DALHOUSIE UNIVERSITY

40th Annual

Cameron Conference

FOR BIOLOGY & MARINE BIOLOGY HONOURS STUDENT RESEARCH

Saturday
28 February 2026
9:00 am - 12:30 pm

Sponsored by the Department of Biology

&

Dalhousie Association of Biology Students

DALHOUSIE ASSOCIATION OF BIOLOGY STUDENTS

Dalhousie Association of Marine Biology Students

DAMS

Organism on Cover:

Jakoba isolate “Jak2”

Scanning electron micrograph by Meredith Rose

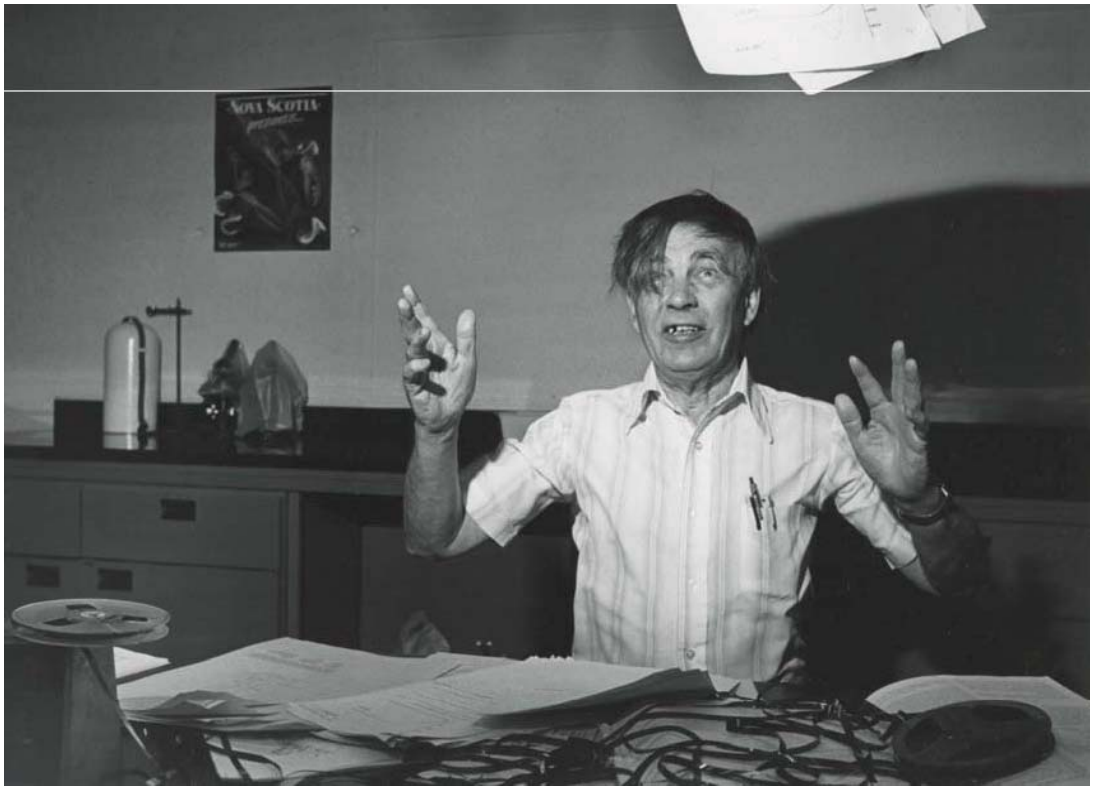
On the Origin of the Cameron Conference

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)

Third Floor Atrium - Life Sciences Centre

8:30 am

Warm drinks and snacks available

8:50 am

Conference Welcome

Professor Patrice Côté,
Chair of Biology Department

9:00-10:00 ~ Poster Session I

1	Seamus Berger-Smale	**Investigating the prey range and feeding preferences of groove-bearing, eukaryote-eating flagellates**
2	Nicholas Brady	**Finding the "Drivers": An agent-based simulation approach to investigating population-level selective pressures favouring Transposable Element carriage.**
3	Zoe Clark	**Interspecific and temporal patterns of environmental contaminants in eggs from four seabird species at Sable Island, Nova Scotia, Canada**
4	Elle Crilly	**Deciphering the role of WAVH1 in response to nitrogen and phosphorus deprivation in Arabidopsis thaliana**
5	Emma Daigle	**Tracking snapping turtles in Nova Scotia using acoustic telemetry**
6	Sofia Day	**Individual locus effects on mortality risk in the endangered St. Lawrence beluga whale**

7	Melina Gobel	**Comparing the effects of exhaustive chasing and lethal TFM lampricide exposure on non-target Great Lakes species**
8	Remi Kowalski	**Overwinter storage of eelgrass (Zostera marina) seeds from a Nova Scotian population for use in coastal habitat restoration**
9	Jayda Kruger	**Bio-receptivity of phytoplankton-enriched concrete: a material that couples wastewater remediation to carbon capture and sequestration.**
10	Vanessa Landry	**Assessing the impact of ocean alkalinity enhancement on benthic microbial communities using eDNA metabarcoding**
11	Jeremy Larsen	**Assessing the germicidal efficiency of UV-LED technology in different wastewater matrices**
12	Cindy Liu	**Characterization of interventricular septal development and perinatal mortality in mice lacking natriuretic peptide receptor A (NPRA)**
13	Eliseo Martignago	**Quantifying the relationship between fat content and Rickettsia sp. bacterial prevalence in the American dog tick (Dermacentor variabilis)**
14	Metyn Rehman	**Estimating Atlantic tomcod (Microgadus tomcod) spawning timing and fecundity in the Minas Basin**
15	Madelyn Richardson	**Characterizing brown trout (Salmo trutta) movement in the Margaree River, Cape Breton using radio telemetry**
16	Daisy Rubenstein	**Melon morphometrics in northern bottlenose whales (Hyperoodon ampullatus)**
17	Maggie Sharpe	**Competitive adaptation in isolated selection lines of female medaka (Oryzias latipes)**
18	Claire Thrower	**Multi-taxa assessment of genetic diversity and differentiation in invasive and non-invasive populations**

10:00-10:15 am

Coffee Break and Transition to…

Life Sciences Centre Room 242

10:15 – 11:15 Oral Presentations

Session Chair - Dr. Jen Frail-Gauthier

Jenny Amsden	**Characterizing background zooplankton assemblages in a potential foraging habitat for North Atlantic Right Whales using situ imaging.**
Ella Colwell	**Using eDNA to reveal the impacts of invasive fish on freshwater communities**
Élise Poirier	**Assessing genetic and environmental drivers of MSX resistance in eastern oysters (*Crassostrea virginica*) in Cape Breton, Nova Scotia**
Katherine Crawford	**The ability of scent-detection dogs to identify and signal VOCs associated with anxiety in humans with PTSD**
Nelene Silva	**Is the sponge loop present in the Makkovik Hanging Gardens?**
Aiden Moore	**Uncovering the relationship between the lampricide 3-trifluoromethyl-4-nitrophenol (TFM) and oxygen consumption in non-target species**
Milena Wilson	**Exploring the variation in marine benthic community composition across the Northumberland Strait**
Hannah Millar	**Characterizing DCX+ round cells in the chickadee hippocampus**

11:30 – 12:30 ~ Poster Session II

19	Lena Chown	**Assessing environmental covariates and ontogenetic and sex-specific patterns in blue sharks (Prionace glauca) off the coast of Nova Scotia**
20	Maeve Cuthbert-Shore	**Temperature-associated movement and hibernacula use in eastern ribbon snakes (Thamnophis sauritus)**
21	Geraldine Fernandez	**Evaluating individual identification of blue sharks (Prionace glauca) using ampullae of Lorenzini and fin morphology**
22	Jessica Fullerton	**Amphibian and reptile richness and abundance in the Backlands**
23	Kevin Glover	**Microbial transformation of organic matter: Linking nitrogen acquisition strategies to δ^{15}N-amino acid fractionation**
24	Ruby Harrington	**Defining histotripsy safety margins for image-guided spinal tumour treatment**
25	Anders Hoffmann	**Behavioral thermoregulation of sea-run brook trout (Salvelinus fontinalis) in the East River of Pictou, Nova Scotia**
26	Eliza MacDonald	**Testing different sporing methods, water flow, and nutrient conditions on the growth of Saccharina latissima in the hatchery phase**
27	Kate McKee	**Investigating muscle repair by inducing cold damage in Drosophila melanogaster**
28	Cora Mitchell	**Investigating the effect of light intensity on programmed cell death in lace plant (Aponogeton madagascariensis) leaves**
29	Hoang Nam Nguyen	**Investigating the effects of ocean alkalinity enhancement towards the surface microbial community in Atlantic Canada**

30	Carter Rice	**Does Bartonella infections alter cold tolerance of the American dog tick Dermacentor variabilis in Nova Scotia?**
31	Meredith Rose	**Isolating and characterizing new evolutionarily important groove-bearing protozoa**
32	Jordan Sampson	**Identification of plasminogen receptors of secretome-stimulated fibroblasts**
33	Madison Sliwa	**Sperm whale (Physeter macrocephalus) clan assignments in the Galápagos Islands from 2013-2023**
34	Ross Torrie	**Effects of trait-urbanization relationships on avian genetic diversity in Europe and North America**
35	Kyra Uyeda	**Aerial photo-identification and mark type analysis of northern bottlenose whales (Hyperoodon ampullatus)**
36	Jessica Wong	**The effectiveness of physical filtration at removing tunicates from aquaculture systems**

LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME

Characterizing background zooplankton assemblages in a potential foraging habitat for North Atlantic Right Whales using in situ imaging.

Author: Jennifer Amsden
Program: Marine Biology
Supervisor(s): Dr. Sarah Fortune, Department of Oceanography, Dalhousie
Dr. Laura Helenius, Department of Oceanography, Dalhousie

Abstract

The North Atlantic Right Whale (*Eubalaena glacialis;* NARW) is an endangered species of baleen whale distributed along the eastern coast of North America. Between 2015 and 2017, NARW shifted their distribution from the Gulf of Maine into the Gulf of St. Lawrence (GSL), tracking a spatial distribution of their primary prey, *Calanus* spp. copepods. This rapid expansion into new waters led to elevated mortality from vessel strikes and entanglement in fishing gear. Therefore, identifying and characterizing previously unknown potential habitats and seasonal use will allow for the creation of protective policies and predictions of future distributional shifts, ultimately increasing the recovery potential for NARW.

Sporadic acoustic presence and prey abundance estimates indicated that the northeastern GSL could be a potential foraging area for NARW throughout a northward expansion. To evaluate this potential, an Underwater Vision Profiler 6 – High Frequency (UVP6-HF) *in-situ* imaging sensor was utilized to characterize zooplankton communities in a known NARW foraging habitat in the southwestern GSL, Shediac Valley, and a potential future foraging habitat in the northeastern GSL, Lark Harbour, Newfoundland. Further, background oceanographic conditions were determined using a Conductivity, Temperature and Depth (CTD) profiler and the energetic density of the zooplankton community was determined using oxygen bomb calorimetry.

Results indicate that (1) areas sampled off the western coast of Newfoundland may not currently constitute suitable foraging habitat for NARW, as the background zooplankton assemblages did not maintain the densities likely required for foraging; (2) zooplankton community composition exhibited consistent seasonal variability in the Lark Harbour / TBB region in comparison to the Bonne Bay fjord; and (3) pronounced spatial differences were observed, with the Lark Harbour / TBB region exhibiting higher *Calanus* spp. biovolume and corresponding energetic density compared to the Bonne Bay fjord. However, this study was spatially constrained to a small area off the western coast of Newfoundland, and further investigation is required for definite inference.

As climate-driven shifts in prey distribution and whale foraging areas are expected to become increasingly common under ongoing anthropogenic climate change, pre-defining potential habitats will be essential for proactive conservation and management of NARW.

