genes, *xbat31-1*, STRF1/ATL63, AT5G37910 and AT2G38920, which have shown differential expression under nitrogen limitation and iron deprivation, were selected for further experimental analysis. Growth of mutant seedlings under nitrogen limitation, nitrogen excess and iron deprivation conditions were compared to that of wild type. In a preliminary trial, growth of *xbat31-1* mutant seedlings was similar to that of wild-type seedlings in all treatments indicating that the gene may not play a role in the process of tolerating iron deprivation or nitrogen limitations/excess stress conditions.

Simulating *Calanus finmarchicus* (copepoda) response to environmental variability with a 1-D individual based model in the Northwest Atlantic Ocean

Author: Emma Leitao

Programme: Marine Biology Co-op

Supervisor(s): Dr. Wendy Gentleman, Engineering Mathematics Department, Dalhousie University

Dr. Catherine Johnson, Bedford Institute of Oceanography

Abstract

Calanus finmarchicus is a marine copepod that dominates the biomass of mesozooplankton in the Northwest Atlantic Ocean and has significant importance as the main prey of the endangered North Atlantic right whale (NARW). In recent years, there have been observed changes in the abundance and distribution of *C. finmarchicus* which could pose a risk for the NARW population. The variability could be linked to changes in the environment, as temperature and food availability have been shown to directly relate to biological processes, such as development rates, within these copepods. This project aims to investigate how food and temperature variability will affect *C. finmarchicus* through the use of a *Calanus* life history model. Models often require a range of parameters, where some are characterized better than others. To estimate some of the less understood parameters, a genetic algorithm was used to optimize a 1-Dimensional Individual Based Model to both the Anticosti Gyre station in the Gulf of St. Lawrence and the Halifax-2 station on the Scotian Shelf. Using food and temperature profiles from characteristically warm and cool years, we then analyzed how these environmental conditions impacted a modelled population of *C. finmarchicus*. While the model optimization did not result in a converged solution of parameters for the model, we were still able to analyze the impacts of environmental variability at the stations. Warm year forcing had negative impacts on *C. finmarchicus* phenology and survivorship between stages while the cool year forcing showed improved timing and abundances in comparison. These results suggest that with the rising of ocean temperatures, *C. finmarchicus* populations will be negatively impacted which in turn will negatively affect North Atlantic right whales.

Determining the Effect of Hurricane Dorian on the Structure and Composition of the Microbial Community in the Bedford Basin

Author: Bailey Levesque
Programme: Marine Biology Co-op
Supervisor(s): Dr. Julie LaRoche, Biology Department, Dalhousie University

Abstract

Microorganisms are essential to biogeochemical processes, photosynthesis, and nutrient cycling in marine environments. Formation of long- term time series analyses using DNA from environmental samples allows for determining baseline structure and composition of specific microbial communities. These analyses also allow for determining the effect of large- and small- scale disturbances on the community. This project aimed to ascertain the effect of Hurricane Dorian on the structure and composition of the microbial community in the Bedford Basin. Weekly water samples were collected from the Bedford Basin in Halifax, Nova Scotia, Canada from 2014- 2019 as a part of the Bedford Basin Microbial Time Series. These samples were filtered through size fractioned filters and DNA was subsequently extracted from the surface of the filters. Extracts were sequenced using Next- Generation Sequencing and data were analyzed through the QIIME 2 pipeline.

Through Non- Metric Multi- Dimensional (NMDS) analysis, samples tended to form clusters based on sampling depth and filter size fraction. The samples formed four distinct clusters. These clusters include the 0.2 µm samples from depths 1, 5, and 10m, the 3 µm samples from depths 1, 5, and 10m, the 0.2 µm samples from 60 m, and the 3 µm samples from 60m. Various amplicon sequence variants (ASV) from Order Flavobacteriales were found only to occur in the 2019 samples following Hurricane Dorian but were not found in the samples taken the year prior. The absence of multiple cyanobacterial ASVs in the 2019 samples surrounding Hurricane Dorian may be indicative of no fall cyanobacterial bloom. This may demonstrate the ability of large disturbances to transiently disrupt annual occurrences within the microbial community. Retrospective analysis will be completed for the time period 2014-2019 for dominant microorganisms present after Hurricane Dorian.

Sperm Whale (*Physeter Macrocephalus*) Social Unit Distribution Around Dominica, Eastern Caribbean

Author: Abbey Lewis
Programme: Biology major, Ocean Sciences minor
Supervisor(s): Dr. Shane Gero, Adjunct Biology, Dalhousie University
Dr. Hal Whitehead, Biology, Dalhousie University
Felicia Vachon, PhD candidate Biology, Dalhousie University

Abstract

Differential population responses to environmental variables and ecosystem changes have been observed across various taxa, including Cetacea. This study explored differential behaviour between social units within the sperm whale (*Physeter macrocephalus*) population living off the west coast of Dominica, Eastern Caribbean. The main objective of this study was to investigate whether these social units occupy different spatial distributions related to habitat type, and if distributions are shifting over time. Data came from photo-identification and GPS location recordings of sperm whale sightings from observational surveys by the Dominica Sperm Whale Project between 2005-2018. Only the first identification of a social unit each day was used for analysis, to account for spatial autocorrelation. Datapoints were mapped using ArcGIS and grouped into north and south categories of canyon, basin, and escarpment bathymetric classes. Where overlap occurred, priority was given to canyons and then basins as sperm whales have been found to prefer these complex bathymetries. Bar plots were created on R to illustrate habitat occupancy for 11 social units. These units primarily occupied the southern escarpment, then the northern escarpment and northern canyon. A chi-square test was performed to determine if social units occupy different habitats, and preliminary results indicate there are no statistically significant differences in habitat preference between units. Further statistical analysis will be done to determine if there are significant differences in habitat preference over time for individual social units, or if unit distributions are shifting over time. The results of this study shed light onto habitat use and spatial distribution of Dominica sperm whales, which holds important consequences for conservation, management, and sustainable tourism efforts around the island.

