DALHOUSIE
UNIVERSITY

38th Annual

Cameron Conference

FOR BIOLOGY & MARINE BIOLOGY HONOURS STUDENT RESEARCH

Saturday
10 February 2024
9:00 am - 12:30 pm

Sponsored by the Department of Biology

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Dalhousie Association of Biology Students	Dalhousie Association of Marine Biology Students
DABS DALHOUSIE ASSOCIATION OF BIOLOGY STUDENTS	DAMS

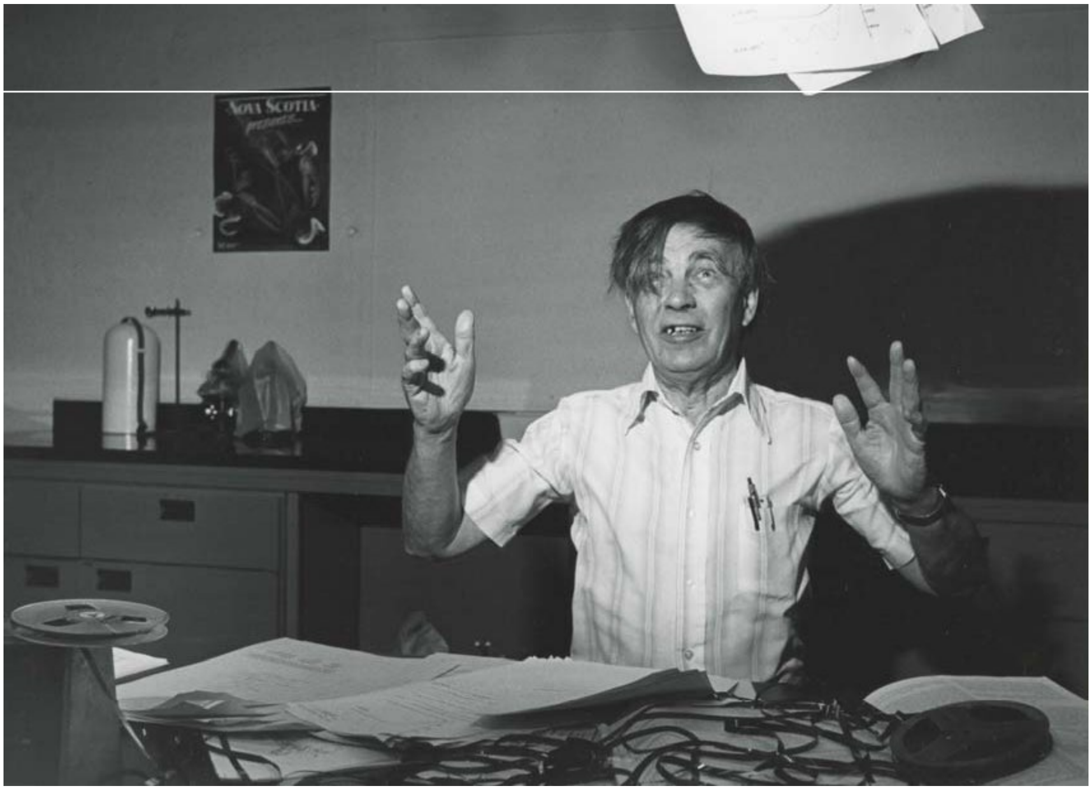
On the Origin of the Cameron Conference

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

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

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

Thanks to Professor Brian Hall for this synopsis



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

Third Floor Atrium - Life Sciences Centre

8:30am
Warm drinks and snacks available

9:00 am
Conference Welcome

Professor Mark Johnston
Chair of Biology Department

9:10-10:00 ~ Poster Session 1

1	Luc Bouchard	Measuring the effects of tagging and transportation on the activity of Atlantic Salmon (*Salmo salar*) using acoustic accelerometers
2	Mackenzie Burke	Effects of acute simulated ocean alkalinity enhancement on natural phytoplankton assemblages in the North Atlantic ocean
3	Chelsea Eldridge	Great White Shark, *Carcharodon carcharias*, presence & residence in the Upper Bay of Fundy
4	Jacob Ferris	Comparing the diving behaviour of four shark species (Blue, White, Porbeagle, and Shortfin Mako) in the Atlantic Ocean
5	Max Gallo-Will	Phytoplankton in changing oceans: The effects of carbon dioxide on phytoplankton abundance, health and community structure

6	Sophia Hibbert	Contributions from A17 amacrine cells to the oscillatory potentials in the full field electroretinogram (ERG) of mice
7	Tatum Johnson	Growth and tissue composition of Atlantic Salmon (*Salmo Salar*) fed novel alternative feeds reared in aquaculture setting
8	Kat Kabanova	Effects of temperature and food availability on feeding behaviour and metabolism in the sea cucumber *Cucumaria frondose*
9	Chris Lord	Growth-dependent changes in elemental stoichiometry and macromolecular allocation of field collected phytoplankton in response to N, P, and Fe nutrient supply
10	Emily McLean	Floral resource utilization by *Bombus* spp. across three distinct garden sites at Dalhousie University: A comparative study
11	Dona Nelson	Examining the role of the *ARI11* gene in plant growth, development, and drought stress tolerance.
12	Amelia Perrin-Pretty	Shifting intersexual dynamics and sexual conflict of Japanese Medaka (*Oryzias latipes*) amongst inverse sex ratios.
13	Madeleine Platt	The Global Meat Project - Shark meat prices driving global fisheries and influencing trade markets
14	Isabel Ross	Using trail cameras to evaluate the source and impact of predation on Leach's Storm Petrels (*Hydrobates leucorhous*)
15	Tessa Schaeffer	Optimizing sterilization and nutrient delivery techniques for sugar kelp (*Saccharina latissima*) seedlings in Dalhousie's Aquatron
16	Jana Sewidan	Development of fibronectin-based protein fibers for promoting cell adhesion to biomaterial textiles

10:00 – 10:50 ~ Poster Session 2

17	Caliyena Brown	Developing a suitable tagging methodology for Atlantic Mackerel *(Scomber scombrus*): The effects of electro-anesthesia on fish mortality
18	Jack de Swart	The influence of hydrologic connectivity on the diversity and the productivity in Arctic thermokarst lakes
19	Joshua Feld	The Effects of plasminogen activation induced by chemotherapy-treated cancer cells on regulating macrophage-mediated phagocytosis
20	Ainhoa Fournier	Testing the tests: analysing and developing methods of characterizing phenotypes of *Saccharina latissima* in Nova Scotia, Canada
21	Shantelle March	Tick-Talk: Quantifying dawn and dusk questing behaviour and pathogen presence in *Ixodes* ticks
22	Paris Mastrodimitropoulos	Using life history traits of Coregonid species to make inferences about Atlantic Whitefish (*Coregonus huntsmani)* anadromy, migratory struggles and spawning behaviour
23	Julia Packer	The phylogeny and taxonomic position of Gem-Kin, a culture representing the evolutionarily pivotal Kinetoplastid taxon Allobodonidae
24	Katie Ryder	Examining herring gull (*Larus Smithsonianus*) diet through noninvasive bolus collection as an index of predation pressure on conspecific nesting seabird species
25	Vanessa Schiliro	Predicting habitat suitability for the basking shark (*Cetorhinus maximus*) in the Northwest Atlantic