Exploring the Prey Range and Feeding Preferences of Eukaryote-Eating Flagellates

Author: Seamus Berger-Smale
Program: Biology
Supervisor(s): Dr. Alastair Simpson, Department of Biology, Dalhousie University

Abstract

Phagotrophy, a feeding mechanism unique to eukaryotes in which whole prey cells are engulfed, was present in the last common ancestor of all eukaryotes. A popular hypothesis proposes that ancestral eukaryotes fed similarly to living 'typical excavates', which capture bacterial prey by generating an efficient feeding current using a vane-bearing flagellum beating within a ventral groove. Interestingly, some living eukaryotes possess a superficially similar vane-and-groove system but instead capture and phagocytose other eukaryotes, which are much larger than most bacteria.

Colponemids (Colponemida) and provorans (Provora) are eukaryote-eating flagellates that share many morphological similarities, including a vaned flagellum associated with a ventral groove. Despite these similarities, the two groups are distantly related and occupy distinct ecosystems, highlighting the need to understand how this feeding architecture evolved and how it influences predator–prey interactions. Additionally, the ecological roles and feeding preferences of both groups are poorly characterized as nearly all described cultures were isolated onto predator-specific kinetoplastid prey species. This study addresses two questions: first, whether each predator group is restricted to specific prey types or can exploit a broader range of prey; and second, which prey species best support predator growth. To address the first question, I tested the prey range of two provorans and two colponemids on a taxonomically and biologically diverse array of new prey species. Di-eukaryotic cultures containing predators and their original kinetoplastid prey were introduced, in triplicate, to high-density cultures of new prey species. The density of all three eukaryotes was qualitatively assessed, and cultures were observed for additional evidence of feeding. Both provoran species fed on 7 of 10 new prey species, suggesting they are generalist feeders. Colponemid trials are currently underway, with similar results expected. To test whether new prey supported better growth of the provorans compared to original kinetoplastid prey, I isolated them using single-cell isolation onto the 3 prey species that best supported predator growth. Exclusion of the original prey was confirmed by PCR with specific 18S rDNA primers. Quantitative measurements of predator density responding to various new prey is underway. These recently described organisms provide an excellent opportunity to study the functional diversity of the vane-and-groove architecture, while clarifying the role that these predatory microbes play in complex aquatic microbial ecosystems.

Finding the "Drivers": An agent-based simulation approach to investigating population-level selective pressures favouring Transposable Element carriage

Author: Nicholas Brady
Program: Biology
Supervisor(s): Dr. Joseph Bielawski, Department of Biology, Dalhousie University

Abstract

Transposable Elements (TEs) are independently replicating genetic entities that exist within host genomes. Current evolutionary theory supports that TEs are maintained within the genomes of their host population via selection on transposition rate and a series of trade-offs that limit the evolution of effective host silencing mechanisms. However, recent research has discovered that TEs have repeatedly been co-opted as host exaptations. These findings show TE-derived sequences with selected effects on chromatin state rewiring, modifications to cis-regulatory networks, and changing the 3D folding of chromosomes as structural DNA. TE sequences may be predisposed for exaptation because the promoters and regulatory sequences they encode are shared with their host cell. It has been suggested that TEs may have a selected effect function as "Drivers of Evolution". This adaptive claim suggests a teleonomic role for TEs contributing to host evolution where the deleterious effects of insertion is offset by a contribution to future adaptation. Doolittle (2022) outlined a verbal model using Multi-level Selection Theory that recasts this function as a selective product at a higher level (e.g. Species). TEs are simultaneously selfish Darwinian individuals with deleterious effects on their hosts and positively selected by the differential persistence/speciation of clades. I explored this model using an *in-silico* simulation where Hosts and TEs act as agents. Within the simulation, host individuals form discrete populations within a patchy environment. Individual host reproduction is dependent on the selective fit of their genotype to their local environment. TE insertion within a host genome can affect the expression of nearby genes to simulate TE interference with the local chromatin state and regulatory environment. Hosts can migrate in groups to empty patches where there is a different selection pressure. Migration is discrete which results in distinct population lineages. My model suggests that TE insertions can contribute genetic variation that enables TE infected populations to spread faster than those with no TEs despite TE deleteriousness for the individual. My findings suggest there is a potential higher level of selection occurring on TE carriage but there may be a "goldilocks zone" that balances the effects of insertion, the insertion rate, and the evolution of silencing mechanisms. This goldilocks zone may be relatively small and requires further exploration.

Assessing environmental covariates and ontogenetic and sex-specific patterns in blue sharks (*Prionace glauca*) off the coast of Nova Scotia

Author: Lena Chown
Program: Marine Biology & Environmental Science
Supervisor(s): Dr. Heather Bowlby, DFO, Bedford Institute of Oceanography

Abstract

Blue sharks (*Prionace glauca*) are found throughout Atlantic Canada and the North Atlantic Ocean. They are considered near threatened by the IUCN, with bycatch and targeted fishing being their two biggest threats. Research in the North Pacific Ocean has found bathymetry and sea surface temperature (SST) to be the two most informative predictors of blue shark presence, with specific SST range preferences observed based on size and sex. However, no studies have looked at these preferences in the Atlantic Canada population. Juvenile blue sharks are known to associate with topographic features like steep bathymetric gradients in the Azores population, but these bathymetric gradient associations have not been examined or compared across size and sex in the Atlantic Canada population. Based on research on other oceans and populations, these environmental factors may be related to blue shark habitat use in the Atlantic Canada population. If this is the case, then different sizes and sexes of blue sharks in Atlantic Canada may have inherently different preferences and thus be primarily found in different habitats. Juvenile blue sharks are the life stage most frequently bycaught by pelagic fishing fleets, so if differences in habitat use are found, then this knowledge can be used to limit bycatch mortality by excluding fishing activities in the habitats most commonly used by juveniles. This study aims to determine what habitat characteristics are associated with blue shark captures off the coast of Nova Scotia and to explore ontogenetic and sex-specific patterns in habitat use. Spatial data of blue shark captures from a long-term charter fishing business in a small area off the coast of Nova Scotia were matched with SST, bathymetry and bathymetric roughness (represented by standard deviation) for each capture location. Captures were separated into four life stage categories based on their sex and size. Levene's tests and Kruskal-Wallis tests were performed for each environmental variable to look for differences in variance and median between life stages. SST was the only variable with significant p-values, showing variation between life stages in the median and range of temperature used. Kernel density maps were used to examine the extent of spatial overlap between life stages based on SST. A contingency table was also used to determine that there were no temporal differences in captures by month for either sex or any life stage, suggesting all components of the population are present for the duration of the fishing season. To evaluate if blue sharks tend to be in habitats with rough bottom types, a regression will be fit between roughness and capture density and between SST and captures per day.

Interspecific and Temporal Patterns of Environmental Contaminants in Eggs from Four Seabird Species at Sable Island, Nova Scotia, Canada

Author: Zoe Clark
Program: Marine biology
Supervisor(s): Margaret Eng, Environment and Climate Change Canada
Glenn Crossin, Department of Biology, Dalhousie University

Abstract

Chemical pollution is a significant threat to wildlife, and the eggs of seabirds are valuable indicators of marine pollution. Seabirds are used as bioindicators due to their tendency to occupy high trophic levels, long life spans, and ability to bioaccumulate pollutants. Sable Island is a remote offshore island located approximately 160km from the nearest landfall and has been designated as an Important Bird Area that supports large numbers of nesting seabirds. Previous studies have found that herring gull (*Larus smithsonianus*) eggs from Sable Island have higher average mercury concentrations and higher ΣPFAS levels compared to other Atlantic study sites. The goal of this study was to investigate these trends further by gaining additional data on interspecific and temporal patterns of contaminants in seabird eggs on Sable Island. In 2012 and 2025, eggs from herring gulls plus three additional species (great black-backed gull [*Larus marinus*], common tern [*Sterna Hirundo*], and arctic tern [*Sterna paradisaea*]) were collected on Sable Island and analyzed for chemical contaminants of concern, including mercury (Hg), polybrominated diphenyl ethers (PBDEs), organochlorine pesticides (OCPs), polychlorinated biphenyls (PCBs), and per and polyfluoroalkyl substances (PFAS). Stable isotopes ($\delta^{13}C$ and $\delta^{15}N$) were also analyzed to investigate links between foraging ecology and contaminant exposure. Stable isotope analysis from 2012 indicated that common and arctic terns occupy similar foraging niches. Great black-backed gulls occupied the highest trophic level, and herring gulls occupied the second-highest. In 2012, contaminant profiles generally aligned with trophic level, and for OCPs, PCBs, and mercury, great black-backed gulls had the highest average total contaminant loads, and both tern species had similarly low contaminant loads relative to both gull species. Average total PBDE load was highest in herring gulls in 2012, and again similarly low in both tern species. The average ΣPFAS burden was the same for great black-backed and herring gulls in 2012, but there was a clear shift in 2025 to great black-backed gulls having the highest ΣPFAS burden among all species. Between 2012 and 2025, ΣPFAS levels decreased across all species, with significant decreases for both tern species. PFOS was the dominant compound among all 4 species, consistently accounting for over 60% of ΣPFAS burden. Over the study period, the proportion of PFOS did not shift substantially.

Using eDNA to reveal the impacts of invasive fish on freshwater communities

Author: Ella Colwell
Program: Biology
Supervisor(s): Dr. Paul Bentzen, Biology Department, Dalhousie University
Beth Watson, Biology Department, Dalhousie University

Abstract

Freshwater ecosystems are among the most at-risk biomes in the world, with higher losses in vertebrate biodiversity than marine or terrestrial environments. One driver of this biodiversity loss is aquatic invasive species (AIS) such as Smallmouth Bass and Chain Pickerel, which are present in Nova Scotia. In my honours thesis, I am investigating if and how these two AIS affect native fish species richness in lakes in Lunenburg County, NS. I conducted water-based environmental DNA (eDNA) surveys across nine lakes. The eDNA from each lake was analyzed using qPCR and metabarcoding to determine AIS presence and overall fish community composition in each lake. Results indicate that lakes with Chain Pickerel tend to have lower species richness compared to lakes with only Smallmouth Bass or no AIS. These findings highlight how different invasive species can have distinct ecological impacts and demonstrate the value of eDNA surveys for monitoring freshwater fish communities. The results provide insights for conservation strategies aimed at protecting native biodiversity.

The Ability of Scent-Detection Dogs to Signal VOC's Associated with Anxiety in Humans with PTSD

Author: Katherine Crawford
Program: Biology
Supervisor(s): Dr. Simon Gadbois, Psychology and Neuroscience Department, Dalhousie University

Abstract

Domestic dogs (*Canis lupus familiaris*) use their extraordinary olfactory abilities to enhance our workforce across many fields. This offers particular advantages for the biomedical detection of disease and the assessment of human metabolic state. There is evidence that dogs can detect infectious and non-infectious diseases by identifying changes in an individual's unique scent profile, composed of volatile organic compounds (VOCs). There is little research on whether the human stress axes (Hypothalamic-Pituitary-Adrenal and Sympathetic-Adrenal-Medullary) alter VOC patterns, inducing specific olfactory biomarkers that dogs could detect. Post-traumatic stress disorder (PTSD) is a trauma stress-related disorder with a high prevalence among veterans. PTSD service dogs are an addition to a primary treatment plan for those who suffer from PTSD. Currently, they are trained to respond to their owners' physical symptoms. If research could support dogs' ability to detect human stress-related VOCs, they could be trained to alert their owners before physical symptoms appear. This study asks if dogs can reliably detect VOCs in human breath associated with early markers of anxiety responses in individuals with PTSD. By following a low saliency training protocol using operant conditioning principles, we trained a small cohort of dogs to detect a training odour. The Mood, Anxiety, Addictions, and Co-Morbidity Lab (MAAC) at Dalhousie University was conducting a simultaneous independent study and provided us with the face masks worn by their participants with PTSD in a stressed and baseline state. Dogs that consistently and reliably detect the odour will move on to testing, where they will identify human breath samples as stressed or baseline in a yes/no detection task. Training sessions are double-blind, and all dogs' correct or incorrect responses will be analyzed using signal detection theory to determine performance measures. We predict that at least some dogs will achieve over 85% accuracy in correctly identifying breath samples. We speculate that the dogs are detecting VOCs from the SAM axis due to the short collection time for breath. These results can be used to alter PTSD dog training protocols, with concurrent research with colleagues that is focusing on the exact VOCs they are detecting.