Design, Assessment and Use of Signal Classifiers in Autonomous Recording Unit Data for Five Bird Species at Risk in Nova Scotia

Author: Jingwen Li (Jenny)
Programme: Marine Biology
Supervisor(s): Dr. Cindy Staicer, Biology Department, Dalhousie University

Abstract

Autonomous Recording Units (ARU) can be used to record animal vocalizations in a non-invasive way. ARUs are being widely used to collect data on bird species, for example to determine the presence of species at risk. ARU recordings generate large amounts of data which can be stored and analyzed to identify target species using algorithms known as species classifiers. The first objective of this study was to build, test, and improve species classifiers to identify the vocalizations in ARU recordings for five bird species at risk: Canada Warbler (*Cardellina canadensis*), Common Nighthawk (*Chordeiles minor*), Eastern Wood-pewee (*Contopus virens*), Olive-sided Flycatcher (*Contopus cooperi*), and Rusty Blackbird (*Euphagus carolinus*). The second objective was to use ARU recordings to identify diel and seasonal patterns in the vocalization activities of the target species. Samples used in this study were 10 min ARU recordings collected in Nova Scotia between 2011-2020. Classifiers were built using Kaleidoscope Pro software, and then used to scan through recordings to identify the target species. Classifier effectiveness were assessed by comparing the species detection and vocalization rates obtained through the classifiers to those from manual analysis. Previous studies used manual analysis to determine true detection rates for a subset of the study samples. Using a confusion matrix, the classifiers for Common Nighthawk showed a high accuracy for detecting the number of samples with at least one target species vocalization, but a lower accuracy for determining the total number of target species vocalizations per sample. The classifiers were then used to determine the diel and seasonal patterns of vocal activity of the target bird species on a new set of 10-min recordings made at different times of the day and season. Results showed that Common Nighthawks were more active 40-60 min before sunrise and 20 min before and after sunset. This procedure of building, testing and applying classifiers will be repeated for the other target species. Results to date show that species classifiers are an effective tool for detecting the presence of a target species within a sample. Determining the diel and seasonal vocal activity patterns for the five bird species will aid conservation efforts by identifying optimal timing for ARU recordings to locate these birds.

Comparative Transcriptome Analysis of Anthocyanin Biosynthesis Genes During Lace Plant *(Aponogeton madagascariensis)* Leaf Development and Programmed Cell Death

Author: Jenna Liang
Programme: Biology
Supervisor(s): Dr. Arunika Gunawardena, Biology Department, Dalhousie University

Abstract

Programmed cell death (PCD) is a genetically controlled or environmentally triggered process, essential to maintain homeostasis in animals and plants by the careful demise of targeted cells. *Aponogeton madagascariensis* or the lace plant is an aquatic monocot endemic to Madagascar. As an emerging novel model organism to study PCD, the lace plant utilizes PCD to form a predictable perforation pattern during leaf development. Leaves emerge in a heteroblastic series where the first three to four leaves do not form perforations during development and are deemed imperforate leaves. All subsequent leaves are perforating, initiating at the pre-perforate stage – characterized by longitudinally furled leaves and an abundance of visible anthocyanin. Window stage leaves are unfurled to reveal a gradient of anthocyanin within leaf areoles and mature stage leaves have completed perforations with no visible anthocyanin pigmentation. Past research has characterized the cellular changes accompanying lace plant leaf morphogenesis however, the underlying genetic information remains to be elucidated. The gradient of anthocyanin, a potent antioxidant, during lace plant leaf development is a visible indicator to cell differentiation and fate and can be used as a basis of investigation to genes involved in regulation of PCD during perforation formation. With the recently sequenced lace plant leaf transcriptome, utilization of Gene Ontology analysis and comparative transcriptome studies, can reveal gene profiles of expression and function. The objectives of this study were to identify differentially expressed genes (DEGs) related to anthocyanin biosynthesis across leaf stages and cell types to understand the molecular mechanisms of developmental PCD during leaf remodelling related to anthocyanin expression. Current results reveal that anthocyanin biosynthesis genes are most upregulated in non-PCD cells, pre-perforate and window stage leaves as compared to PCD cells, imperforate and mature stage leaves. Using GO analysis, the molecular function of 172 up-regulated anthocyanin genes in the global lace plant transcriptome was elucidated to be involved in transcription factor activity, bHLH binding, and protein binding. Ongoing work is focused on cross-species comparisons and the identification of unique anthocyanin species. This study provides a basis of using comparative bioinformatics analysis to identify anthocyanin genes promoting leaf morphogenesis and cell fate.

Aerobic Capacity Predicts Breeding Success in Giant Petrels (Macronectes spp.)

Author: Theodore Lownie
Programme: Biology
Supervisor(s): Dr. Glenn Crossin, Department of Biology, Dalhousie University

Abstract

Life-history theory holds that parents should preserve their own lives over that of their offspring if they have ample opportunity for future reproduction. This can result in failed breeders, or parents who prove unsuccessful in rearing their offspring due to their inability to manage the costs of reproduction. These breeders are thought to represent the least viable and often competitively excluded individuals of a colony. Their relative deficiency should theoretically be reflected in physiological signatures, but we know little about the effects of the specific physiological costs of reproduction. Many studies have identified costs associated with the provisioning of offspring, but interestingly, many have not. This widespread discrepancy highlights the need for further evaluation of reproductive costs and the necessity of accounting for species-specific traits when interpreting findings. For central-place foraging seabirds, aerobic capacity (i.e. the oxygen-carrying capacity of blood) can explain variation in foraging effort and success, and may represent a potential cost of reproduction. Aerobic capacity is critical for providing working muscles with an adequate supply of oxygen. I examined whether aerobic capacity measures (as indexed by hematocrit or the percentage of red blood cells in blood, and reticulocyte index or the percentage of new red blood cells in circulation), differed between failed and successful breeders in northern and southern giant petrels (*Macronectes halli* and *M. giganticus* respectively). Results show that both hematocrit and reticulocyte index differed significantly between breeding fates. In both species and sexes, failed breeders exhibited markedly lower aerobic capacities than successful breeders, especially hematocrit, and with similar patterns in reticulocyte index. I will discuss the ecological implication of this physiological cost of reproduction.