26	Wendy Shue	Movement behaviour of young-of-year porbeagle sharks (*Lamna nasus*) in comparison with older animals in Northwest Atlantic
27	Davjit Sidhu	Sperm whale (*Physeter macrocephalus*) movement across temporal scales around the Galápagos between 2013-2014 and 2022-2023
28	Emma Stainforth	Presence of *Borrelia burgdorferi, Anaplasma phagocytophilum, Babesia spp.,* and Powassan virus within *I. scapularis* in the Halifax Regional Municipality, Nova Scotia, Canada
29	Kylie Van Dyke	Investigating the effect of spermidine on chemotherapy-induced oral mucositis in a 2D co-culture model
30	Shwayam Vinayak	Genomic Analysis of the Bacterium *Roseibium aggregatum* and its Role as a Symbiont of *Oxyrrhis marina*
31	Monica Wright	At-sea associations in an upper-trophic level predator, the grey seal (*Halichoerus Grypu*s)

Life Sciences Centre Room 242

11:00 - 12:30 Oral Presentations

Session Chair - Dr. Patrice Côté

1	Kestrel Adams Unger	Investigating Secondary Metabolites of the Lace Plant
2	Stephanie Agnew	Developmental and behavioural responses of the obliquebanded leafroller (*Choristoneura rosaceana*) to heat waves and insecticide
3	Emilia Cordova	Correlating Protein Architecture to Recombinant Spider Silk Fiber Properties Using Engineered Fusion Proteins with Units from Aciniform and Pyriform Silks
4	Anna Gleason	The influence of cobalamin availability on metabolite production in phytoplankton isolates from the Scotian Shelf
5	Ahsan Malick	Characterizing a model of exercise-induced muscle damage in *Drosophila melanogaster*
6	Lauren LaPorte	Examining the effects of temperature and salinity on the germination success of *Zostera marina* (eelgrass) seeds.
7	Kate Pennyfather	Evolution of genome size and repetitive DNA in *Lobelia cardinalis*
8	Kylee Lightbody	The impacts of scale on kelp abundance estimates
9	Meg Smith	Identifying the glacial lineage of North Mountain Brook Trout (*Salvelinus fontinalis*): a mtDNA whole-genome analysis
10	Kendra Mainprize	Compounding interactive effects of warm temperature and aerial exposure on the physiology of blue mussels (*Mytilus edulis*)

Abstracts

LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME

Investigating Secondary Metabolites Of The Lace Plant

Author: Kestrel Adams Unger
Programme: Biology
Supervisor(s): Dr. Arunika Gunawardena, Department of Biology, Dalhousie University

Abstract

Secondary metabolites are compounds produced by various eukaryotic organisms that do not play a shared direct role in their growth and reproduction. Within plants, they play roles in development and protect from environmental stressors. This is possible because of the plasticity of secondary metabolite production and their diversity of function and chemical composition. The three most abundant types of secondary metabolite are terpenes, phenolics and alkaloids.

The lace plant, *Aponogeton madagascariensis*, is an ideal model for studying developmental programmed cell death (PCD) because of the predictable perforations which form in its leaves. These perforations start to form during an early stage of leaf development known as the window stage and are fully formed at the mature stage. Window stage leaves show a visible accumulation of anthocyanins, a type of phenolic compound, which plays a vital role in PCD in the lace plant. The identities of the anthocyanin species and other secondary metabolites involved in PCD induction and perforation formation are unknown.

This research project aims to profile the secondary metabolites produced in window and mature stage lace plant leaves and, second, to identify significant differences between the two leaf stages. Profiling was undertaken through untargeted LC-MS-MS and analyzed through MS-DIAL. The extracts from both leaf stages were statistically compared using MetaboAnalyst.

This analysis finds 22,367 features, or possible compounds, produced by lace plant leaves, of which 6,967 are tentatively identified. The most abundant secondary metabolite in both leaf stages is a compound similar to honokiol, a phenolic. Significant differences exist in abundance and type of secondary metabolites between the two leaf stages. Specifically, 753 features are over two-fold higher in the window than in mature, whereas 413 features are over two-fold higher in mature than in window stage leaves. The most significantly different tentatively identified species is [7-(hydroxymethyl)-4-methyl-1-[3,4,5-trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxy-1,4a,5,6,7,7a-hexahydrocyclopenta[c]pyran-5-yl] (E)-3-(4-hydroxyphenyl)prop-2-enoate, a terpene.

Ongoing work is being undertaken to confirm the identity of the most significant and abundant features through targeted LC-MS-MS. Work is also being undertaken to investigate how sucrose and light availability, as environmental stressors, affect the production of these secondary metabolites.

Developmental And Behavioural Responses Of The Obliquebanded Leafroller (*Choristoneura rosaceana*) To Heat Waves And Insecticide

Author: Stephanie Agnew
Programme: Combined Honours in Biology and Psychology
Supervisor(s): Dr. Shelley Adamo, Neuroscience Department, Dalhousie University
Dr. Laura McMillan, Neuroscience Department, Dalhousie University

Abstract

Climate change has increased extreme weather events all over the world. In Nova Scotia, heat waves are expected to become longer, hotter, and more frequent by the end of the century. This may have unpredictable effects on agriculture, particularly around insect pests. Temperature plays a significant role in both the development and growth of insects as well as the efficacy of pesticides, many of which are temperature dependent. Thus, the relationship between heat waves and insecticides within insect pests is of great importance for the future of agriculture in both Nova Scotia and across the world. I investigated how heat waves and insecticide may interact to affect the growth, development, and foraging behaviour of the caterpillar *Choristoneura rosaceana*, or the obliquebanded leafroller (OBLR). OBLR are already a common apple pest across North America (including Nova Scotia), and both their numbers as well as their impact on orchards only increase with warmer climate. I separated third instar OBLR into groups comparing those experiencing a simulated heat wave with those in control temperatures. Then either during the heat wave (or equivalent), or after, each caterpillar was placed on food with the choice of either insecticide (DiPel) or nothing, or on food with the choice of water (control) or nothing. Caterpillar location (on the food), weight, and development were measured daily after treatment. Preliminary results suggest that regardless of treatment (heat vs no heat, during or after heat wave), there were no differences in location or foraging behaviour, suggesting OBLR do not actively avoid ingesting DiPel. The data further suggest that heat waves accelerate the growth and development of OBLR, and that DiPel administration before or early in the heat wave may negate some of these effects. This could help guide the timing of pesticide use for greatest efficiency in a future likely to feature more and longer heat waves.