Deciphering the Role of *WAVH1* in Response to Nitrogen and Phosphorus Deprivation in *Arabidopsis thaliana*

Author: Elle Crilly
Program: Biology
Supervisor(s): Dr. Sophia Stone, Department of Biology, Dalhousie University

Abstract

Plant survival and reproduction largely depend on the ability to detect and acquire bioavailable nitrogen (N) and phosphorus (P) macronutrients from the soil. Plants have evolved diverse strategies to circumvent N and P deprivation in soil systems, involving transcriptional regulation that favours survival and adaptive growth in nutrient-poor soils. The Ubiquitin-Proteasome System (UPS) is also essential for facilitating tolerance to nutrient stress by mediating changes to cellular protein content via degradation. For example, by regulating the abundance of transcriptional regulators, the UPS can mediate changes in gene expression required for promoting nutrient uptake. Central to the UPS are ubiquitin ligases (E3S) that confer substrate specificity, covalently attaching ubiquitin molecules to selected proteins, marking them for degradation by the 26S Proteasome complex. Members of the Wavy Growth 3 (WAV3) gene family encode for E3s involved in the regulation of root gravitropism and changes in root system architecture, including lateral root emergence and primary root growth. Here, we investigate Wavy Growth 3 Homolog 1 (*WAVH1*), a homolog of Wavy Growth 3 (*WAV3*), as a candidate modulator of nutrient stress responses. Using RNA sequencing data, real-time PCR (RT-PCR), and quantitative PCR (qPCR), we assess how loss of *WAVH1* function (*wavh1*-1) alters gene expression under nitrogen-deficient (-N) and phosphorus-deficient (-P) conditions. Additional phenotypic assays are used to elucidate how the loss of *WAVH1* influences growth vigour under -N and -P. We predict that the loss of *WAVH1* will impair the plant's ability to mount a proper coping response to nutrient deficiency stress. Preliminary results demonstrate that *WAVH1* function is required for an appropriate response to -P conditions, but may not play an integral role in mediating responses to -N. Although the *wavh1-1* mutant is phenotypically insensitive to nitrogen and phosphorus deprivation, it exhibits an attenuated transcriptional expression of genes that respond to phosphate deficiency compared to the wild-type (WT). The characterization of the E3 WAVH1 provides invaluable insight into how UPS-mediated tolerance to nutrient stress is achieved and may inform strategies to improve crop yields, while decreasing reliance on the excessive use of harmful inorganic fertilizers. Decreases in arable land, coupled with increasing global population levels, necessitate agricultural innovations that reduce dependence on synthetic fertilizers while maintaining crop productivity.

Temperature-Associated Movement and Hibernacula Use in Eastern Ribbon snakes (*Thamnophis sauritus*)

Author: Maeve Cuthbert-Shore
Program: Biology and Creative Writing
Supervisor(s): Carter Feltham, Mersey Tobeatic Research Institute
Dr. Robert Lennox, Department of Biology, Dalhousie University

Abstract

Overwintering behaviour and habitat are critical yet poorly understood components of snake ecology, particularly for species of conservation concern such as the Atlantic population of the Eastern Ribbonsnake (*Thamnophis sauritus septentrionalis*). This study investigated fall ingress movements using Passive Integrated Transponder (PIT) tag detections across four suspected hibernacula in southwestern Nova Scotia. The date and timing of detections in relation to environmental temperatures were assessed to identify seasonal patterns and variation in site use.

Detections at overwintering sites generally increased as air temperatures declined, with activity ceasing at approximately 10 °C air temperature, suggesting a thermal threshold for late-season surface activity and supporting the minimum temperature for visual surveys to be around 8°C. Movement patterns were highly variable between sites, one location suggested early-season ingress, while another recorded above-ground activity later in the season and at cooler temperatures. Notably, one historically active site recorded no detections during the fall ingress period, indicating recent shifts in habitat suitability or a lack of annual site fidelity. These findings suggest that conservation strategies cannot rely on static overwintering and locations and highlight the need for flexible conservation management that account for annual variation in site use, ensuring that a diverse range of potential hibernacula are protected to support seasonal survival and population recovery.

Tracking Snapping Turtles (*Chelydra serpentina*) in Nova Scotia Using Acoustic Telemetry

Author: Emma Daigle
Program: Biology
Supervisor(s): Dr. Robert Lennox, Biology Department, Dalhousie University

Abstract

The common snapping turtle (*Chelydra serpentina*) is a freshwater turtle species that spends most of its time in the aquatic environment. Snapping turtles are relatively abundant; however, snapping turtles have long lifespans associated with low recruitment and delayed maturity. This trait served snapping turtles well in the past, but with today's anthropogenic factors (e.g., urbanization, conversion to agricultural land, road mortality, etc.), this life trait hinders their persistence. Due to snapping turtles' susceptibility to anthropogenic factors, they have been listed as Special Concern under the Species at Risk Act and as a Vulnerable species under the Nova Scotia Endangered Species Act. Knowledge of their movement ecology in freshwater habitats is limited, yet understanding movement is crucial for habitat protection. Acoustic telemetry, a common method for tracking aquatic animals, is increasingly being applied to freshwater turtle research. This study aims to determine when snapping turtles are active in the aquatic environment, and to observe the connectivity between lakes in the Petite Rivière watershed in Nova Scotia occupied by snapping turtles using acoustic telemetry. The Petite Rivière is a watershed located in Lunenburg County on the south shore of Nova Scotia. Acoustic receivers were deployed in Minamkeak Lake, Hebb Lake, and Milipsigate Lake, which are interconnected in the Petite Rivière. Acoustic tags were attached to 12 snapping turtles from late May to late June 2025 using plumbing epoxy. The turtles were tracked for six months from July to December 2025. All turtles were detected on receivers during this study period for a total of 23164 times. Turtles were observed moving from their release location across lakes and to other lakes. Snapping turtles moved between Minamkeak and Milipsigate Lakes and were not detected in Hebb Lake. The number of detections varied across individuals; however, daily peak detection periods occurred mid-day (around 12pm). These findings represent the first study of snapping turtle movement ecology in Nova Scotia. Next steps include modeling the time spent in aquatic environments to determine how use of this habitat varies across individuals and time using generalized additive models (GAMs). Our findings will fill critical knowledge gaps of the species' seasonal movements to inform conservation efforts of this at-risk species.

Individual Locus Effects on Mortality Risk in the Endangered St. Lawrence Beluga Whale

Author: Sofia Day
Program: Marine Biology and Oceanography
Supervisor(s): Dr. Tim Frasier, Biology Department, Saint Mary's University

Abstract

Small and isolated populations are particularly vulnerable to harmful genetic effects, such as inbreeding depression, which can hinder recovery and reproductive success. The St. Lawrence Estuary beluga population has been listed as Endangered by COSEWIC due to their small population size, lack of recovery despite protection from hunting, and increased calf and peripartum mortality. Although cancer from PAH exposure appeared to be limiting population reestablishment in the past, no cancer-related mortalities have been observed since 2011. Therefore, current research is focused on identifying what other factors may be hindering recovery. To assess the effects of low genetic diversity, recent analyses compared ddRADseq and whole-genome data from individuals within the population and found no correlation between inbreeding coefficients and mortality risk, as well as no evidence of recent inbreeding. However, several regions of the genome in neonates showed reduced heterozygosity at sites associated with processing environmental contaminants. To further this finding, I aimed to identify whether specific regions of the genome were associated with mortality risk from different causes. This was carried out by analyzing ddRADseq data using 15,452 SNPs across 143 individuals in combination with phenotype mortality data. Genome-wide association analyses, conducted using logistic regressions within PLINK, revealed no significant allelic or genotypic associations to mortality risk from the assessed causes. However, both theory and previous studies suggest that mortality risk may be influenced by the interaction of multiple loci. Therefore, I took subsequent steps to reexamine the dataset for epistatic interactions and identify clusters of alleles associated with a given phenotype. Of the eight total tests, unique gene modules were identified from genotypic comparisons associated with mortality due to infectious disease and neoplasia. Further work is being done to understand the biological processes associated with these regions and their potential correlation to cause of death. This research contributes to a broader understanding of conservation genetics, particularly how genes interact with their environment, and possible outcomes may help inform conservation strategies to better protect this endangered population.

Evaluating Individual Identification of Blue Sharks (*Prionace glauca)* Using Ampullae of Lorenzini and Fin Morphology

Author: Geraldine Fernandez
Program: Concentrated Honours in Marine Biology; Minor in Statistics
Supervisor(s): Dr. Derek Tittensor, Biology Department, Dalhousie University
Dr. Manuel Dureuil, Biology Department, Dalhousie University

Abstract

Accurate representation of elasmobranch populations is essential for monitoring and effective conservation assessments. Such representation requires reliable identification of individuals yet conventional methods, such as physical tagging, can cause stress, tissue damage, and harm. While not a direct substitute for physical tagging, photographic identification (photo-ID) offers a non-invasive alternative for individual identification and is therefore increasing in usage. Photo-ID relies on natural markings to distinguish individuals and has been applied to many species but remains underexplored in pelagic and migratory species. The blue shark (*Prionace glauca*) is a highly migratory species, aggregating on coastal shelves, and is highly exploited, making effective monitoring critical. However, it remains unknown whether there are sufficient morphological differences to allow for the identification of these individuals. To address this gap, my project evaluates the feasibility of using underexplored markings in the identification of individual blue sharks using two separate morphological features: (1) the arrangement of ampullae of Lorenzini and (2) combined fin morphology and intermediate body contours. I further assess whether existing photo-ID applications can automate identification using one or both features.

Underwater video footage of blue sharks was collected using the prototype "Shark Bar" created by the FOME lab of Dalhousie University from July to September 2025 during Atlantic Shark Expeditions off Sambro Harbour, Nova Scotia. Frames were extracted from the videos to construct a photo-ID database including only individuals that provided clear views of ampullae and complete lateral fin profiles. Ampullae within a predefined triangulated area were manually annotated and visually compared to evaluate individual distinctiveness. Fin contours were traced and then compared to other individuals to determine uniqueness. The Interactive Individual Identification System (I^3S) in both Classic and Contour modes were tested to evaluate the automated individual matching performance of both ampullae and fin contours. Results of these methods are still underway. In brief, my project explores a novel, non-invasive approach for identifying individual blue sharks and aims to expand photo-ID applications for sharks that lack conventional markings to ultimately aid ethical and non-invasive conservation monitoring.

Amphibian and Reptile Richness and Abundance in the Backlands

Author: Jessica Fullerton
Program: Marine Biology Co-op; Minor in Statistics
Supervisor(s): Boris Worm, Biology Department, Dalhousie University

Abstract

Urban wilderness areas in Nova Scotia, such as the Halifax Backlands, are important for supporting a variety of species and ecosystems. These areas are at risk of environmental degradation and development due to growing human populations. Amphibians and reptiles are particularly vulnerable to habitat loss, and they are critically understudied despite their significant ecological roles. Amphibian and reptile populations are declining as human driven disturbances increase. Human activity can worsen freshwater quality, making pH more acidic and increasing salinity, possibly leading to lower species richness and total abundance. Human activity can also directly disturb normal amphibian and reptile behaviors; amphibians and reptiles may therefore avoid areas of frequent human use. To assess anthropogenic effects on amphibians and reptiles in the Halifax Backlands, water quality and human use of the trails were compared with amphibian and reptile species richness and total abundance. During the summer of 2025, species richness and total abundance were measured using repeated visual and auditory surveys, along with measuring water pH, temperature, and conductivity as a proxy for salinity. Trail use by humans during the time of the survey was also recorded. Average total abundance and average species richness did not differ significantly when people were on the trail and when there were no people on the trail. Although there was no statistical significance, the site with the greatest difference had a higher average richness and average total abundance when no people were on the trail. Single variable regression analyses conducted for environmental parameters (water and weather conditions) against total abundance had no significant predictors for total abundance. Conductivity, humidity and visibility were significant in predicting species richness. Each of these parameters only accounted for a small proportion of the variation seen in species richness with visibility accounting for the highest proportion. This study suggests there may be a trend between human activity and lower amphibian and reptile species richness and total abundance in the Backlands, but there is limited data collected over a short period of time meaning further studies are needed to properly assess significance and draw conclusions.