Analysis of *Arabidopsis thaliana* RING-type Ubiquitin Ligases Using Protein-Protein Interaction Datasets.

Author: Tessa Macaulay
Programme: Biology
Supervisor(s): Dr. Sophia Stone, Biology Department, Dalhousie University

Abstract

Eukaryotes utilize an essential post-translational modification system, called ubiquitination, to regulate protein localization, activity, and abundance. In ubiquitination, the ubiquitously expressed protein ubiquitin is carried along an enzyme cascade, from a ubiquitin- activating (E1) to a ubiquitin-conjugating (E2) to a ubiquitin ligase (E3), which then transfers the ubiquitin to a substrate protein. RING (Really Interesting New Gene)-type E3s are a group of approximately 500 ubiquitin ligases that play important roles in plant growth, development, reproduction, and response to abiotic and biotic stresses. However, the majority of RING E3s are uncharacterized and their substrates unknown. This study provides an analysis of *Arabidopsis thaliana* RING-type E3s via the identification of potential substrates using an interactome built from high-throughput protein-protein interaction databases and low-throughput studies. To further identify potential substrates, the interactome was cross-referenced with a merged ubiquitinome dataset curated from 13 independent high-throughput studies.

Our results reported 1,551 interactions between 210 RING E3s and 842 unique interactors. RING E3s were versatile and found mostly interacting with multiple unique interactors, while the interactors were more specific and reported mainly to interact with single RING E3s. Of the 4,268 proteins reported from the merged ubiquitinome, 191 were also identified as interactors for the RING E3s and therefore supported as potential substrates. The largest subgroup of RING E3s, Arabidopsis Tóxicos en Levadura (ATL), was reported in 275 interactions between 37 ATL E3s and 145 unique interactors. Many of the unique interactors for the ATLs are in gene families of regulatory proteins, such as the 14-3-3-like family of signaling regulators. Interactors of the 14-3-3-like family were highly targeted by the ATL E3s and all 13 members were also found to be ubiquitinated. Interaction assays will be used to confirm select interactions, such as the interaction between XBAT32 and NDL1 along with XBAT32 and ACS7**.** This study provides valuable insight into the process of ubiquitination in Arabidopsis through the characterization of RING E3s and their potential substrates. Further study of the RING E3s and their substrates being ubiquitinated, could widen our understanding of the molecular mechanisms for plant stress responses.

Molecular Dynamics and Enhanced Pathogenicity in Human Coronaviruses

Author: Georgia MacDonald
Programme: Biology
Supervisor(s): Dr. Joseph P. Bielawski, Biology and Statistics Departments, Dalhousie University

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus causing the respiratory disease COVID-19, continues to pose a major threat to global public health. Its enhanced pathogenicity, as compared to other human coronaviruses responsible for a 15-29% of common colds each year, is key to the devastating medical consequences the virus has on those infected. Existing research highlights modulating proteins of the JAK/STAT pathway of the innate immune response and the spike protein allowing attachment to host cells as two factors believed to be important to the pathogenicity of coronaviruses. Furthermore, coronaviruses are shown to have relatively high mutation rates making them one of the most diverse and genetically distinct groups of viruses. This study addresses the gap in research linking pathogenicity and molecular evolutionary dynamics of coronaviruses by analysing the association between the enhanced pathogenicity and molecular evolutionary dynamics of SARS-CoV-2, and other highly pathogenic human coronavirus strains SARS-CoV and MERS-CoV. Sequence data were modelled using traditional models of codon evolution and a novel framework for joint modelling of gene sequences and phenotype evolution. In the latter case pathogenicity was specified as the phenotype of interest within the model. Maximum likelihood methods were used to test for (i) the canonical signal of adaptive molecular evolution and (ii) a significant association between molecular evolution and pathogenicity score. Where applicable, sites associated with positive selection or enhanced pathogenicity will be assessed using empirical Bayes methods and discussed in the context of protein 3D structure.

Validating Species Distribution Models for Aquatic Invasive Species

Author: Zachary MacMillan-Kenny
Programme: Marine Biology
Supervisor(s): Dr. Claudio DiBacco, Bedford Institute of Oceanography

Abstract

Species distribution models (SDMs) are a relatively new statistical tool used in ecology to help identify and predict a species' suitable habitat, often based only on local environmental predictors like temperature and salinity. SDMs are used increasingly in invasion ecology to help assess the risk of introduction and impact posed by non-indigenous species (NIS) of concern. SDM-based risk is expressed probabilistically with values ranging from 0 to 1, corresponding with lower to higher risk. Along this probability scale, suitability thresholds (T_S) estimated by SDM models are used to define probabilities that predict whether a species is likely to establish ($p > T_S$) or not ($p < T_S$). As such, T_S accuracy is recognized as an important potential source of SDM prediction error, yet there have been no studies that have assessed this source of error to date. The overarching objective of this study is to compare and assess the relative accuracy of SDM-based T_S estimates ($T_{S\text{-}SDM}$) against our best T_S estimates, which are based on empirical observations ($T_{S\text{-}EMP}$) that most closely reflect the true distribution of target NIS. Therefore, the accuracy of $T_{S\text{-}SDM}$ will be assessed by (i) quantifying the magnitude of the difference between $T_{S\text{-}SDM}$ and $T_{S\text{-}EMP}$, and (ii) comparing $T_{S\text{-}SDM}$ and $T_{S\text{-}EMP}$ prediction error rates (i.e., false negatives and positives) against empirical observations. The empirical data employed in this study was collated from Fisheries and Oceans Canada's (DFO) aquatic invasive species (AIS) monitoring program and uses sentinel sites spanning the Bay of Fundy (Nova Scotia) to the northern Gulf of St. Lawrence (Quebec) since 2008. Suitability thresholds based on empirical field data ($T_{S\text{-}EMP}$) are hypothesized to result in fewer prediction errors. Understanding the potential distribution of NIS is necessary to identify species and areas of concern for invasion, and support the development of mitigation and management strategies against AIS. Results from this study will help to better define the limitations of SDMs, improve habitat suitability predictions in Atlantic Canada, and assist in AIS management and mitigation efforts.