Measuring The Effects Of Tagging And Transportation On The Activity Of Atlantic Salmon (*Salmo salar*) Using Acoustic Accelerometers

Author: Luc Bouchard
Programme: Marine Biology
Supervisor(s): Dr. Robert Lennox, Biology Department, Dalhousie University

Abstract

The Atlantic salmon (*Salmo salar*) in Cape Breton Highlands National Park, Nova Scotia are an endangered population that have undergone a continued decrease in numbers in recent decades. The recovery program through the collaboration of Parks Canada and the Aquatron laboratory at Dalhousie University aims to restore the population by catching, rearing, and transporting the salmon back to their native watercourse, the Clyburn brook. This study focuses on internal tag insertion, transportation, and the environmental parameters of feeding and light regime and their effects on changing behavior and activity in Atlantic salmon. Tri-axial acoustic accelerometers, measuring acceleration in three-dimensions, were internally implemented in 20 adult salmon to track changes in activity. Such changes in activity can be a strong indication of changes in an individuals' immediate environment. Preliminary results show correlations between increased activity with feeding events and vehicular transportation, but continued statistical analyses are needed to verify the significance of the correlation between changes in activity and the selected parameters. The continued analyses will also determine the correlation on both an individual and sample-wide scale. The results from this research will provide a greater understanding of the ecology of Atlantic salmon populations in Cape Breton and create greater opportunities for management strategies to support conservation efforts.

Developing a Suitable Tagging Methodology for Atlantic Mackerel (*Scomber scombrus*): The Effects of Electro-anesthesia on Fish Mortality

Author: Caliyena Brown
Programme: Marine Biology
Supervisor(s): Dr. Robert lennox, Biology Department, Dalhousie University

Abstract

Effective fisheries management requires accurate assessments of fish abundance and an understanding of the distributional limits of exploited species. Acoustic telemetry can provide valuable insights into population dynamics and migration patterns, supplementing stock assessments that rely on fisheries-dependent data. Atlantic Mackerel (*Scomber scombrus*) is a species that requires conservation action and would greatly benefit from a tagging program. Conventionally, transmitter implantation and the use of chemical anesthesia can negatively impact fish behaviour and the kinematic components that prey species use in escape responses. Atlantic mackerel are a challenging species to tag because they are sensitive to handling and vulnerable to post-release predation. This study evaluates a novel approach that could reduce handling and eliminate chemical withdrawal by using electro-anesthesia facilitated by electronic fish handling gloves. This method aims to minimize post-operative performance deficits associated with chemical anesthesia and offer insights into a viable tagging methodology for this species. Mackerel sourced from Sambro, NS, Canada, were transported to a holding facility for 30-day acclimation, and then a subset underwent tagging with dummy transmitters. Each fish was sedated using electronic fish handling gloves and surgically implanted with a dummy acoustic tag (7 x 28mm). The mackerel were monitored for 30 days to evaluate survival rates, the relationship between fish size and tagging order with mortality, and wound healing. Preliminary findings indicate that electro-anesthesia is not a viable alternative to chemical anesthesia for tagging Atlantic mackerel, likely due to skin lesions developed by the fish after handling with the gloves. The fish did not, however, exhibit discernible adverse consequences from the electric treatment itself. This new knowledge is a significant advancement in the development of an optimal tagging method for this species, which is needed to establish more effective management given the ongoing stock crisis in Canada.

Effects Of Acute Simulated Ocean Alkalinity Enhancement On Natural Phytoplankton Assemblages In The North Atlantic Ocean

Author: Mackenzie Burke
Programme: Marine Biology Co-op, Statistics Minor
Supervisor(s): Dr. Hugh MacIntyre, Oceanography Department, Dalhousie University

Abstract

Climate change poses a significant environmental and economic threat. To reach the 1.5 °C target set by the Paris Agreement, we must restrict CO_2 emissions and invest in CO_2 removal (CDR) techniques (IPCC, 2018). One CDR strategy is Ocean Alkalinity Enhancement (OAE), in which an alkaline substance is added to the surface ocean to draw down CO_2 for long-term storage as bicarbonate. As part of a collaboration with industrial partner Planetary Technologies and the National Research Council of Canada (NRC), I tested the potential impacts of acute simulated OAE on natural phytoplankton assemblages in three separate mesocosm experiments. Each was run in duplicate with controls and NaOH-dosed treatments as follows: 1) to test the effect of exposure time and high alkalization, treatments were dosed to reach a pH of 8.8 and neutralized at different times (10, 60, 120 and 180 mins post addition); 2) to test the effect of alkalinity concentration, treatments were dosed to achieve a range of pHs (8.05, 8.3, 8.55 and 8.8) for 10 mins before neutralization; and 3) to assess the potential impact of high alkalization on trophic interactions, growth and grazing rates were measured using the serial dilution method in control and alkalized tanks dosed to pH 8.8, with no neutralization. In all cases, sampling occurred before and after dosing and at the experiment's end, 24 hours later. For all, metrics of abundance (chlorophyll-a, particle counts, biovolume) and community structure (classified from flow cytometry) were compared to the physiochemical parameters (pH, dissolved inorganic carbon, total alkalinity). Additional measurements of particulate carbon, nitrogen and phosphorous were taken for the benchtop experiments (#1 and #2). Metric multidimensional scaling (mMDS) was used to visualize dissimilarity in all measured parameters between treatments. Statistical tests for treatment effects on abundance metrics were done using analysis of similarity (ANOSIM) and analysis of variance (ANOVA). No significant treatment effect was detected for abundance metrics across experiments. Significant differences ($p<0.05$) in dissolved inorganic carbon and total alkalinity were observed between OH^--dosed and control tanks at harvest for the serial dilution experiment, #3. In this study, simulated OAE resulted in CO_2 capture but had no detectable effect on the growth rates, composition, and grazing loss rates of the phytoplankton assemblages studied.