Microbial Transformation of Organic Matter: Linking Nitrogen Acquisition Strategies to δ^{15}N-Amino Acid Fractionation

Author: Kevin Glover
Program: Marine Biology
Supervisor(s): Dr. Owen Sherwood, Earth and Environmental Sciences Department, Dalhousie University

Abstract

Dissolved organic matter (DOM) is a major oceanic carbon sink whose components can persist for millennia. However, the cycling of DOM in the ocean is poorly understood. This limits our ability to predict how global biogeochemical cycling may shift with climate change. Microbes (bacteria, archaea, and fungi) are major contributors to the DOM pool as the degrade particulate organic matter (POM) into DOM. However, the impact of microbially mediated biogeochemical cycling remains unclear. To better understand the effect of microbial degradation of organic matter we conducted a series of feeding trials on eight species of bacteria grown on three different forms of nitrogen (ammonium, peptides, free amino acids). We aimed to isolate the different nitrogen isotopic composition of amino acids ($\delta^{15}N_{AA}$) produced by the intake of different nitrogen sources using compound specific isotope analysis of amino acids (CSIA-AA). We found that the $\delta^{15}N_{AA}$ pattern of bacteria consuming ammonium resembled that of phytoplankton and the $\delta^{15}N_{AA}$ pattern of bacteria consuming preformed AA resembled that of metazoans as described in previous literature. We expected to see distinct $\delta^{15}N_{AA}$ patterns for bacteria consuming performed AA in peptides and preformed free AA. While there appear to be subtle differences, the statistical significance of these patterns has yet to be confirmed. Through comparison of our data with other bacterial $\delta^{15}N_{AA}$ data we have isolated heterotrophic bacteria from the other end-member categories described by in previous studies, expanding on the known end-members identified in POM. These findings add to a growing database for interpreting $\delta^{15}N_{AA}$ values for organisms and organic matter in natural environments.

Comparing the effects of exhaustive chasing and lethal TFM lampricide exposure on non-target Great Lakes species

Author: Melina Göbel
Program: Concentrated Honours Marine Biology (Co-op)
Supervisor(s): Dr. Hugo Flávio, Lennox Lab, Dalhousie University
Dr. Robert Lennox, Department of Biology, Dalhousie University

Abstract

The invasive parasitic sea lamprey (*Petromyzon marinus*) once decimated important commercial and recreational fisheries in the Laurentian Great Lakes, impacting ecosystem services and the local economy. Today, sea lamprey populations are primarily kept under control by the periodic dosing of the lampricide 3-trifluoromethyl-4-nitrophenol (TFM) in streams and tributaries containing benthic-living larvae. Commonly, toxicity experiments used to determine the sensitivity of both sea lamprey and non-target species to TFM require killing large numbers of study animals. As part of an effort to develop a non-lethal method to determine TFM sensitivity, I used intermittent flow respirometry to determine the maximum metabolic rate following exhaustive chasing of four Great Lakes species; lake sturgeon (*Acipenser fulvescens*), rainbow trout (*Oncorhynchus mykiss*), smallmouth bass (*Micropterus dolomieu*), and giant floater (*Pyganodon grandis*), and compared these to each species' oxygen consumption rates during exposure to lethal TFM concentrations. Preliminary results indicate that species-specific maximum metabolic rate may be used as a predictor for the change in oxygen consumption imposed by exposure to lethal TFM concentrations. Specifically, this method appears to be more reliable for species sensitive to TFM than for highly tolerant species. This method has the potential to supplement and reduce testing that results in animal mortality, which is essential when studying vulnerable Great Lakes species.

Defining Histotripsy Safety Margins for Image-Guided Spinal Tumour Treatment

Author: Ruby Harrington
Program: Biology
Supervisor(s): Dr. Jeremy Brown, Department of Electrical Engineering, School of Biomedical Engineering, Dalhousie University
Dr. Thomas Landry, School of Biomedical Engineering, Dalhousie University, Nova Scotia Health Authority

Abstract

Spinal metastases are a major cause of morbidity in cancer patients, and frequently lead to spinal cord compression, neurological deficits, and reduced quality of life. Surgical decompression and radiotherapy remain the primary treatment options. However, many patients are ineligible for surgery due to poor health, limited life expectancy, and procedural risks. Radiotherapy is constrained by the spinal cord's extreme radiosensitivity, which often results in insufficient radiation dosing when tumours are located adjacent to neural tissue. These limitations highlight the need for a minimally invasive, highly precise therapeutic alternative.

Histotripsy is a minimally invasive, non-thermal focused ultrasound ablation technique which mechanically disrupts tissue through acoustic cavitation. Due to its high spatial precision histotripsy shows promise for tumour ablation near critical structures, like the spinal cord. However, safe application requires a clear understanding of distance thresholds for ultrasound ablation to prevent off-target damage in neural tissue.

This study aims to determine the distance at which focused ultrasound ablation can be delivered without causing damage to spinal tissue. Ex vivo porcine spinal cord samples with intact dura were embedded in tissue-mimicking phantoms and histotripsy treatments were applied incremental distances, ranging from 5mm outside to 1mm within the spinal cord. Treatments were applied using a 1.5MHz histotripsy transducer equipped with real-time ultrasound imaging. Tissues were then sectioned and stained for histological analysis. Damage was quantified using digital image analysis, with damage classified as either present or absent each site.

It is hypothesized that the probability of seeing damage will increase as the spinal cord is approached, and that there will be a sudden shift seen when significant damage occurs. These results will help guide safe use of histotripsy in spinal tumor treatments, supporting clinicians in making informed decisions about its use near neural structures.

By defining reliable proximity limits, this study contributes to the development of image guided, minimally invasive alternatives to conventional spinal tumour surgery. These findings may improve access to treatment for patients who are unsuitable for existing options and contribute to the safe clinical translation of histotripsy.

Behavioral thermoregulation of sea-run brook trout (*Salvelinus fontinalis)* in the East River of Pictou, Nova Scotia

Author: Anders Hoffmann
Program: Marine Biology
Supervisor(s) Dr Robert Lennox, Biology Department, Dalhousie University

Abstract

Brook trout *(Salvelinus fontinalis)* are a species of cold-water salmonid that is native to much of Eastern Canada, where they face the threat of warming water temperatures throughout the southern extent of their range. Our understanding of sea-run brook trout oversummering thermal refuge sites is lacking in Atlantic Canada, and research typically focuses on their movements in the marine environment. This study uses acoustic telemetry to investigate sea-run brook trout thermal experience and movements over summer in the East River of Pictou, Nova Scotia. I aim to determine whether sea-run brook trout exhibit thermoregulation and the location of thermal refuge sites over the summer, following their upstream migration. Brook trout (n = 30) were caught and implanted with acoustic transmitters that included temperature sensors, and acoustic receivers were deployed throughout the river. Brook trout were tracked between May and November 2025 to ensure that the full oversummering period could be characterized. Results from this study show that these fish are using specific cold-water habitats to thermoregulate during the summer months when water temperatures warm. These findings will help us understand more about the ecology of these valuable migratory fish in order to better protect and manage populations and habitats in both this river system and others across the southern range of sea-run brook trout.

Overwinter storage of eelgrass (*Zostera marina*) seeds from a Nova Scotian population for use in coastal habitat restoration

Author: Remi Kowalski
Program: Concentrated Honours in Marine Biology
Supervisor(s): Dr. Kristina Boerder, Biology Department, Dalhousie University
Dr. Derek Tittensor, Biology Department, Dalhousie University

Abstract

Eelgrass (*Zostera marina*) meadows play an important role in mitigating the climate crisis due to their ability to capture organic carbon, protect against coastal erosion, and form highly biodiverse habitat. However, anthropogenic pressures such as coastal development, invasive species, and warming sea temperatures are causing worldwide declines of all seagrasses, eelgrass included.

Eelgrass restoration typically involves transplanting shoots from healthy donor beds to grow new meadows. However, using seeds instead is likely to have lower impact on the donor meadows and can increase genetic diversity in the restored meadows. In Nova Scotia, Canada, eelgrass populations go into seed mid-late summer, but the seeds don't germinate until the following spring after a cold period. Therefore, eelgrass seeds need to be stored overwinter to be used in restoration efforts. Although multiple seed storage experiments have been conducted on *Z. marina*, parameters impacting the success of long-term storage appear to vary by population and region, and overwinter seed storage has not yet been studied for Nova Scotian populations.

To investigate what storage conditions will minimize seed mortality and avoid premature germination for an NS population, I conduct an exploratory pilot experiment on *Z. marina* seeds from a subtidal meadow at Cliff Cove, NS. Seeds were divided into 12 distinct treatments crossing 4°C, 0°C, 40 ppt, and 50 ppt with 1 ppm copper sulfate, constant aeration, and control. Seeds were stored in their respective treatments for 14 weeks. Every 2 weeks, a subsample of seeds was removed from each replicate and tested for viability by staining with triphenyl tetrazolium chloride (TTC).

Treatments at 0°C appear to have the highest proportion of viable seeds, particularly for 0°C, 50 ppt, and 1 ppm copper sulfate. These preliminary results can guide future long-term eelgrass seed storage experiments for NS populations, potentially enhancing vital ecosystem restoration around the province.

Reusing Waste, Capturing CO_2, and Restoring Habitat With Algal-Enriched Concrete

Author: Jayda Kruger
Program: Marine Biology, Ocean Science Minor
Supervisor(s): Dr. Hugh MacIntyre, Department of Oceanography, Dalhousie University

Abstract

Climate change causes larger storms, rising sea levels, and habitat loss, driving an increased need for coastal armoring and reef restoration. Seawalls and Artificial Aquatic Habitats are normally made of concrete, however, concrete production accounts for approximately 8% of anthropogenic greenhouse gas emissions (Monteiro et al., 2017). To avoid a positive feedback loop, the concrete industry must be decarbonized. We have formulated a concrete mixture enriched with an algal admixture – Phycocrete – that sequesters the CO2 captured during growth without decreasing the strength of the material. The alga is an extremophilic isolate from Nova Scotia and is grown in a medium of amended tertiary-treated municipal wastewater. To assess the marine applications of this material, we compared the bio-receptivity of pucks made of Phycocrete to control pucks made of regular concrete. Seventy-two pucks were submersed for five weeks at a shallow water mooring in Mahone Bay, Nova Scotia, and sampled weekly to assess biofilm growth. Biomass accumulation on the pucks was measured using extracted chlorophyll a and spectral reflectance. Physiological status was interrogated using variable fluorescence. We measured vigorous periphyton growth on the pucks over time, with chlorophyll concentrations reaching an average concentration of 7.49 ± 0.86 mg/m^2 after one month. Importantly, through a nested ANOSIM, we determined there was a significant increase in the biofilm over time ($p < 0.001$) but no significant difference in biomass accumulation or periphyton photo-physiology between regular concrete and Phycocrete within sampling intervals ($p = 0.48$). This preliminary experiment suggests that Phycocrete could be used in marine applications – including Artificial Aquatic Habitats and seawalls – to couple wastewater remediation, carbon capture, and sustainable building.