A Metagenomic Analysis of the Arctic

Author: Olivia Melville
Programme: Marine Biology Honours, Minor in Chemistry
Supervisor(s): Dr. Julie LaRoche

Abstract

Marine ecosystems are changing rapidly due to global warming. Arctic waters are shifting more quickly than other places, making them valuable indicators of biogeochemical shifts within the pelagic environment. In fact, as waters warm in arctic ecosystems, we may see drastic changes in upwelling, ocean circulation, stratification and nutrient availability. Changes in pelagic ecosystems will affect microorganism assemblages which are responsible for nutrient cycling in the ocean, including nitrogen cycling (Moore et al. 2013). Nitrogen is a key nutrient in oceans and is essential for the success of all organisms. Indeed, it is necessary to the creation of important cellular components such as nucleic acids and proteins. It is most broadly found as N_2 gas, however most organisms can only access bio-available nitrogen in the form of compounds like ammonia and nitrate (Kuypers et al. 2018). Many microorganisms have been classified by the role they comprise in the cycle. These roles include nitrogen-fixation, ammonification, assimilation, nitrification, denitrification and annamox. In this study, we analyzed two study sites from an Arctic GEOTRACES cruise from 2015. The sites are in Baffin Bay (BB1) and in the Labrador Sea (K1). The aim of the study was to examine the differences in microbe structure between sites and to identify potential causes for differences based on environmental parameters. Environmental data was retrieved from the GEOTRACES team. Water samples were taken at 3 depths per station and filtered through 3.0µm and 0.2µm filters. DNA was extracted using QIAGEN extraction kits, sequenced with Illumina shotgun sequencing and the metagenomes re-constructed using Megahit and Anvio'o. The study showed that the environments at each site are significantly different and that Baffin Bay had a lower N:P ratio than the Labrador Sea. In Baffin Bay, the most abundant (>5%) organisms were Proteobacteria, Planctomycetes and Actinobacteria. In the Labrador Sea, the most abundant (>5%) organisms were Proteobacteria, Thiotrichales, Verrucomicrobiaceae and Nitrosopumilaceae. Nitrogen cycle functions fulfilled at both sites were ammonia assimilation, allantoin utilization, ammonification and denitrification, based on the SEED and RAST annotation. The results indicate that while the most abundant organisms are different at each site, both sites have members which fulfill all elements of the nitrogen cycle.

Can Biomonitoring the Northwestern Atlantic Scotian Shelf with eDNA Metabarcoding Reveal Interactive Communities and Keystone Species?

Author: Shannon Myles
Programme: Biology
Supervisor(s): Dr. Julie LaRoche, Biology Department, Dalhousie University

Abstract

A recent advancement in molecular ecology, namely the development of environmental DNA (eDNA) metabarcoding, allows for holistic and nonintrusive biomonitoring of ecosystem dynamics. This pilot study makes use of the technique to assess the community of the Scotian Shelf, North West Atlantic Ocean across the entire tree of life – from prokaryotes to higher eukaryotes. Precisely, from analyses of co-occurrences and trends in relative abundances of recovered taxa, our study will attempt to reveal linkages between organisms. My hope is that these linkages segregate taxa into subnetworks of organisms whose prevalence are correlated, which I would infer as interactive communities. Previous studies have found that responses to temporal, spatial or environmental changes by the most correlated taxa within such subnetworks was mirrored, to an extent, by their owning interactive community. Similar findings would allow inferring these ecologically informative taxa as keystone species.

To perform this study, water samples were collected by the Atlantic Zone Monitoring Program (AZMP) cruises and filtered through small-pore filters by lab members to collect eDNA. In a previous microbial ecology study of the site, scientists have amplified (with PCR) targeted variable regions of two marker genes (16S ribosomal RNA, 18S ribosomal RNA). To capture diversity across the entire tree of life, PCR amplification with a new set of primers will be performed, targeting the cytochrome c oxidase sub-unit 1 gene (COI). Next, reads from next-generation high-throughput sequencing of the amplicons will be processed through a bioinformatics pipeline to cluster them into Amplicon Sequence Variants (ASVs). After taxonomic identification of ASVs, proportional abundance indices will be computed for each taxon varying (across samples) between 0 & 1. It is the dynamics of these indices, captured by a correlation matrix, that will allow a weighted correlation network analysis to cluster taxa into subnetworks, or in other words, interactive communities.

The simplicity and non-intrusiveness of this sampling method, which can later yield unparalleled information about marine communities, has important implications for biomonitoring efforts. I hope this new lens on the dynamics of broad-scale ecosystems can complement current monitoring techniques used in Marine Protected Areas and other relevant regions.

Faunal Communities at Inactive Hydrothermal Vents

Author: Monika Neufeld
Programme: Marine Biology
Supervisor(s): Dr. Anna Metaxas, Department of Oceanography, Dalhousie University

Abstract

There has been increasing interest in mining polymetallic sulfide deposits at deep-sea inactive hydrothermal vents, leading to the development of environmental regulations to minimize risk to the marine environment. While an extensive body of literature exists on the ecological communities at active vents, fauna at inactive hydrothermal vents are poorly described and their vulnerability to disturbance is unknown. This research documents epibenthic megafauna on inactive sulfides on two segments of the Juan de Fuca Ridge, NE Pacific. Video footage was collected by the remotely operated vehicle ROPOS during six dives at the Endeavour vent field and Middle Valley in August 2016. I compared patterns in abundance of non-vent faunal assemblages along gradients from active chimneys to inactive sulfide deposits and peripheral hard substrate. Inactive sulfides support dense communities of species including deep-sea corals, sponges, and crinoids. However, abundance of fauna varies with proximity to hydrothermal fluid flow, a factor which may limit colonization on sulfide features. This study will contribute much needed data for the development of sustainable management plans for the emerging deep-sea mining industry.