Correlating Protein Architecture To Recombinant Spider Silk Fiber Properties Using Engineered Fusion Proteins With Units From Aciniform And Pyriform Silks

Author: Emilia Córdova
Programme: Biology & Chemistry
Supervisor(s): Dr. Jan Rainey, Department of Biochemistry and Molecular Biology, Dalhousie University

Abstract

Spider silks are desirable protein-based biomaterials due to their mechanical properties and their promising applications ranging from textiles to regenerative medicine. Spiders produce seven types of silks with different mechanical properties and functions. To date, available literature on silks focuses on native and recombinant dragline silks. This study encompasses two less-characterized silks: pyriform and aciniform. Pyriform (Py) silk adheres the spider web to various materials and aids in web construction by bonding threats together; aciniform or wrapping (W) silk is the toughest of all silks and is used to wrap prey and line the egg sacs. Research on spider silks aims to replicate natural silk properties using recombinant spider silk proteins termed spidroins. Pyriform and aciniform recombinant silks have been studied separately. However, a fusion of these two silk proteins has not been explored yet. Here, a recombinant hybrid protein with repeat units of pyriform and aciniform spidroins named $(PyW)_2$ is produced in *Escherichia coli*, purified with a Ni^{2+}-NTA affinity column, and spun into fibers using a wet-spinning method. Far-UV circular dichroism spectroscopy analysis showed a predominant alpha helicity when the protein was dissolved in an aqueous buffer or a fluorinated acid and alcohol-based spinning dope. Recombinant $(PyW)_2$ was solubilized in a trifluoroacetic acid (TFA)/2,2,2-trifluoroethanol (TFE)/water mixture forming a viscous spinning dope. Wet-spinning into an ethanol/water coagulation bath yielded fibers with no visible defects on the surface. The spun fibers were collected either immediately after the coagulation bath, following a post-spin stretch in air, or following a water immersion with a post-spin stretch in air. The mechanical behavior of the fibers is hypothesized to vary as a function of post-spinning stretching conditions, which is correlated to the loss of alpha helicity in the fibrous state in contrast to the spinning dope. The transition from alpha-helix to beta-sheet conformation after stretching would be shown through enhanced birefringence in polarized light microscopy and band shifts in Fourier-transform infrared spectroscopy. The resulting $(PyW)_2$ fibers will be compared to other recombinant silks, synthetic materials, and native silks. Characterizing and understanding the properties of hybrid silks will allow us to determine their suitability and tunability for distinct applications.

The Influence Of Hydrologic Connectivity On The Diversity And The Productivity In Arctic Thermokarst Lakes

Author: Jack de Swart
Programme: Marine Biology
Supervisor(s): Dr. Andrew Medeiros, Department of Resource & Environmental Management, Dalhousie University

Abstract

Thermokarst lakes are heavily influenced by climate change in the Arctic. The tundra uplands, north-east of the Mackenzie River Delta (NWT) contain several several of these lakes. The region is covered by a south to north gradient of increasing permafrost depth beneath a thin active layer. Characterizing and categorizing the lakes' primary producers like algae and bacteria, and their change in abundance and diversity to increased variance in the surrounding hydrography is needed to add increased understanding of the imminent effects of climate change on freshwater tundra ecosystems, fill knowledge gaps, and prepare for further anthropogenic effects in other Arctic thermokarst lake research. To investigate this, 60 lakes, as well as several polygons, rain water sources, and a few streams were sampled and analyzed for oxygen/hydrogen isotope ratios to help determine lake water source and stress factors (like evaporation without intermittent precipitation) in July of 2023. Sampling was preformed by researchers of Dalhousie University and Northwestern University. simultaneously, the 60 lakes were analyzed for water chemistry, chlorophyll-a cover (Chl-a), nutrients, temperature, and FDOM (fluorescent dissolved oragnic matter). Chl-a was used to estimate algae coverage and FDOM data was used to interpret organic carbon structure and input into the lake as well as bacterial modification to lake DOM (dissolved organic matter), and DOM input from weathering or ground water/permafrost melt. Analysis of this data was done using is currently being conducted.

Great White Shark, *Carcharodon carcharias*, Presence & Residence In The Upper Bay Of Fundy

Author: Chelsea Eldridge
Programme: Marine Biology
Supervisor(s): Dr. Charles Bangley, Research Associate, Dalhousie University

Abstract

The Minas Basin, situated in the upper Bay of Fundy, Nova Scotia is acknowledged as a noteworthy marine energy site due to its considerable commercial potential. Additionally, the Minas Passage serves as an important habitat for numerous marine species, including white sharks. Understanding the presence and residence of white sharks at this site can aid in the assessment of the risk of encounter with tidal power infrastructure. Acoustic telemetry data were used to determine the locations of white sharks, providing insights into their spatial distribution within Minas Basin and confirming their presence in Minas Passage. Abacus plotting the years, months, and Julian days associated with individual white shark tag detections illustrated the presence of white sharks by visualizing the frequency of their visits and the potential for recurrence in consecutive years. Plotting revealed that white sharks were present in the Minas Basin during the warmer summer months, beginning in June and extending into early fall, as late as October. Additionally, some individuals exhibited a pattern of making repeated visits year after year. Residence time analysis was used to identify specific areas of Minas Basin that white sharks most frequently utilize. Using the Glatos package, we calculated the duration (measured in seconds) during which the animal was detected at a specific site within the Minas Basin without a gap of at least one hour between tag detections. This information was comparied with periods in which no detections occurred. Comparison between the Avon River, Main Basin, and Minas Passage regions of Minas Basin showed that the Main Basin was identified as the region with the longest residence time for white sharks. Further investigation into the size class of white sharks inhabiting these areas of interest will be undertaken using the age and growth equation developed by Natanson & Skomal (2015). Here, we presented the potential ability to use acoustic telemetry data to provide information on white shark habitat utilization within the Minas Basin, aiming to enhance understanding of the risks associated with the proposed tidal power development.

The Effects Of Plasminogen Activation Induced By Chemotherapy-Treated Cancer Cells On Regulating Macrophage-Mediated Phagocytosis

Author: Joshua Feld
Programme: Biology
Supervisor(s): Dr. David Waisman, Department of Pathology, Dalhousie University
Dr. Dharini Bharadwaj, Department of Pathology, Dalhousie University

Abstract

Introduction: Cancer represents the second largest burden of disease globally in terms of number of deaths, years of life lost and disability adjusted life years. Chemotherapeutics remain the most effective and widely used cancer modality. Of emerging importance, is the role of chemotherapy in eliciting an immune response against cancer cells through immunogenic cell death (ICD). This report investigates the role of plasmin, and its zymogen, plasminogen (plg), in chemotherapy-induced phagocytosis of cancer cells, providing insight into plasmin's role in chemotherapy-induced immune modulation and ICD. Preceding these analyses, this study analyzes the regulation of plasmin following chemotherapy and assesses plasmin's role in mediating the phagocytic capacity of macrophages.

Methods: To determine plasmin regulation following chemotherapy, plg activation was quantified using a chromogenic assay in which cultured murine fibrosarcoma, MCA205, cells were pre-treated with serial dilutions of chemotherapeutics, doxorubicin, mitoxantrone, oxaliplatin, or DMEM for 20 hours. This was followed by measuring the conversion of inactive plasminogen to active plasmin in the presence of plasminogen activators. Phagocytic capacity of murine macrophage, J774A.1 cells, was assessed by incubating cells with fluorescent bioparticles in the presence or absence of Plg and tissue-type plasminogen activator (tPA), with and without plasmin activation inhibitors, epsilon-aminocaproic acid (eAPA) or tranexamic acid (TXA) for two hours and compared to the no-treatment control.