Assessing the Impact of Ocean Alkalinity Enhancement on Benthic Microbial Communities Using eDNA Metabarcoding

Author: Vanessa Landry
Program: Concentrated Honours in Marine Biology
Supervisor(s): Dr. Julie LaRoche, Department of Biology, Dalhousie University

Abstract

Climate change is impacting countless ecosystems worldwide and it is becoming increasingly evident that something needs to be done about it. Since climate change is largely caused by an increase in CO_2 in the atmosphere, several projects have been proposed to reduce atmospheric CO_2. One of these projects is the Ocean Alkalinity Enhancement (OAE) project, which consists of increasing the pH of the ocean by dosing alkaline material in it to enable it to sequester more CO_2. However, the environmental impacts of this project have yet to be studied in natural ecosystems. In September of 2023, a fully operational OAE pilot plant was implemented in the Halifax harbour, which provides a unique opportunity to study how ecosystems respond to OAE. This present study assesses the impact of OAE dosing on benthic microbial communities. Sediment samples were taken before the dosing started, ~1 week, and several months after it started, in different locations, including Tuft's Cove where the dosing is happening. eDNA metabarcoding techniques were used to determine the composition of the communities for each date and each station. A significant shift in the microbial composition and a major drop in alpha-diversity was observed in sediments nearest to the dosing release site in June 2025, several month after the beginning of the dosing, There were also significant differential abundances of some microbial taxa; notably, members of the genera *Lutibacter* and *Desulfoconvexum* became significantly more abundant. These changes in community composition and diversity might indicate that the dosing did have an impact on the microbial communities. Although the results are preliminary and await additional time points to support the findings, these results provide a necessary insight into the biological impact of OAE and could help policymakers and industries work together to take action against climate change.

Assessing the Germicidial Efficiency of UV-LED Technology in Different Wastewater Matrices

Author: Jeremy Larsen
Program: Biology (Co-op), Minor in Environmental Science
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Dr. Sean MacIsaac Department of Engineering, Dalhousie University

Abstract

Ultraviolet Disinfection (UV) has been utilized effectively for years as the final step of the wastewater disinfection. Conventional wastewater systems rely on mercury to power their UV disinfection, which comes with negative environmental and health impacts. The UN Minamata convention on Mercury has banned the use and production of mercury by 2032, leaving the wastewater industry in a bind to find a disinfection alternative. UV-LEDs have shown promise to replace the mercury bulbs in the UV disinfection. UV-LEDs have shown similar disinfection to the conventional system on both the bench scale and full-scale experiments. This study assesses the germicidial efficiency of several UV-LED wavelengths on a selection of challenge organisms, including *Escherichia coli (E. coli)*, in two different wastewater matrices. Water was collected from wastewater facilities in Eastern Passage (EP) and Chicago, filtered, sterilized to avoid unwanted microbial activity, and spiked with *E. coli* K12. Each sample was dosed under three different wavelengths of LED (255 nm, 265 nm, and 280 nm), as well as a medium pressure (MP) lamp (254 nm) and a low pressure (LP) lamp (275 nm) to represent the conventional system. Preliminary results show that on Chicago wastewater spiked with *E. coli* K12, UV-LEDs had a lower k-values (k_{255} = 0.39, k_{265} = 0.41, k_{280} = 0.30, k_{LP} = 1.77), while having similar or higher log reduction values. Preliminary results on Eastern Passage water showed similar results with lower k values in LEDs, but higher log reduction values (k_{255} = 0.40, k_{265} = 0.41, k_{280} = 0.30, k_{LP} = 1.63), however similar or higher log reduction values in UV-LEDs. Medium Pressure showed a low k-value in each of the water matrices. Additional statistical analysis will show the differences between disinfection values at each of the different UV sources. The results of this research will provide a greater understanding on whether the use of UV-LED technologies to replace conventional mercury systems is viable in varying water matrices. Next steps include repeating this work on an additional challenge organism, F-type Bacteriophage, MS2, which has a substantially higher resistance to UV exposure compared to *E. coli*.

Characterization Of Interventricular Septal Development and Perinatal Mortality in Mice Lacking Natriuretic Peptide Receptor A (NPRA)

Author: Cindy Liu
Program: Biology
Supervisor(s): Dr. Kishore Pasumarthi, Department of Pharmacology, Dalhousie University

Abstract

Natriuretic peptide receptor A (NPRA) is a high-affinity receptor for cardiac hormone atrial natriuretic peptide (ANP), and it is known to play an essential role in embryonic heart development and the maintenance of normal cardiac function. Previous research has shown that NPRA Knockout (KO) mice exhibit perinatal mortality, and recent findings from our lab show that stillborn neonatal NPRA KO mice display a ventricular septal defect (VSD) phenotype. VSD is the most prevalent type of congenital heart disease (CHD), which is the most common type of birth defect worldwide. Despite advancements in clinical interventions treating VSDs, the cellular mechanism responsible for VSD are still unclear.

To decipher the underlying mechanism of septal malformation, this research aims to characterize septum development and VSD formation in NPRA KO mice. Specifically, this study investigates whether altered cell proliferation and metabolic regulation in the developing interventricular septum disrupt progenitor cell fate and metabolic status, ultimately leading to septal defects, perinatal mortality or cardiac dysfunction. Ventricular septal development will be evaluated in the neonatal day 1 hearts using cryosections obtained from three wildtype, three live NPRA KO, three stillborn NPRA KO hearts (N=3 per group). Cell proliferation and apoptosis will be assessed through immunostaining. Cardiac progenitor cell distribution and metabolic markers will also be examined through immunofluorescence, confocal microscopy and analyzed using intensity analysis. Further histology and fibrosis staining will be performed to identify whether there is abnormal accumulation of collagen in the KO neonate compared with the WT.

Result to date found a significant increase in the heart/body weight ratio in neonatal NPRA KO mice compared to WT littermates. Immunostaining experiments revealed a significant reduction in the proliferating of septal cardiomyocytes in KO vs WT hearts with no changes in apoptosis levels. Histological staining revealed no significant differences in collagen accumulation between two groups.

This honours research reveals the effects of NPRA loss on early septal development; and helps identify the mechanisms underlying ventricular septal defects and perinatal mortality. These results will provide mechanistic insights into the ventricular septal malformation in CHD patients and ultimately facilitate discovery of new drug targets.

Testing Different Sporing Methods, Water Flow, and Nutrient Conditions on the Growth of *Saccharina latissima* in the Hatchery Phase

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Program: Marine Biology
Supervisor(s): Dr. Carolyn Buchwald, Department of Oceanography, Dalhousie University

Abstract

Sugar kelp (*Saccharina latissima*) is one of the most widely cultivated macroalgae species and is native to Atlantic Canada where it has strong potential for aquaculture development. However, warming ocean temperatures influence the natural sporulation in wild populations, altering the traditional seeding windows for farmers. These changes have increased the need for alternative, climate-resilient hatchery practices. This study investigates the hatchery-stage growth of *S. latissima* using three seeding methods: spores released from artificially matured sporophytes, spores from wild-caught mature sporophytes, and direct seeding using cultured gametophytes. In addition, three hatchery nutrient delivery systems are tested: continuous flow-through seawater, recirculated seawater, and static seawater tanks. Induced sporogenesis was achieved by exposing immature blades to short-day photoperiod conditions, allowing controlled spore production to be independent of natural seasonal timing. Development of sporogenetic tissue in force-matured kelp blades was tracked using image analysis software to produce a timeline of sorus growth. Growth in the hatchery phase was assessed 40 days after inoculation of spools by measuring sporophyte density and length on twine samples using image analysis. Through two-way ANOVA testing and pairwise comparisons, analysis revealed that seeding method and nutrient delivery both influenced early sporophyte growth. Spools seeded with spores from force-matured blades produced significantly higher sporophyte densities than both gametophyte and wild-matured treatments, while densities did not differ between gametophyte and wild-matured groups. Significant differences in sporophyte length were also observed among seeding methods, with the largest differences occurring between the force-matured treatment and the other methods. Hatchery condition affected growth outcomes, with recirculated systems producing significantly different sporophyte densities compared to both flow-through and static tanks. For blade length, differences were detected between flow-through and recirculated systems, while other pairwise comparisons were not significant. However, differences could be attributed to increased contamination on the spools seeded with gametophytes and wild-matured spores, as well as varying levels of contamination between tanks. The results demonstrate that lab-matured spores and gametophytes can support equally strong hatchery performance and provide practical insight for improving hatchery efficiency, supporting the development of sustainable sugar kelp aquaculture under changing environmental conditions.

Quantifying the relationship between fat content and *Rickettsia sp.* bacterial prevalence in the American dog tick, *Dermacentor variabilis*

Author: Eliseo Martignago
Program: Biology
Supervisor(s): Dr. Tatiana Rossolimo, Biology Department, Dalhousie University
Dr. James Kho, Biology Department, Dalhousie University

Abstract

The American Dog tick (*Dermacentor variabilis)* is a hard-bodied tick distributed across eastern North America and is a known vector of many tick-borne pathogens. Previous studies performed on other species of hard bodied ticks, mainly from Ixodes genus, indicate there may be a correlation between bacterial prevalence and tick fat reserves, giving infected ticks more energy for questing behaviour. This study aims to find if local *Dermacentor variabilis* ticks that are infected with *Rickettsia sp.,* a major tick-borne pathogen and the causative agent of Rocky Mountain Spotted Fever (RMSF), exhibit a similar pathogen-host relationship. Adult ticks were collected from established populations around Halifax Regional Municipality area in Nova Scotia. Each tick was cut in half with one half used to measure body size and fat content, while the other is used to examine *Rickettsia sp.* infection. Preliminary results suggest *D. variabilis* ticks infected with *Rickettsia sp.* have a higher fat content. This would suggest that *Dermacentor variabilis* ticks follow similar patterns seen in previous studies, providing insight into the physiology of local hard-bodied ticks. Data processing is ongoing but are predicted to further support this hypothesis. *D. variabilis* is a growing concern in Nova Scotia community in part due to their role as disease vectors of human diseases such as RMSF. *Dermacentor variabilis* is expected to undergo a large northern range expansion in the coming years due to climate change. These findings provide key information on how bacterial pathogens can potentially influence tick physiology, thereby helping us to better understand the role of ticks as carriers of human pathogens.

Investigating Muscle Repair by Inducing Cold Damage in *Drosophila melanogaster*

Author: Kate McKee
Program: Concentrated Honours in Biology
Supervisor(s): Dr. Nicanor González-Morales, Department of Biology, Dalhousie University

Abstract

Insects frequently encounter freezing temperatures that threaten cellular stability and locomotor performance, yet the tissue-level consequences of freezing and the potential for muscle repair remain poorly understood. This study investigates whether freezing induces structural damage in *Drosophila melanogaster*, whether damaged fibres recover over time, and how age and sex shape these outcomes. Flies expressing Zasp52-mCherry and ObscurinGFP were used to visualize Z-discs and M-lines, enabling direct assessment of sarcomere integrity. Experimental flies were grouped by sex and aged into four cohorts (1-4 weeks). Baseline walking speed and femur muscle structure were measured prior to freezing. Flies were then subjected to a two-phase cold-hardening and freezing protocol (3°C for 3.5h, -4°C for 6h), followed by seven days of recovery during which locomotor performance and muscle morphology were repeatedly assessed. Freezing caused an immediate and dramatic reduction in walking speed, with repeated-measures ANOVA confirming a highly significant effect of time. Flies recovered substantially over the seven-day period, though recovery trajectories varied strongly with age. Age was the dominant predictor of locomotor performance both before and after freezing, and post-hoc tests showed that 4-week-old flies were consistently slower than all younger groups at every time point. In contrast, sex had no significant effect on walking speed at baseline, immediately after freezing, or during recovery, and males and females recovered at similar rates. Confocal imaging revealed structural muscle disruption immediately after freezing, followed by progressive restoration of sarcomere organization over several days, consistent with functional recovery. Together, these results demonstrate that freezing induces measurable muscle damage in *D. melanogaster*, that muscle fibres exhibit clear evidence of repair, and that locomotor recovery parallels structural restoration. This work provides an integrated view of how freezing impacts muscle structure and function, offering new insight into the mechanisms underlying insect cold tolerance and post-freeze resilience.