Developmental Differences and Reproductive Consequences of Submerged and Aerial Floral Morphologies in the Aquatic Plant *Lobelia dortmanna*

Author: Hannah Nickel
Programme: Biology & History of Science and Technology
Supervisor(s): Dr. Mark Johnston, Biology Department, Dalhousie University

Abstract

Mixed mating systems occur when a species performs both self-fertilization and outcrossing to produce progeny. Although the benefits of retaining two mating strategies in a population remain unclear, the phenomenon occurs frequently in nature. *Lobelia dortmanna*, a fresh water aquatic species of the Campanulaceae family, produces both submerged and aerial flowers. While it is known that the aerial flowers of *L. dortmanna* are chasmogamous (open), it is hypothesized in this study that the submerged flowers of the species are cleistogamous (closed) and make *L. dortmanna* a cleistogamous species. Cleistogamous species by definition produce both chasmogamous potentially outcrossing flowers and autonomously self-fertilizing cleistogamous flowers, sometimes on the same individual. Cleistogamous species offer an opportunity to explore why mixed mating systems persist in natural populations. In this study, I examine the causes of developmental differences and the reproductive consequences of the two floral morphologies—submerged and aerial—in *L. dortmanna*. Approximately 40 *L. dortmanna* flowers of varying ages from five populations were collected and dissected under a dissecting scope for a total of 200 dissections. Photographs were taken of the dissections and 42 flower traits were measured using imageJ software. Using style length as a measure of time, developmental timing differences between the submerged and aerial flowers were found. Smaller traits in the submerged closed flowers, particularly in the androecium and corolla support the hypothesis that *L. dortmanna* exhibits cleistogamy. To investigate the reason for mixed mating in the species several tests were undertaken. These tests included the calculation of self-fertilization rates by genotyping 14 microsatellite loci from six populations. Additionally, an overall maximum potential outcrossing rate was derived from observing the total number of exserted stigmas from mature flowers. Sex allocation, seed production, and germination rates were also explored. Overall, high but not absolute rates of self-fertilization were found in the species, indicating that some amount of outcrossing is retained. The possible reason for retaining this mixed mating dimorphism is explored and considered in the context of other mixed mating research.

Effects of Nutrient Deficiency and High-Fat Diet Exposure on Maternal and Fetal Hypothalamic Transcriptome

Author: Oguz Kaan Ozgoren
Programme: Biology and Neuroscience
Supervisor(s): Dr. Ian Weaver, Neuroscience Department, Dalhousie University

Abstract

In mammals, embryogenesis is shaped by interactions between the genotype inherited form each parent and the uterine conditions during fetal development. Past research has shown that maternal nutrition exposure during pregnancy can influence specific neural gene networks in the offspring, underlying brain, and behavioral development. The hypothalamus is a region of the brain that involved in regulation of metabolism, endocrine function, and social and emotional behavior. Herein, gestational nutrition and uterine conditions potentially play key roles in the development of developing circuits, neural function, and health outcome. We hypothesize that: maternal nutrient deficiency and high-fat diet exposure during pregnancy will affect both the mother and fetal hypothalamic transcriptome in C57/B6 mice.

Previously, adult female C57BL/6J mice were randomly assigned to either a calorie restricted diet (CRD, 30 kcal%), high-fat diet (HFD, 60 kcal%) or protein/carbohydrate matched control diet (CD, (45 kcal%), 4 weeks prior to conception and during pregnancy. At the end of the third trimester, total RNA was extracted from the paraventricular nucleus (PVN) of the hypothalamus of pregnant mothers and their fetal offspring and the expression of 23,188 unique RNA transcripts was monitored by Affymetrix HT Clariom assays.

Using the above transcriptome data, we examined distributions of individual responsive genes over different classes of molecular function, biological function, and cellular function, as well as heatmaps from GO enrichment-based cluster analysis of KEGG pathways. We also randomly assigned 4 gene targets and analyzed their expression by RT-qPCR using total hypothalamus RNA from each treatment group. The RT-qPCR expression analysis will be used to confirm the Clariom assay results and the magnitude of the effects between the three different maternal diets (CD, CRD, HFD) on PVN differential gene expression were similar in the fetal female and male offspring. Together, these findings demonstrate generation- and sex-specific effects of maternal CRD and HFD.

Using Sportfishing Tournament Data to Determine Factors Influencing Black Bass (*Micropterus* spp.) Catches and Catch Trends

Author: Victor Papaiz
Programme: Marine Biology Co-op
Supervisor(s): Dr. Heike Lotze, Biology Department, Dalhousie University

Abstract

In 2016, Black Bass species (*Micropterus* spp.) were the most targeted freshwater fish in the United States with 9.6 million anglers targeting them for a combined total of 117 million days. Black Bass sportfishing tournaments are a competition-oriented derivative of this recreational fishery. Previous studies have found that these tournaments are a source of extensive catch data that can be used to assess population trends in the waterbodies in which the events take place. This study evaluated the usefulness of sportfishing data in determining the impact of factors such as stocking, predator presence, latitude, water body, and the presence of different target species on average catches and catch trends over time. Publicly available sportfishing data from 896 tournament events occurring over 110 different waterbodies in the United States between 1976 and 2020 were analysed. For each tournament event, the data was used to calculate values for stock-related variables such as mean fish size and biggest fish caught for average catches over the past 10 years and for catch trends over time. Data was also compiled on 11 biological, physical, and stock management characteristics that were hypothesized to influence the stock-related variables. Random forests and correlation matrices were used to determine which factors were most influential for each variable across all waterbodies. These influential factors were then used to create generalized linear models (GLMs) to determine which factors had significant positive or negative effects on each variable. Results indicate that the presence of Florida-strain largemouth bass had significant positive effects on the size of the average and the biggest fish caught during tournament events over the last 10 years. It was also found that the presence of largemouth bass had a significant negative effect on the size of the average fish caught while latitude had a significant positive effect. In contrast, the presence of smallmouth bass and spotted bass had significant positive and negative effects, respectively, on trends in the size of the biggest fish caught over time. These results suggest that sportfishing data can be useful in evaluating the impacts of various biological, physical, and management factors on fish catches and stock-related variables and could be used to supplement independent scientific and monitoring data to ensure the sustainable management of these important recreational fisheries.