Results: Preliminary data showed that chemotherapeutics led to an increase in plg activation compared to the no-treatment control in MCA205 cells in a dose-dependent manner. The phagocytic uptake of fluorescent bioparticles by J774A.1 cells was increased with plg and tPA. This increase was attenuated by plg activation inhibitors, eAPA and TXA, indicating that active plasmin enhances the phagocytic capacity of murine macrophages.

Conclusion: Overall, this study will provide a mechanistic understanding of the role of plasmin in cancer progression following chemotherapy which will build the foundation for further studies of the role of plasmin in ICD. Therefore, this report may provide important insight in the understanding and development of cancer cure strategies.

Comparing The Diving Behaviour Of Four Shark Species (Blue, White, Porbeagle, And Shortfin Mako) In The Atlantic Ocean

Author: Jacob O. Ferris
Programme: BSc Combined Honours, Marine Biology & Env Science
Supervisor(s): Dr. Heather D. Bowlby, Bedford Institute of Oceanography
Research Lead, Canadian Atlantic Shark Research Laboratory

Abstract

As apex predators, sharks play a crucial role in maintaining the health and balance of marine ecosystems. Understanding the behaviour and movement patterns of sharks is pivotal for advancing our comprehension of these species and the ecosystems they influence. One aspect of shark behaviour that has garnered substantial attention is their diving habits since a variety of behaviour-influencing factors (e.g., access to prey and temperature) vary throughout the water column. The use of habitat selection theory, which examines a comprehensive web of factors (e.g., life-history traits and community dynamics), to explain behaviour and niche use rather than singular drivers, in animal behaviour studies ensures the use of a holistic framework to accurately describe behaviour. This research aims to characterize and compare the diving behaviour of four shark species (Blue - *Prionace glauca*, White - *Carcharodon carcharias*, Shortfin Mako - *Isurus oxyrinchus*, and Porbeagle - *Lamna nasus*) in the Atlantic Ocean. We used data from pop-up satellite archival tags (n_{total}=104; n_{blue}=37; n_{white}=14; $n_{porbeagle}$=43; n_{mako}=20) deployed between 2001 and 2019 to produce time series, time-at-depth, and time-at-temperature distributions for each species group. Differences between species distributions were statiscally compared to make inferences regarding the sharks' behaviours both independently and in relation to one-another using habitat selection theory.

Testing The Tests: Analysing And Developing Methods Of Characterizing Phenotypes Of *Saccharina latissima* In Nova Scotia, Canada

Author: Ainhoa Fournier
Programme: Marine Biology (Co-Op) & Ocean Sciences;
Supervisor(s): Dr. Flora Salvo, Merinov
Dr. Carly Buchwald, Department of Oceanography, Dalhousie University

Abstract

A promising sustainable solution to the increasing global demand of aquatic products is aquaculture. The diversification of refined bioproducts derived from aquatic plants, such as algae, has further increased this global demand. In Atlantic Canada, the main cultivated seaweed is Sugar Kelp (*Saccharina latissima*), also known as sea lasagna. The current practices of *S. latissima* are not self-sustaining and rely heavily on the collection of natural broodstock. Due to *S. latissima*'s reproductive temperature dependence, its cultivation and production is susceptible to increasing seawater temperatures caused by climate change. In attempts to improve the artificial cultivation of *S. latissima*, collaborative research between the National Research Council of Canada and Merinov aims to identify and biobank the optimal phenotype of *S. latissima* for cultivation. The optimal phenotype will be suitable for farming, yield the most biomass, and potentially possess resistance to climate change. This project, specifically, will test the efficiency and accuracy of the 1-dimnesional (1D metric measurements), 2-dimensional (2D pictures), and novel 3-dimensional (3D scans) methods used to identify and characterize these phenotypes. It is hypothesized that using a 3D scanner and software to physically characterize phenotypes of *S. latissima* may be the most effective and efficient method, comparatively.

Phytoplankton In Changing Oceans: The Effects Of Carbon Dioxide On Phytoplankton Abundance, Health And Community Structure

Author: Maxwell Gallo-Will
Programme: Marine Biology & History of Science and Technology
Supervisor(s): Dr. Caroline Chenard, AGSB, NRC-CNRC

Abstract

Phytoplankton are important drivers of ocean biogeochemical cycles such as carbon sequestration, produce around 50% of the earth's oxygen, and act as the base of the trophic web in nearly every oceanic environment. Phytoplankton are key drivers of biogeochemical cycles in the oceans as well as globally, they have important roles in nitrogen fixation, phosphorous transport silica and carbon cycles. Despite their importance the effects of CO_2 (carbon dioxide) on the health of phytoplankton species and populations is not fully understood especially in local contexts. Typically CO_2 in the environment isn't great but in the ocean it leads to unique environmental changes such as ocean acidification which can have their own major knock-on effects. Understanding the effects of increased CO_2 concentrations on local phytoplankton health and community structure may give us insights into the future condition of the ocean environment around Halifax. Theoretical models as well as previous experiments have shown that different species of phytoplankton even within the same general groups have varying responses to heightened levels of CO_2 when in a mixed culture. Unlike many previous experiments we sampled and experimented on wild populations which may give greater insight into the actual responses in nature. By filtering seawater into four different experimental treatments and sampling them at the beginning and end of a 24 hour period we are able to examine the differences between populations at different levels of CO_2 through metagenomics as well as take a snapshot of phytoplankton health using fluorescence.

Different phytoplankton species have varied responses to increases in CO_2 concentrations. There is evidence that some diatoms such as *Coscinodiscus sp.* grow better at higher CO_2 concentrations when free of competition, as they are capable of downregulating energy consuming mechanisms that create CO_2 for use in RubisCO when environmental levels CO_2 are too low for the enzyme to run efficiently. However, the growth provided by this newly acquired energy may be pyrrhic in nature, as some studies suggest that without their advantage at low CO_2 levels they are outcompeted by coccolithophores and dinoflagellates, whose RuBisCO is naturally more efficient at these higher levels of CO_2. Understanding the effects of these CO_2 concentrations on differ

The Influence Of Cobalamin Availability On Metabolite Production In Phytoplankton Isolates From The Scotian Shelf