Characterizing DCX+ Round Cells in the Chickadee Hippocampus

Author: Hannah Millar
Program: Biology and Neuroscience Co-op
Supervisor(s): Dr. Leslie Phillmore and Brodie Badcock-Parks, Psychology and Neuroscience Department, Dalhousie University

Abstract

Neurogenesis, the process of creating new neurons, occurs both throughout the brain and throughout adulthood in birds. Mammals, in comparison, show lower levels post-development and it is highly localized. This makes the avian brain a valuable model for studying neural plasticity. Doublecortin (DCX) is a microtubule-associated protein used as a marker to quantify neurogenesis because it is expressed in neurons that are under 30 days old. In the avian brain, some DCX-immunoreactive (DCX+) cells have typical neuronal morphologies, namely a central cell body and external projections. However, in certain brain regions, including the avian hippocampus, we have documented DCX+ cells that do not have this classical neuronal morphology. Instead, these cells are small, punctate, round, and have no external projections. Similar DCX+ cells have been reported across avian species and brain regions, but their identity has not yet been confirmed. Given the role of the hippocampus in avian spatial behaviour, and given that many species, including black-capped chickadees (*Poecile atricapillus*), rely heavily on the hippocampus for their food-storing spatial memory, it is therefore especially important to understand the cell types that comprise this critical structure.

In mammals, DCX, in addition to a marker for neurogenesis, is understood to be a marker of general cellular plasticity; it is expressed in several cell types undergoing structural or functional changes. Given this, it is possible that the DCX+ "round" cells are not neurons, but instead are oligodendrocyte precursor cells (OPCs), a highly plastic population of glial progenitor cells. This talk will describe our approach to test whether these DCX+ round cells in the chickadee hippocampus represent this unique non-neuronal cell population. This research will determine the specificity of DCX as a marker of neurogenesis in birds, establish the identity of the abundant DCX-positive round cells, and improve our understanding of which cell populations contribute to specialized avian brain regions.

Investigating the Effect of Light Intensity on Programmed Cell Death in Lace Plant (*Aponogeton madagascariensis)* Leaves

Author: Cora Mitchell
Program: Concentrated Honours in Biology
Supervisor(s): Dr. Arunika Gunawardena, Biology Department, Dalhousie University
Dr. Srinivas Sura, Agriculture and Agri-Food Canada, Government of Canada

Abstract

The lace plant (*Aponogeton madagascariensis)* is a flowering aquatic monocot that forms uniquely perforated leaves. These perforations result from programmed cell death (PCD), a process in which cell death occurs in a temporally and spatially predictable manner. The lace plant is an excellent model for studying PCD because of the predictability of cell death, an established sterile culture system, and its thin, semi-transparent aquatic leaves, which are ideal for live cell imaging. Anthocyanins, a type of phenolic compound located in the plant cell vacuole, are responsible for the red, purple, and blue colouration of plant tissues and possess strong antioxidant activity. In the lace plant, young leaves, known as window leaves, are pink due to the presence of anthocyanin, which later becomes masked by chlorophyll as the leaves mature.
Environmental factors, such as light intensity, pH, nutrient availability, and overgrowth, can influence these pigments. Anthocyanin vacuolar inclusions (AVIs) are condensed bodies of pigment found within the vacuole of plant cells. However, their role and function in the lace plant are unknown.

This study aims to determine the effects of different light intensities on PCD during leaf development in the lace plant. This will be conducted by comparing the phenolic compound profiles in leaves grown under different light intensities using LC-HRMS and examining the quantity and localization of AVIs in window stage leaves using light and transmission electron microscopy. Sterile lace plant cultures with 1-2 perforated leaves were randomly assigned to one of four treatments: low (35 ± 5 PPFD), control (125 ± 5 PPFD), high (225 ± 5 PPFD), or overgrown plants (125 ± 5 PPFD). After 3-4 weeks, leaves were harvested for morphological, LC-HRMS, and microscopic analysis. LC-HRMS data showed that the most abundant compounds are caffeic acid, catechin, cyanidin chloride, and rutin. The data processing is currently underway to determine the significance between treatments and developmental stages. Pre-liminary microscopic analysis demonstrated that overgrown window leaves have a higher number of AVIs. These findings will advance our understanding of the role of phenolic compounds in PCD and may be applied in agricultural and medicinal research to harness potential benefits.

Uncovering the relationship between the lampricide 3-trifluoromethyl-4-nitrophenol (TFM) and oxygen consumption in non-target species

Author: Aiden Moore
Program: Honours Conversion in Biology
Supervisor(s): Dr. Hugo Flávio and Dr. Robert Lennox, Department of Biology, Dalhousie University

Abstract

The invasive sea lamprey entered the Laurentian Great Lakes through a series of manmade canals and quickly led to considerable declines in the populations of culturally and economically significant fish species. TFM (3-trifluoromethyl-4-nitrophenol) was found to be an effective lampricide for its ability to selectively target sea lamprey. Recently, D'Souza et al (2025) found that increasing concentrations of TFM led to stepwise increases in oxygen consumption in larval sea lamprey. Whether this same relationship occurs in non-target species remains unclear. In this study, we investigate a potential relationship between TFM exposure and oxygen consumption in four non-target species found in the Great Lakes: lake sturgeon (*Acipenser fulvescens*), rainbow trout (*Oncorhynchus mykiss*), smallmouth bass (*Micropterus dolomieu*), and giant floater (*Pyganodon grandis*). Using intermittent-flow respirometry, we measured the oxygen consumption of each species during exposure to varying concentrations of TFM. Preliminary results suggest that TFM leads to stepwise increases in oxygen consumption in all four non-target species, which is in line with the earlier findings for sea lamprey. This work establishes intermittent-flow respirometry as a non-lethal method of determining the toxicity of TFM for non-target species, reducing the need for lethal toxicity experimentation. Further, by showing the impacts of TFM in real time, this method may inform conservation agencies on the sensitivity of non-target fishes during field applications of TFM, avoiding accidental overdoses.

Investigating the Effects of Ocean Alkalinity Enhancement on the Surface Microbial Community in Atlantic Canada

Author: Nam H. Nguyen
Program: Biology
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Abstract

Carbon dioxide (CO_2) is a potent greenhouse gas that drives climate change by trapping radiation leaving earth and reflecting them back to the surface, therefore increasing earth's temperature. Ocean Alkalinity Enhancement (OAE) is a method of carbon dioxide removal (CDR) aimed at enhancing the ocean's ability to draw down atmospheric CO_2 to combat the effects of global warming. To assess the viability of OAE, we need to understand what effects it can have on marine microbial communities, which play a vital role in the marine food web as well as oxygen production. We conducted a 19-day experiment from late September to mid-October by collecting water samples from McNabs island in Halifax harbor and enclosed them in nine microcosms consisting of 55L keg bottles. The microcosms were divided into three groups: the control, the unequilibrated treatment, where seawater CO_2 is not yet in equilibrium with atmospheric CO_2 after alkalinity addition, and the equilibrated treatment, where seawater CO_2 is in equilibrium with atmospheric CO_2 with the addition of sodium bicarbonate. Flow cytometry results revealed that the experiment produced the same overall trend in all treatment conditions regarding cell counts per microliter. Nonetheless, the unequilibrated treatment had a slight effect on phytoplankton biomass and composition while the equilibrated treatment showed even less changes when compared to the control. GAMM analysis showed treatments had an effect on Picoeukaryotes and Microeukaryotes' temporal trends and absolute counts. Nanoeukaryotes and Synechococcus, on the other hand, exhibited a shift in absolute counts. Other results that also supported the change in biomass included the increase in chlorophyll-a, particulate organic carbon & nitrogen (POC/PON), and biogenic silica (Bsi). OAE is a promising method of carbon removal due to its scalability and longevity of carbon storage. In collaboration with 19 other institutions across the world, the impact of OAE on the global marine microbial community is being assessed to determine its usage as a solution to increase the CO_2 absorption capability of the ocean.

Assessing Genetic and Environmental Drivers of MSX Resistance in Eastern Oysters (*Crassostrea virginica*) in Cape Breton, Nova Scotia

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Supervisor(s): Dr. Ramón Filgueira, Marine Affairs Program, Dalhousie University
Dr. Eric Ignatz, Marine Affairs Program, Dalhousie University

Abstract

Eastern oysters (*Crassostrea virginica*) are benthic filter feeders that provide socioeconomic value to coastal communities. However, the spread of *Haplosporidium nelsoni*, the causative agent of Multinucleate Sphere Unknown X (MSX), threatens both wild and farmed oyster populations in the Maritimes. MSX was first detected in Cape Breton's Bras d'Or Lake in 2002 and subsequently detected in Prince Edward Island and New Brunswick in 2024. Currently, no treatment exists to control or eliminate the disease, and resistance through selective breeding remains the most promising management strategy. This project investigated oysters from MacDonald's Pond, NS, where MSX prevalence without disease-associated mortality has been documented for over a decade. To test whether this unique survival is due to genetic resistance or environmental factors, 360 oysters from MacDonald's Pond were transplanted to Nyanza Bay, NS, a site with a history of MSX-induced mortality. A control group of 120 oysters remained in MacDonald's Pond. Oysters were separated in equal numbers between surface and bottom cages to additionally assess the effect of culture depth. Mortality, growth, and environmental conditions were monitored throughout the summer, with oyster cages first deployed on May 21st (MacDonald's Pond) and May 22nd (Nyanza Bay), 2025. Environmental conditions differed between sites, with Nyanza Bay being warmer and less saline than MacDonald's Pond. Despite these environmental differences and the documented history of MSX-associated mortality at Nyanza Bay, survival probability in both control and transplanted oysters remained above 90%, with no statistically significant differences among groups (p-value = 0.6). These results suggest that oysters in MacDonald's Pond are potentially MSX-resistant. If further experiments corroborate these findings, the MacDonald's Pond oyster population could be used in selective breeding programs and support sustainable oyster aquaculture amid rising disease threats.

Estimating Atlantic tomcod (*Microgadus tomcod*) spawning timing and fecundity in the Minas Basin

Author: Metyn Rehman
Program: Marine Biology
Supervisor(s): Dr. Aaron MacNeil, Biology Department, Dalhousie University

Abstract

Species that are not commercially important tend to be poorly researched, which makes their ecological significance difficult to quantify. One such species is the Atlantic tomcod (*Microgadus tomcod*), an anadromous fish that lives along the eastern coast of North America. Since little information is available regarding *M. tomcod*, the anthropogenic threats that they now face, such as habitat disturbance and climate change, could negatively impact their population. Consequently, we have quantified the fecundity, reproductive timing and gonadosomatic index (GSI) of tomcod populations in four rivers near Windsor, Nova Scotia, Canada, as well as the potential differences between these rivers using hierarchical Bayesian models. One of the rivers in this study (Halfway River) is partially blocked by a culvert and therefore serves as a good model to study the potential impacts that structures inhibiting fish passage might have on a tomcod population. We found that the peak of tomcod reproduction occurs at the end of November/beginning of December, that the annual maximum GSI was approximately 20%, and estimated that the average female fecundity was about 18,000 eggs. Neither reproductive timing, GSI, nor fecundity varied between the different rivers in this study, even amongst those that spawned above and below the culvert on Halfway River. The lack of variation in the maximum GSI between rivers supports the finding that there was no inter-river variation in fecundity. This indicates that the subpopulations in these rivers could be treated as one large population due to the lack of variance in their reproductive parameters, and that a barrier to migration has little to no impact on the reproductive timing and magnitude of this species. A future study to determine if spawning above the culvert on Halfway River negatively impacts future reproductive success could solidify this conclusion. This information will be used to inform decisions regarding the Avon River Highway Twining Project, which is trying to establish the best way to manage fish passage when the aboiteau under the highway that controls the flow of the Avon River is modified during the renovation.