Elevation of Lobster and Crab Fishery Groundlines and the Associated Entanglement Risk to North Atlantic Right Whales in the Gulf of St. Lawrence

Author: Jaime Rae
Programme: Marine Biology & Oceanography
Supervisor(s): Dr. Sean Brillant, Canadian Wildlife Federation and Department of Oceanography, Dalhousie University

Abstract

The North Atlantic right whale (NARW) is a critically endangered species, with entanglements in fixed fishing gear identified as the most significant cause of serious injury and human-caused mortality in the species. Beginning in 2017, NARWs began showing up in large numbers in the Gulf of St. Lawrence (GoSL) and there has been an increase in the frequency and severity of fixed fishing gear entanglements in recent years. Groundlines are a primary component of fixed fishing gear that pose an entanglement risk, but little is known about groundline elevations and the factors affecting them in the GoSL. This study uses temperature depth-sensor data from Cape Island and Little River to examine the elevations of groundlines on commercially active gear above the seafloor in relation to how they may affect the likelihood of a NARW becoming entangled. We also examine factors that may influence groundline elevations, including order of the groundlines on the trawl, depth of the water the trawl is set in, and factors associated with tidal current velocities. This research will provide a better understanding of the risk to NARWs posed by groundlines in the GoSL,and identify various factors within a fisher's control to reduce groundline elevations.

Estimating the Current Global Population of Sperm Whales (*Physeter macrocephalus*)

Author: Megan Shin
Programme: Marine Biology Co-Op
Supervisor(s): Dr. Hal Whitehead, Biology Department, Dalhousie University

Abstract

Sperm whales are one of the most widely distributed marine mammals, with their habitat ranging from 60˚N to 60˚S, limited to depths of more than 1000m. Their biomass and position in the ocean food chain make them important actors in deep ocean nutrient cycling. However, their widespread habitat and elusive behaviour make it difficult to understand population size and dynamics. As an update to Dr. Whitehead's 2002 population estimate model, this study estimates global sperm whale population, scaling by habitat area, sightings by open-boat whalers, primary productivity levels, depth, distance to shore, water temperature, salinity, and benthic dissolved oxygen. Based on parameter values within study areas, global population estimates are calculated for each variable, based on measurements across all sperm whale habitat. These scaling factors are then individually regressed on existing visual survey numbers and stepwise selection is used to find the most accurate multivariate linear model. Preliminary results based on scaling by habitat area suggest there are 415,700 sperm whales globally, this estimate is subject to change based on other predictors contribution to the final model. This study will help contribute to population assessments, conservation measures, and further research on sperm whales that reference habitat parameters.

Determining Habitat Use of Baleen Whales in the Northwest Atlantic Ocean That Overlap With Human-Use Patterns

Author: Hannah Solway
Programme: Marine Biology
Supervisor(s): Dr. Boris Worm, Biology Department, Dalhousie University
Olivia Pisano, Biology Department, Dalhousie University

Abstract

While many Northwest Atlantic Ocean (NWA) baleen whale populations are now recovering from previous overhunting, new human pressures related to vessel activity are threatening the survival of baleen whales. Vessels can be dangerous to slow-moving whales, as collisions may cause sharp or blunt trauma. The interactions between NWA baleen whales and vessel activity are not well known. This project will mainly determine the baleen whale spatiotemporal distributions and aggregations in the NWA relative to vessel activity. An automated machine learning algorithm is being used to determine baleen whales' spatial and temporal locations in the NWA. This algorithm is currently being developed at Dalhousie University using aerial survey images from Fisheries and Oceans Canada (DFO). Data on vessel density and distribution in the NWA has been obtained from Global Fishing Watch (GFW) via Automatic Identification System (AIS) technology. Distributions of the vessel activity and the baleen whales will be mapped using GIS technology. Hot spots of baleen whale and human pressure interaction will be identified. From a manual analysis of approximately 40,000 aerial images taken in the Gulf of St. Lawrence (GSL), 147 whales have been observed. Of these detections so far, several Minke Whales, Right Whales, and Blue Whales, among other species, have been identified. Preliminary GIS results suggest there is a high degree of correlation between vessel activity and baleen whales in the GSL.

Physiological Response of Pacific Auklets to Interannual Variations in Marine Climate

Author: Heidi Tate
Programme: Marine Biology
Supervisor(s): Dr. Glenn Crossin, Biology Department, Dalhousie University

Abstract

The formation of “The Blob”, a mass of warm water in the Northeast Pacific Ocean emerged and lasted from 2013 to 2015, causing a decrease in primary productivity, which negatively impacted predators at higher trophic levels, including sentinel species like seabirds. For seabirds, this climate pattern had far-reaching effects, including breeding mismatches and die-offs. Recent studies on birds have used feather corticosterone (fCort) as an indicator of physiological stress in response to environmental stressors. In this study, feathers were collected from females of two sentinel Pacific auklet species (family Alcidae) over a 7-year period spanning The Blob and other anomalously warm and cool years. As Pacific auklets moult and grow new feathers during the winter period of migration at sea, measures of fCort can provide an accumulated, physiological measure of nutritional stress experienced during this period of non-breeding feather growth. Via AIC_C model selection, we show that rhinoceros auklets (*Cerorhinca monocerata*) were virtually unaffected by warming events, with fCort values stable across years. In contrast, Cassin’s auklets (*Ptychoramphus aleuticus*) showed an increase in fCort during The Blob and El Niño years, suggesting a greater physiological sensitivity to ocean climate. This study provides insight into how Pacific auklets may respond to future climate change and provides a means for monitoring the population level responses to climatological variation.