Author: Anna Gleason

Programme: Marine Biology Co-op

Supervisor(s): Dr. Erin Bertrand, Biology Department, Dalhousie University

PhD Candidate Catherine Bannon, Biology Department, Dalhousie University

Abstract

Cobalamin, or vitamin B_{12}, is required by half of all surveyed phytoplankton (auxotrophs) but is produced only by select bacteria and archaea. Cobalamin has been shown to be a critical currency for microbial interactions and cobalamin availability has important implications for community composition and primary productivity in various regions of the ocean. Cobalamin auxotrophy cannot be determined solely from taxonomic information and can vary even between closely related species. Here, we cultivated and leveraged 18s and 16s rRNA gene sequencing to identify diatoms, *Bacterosira constricta* and *Chaetoceros neogracile* from the Scotian Shelf in the Northwest Atlantic Ocean. We grew both diatoms over a range of different cobalamin concentrations. Then, using mass spectrometry, we quantified cobalamin quotas and cobalamin in spent media to confirm each isolate's functional role in cobalamin dynamics. We found that the hypothesized auxotrophic status assigned to our isolates based on their taxonomic identification was incorrect, and that these diatoms are in fact non-auxotrophs. Additionally, we observed that in these non-auxotrophic organisms, cobalamin availability did not influence growth rate but did significantly alter the concentrations of key intracellular metabolites. This work demonstrated how sequencing can be coupled with culture studies to quantify cobalamin use and production in marine microbes and understand the metabolic consequences of auxotrophy, both of which can influence microbial community dynamics and productivity.

Contributions From A17 Amacrine Cells To The Oscillatory Potentials In The Full Field Electroretinogram (ERG) Of Mice

Author: Sophia Hibbert
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Supervisor(s): Dr. Patrice Côté , Biology Department, Dalhousie University
Jeffrey Locke, Dalhousie University

Abstract

A17 amacrine cells in the inner plexiform layer of the retina are fundamental in visual processing under scotopic conditions. They play a key role in the rod pathway by creating an inhibitory circuit, channeling their synaptic output back onto rod bipolar cells. The precise role of GABAergic A17 feedback in scotopic processing is unclear as rod bipolar cells receive input from multiple classes of amacrine cells. The synapses between rod bipolar cells and GABAergic A17 amacrine cells are believed to be the main mechanism underlying oscillatory potential (OP) generation on an electroretinogram (ERG) of dark adapted mice. This study investigates the hypothesis that the pharmacological ablation of A17 cells will have a de-inhibitory effect under scotopic conditions, resulting in a larger amplitude and shorter implicit time.

An auto-fluorescent serotonergic neurotoxin, 5,7-dihydroxytryptamine hydrobromide (5,7-DHT) dissolved in Phosphate-buffered saline (PBS), was administered intravitreally to the right eye of wild-type mice (Scn8a-flox) in the experimental group to ablate A17 amacrine cells. PBS alone was administered intravitreally to the right eye of the control group. Both eyes of C57BL/6 normative mice were left intact and used to create baseline recordings. Effects on OPs were then observed on scotopic flash ERG recordings taken after dark-adapting the mice. To confirm the success of A17 cell ablation, histology and immunohistochemistry analyses will be performed. The results will lead to an improved understanding of the cells involved in OP generation, and may help ophthalmologists and researchers to determine if A17 amacrine cell inhibitory circuits are involved in human retinal dysfunctions.

Growth And Tissue Composition Of Atlantic Salmon (*Salmo salar*) Fed Novel Alternative Feeds Reared In Aquaculture Setting

Author: Tatum Johnson
Programme: Marine Biology
Supervisor(s): Dr. Stefanie Colombo, Dept. Animal Science and Aquaculture, Dalhousie University

Abstract

One of the biggest challenges in aquaculture production is formulating feeds that are suitable for the species, in terms of meeting nutritional requirements for optimal health and growth, while also being economically and sustainably productive. Fish meal and fish oil-based feeds are commonly used as aquafeeds because they are closest to what would be consumed in natural settings and therefore produce the most efficient growth rates. However, because of the rapidly growing aquaculture industry, they are an unsustainable feed source. This study looks at a combination of three alternative feeds: Black solider fly meal, micro-algae biomass, and alternatively sourced fish meal from co-culture for Atlantic salmon (*Salmo salar*) feed. Atlantic salmon (n=198) were measured initially for weights and lengths, randomly assigned to nine tanks and fed one of three diets (two experimental diets and one control). After a grow out period of two months, all individuals were sampled to determine growth performance (including condition factor, specific growth rate and feed conversion ratio). Five individuals from each tank were sampled for further biochemical analysis of amino acid profile and fatty acid profile of the tissues, as well as visceral somatic index, hepatosomatic index and gonadal somatic index. If the hypothesis that Atlantic salmon fed with sustainable feed will have the same growth rates and tissue composition compared to those fed with the industry standard feed is correct, then we can make the case to shift aquafeeds to a more sustainable product.

Effects Of Temperature And Food Availability On Feeding Behaviour And Metabolism In The Sea Cucumber *Cucumaria frondosa*

Author: Kat Kabanova
Programme: Marine Biology
Supervisor(s): Dr. Ramón Filgueira, Department of Marine Affairs, Dalhousie University

Abstract

Cucumaria frondosa are the largest and most abundant species of sea cucumber in the North Atlantic and Arctic oceans. They are commercially exploited in Maine and the Canadian Maritimes; however, the catch per unit effort and the average size of harvested individuals have started declining, particularly near the southern limit of the fishing operations. To be able to understand and predict individual growth and population dynamics, sustainable stock management requires addressing knowledge gaps in *C. frondosa*'s ecophysiology and bioenergetics. While temperature is commonly assumed to be the principal factor affecting the metabolic rates of aquatic ectotherms, food availability determines the feeding ecology and, ultimately, growth rates of suspension feeders such as *C. frondosa*. Effects of temperature and food availability on individual feeding rates, metabolism, and population-level feeding activity were investigated in *C. frondosa* collected from Halifax Harbour. Two independent experiments were carried out in which 10 sea cucumbers were held in each of 2 mesocosms with seawater flowing at 150L h-1 and live phytoplankton (*Chaetoceros muelleri*) continuously supplied via peristaltic pumps. In the first experiment, temperature was increased from 5°C to 16°C by 1°C every 3 days. Maximum tentacle insertion rates (TIRmax, a proxy for food intake) and cloacal opening rates (COR, a proxy for respiration) increased with temperature, while the total proportion of feeding individuals decreased. Beyond 12°C, novel abnormal behaviors – rhythmic openings of the mouth and incomplete TIR – emerged and became increasingly common at higher temperatures, suggesting thermal stress. In the second experiment, phytoplankton concentration was increased from 2 000 cells ml^{-1} to 50 000 cells ml^{-1} by ~10 000 cells ml^{-1} every 3 days. TIRmax increased until 30 000 cells ml^{-1}, then plateaued, suggesting that ingestion in *C. frondosa* may follow a Holling's type 3 functional response, in which food intake accelerates at low prey densities. Further research would be needed at higher phytoplankton concentrations to determine how saturation manifests. The proportion of feeding individuals increased with food availability, with all individuals feeding at concentrations above 40 000 cells ml^{-1}. These findings provide insight into the physiological performance of *C. frondosa* under different environmental conditions and can help inform fisheries management.