Does *Bartonella* Infections Alter Cold Tolerance of the American Dog Tick *Dermacentor variabilis* In Nova Scotia?

Author: Carter Rice
Program: Bachelor of Science Honours in Biology
Supervisor(s): Dr. Tatiana Rossolimo, Dr. James Kho,

Abstract

As climate change makes the climate warmer there is a chance where ticks and the pathogens they carry can survive, but we still don't fully understand how being infected might change a ticks own physiology. In Nova Scotia, the American dog tick *Dermacantor variabilis* commonly bites humans and can carry *Bartonella* bacteria. For my honours project, I tested whether *Bartonella* infection is linked to differences in cold tolerance in adult *D. Variabilis.* I measured three traits that describe lower thermal limits critical thermal minion (CTmin) the temperature at which ticks loose coordinated movements during gradual cooling, chill coma recovery (CCR) how long it take to resume movement after cold exposure and supercooling point (SCP) the temperature at which body fluids freeze. Adult ticks of both sexes were screened for *Bartonella* using PCR then assigned to *Bartonella*-positive (B+) or *Bartonella*-negative (B-) groups. I compared cold tolerance between infection groups using t-tests. Overall, *Bartonella* prevalence was 49%. B+ ticks had a significantly higher CTmin than B- ticks approximately -8.5 vs -9.4 degrees celsius P= 0.02, suggesting that infected ticks become inactive at slightly warmer temperatures and therefore may be less able to stay active in the cold. In contrast CCR and SCP did not differ significantly between infection groups, both P>0.5. Together these results indicate that *Bartonella* infection is associated with a modest but measurable chance in one aspect of cold tolerance in *D. Variables* while other cold hardiness traits remain unchanged. Understanding how pathogen infection interacts with tick thermal physiology can improve predictions of overwinter survival and disease risk under future winter climates in Atlantic Canada.

Characterizing brown trout (*Salmo trutta*) movement in the Margaree River, Cape Breton using radio telemetry

Author: Madelyn Richardson
Program: Co-op Marine Biology
Supervisor(s): Dr. Robert Lennox, Biology Department, Dalhousie University & Ocean Tracking Network

Abstract

Atlantic salmon (*Salmo salar*) are native to Atlantic Canada and are of conservation concern, while Brown trout (*Salmo trutta*) are non-native. Atlantic salmon in Nova Scotia did not evolve in sympatry with brown trout, suggesting a lack of effective mechanisms for co-existence, increasing hybridization risk and disadvantaging Atlantic salmon in habitat competition. The Margaree River hosts a stable population of Atlantic salmon, though Brown trout have colonized and there is little understanding of their impact. This project aimed to characterize the movement of adult brown trout and assess their potential interference with Atlantic salmon during spawning migrations. Fish were caught by fly fishing, affixed with radio transmitters and tracked throughout the Margaree River. Fish showed three general movement patterns: contained within middle or lower river (~58% of trout, ~33% of salmon), downriver (~21%/~9%), and upriver (~16%/~45%). A Generalized Additive Model showed a significant interaction between date and species on distance from the Margaree estuary. Partial effects were similar between species for most of the study period, indicating overlap in river use, while salmon had a greater partial effect than trout late in the spawning season, indicating migration further upriver. Fewer brown trout utilized the upper and sanctuary sections than Atlantic salmon, indicating potential for distinct spawning habitat between species. However, there was considerable overlap in the middle and lower Margaree, indicating a potential source of brown trout interference with Atlantic salmon. This project provides a baseline understanding of brown trout movement in the Margaree, which can inform more targeted assessments of spawning interference for trout management and Atlantic salmon conservation.

The isolation and characterization of new evolutionarily important groove-bearing protozoa

Author: Meredith Rose
Program: Biology
Supervisor(s): Dr. Alastair Simpson, Biology Department, Dalhousie University

Abstract

The eukaryotic tree of life spans all multicellular lineages, as well as many more unicellular organisms. As technology has improved, most of these groups have been placed with high certainty; however, the Excavates' position has yet to be confidently resolved. The isolate 'SSEX' is a novel 'typical excavate' isolated by Liz Weston (at Dalhousie), that showed unusual gliding behaviour on its anterior flagellum. Preliminary DNA sequence analysis unexpectedly placed SSEX as related to Jakoba (Jakobida; Discoba), though it has behavioural and morphological differences compared to J. libera, the only described species. I aimed to characterise the isolates' morphology and establish their placements within Jakobida. Two isolates previously identified morphologically as J. libera - 'Jak2' and 'J.lib' - were examined together with SSEX in order to determine differences between them, and to better resolve species-level diversity. Phylogenetic analysis of SSU rDNA placed all three isolates as more closely related to one another than to the only other 'J. libera' sequence. Morphological data from Differential Interference Contrast (DIC) light microscopy and Scanning Electron Microscopy (SEM) revealed that the three isolates have largely similar cell body plans, though they differed significantly in cell body and flagellum lengths. Two isolates (SSEX and Jak2) possessed a novel structure visible by SEM: a 'grate' of cytoplasmic threads at the posterior end of the groove, hypothesized to play a role in prey capture. The lack of phylogenetic distinction between J. libera isolates and SSEX, along with the morphological differences among isolates, suggest that the Jakoba genus has more (meaningfully distinguishable) species within it than previously accepted. Appreciation of this diversity may be useful for analyses to resolve phylogenetic relationships within Jakobida, as well as for comparative examinations of the functional ecology of typical excavates. aiding in resolving Excavata's position on the eukaryotic tree of life.

Melon Morphometrics in Northern Bottlenose Whales (*Hyperoodon ampullatus*)

Author: Daisy Rubinstein

Program: BSc Honours in Marine Biology

Supervisor(s): Dr. Laura Feyrer, Biology Department, Dalhousie University, Fisheries and Oceans Canada

David Gaspard, MSc Candidate, Biology Department, Dalhousie University

Abstract

Northern bottlenose whales (*Hyperoodon ampullatus*, NBW) are a species of beaked whale (family Ziphiidae) found in the North Atlantic. There are two genetically and geographically distinct NBW populations of concern in Canada: the Scotian Shelf (SS) population and the Davis Strait-Baffin Bay-Labrador Sea (DS-BB-LS) population. Both are relatively small, were impacted by commercial whaling, and face poorly understood contemporary threats such as entanglements and vessel collisions, making continued monitoring essential for assessing population health and stability. A key component of population monitoring involves understanding demographic structure, which requires the ability to reliably sex individuals. When mature, NBWs exhibit sexual dimorphism in both body length and melon (forehead) curvature. This dimorphism has successfully been used to infer sex using vessel-based photo-identification (photo-ID). An alternative method is drone-based aerial imagery. Drones are a minimally invasive tool increasingly common in cetacean research and are currently being implemented to monitor NBWs. For my project, I evaluated whether drone-derived morphometrics can reliably determine sex in mature NBWs, detect sex prior to maturity in male NBWs, and produce classifications consistent with photo-ID and genetic sexing methods. I analyzed 2025 drone footage from both populations, including 293 stills from 99 individuals. I extracted averaged body length, melon length, and melon width (posterior and anterior) measurements which I used to calculate melon width ratios for each individual. I then used linear regression to examine the relationship between these melon ratios and body length, and principal component analysis (PCA) to assess overall patterns in morphometric variation associated with sex. Finally, I compared these results to known sex classifications to evaluate how drone-based morphometrics performed relative to photo-ID and genetic sexing. My results suggest that drone-based morphometry is an accurate method to probabilistically infer sex in mature NBWs, with classifications that are largely consistent with photo-ID and genetic sexing. This method ultimately provides a practical, minimally invasive means of inferring sex in NBWs, improving population monitoring and conservation for this vulnerable species.

Identification of Plasminogen Receptors of Secretome-stimulated Fibroblasts

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Supervisor(s): Dr. David Waisman, Pathology Department, Dalhousie
Dr. Gillian Okura, Pathology Department, Dalhousie

Abstract

Metastasis is facilitated through the establishment of pre-metastatic niches (PMNs), permissive microenvironments formed at distant sites prior to tumour cell arrival. Primary tumour cells create these sites through the release of secretomes, which can alter stromal cells into pro-metastatic phenotypes. Of interest are altered fibroblasts, called cancer-associated fibroblasts (CAFs). Fibroblasts may serve as targets of tumour-derived secretomes, as they express plasminogen receptors, which facilitate the activation of plasminogen into plasmin. Although tumour cells do not produce plasmin, plasmin has been identified as playing a key role in establishing the PMN; therefore, this study aims to link tumour-derived secretomes to fibroblast-mediated plasmin generation. This paper hypothesizes that breast tumour secretomes actively prime PMNs by upregulating plasminogen receptor levels in lung fibroblasts. To test the hypothesis, this study measured plasmin activity in secretome-treated and control fibroblasts using a fluorescent plasmin-generation assay and used a one-way ANOVA to test significance. Present plasminogen receptors were identified in treatment and control fibroblasts using Western blotting. It is expected that fibroblasts treated with breast tumour secretomes will exhibit increased plasmin activity and an upregulation of plasminogen receptors compared to control fibroblasts. These changes would indicate that primary tumour cells mediate metastatic spread through fibroblast-driven plasmin generation during PMN formation. Such findings could provide insight into early metastatic events, potentially revealing novel therapeutic targets.

Competitive adaptation in isolated selection lines of female medaka (*Oryzias latipes*)

Author: Maggie Sharpe
Program: Biology
Supervisor(s): Dr. Laura Weir, Biology Department, Saint Mary's University

Abstract

As a common model organism in population dynamics studies, Japanese medaka (*Oryzias latipes*) have significantly influenced our understanding of mating systems. Despite their importance in the evolution of reproductive behaviour, female medaka have been relatively understudied compared to their male counterparts. Failure to adequately characterize female competition results in a sizable knowledge gap in our understanding of the evolution of mating systems. In this study, I characterize competitive behaviours unique to female medaka and determine their adaptive response to the selection pressure of differing sex ratios. To do so, female medaka have been isolated in four sex ratios of 0.5, 1, 2, & 5 (male:female) for eight generations. Intrasexual competitive and intersexual conflict behaviours were recorded during discrete 2-minute observation windows. Observations both included "overt" aggression traditionally used to measure medaka competition and introduced "subtle" dominance behaviours more suited to female competition. Rates of traditional "overt" competitive behaviours were compared with those of females initially placed in the same sex ratios pre-reproductive isolation to determine their adaptive response to selection. The rate of "subtle" competitive behaviours was compared against that of "overt" behaviours to characterize the unique competitive strategies of these isolated populations. Identifying the competitive strategies of female medaka and their adaptive response to different selective pressures can improve our understanding of female influence on mating systems and the evolution of behavioural competition.

Is The Sponge Loop Present in The Makkovik Coral Gardens?