Comparing Spatial and Temporal Patterns in Trait Diversity Between Fisheries Landings and Observed Coral Reef Communities.

Author: Emma Touchie
Programme: Marine Biology
Supervisor(s): Dr. Aaron MacNeil, Biology Department, Dalhousie University
Dr. Matthew McLean, Biology Department, Dalhousie University

Abstract

The resilience and diversity of coral reefs have been severely impacted in recent decades by stressors such as unsustainable fishing and global warming. As commercial fishing pressure increases, adaptive fisheries management encompassing organism functionality is increasingly important for conserving the health of these highly productive ecosystems. Trait-based approaches, which link species' traits to ecosystem process, may be particularly useful for assessing the effects of altering species assemblages on ecosystem functioning. The goal of this study was to uncover differences in, and drivers of, trait diversity of fish assemblages observed on reefs and in fisheries landings sold in markets around the island of Kosrae, Micronesia. Data from underwater visual censuses of fish communities on the surrounding reefs and a year-long daily survey of market landings were used to compare trait assemblages. Ten morphological traits related to swimming and feeding were measured on 71 species present in both reef observations and market landings. These measurements were used to calculate functional diversity indices and to characterize community trait composition. A generalized linear mixed-effects model was used to determine whether trait diversity observed in the landings was related to the diversity present on reefs, or if landings were driven by other forces such as reef accessibility or fisher preferences. We observed strong mismatches between trait diversity on the reefs and within the landings. Across all locations, the proportions of large-bodied species with traits relating to piscivorous diets and predatory feeding were greater within the landings than on the reefs, indicating that fishers were not fishing in accordance to reef composition, but selectively targeting desirable species. Alarmingly, species that were more commonly targeted (i.e., had greater catch biomass) were also classified as highly vulnerable to fishing pressure, and many of these species are considered 'functionally distinct,' i.e., having unique traits. In some locations, species with high functional distinctiveness were fished at much greater proportions than they were observed, potentially removing unique and uninsured functions. To sustainably manage small scale coral reef fisheries in the face of increasing commercial demand, alternative species should be harvested that are less vulnerable and that do not support unique and uninsured ecological roles.

Genetic Diversity in Resident *Galaxias maculatus* in Patagonia

Author: Kristen Tymoshuk
Programme: Biology, Oceanography (minor)
Supervisor(s): Dr. Daniel Ruzzante, Biology Department, Dalhousie University
Lisette Delgado (PhD), Biology Department, Dalhousie University

Abstract

Genetic divergence within a species can arise through a variety of evolutionary mechanisms. For instance, geographic changes throughout history can play a large role in creating genetic differences among environmentally isolated populations of a species. This study focuses on *Galaxias maculatus*, a fish widely distributed throughout the Southern Hemisphere. *G. maculatus* has two life histories: an ancestral diadromous form and a derived freshwater resident form. We examined the genetic differentiation among 5 *Galaxias maculatus* resident populations in the Manso River system and a resident and a diadromous population in the Puelo River system, into which the Manso River drains. We used the RADcap approach to obtain single nucleotide polymorphism (SNP) markers for 100 individuals. We expect the Manso resident populations to be highly differentiated from each other and the Puelo populations. Resident populations are environmentally isolated and are thus expected to be highly genetically differentiated from each other through the combined effects of genetic drift and local adaptation. This study aims to provide further evidence that environmental changes can inform species adaptation and genetic divergence.

Localization of North Atlantic Right Whales using a Deformable Array of Passive Acoustic Monitors

Author: Zachary Wallot-Beale
Programme: Marine Biology
Supervisor(s): Dr. David Barclay, Oceanography Department, Dalhousie University
Dr. Carolyn Binder, Defense Research and Development Canada

Abstract

Rising global temperatures have shifted the habitat range of many marine species towards the poles. The endangered North Atlantic Right Whale is among these species. With the expansion of their range has come an increased mortality rate largely attributed to ship strikes and entanglements in fishing gear. If the positions of whales were known, large vessels could actively avoid them, reducing ship strikes and noise emission impacts without widely imposing remarkably strict regulations on industry. In July 2018, a two-day data-blitz effort was put together in the Gulf of Saint Lawrence with members of the Royal Canadian Airforce and Dalhousie University. 32 DIFAR sonobuoys, two acoustic gliders, two planes, and a vessel were deployed to collect visual and acoustic data of North Atlantic Right Whales. The aim of this research is to describe the performance of large deformable arrays for passive acoustic monitoring and to quantify the array's effective detection range, localization accuracy and uncertainty as a function of size and number of elements. Bearing information was extracted and cross-referenced between characteristically similar acoustic detections, with the help of a parabolic equation model for calculating the probabilistic range of detection and the visual detections for ground truthing, in order to produce estimates of North Atlantic Right Whales positions through time. Preliminary results will be presented focusing on extracting and visualizing the bearing information and generalizing the probabilities of detection inside and outside of the deformable array through time.

Sediment Grain Size as an Alternative Indicator of Suitable Habitat for *Zostera marina*

Author: Taylor Watts
Programme: BSc. Marine Biology
Supervisor(s): Dr. Jon Grant, Department of Oceanography, Dalhousie University

Abstract

In Atlantic Canada, *Zostera marina* (eelgrass), has been deemed an ecologically significant species as it provides important ecosystem services such as carbon sequestration and suitable habitat for many marine organisms along the coastlines of Nova Scotia (Cullain *et al.* 2018). Unfortunately, *Zostera marina* continues to be heavily impacted and degraded due to nutrient run off from land. There are suggestions that the release of nutrients from marine fish farms causes similar eutrophication and harm to eelgrass. In Port Mouton, a bay on the South Shore of Nova Scotia, it is suggested that nutrient runoff from a previously established finfish aquaculture pen has led to the degradation of local eelgrass beds within the bay. Yet, it has been shown that nutrients from these aquaculture pens have not reached nutrient levels toxic to eelgrass and thus should not be causing the decline of *Zostera marina* in Port Mouton (Filgueira *et al.* 2020). The following research project looks to sediment grain size as an environmental parameter that may be responsible for limiting the density and growth of *Zostera marina*. Namely, widespread unsuitable substrate (gravel and cobble) provides marginal habitat for eelgrass, leading to commonly observed sparsity in shoot density and health. Depth, temperature, salinity, and light have all been studied extensively in terms of their impacts on the health of *Zostera marina,* however, research pertaining to the relationship between sediment grain size and the density of *Zostera marina* is scarce (Kraus – Jensen *et al.* 2011 & Benson *et al.* 2013).