Examining The Effects Of Temperature And Salinity On The Germination Success Of *Zostera marina* (Eelgrass) Seeds.

Author: Lauren LaPorte
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Dr. Kristina Boerder, Biology Department, Dalhousie University

Abstract

Eelgrass (*Zostera marina*) is an important ecosystem engineer species in Atlantic Canadian nearshore environments. Found in sandy subtidal habitats, eelgrass is a marine flowering plant that forms dense meadows that support numerous species. As they form hotspots for biodiversity and productivity, the state of eelgrass meadows can influence local economies such as fisheries relying on eelgrass-associated species (e.g. lobster, crabs, flatfishes) on regional scales. In addition to buffering wave action, improving water quality and producing oxygen, healthy meadows also play an important role in mitigating climate change through efficient sequestration of carbon into biomass and sediments. Despite these benefits, eelgrass populations are experiencing global declines due to a complexity of natural and anthropogenic factors, and losses are only predicted to be exacerbated by climate change. In response, various restoration methods are being conducted to restore declining eelgrass populations. The harvest and distribution of maturing seeds from healthy locations is gaining popularity due to the feasibility of large scale restoration and reduced impact on donor meadows. However, seeds have low germination rates in the wild (around 1%), which may limit restoration success relative to other approaches. To understand germination cues in the study population, I conducted laboratory experiments to evaluate the combined effects of temperature and salinity on *Z. marina* seed germination success. Reproductive shoots containing seeds were collected from an eelgrass meadow near Owls Head, Nova Scotia. After natural maturation and subsequent seed release in vitro, germination was artificially suspended for three months prior to trials. Seeds were then exposed to combinations of five temperatures (5°C, 10°C, 15°C, 20°C and 29°C) and four salinities (5, 15, 27, 30) under constant aeration and 16h:8h light:dark cycle for five-weeks. I hypothesize that *Z. marina* seeds germination success will be inversely correlated with salinity and reach a maximum at 15°C. The outcomes of this study will not only provide important information on climate-induced impacts on the reproductive success of *Z. marina* but also support applied conservation projects by determining conditions to artificially raise germination levels, thus ultimately supporting the establishment of Nova Scotia's first artificial eelgrass seed bank.

The Impacts Of Scale On Kelp Abundance Estimates

Author: Kylee Lightbody
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Alexis Savard-Drouin, Oceanography Department Dalhousie University

Abstract

Emerging evidence suggesting long-term storage through sequestration by kelp beds has resulted in increased focus on kelp beds as a potential source of blue carbon. To better understand their potential role in carbon sequestration and manage their conservation, the distribution of kelp species must be well quantified. However, because of the extensive distribution of kelps globally, coarse-scale studies (100s km) are often favoured over fine-scale assessments (100s m – 10s km). This bias towards coarse-scale sampling could overlook important patterns in species distribution and abundance that occur at smaller scales. My research aims to address the contribution of site-specific (100s m) variability in kelp abundance and its relation to larger scale patterns in kelp distribution. To do so, I am investigating the contribution of different spatial scales in kelp abundance variance. I measured density, percent cover, and biomass as metrics of kelp abundance at 6 and 9 m depth at Long Island, Tuffin Island, and The Moll, on the Eastern Shore of Nova Scotia. To compare the contribution of site-specific and island-wide scales in explaining the variance in kelp abundance, models were run for each of two numerically dominant kelp species using sites and islands as random predictors. Preliminary results show notable differences between site and island scale factors in explaining variability in density. Following deeper analysis, these results will improve our understanding of kelp abundance variability and assist in refining current and future kelp abundance estimates.

Compounding Interactive Effects Of Warm Water And Aerial Exposure On The Physiology And Survival Of Blue Mussels (*Mytilus edulis*)

Author: Kendra Mainprize
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Supervisor(s): Dr. Ramón Filgueira, Marine Affairs Program, Dalhousie University
Jasmine Talevi, Department of Biology, Dalhousie University

Abstract

Blue mussels (*Mytilus edulis*) contribute substantially to Canada's aquaculture industry and provide important ecosystem services, such as improving water quality, providing habitat for other species, facilitating benthic-pelagic coupling, and driving primary production through excreting ammonia and stimulating phytoplankton production. Recent observations have shown declines of intertidal blue mussels in the North Atlantic, which are suggested to be correlated with rising temperatures associated with climate change. In this study, the interactive effects of increased temperature and aerial exposure were examined to better understand how the physiology and survival of subtidal and intertidal mussels will be impacted by climate change. In a 2x2 factorial design, intertidal and subtidal mussels from the same bay (West River, Prince Edward Island) were held under both moderate (20°C) and stressful (25°C) temperatures for four weeks, during which oxygen consumption rate and condition index were measured weekly, and mortality was monitored daily. The effect of increased temperatures and aerial exposure, as well as the interaction between the two factors, were analyzed using a Bayesian model. Intertidal conditions had a negligible effect on oxygen consumption rate; contrarily, increased temperature and the interaction between increased temperature and aerial exposure had a strong impact on increasing oxygen consumption rate. Intertidal conditions and increased temperature both had an effect in decreasing condition index, though the effect of intertidal conditions was much stronger than the effect of temperature, and there was negligible interaction between the two factors. The results of this study suggest that the combination of aerial exposure (intertidal) and warmer temperatures (25 °C) negatively impacted the physiological functioning of mussels, resulting in the highest mortality among the four treatments. This data is important in understanding how blue mussels will be affected by climate change in Atlantic Canada and can help inform industry management decisions and conservation measures.

Characterizing A Model Of Exercise-Induced Muscle Damage In *Drosophila melanogaster*

Author: Ahsan Malick
Programme: Biology
Supervisor(s): Dr. Nicanor González-Morales, Biology Department, Dalhousie University

Abstract

Muscles consist of small contractile units called sarcomeres. Continuous contraction of sarcomeres during exercise causes strain which leads to structural damage. This phenomenon results in Delayed Onset Muscle Soreness (DOMS), yet the precise mechanisms underlying muscle damage, repair, and the subsequent onset of DOMS remain elusive. Due to the limitations of human muscle damage research, *Drosophila melanogaster* provides an alternative model to investigate muscle damage and repair. However, consistently exercising flies has proven difficult. Here we turn to optogenetics to directly stimulate muscle contraction and circumvent the issue. Optogenetics uses transgenic flies that express light-gated ion channels in specific cells (e.g., channelrhodopsins), this approach allows the induction of muscle contractions through light exposure. In this study, optogenetic flies experienced 2 hours of light exposure and were provided with water, sugar water, or no sustenance during the wake-up period. Subsequently, their walking patterns were examined to detect signs of muscle damage, with continuous monitoring until the restoration of a normal walking pattern. Results revealed that flies require at least 3 hours to fully awaken after 2 hours of light exposure, and they exhibit complete recovery of walking patterns within 2-3 days. This project contributes to establishing a robust model for optogenetic muscle damage research in Drosophila.