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Abstract

Deep-sea coral and sponge communities are biodiversity hotspots often found within nutrient-starved areas of the ocean. Corals and sponges sequester nutrients which are transferred to higher trophic levels and contribute to overall carbon cycling. Corals also form complex three-dimensional structures that increase substrate and habitat complexity, further supporting biodiversity. Food sources in these deep-sea communities are often assumed to derive primarily from surface primary productivity as particulate organic matter (POM). A clearer understanding of these nutrients pathways is required as ongoing climate-driven shifts in phytoplankton communities and surface productivity pose poorly constrained threats to deep-sea habitats. Dissolved organic matter (DOM) represents an alternative large and relatively stable reservoir of organic carbon. This highly recalcitrant pool of DOM is largely inaccessible to most animals, but laboratory feeding experiments suggest that sponges can consume DOM and transfer these nutrients to higher trophic levels through the production of detritus or direct predation (i.e. the sponge loop). The goal of this project it to establish in situ evidence for the sponge loop at the Makkovik Hanging Garden. This is a deep-sea vertical wall habitat located ~30 km off the coast of Labrador, Canada, within Nunatsiavut. Based on remotely-operated-vehicle (ROV) footage, sea stars appear to directly predate on sponges. This hypothesis was tested using Nearest Neighbour analysis of orthomosaic images which were generated from ROV footage. This revealed a statistically significant relationship between sea stars and sponges. Compound-specific isotope analysis of amino acids (CSIA-AA) demonstrates tight isotopic affinity between sea stars and sponges. These two lines of evidence strongly support in situ evidence of the sponge loop at the Makkovik Hanging Gardens. These results support Nunatsiavut's marine planning efforts by identifying ecologically and culturally significant environments and contribute to Canada's commitment to conserve 30% of marine habitats by 2030.

Sperm Whale (*Physeter macrocephalus*) Clan Assignments in the Galápagos Islands from 2013 – 2023

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Ana Eguiguren, PhD Candidate, Dalhousie University

Abstract

Culture is the information or behaviour transmitted between conspecifics and cultural differences arise through social learning. It is assumed that individuals who commonly associate together, preferentially learn from each other which gives rise to the creation of isolated groups and unique behaviours. The sperm whale, *Physeter macrocephalus*, is a unique example of culturally distinct groups. Sperm whales are highly social creatures that exist in primarily matrilineal societies comprised of such groups – social units, groups, and clans. Sperm whales only ever associate with individuals of their same clan, which can be described as hundreds to thousands of whales that share culturally transmitted behaviours, including vocal dialects. Dialects are made up of codas, series of patterned clicks used for communication, and are distinct between clans. Therefore, patterns of codas used are employed to distinguish clan identity of sperm whales in the field. In the Galápagos Islands, there are six identified clans: Slow Increasing, Short, Regular, Plus-One, Palindrome, and Four-Plus. Between 1985 – 2003, the dominant Regular and Plus-One clans in the region were replaced by other clans from the region. Given that our knowledge is based on clans present before the turnover, the objective of my project is to evaluate the validity of acoustic-based clan assignments to individuals. To investigate this, photographs of individuals' flukes were collected across the 2013 – 2023 field seasons. The unique trailing edge of each individual's fluke was used for photoidentification. Clan identity was assigned to individuals based on the coda repertoires for each date sighted. It is expected that individuals sighted on multiple days should be assigned the same clan. When this was not the case, the possibility of a photoidentification error, uncertainty of clan identification, and meeting of clans were investigated to explain the misidentification. If none of these reasons applied to the individual, the possibility of a change in vocal clans was considered. As this aspect of social biology has not been researched following the turnover, this project will contribute to the greater understanding of the Galápagos Island sperm whale population.

A Multi-Taxa Assessment of Genetic Diversity and Differentiation in Invasive and Non-invasive Populations

Author: Claire Blackwell Thrower
Program: Marine Biology
Supervisor(s): Dr. Chloé Schmidt, Biology Department, Dalhousie University

Abstract

Biological invasions are increasingly common, and ecologically and economically disruptive. Successful invasions often originate from small founding populations with reduced genetic diversity and thus decreased adaptive potential, yet they persist and spread. This is known as the genetic paradox of invasion. Here we tested whether invasive populations differ in genetic diversity and population differentiation relative to non-invasive populations across 6 phyla: Arthropoda, Chordata, Ctenophora, Gyrista, Magnoliophyta and Mollusca. Using published microsatellite data from >20,000 individuals spanning 30 species, we compared gene diversity, allelic richness, effective population size (Ne), and population specific F_{st} between invasive and non-invasive populations using Bayesian generalized linear mixed models. Invasive populations exhibited lower gene diversity and allelic richness compared to non-invasive populations, while population specific F_{st} was higher in invasive populations. We investigated whether species dispersal method or habitat type had effects on patterns of genetic diversity and differentiation but found no consistent effects of either factor. Furthermore, the number of introduction pathways was not associated with a change in gene diversity, allelic richness, population specific F_{st} or Ne. These findings suggest that in general, invasive populations have lower genetic diversity and are more genetically differentiated from populations in species native ranges, but the extent to which genetic diversity is reduced in invasive populations is largely species-specific. Overall, invasive populations have reduced capacity to respond to environmental change.

Effects of Trait-Urbanization Relationships on Avian Genetic Diversity in Europe and North America

Author: Ross Torrie
Program: BSc Biology; Co-op
Supervisor: Dr. Chloé Schmidt, Biology Department, Dalhousie University

Abstract

Human development and infrastructure introduce novel threats, species, and habitats into ecosystems, reshaping environments and imposing new selective pressures on wildlife. Urbanization is one of the most immediate and extreme forms of human-induced habitat transformation, where natural ecosystems are made glaringly different. While declines in species richness and abundance in urban environments are well documented, far less is known about how urbanization affects genetic diversity, an important consideration in conservation as it determines adaptive potential, population persistence, and extinction risk. In birds, previous studies have reported inconclusive relationships between urbanization and genetic diversity, suggesting that species-specific traits may play an important role in shaping genetic responses to human development. In this study, I used a large-scale macrogenetic approach to examine how urbanization relates to population genetic metrics in birds and whether ecological and morphological traits mediate these relationships. I compiled microsatellite data for avian populations across North America and Europe from publicly available datasets on the Dryad database. With this data, I estimated per-population gene diversity, rarefied allelic richness, population-specific FST, and contemporary effective population size. Urbanization was quantified using human population density and a Human Footprint Index around each sampling location. I integrated species-level trait data from the Avonet database, focusing on body mass, dispersal ability, and native habitat. Using Bayesian mixed-effects models with species-level random effects and trait-urbanization interactions, I tested whether genetic responses to urbanization differed systematically among species with different traits. By examining avian populations across two heavily developed continents and incorporating species traits, this study aims to identify whether certain groups of birds are more resilient or vulnerable to genetic impoverishment in urban settings.

Aerial photo-identification and mark type analysis of northern bottlenose whales (*Hyperoodon ampullatus*)

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Supervisor(s): David Gaspard, Biology Department, Dalhousie University
Dr. Sam Walmsley, Biology Department, Dalhousie University

Abstract

The ability to reliably identify individual animals over time is a valuable tool for long-term ecological and demographic studies, particularly for long-lived and elusive marine mammals. Northern bottlenose whales (*Hyperoodon ampullatus*; NBW) often have distinctive markings making them a great candidate for photo-identification (photo-ID). The endangered Scotian Shelf population of NBW represents a small, genetically distinct population that inhabits deep submarine canyons off the Scotian Shelf. This population has been monitored by the Whitehead Lab through boat-based photo-ID since 1988, producing the longest continuous dataset for any beaked whale species. However, traditional photo-ID images are largely restricted to the dorsal fin region, limiting the assessment of markings and external health indicators across the full body. Recent advances in the usage of drones provides a novel perspective of the dorsal plane of the whales which may complement and extend existing photo-ID methods. Yet the integration of aerial imagery into long-term photo catalogs remains underexplored. The goal of this study is to evaluate the suitability of drone imagery for individual identification and examine patterns of external markings across the body of NBW. Using drone footage collected in the Gully Marine Protected Area during the summers of 2024 and 2025, stills and video sequences were examined to match 104 individuals to the existing longitudinal dorsal catalog using markings, particularly in the dorsal region. Mark types were classified and quantified across four body sections (head, torso, dorsal, and peduncle) and patterns of markedness were compared across location on the body, mark type, sexes, and between the dorsal regions of the aerial and dorsal catalogs to assess the consistency between the two methods. I successfully matched 25 individuals in 2024 and 61 in 2025 with a matching rate of 75.8% and 85.9% respectively. Among the 27 individuals analyzed for mark types, circular scars were the most prevalent, present on 92% of individuals. Being able to reliably link the individuals in the aerial catalog, which provides details on health metrics and fine scale behaviours, to the longitudinal dorsal catalog, which spans decades and has important associated metadata such as sighting history and sex, increases the scope of possible research and enhances the relevancy of drone photogrammetry data as monitoring method for the species.

Exploring the variation in marine benthic community composition across the Northumberland Strait.

Author: Milena Wilson
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Supervisor(s): Dr. Craig J. Brown, Department of Oceanography, Dalhousie University
Dr. Trevor Bringloe, Fisheries and Oceans Canada, Government of Canada

Abstract

Located in the southern Gulf of Saint Lawrence, the Northumberland Strait is home to a diversity of marine species. In 2017, Fisheries and Oceans Canada (DFO) designated existing scallop fishery closures in costal sections of the strait (Scallop Buffer Zones) as marine refuges. Bottom-contact fishing gear, utilized in scallop harvesting, has been shown to decrease community diversity and cause significant changes in benthic species composition. The scallop harvesting exclusion of these marine refuges aim to protect juvenile American Lobster (*Homarus americanus*) and their habitat, with the added benefit of preserving regional benthic biodiversity. Presently there are limited studies that investigate how community composition varies spatially across benthic environments within the Northumberland Strait, and across the fisheries exclusion zones (inside and outside). This study describes the spatial distribution of marine benthic communities across different seafloor substrates and compares the communities inside and outside the marine refuges. From 2023 to 2025 teams from DFO and Dalhousie University conducted 155 drop camera transects across the strait with a 4K drop camera system. The videos were annotated through the platform BIIGLE to identify and quantify epifaunal species and visually classify seabed substrates using a modified Folk 5 classification. Camera transects were standardized by length, and species counts within each transect were used to evaluate patterns in the spatial distribution of biodiversity using a variety of multivariate statistical methods. Bray-Curtis dissimilarities were calculated for benthic assemblages between transects then visualized using multidimensional scaling ordinations, revealing clustering of different benthic assemblages. These assemblages were mapped geographically to understand their spatial distribution relative to environmental variables within the strait based on available geospatial bathymetry, substrate characteristics, and oceanographic variables. Results of this study aid in understanding the efficacy of the Scallop Buffer Zones in protecting epifaunal species and can inform future management decisions in the region.

The Effectiveness of Physical Filtration at Removing Tunicates from Aquaculture Systems

Author: Jessica Wong
Program: Marine Biology (Co-op)
Supervisor(s): Dr. Ramón Filgueira, Marine Affairs Program, Dalhousie University
John Batt, Aquatron Laboratory, Dalhousie University

Abstract

Tunicates are a commonly invasive species that can pose formidable threats to both natural ecosystems and aquaculture practices. In Canada, there are currently 7 invasive tunicates that threaten shellfish aquaculture through competition for plankton in the water column, thus decreasing total shellfish yield. For land-based aquaculture, water filtration systems are used to ensure proper water quality by removing particulates which may include the larvae of unwanted species such as tunicates. However, in some instances particulates have been shown to get past the filters, subsequently interfering with cultured species. For example, in the Dalhousie Aquatron, which draws its water from the Northwest Arm, tunicates have been seen in various tanks that had filtered water. This study looks at the effectiveness of different size cartridge filters at removing tunicates from the water column and how the effectiveness changes over a filter's life span. In the Aquatron, 3 different filtration treatments (raw water, water filtered at 1 μm, and water filtered at 0.35 μm), each with 3 replicates were set up among 9 different tanks. Within each tank a PVC plate was set to hang for tunicates to settle on. Additionally, PAMAS particle counts were taken immediately following a filter change as well as 6, 12, 24, and 48 hours after the filter change to determine the number of particles within different size bins that pass through each filtration level. It is hypothesized that increased levels of filtration will yield the smallest number of tunicates and particles, with the amount increasing over the filter's life span. The experiment is still ongoing; however, no tunicates have been observed on the PVC plates. Once completed, this data will benefit aquaculturists by informing them of the effectiveness of their filters and how the effectiveness may change over time.