This research project is rooted in the realm of benthic ecology and aims to define the marginal sediment type for the growth and inhabitation of *Zostera marina* so as to help examine the hypothesis that aquaculture is leading to the degradation of eelgrass. Rather, it is hypothesized that the sediment type within Port Mouton is not suitable for *Zostera marina* and that with increasing sediment grain size, the density of *Zostera marina* will decrease.

Sediment samples and images to assess eelgrass density were collected from Port Mouton and Port Joli on the South Shore of Nova Scotia. The images have been analyzed to calculate percent cover while future analyses will include sieve analysis to categorize grain size, as well as high temperature ashing to quantify organic matter content of the sediment (Cammen 1982 & Zhou *et al.* 2003). Finally, a regression analysis will be conducted to help define the relationship between grain size and *Zostera marina* density.

Gastropod Buoyancy Behaviour and Regulation using *Biomphalaria alexandrina*

Author: Kayla Young-Daigle
Programme: Marine Biology
Supervisor(s): Dr. Roger P. Croll, Physiology and Biophysics Department, Dalhousie University

Abstract

Negatively buoyant aquatic animals require using energy to avoid sinking. Buoyancy regulation has been studied in many organisms, but this study explores it in a novel species, the freshwater pulmonate gastropod, Biomphalaria alexandrina. Preliminary observations suggest that under normal lab conditions, these snails are generally neutrally/positively buoyant, despite having dense shells. Also, when weighted, they appear to adjust and regulate their buoyancy. This study aims to confirm these observations and hypothesizes that snails regulate buoyancy by increasing lung size. Per trial, 5 control snails, 5 weighted with a full split shot sinker glued to their shell, 5 with half a split shot, and 5 with glue only were housed together. At times after weighting, each snail was held at the water surface and let go to see if they sank. At week 3, 20% of glued and control snails, 73.7% half weighted, and 100% fully weighted sank. At week 6, no significant changes were seen in glued, controls, and fully weighted snails, while in half weighted snails sinking frequency declined to 50%. At week 3, glued and control snails average sinking rate was 3.5 cm/s, half weighted 9.7 cm/s, and fully weighted 13.3 cm/s. At week 6, no significant changes were seen in glued and controls, while in half and fully weighted snails, rates declined to 6.7 cm/s and 10.4 cm/s, respectively, indicating that with time, the number and rates of sinking of weighted snails declined. Snails that floated were held below the water surface and let go to measure floating rates. At week 3, glued and control snails floating rate averaged 8.5 cm/s and half weighted at 4.4 cm/s. At week 6, glued and control snails had no significant changes, while half weighted snails floating rates doubled, showing that already neutrally/positively buoyant weighted snails, increased their buoyancy. Together, these results suggest that weighted snails adjust and regulate their buoyancy. To detect possible changes in lung size, photos of snails were taken prior to weighting and at 6 weeks. Initially, the lung occupied 30.1% of the lateral shell surface area. At week 6, glued and control snails had no significant changes, while lungs of half weighted snails increased to 40.6% and of fully weighted to 45.2%. Overall, there is evidence that snails are regulating buoyancy by increasing their lung size. Future experiments will address survivorship and possible advantages of buoyancy regulation in this novel species.

Covalent Probes for Glucocerebrosidase (GBA) and β-Glucosidase 2 (GBA2)

Author: Ziyang Zhang
Programme: Biology & Chemistry
Supervisor(s): Dr. Aarnoud C. van der Spoel, Department of Pediatrics & Department of Biochemistry and Molecular, Dalhousie University

Abstract

Heterozygous mutations in the glucocerebrosidase gene (*GBA*) are the most common genetic risk factor for Parkinson's disease (PD). The lysosomal gluocerebrosidase (GBA) and non-lysosomal β-glucosidase 2 (GBA2) account for nearly all β-glucosidase activities in the cell. GBA is a therapeutic target in the treatment of PD. Precisely and separately measuring GBA and GBA2 activities *in vivo* and *ex vivo* would greatly help determine efficacy of GBA-enhancing treatments of Parkinson's disease. Meanwhile, there is an urgent need for efficient and selective inhibitors to produce GBA-deficient animal models for Parkinson's research without interrupting GBA2. In this research, we investigated the detection ability, efficiency and selectivity of newly developed fluorescent probe and probe precursors which are essentially mechanism-based GBA and/or GBA2 covalent inhibitors. Efficiency and selectivity were obtained by measuring remaining β-glucosidase activities in mouse brain membranes at pH 4.0/5.8, which are pH optima of GBA/GBA2, under titration of different concentrations of each inhibitor. Current results showed a lot better efficiencies of all inhibitors to GBA than conduritol B epoxide, the most widely used GBA inhibitor. Some of those also shown high selectivity to GBA. Fluorescent probe treated recombinant GBA or mouse brain membranes were separated by SDS-PAGE and then scanned by imager to test detection ability. A linear relationship between recombinant GBA quantity and fluorescent band intensity was observed but currently no good result shown from fluorescent probe treated membranes which is possibly due to quenching by other contents in brain membranes. Our probes are excellent as inhibitors to GBA and/or GBA2 but the fluorescent probe is not powerful enough to detect GBA or GBA2 in tissue membranes.