Tick-Talk: Quantifying Dawn And Dusk Questing Behaviour And Pathogen Presence In *Ixodes* Ticks

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Abstract

Vector-borne diseases pose significant health risks to humans, with both the pathogens and their vectors serving as active areas of health research globally. In Canada, the tick genus *Ixodes* is of special concern for its ability to transmit not only *Borrelia burgdorferi* (the causative agent of Lyme disease), but also other harmful viruses and bacteria responsible for Anaplasmosis, Babesiosis, Bartonellosis, and Powassan virus. Often, ticks are found to be co-infected with multiple different pathogens which further underscores the need to better understand the mechanisms of transmission to humans. As ectoparasites, ticks transmit pathogens while feeding. Ticks engage in a sit-and-wait food-seeking behaviour known as questing where they will climb to the distal end of vegetation and wait with forelimbs extended until a food source brushes against them, at which time they will climb onto their victim and attempt to take a blood meal. As questing is the primary strategy in which ticks hunt for hosts, a better understanding of this behaviour becomes imperative. Ticks are susceptible to desiccation, and it is hypothesized that less questing activity occurs at midday when temperatures are high and humidity is low. Previous lab-based research has demonstrated the microclimate parameters in which tick genera may be more likely to quest. This field-based research initiative seeks to determine if Ixodes ticks are more likely to quest during the early morning after sunrise or at dusk, and to attempt to correlate this questing preference with pathogenic-load. Ixodes ticks were collected twice per day (dawn and dusk) using the flag and drag method of collection from September to November at three locations in Halifax, NS. Environmental parameters were recorded during field collections which included temperature, relative humidity, time of collection, and local sunrise and sunset times. DNA and RNA were extracted from the specimens, and PCR and gel electrophoresis were performed to determine pathogenic loads. By studying the specific feeding behaviours of ticks in a field setting, this research will contribute to knowledge gaps in the current literature in questing behaviours.

Using Life History Traits Of Coregonid Species To Make Inferences About Atlantic Whitefish (*Coregonus huntsmani*) Anadromy, Migratory Struggles And Spawning Behaviour

Author: Paris Mastrodimitropoulos
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John Batt, Aquatron Laboratory, Dalhousie University

Abstract

Considered to be one of Canada's most endangered species, the Atlantic Whitefish (*Coregonus huntsmani*) is a fish endemic to the province of Nova Scotia. In recent centuries, threats such as poaching, over-harvesting, invasive species, habitat acidification, shoreline degradation, and migration barriers have reduced its habitat to a singular watershed consisting of three lakes, only a $16km^2$ area. As a salmonid, this species is facultatively anadromous, however the construction and operation of dams beginning in the 1700s has effectively eliminated its migratory ability, restricting its potential to grow and reproduce. Mitochondrial DNA analysis has showcased that this species is genetically distinct from all other Coregonids, and exists as a basal lineage of the genus, predating the Pleistocene epoch. Despite imminent threats, as well as its genetic, evolutionary, and cultural significance, very little is known about the Atlantic Whitefish. This study aims to help fill in the knowledge gaps surrounding the Atlantic Whitefish's life history traits using trait-based phylogenetic imputation and inference. Using the published phylogeny of Coregonids, a literature review was conducted to compile information about the life history traits of 24 related Coregonids, such as lifespan, maximum length, spawning time, and spawning behaviour. The data were then input into a Principal Components Analysis (PCA) to determine how traits cluster within the genus. If the traits of species within a closer genetic proximity to the Atlantic Whitefish cluster together, then we can make inferences that the life history traits of the Atlantic Whitefish would be similar to the traits of these closely ordinated species. The synthesis of this information can inform experiments to confirm these traits and in future will be applied to inform management strategies to protect the species from increasing its threat level to Extinct in the Wild.

Floral Resource Utilization By *Bombus spp.* Across Three Distinct Garden Sites At Dalhousie University: A Comparative Study

Author: Emily McLean
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Supervisor(s): Dr. Heather Cray, Resource and Environmental Studies, Dalhousie University

Abstract

Widespread species loss and ecosystem changes are occurring at an unprecedented rate due to human activities, including habitat loss and climate change. Insect pollinators face significant threats from these anthropogenic stresses. Understanding the floral resources that native insect pollinators utilize is essential for developing strategies to support their populations. Due to their global presence and specialized pollination adaptations, bumble bees (*Bombus spp.*), play a crucial role in pollination. Bumble bees are particularly efficient pollinators in various temperature conditions due to their physiological adaptations. They also exhibit unique pollination adaptations, such as buzz pollination, allowing them to pollinate certain plants that other species cannot. Native plants, being well adapted to their ecosystems, possess characteristics that make them resilient. They typically require minimal watering, boast natural pest resistance, and are generally low maintenance. Recognizing the importance of floral resources for native pollinators, this study investigates the relationship between native bumble bee species and their floral preferences within three distinct garden sites at Dalhousie University's Studley campus. Consistent sampling of these gardens from spring to fall 2023 facilitated an understanding of the predominant flower types present, providing the context to compare bumble bee preferences. The garden sampling results indicate a higher abundance of non-native plants in the spring, with a shift towards a higher abundance of native plants during late season fall. At the peak of summer, both native and non-native plants were observed in abundance. Preliminary analysis of bumble bee behaviour revealed an overall preference for native plants, along with selective foraging behaviour. Notably, bumble bees exhibited a tendency to revisit the same plant species, even when presented with opportunities to forage on different species. These results can guide best practices for planting strategically to increase pollinator resource availability, which is important for enhancing biodiversity, promoting ecosystem stability, and ensuring the long-term sustainability of both native pollinator populations and the ecosystems they inhabit.

Microbial Diversity And Functional Potential Of Sediment Microbial Fuel Cells

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Supervisor(s): Dr. Christopher Algar, Oceanography Department Dalhousie University
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Abstract

Sediment microbial fuel cells (SMFCs) are a novel technology that exploit some microbe's ability to conduct external electron transfer by spatially decoupling redox reactions in the sediment profile. SMFCs ability to connect contaminants in the sediment profile and harness favourable redox pairings has been suggested as a mechanism by which they could remediate sediments contaminated by open pen aquaculture. However, the exact microbes and mechanism of electron transfer in these systems are not well understood. Using 16S rRNA and metagenomic samples from a previous microcosm experiment outlined in Algar et al. (2020), I sought to describe the compositional and functional changes in microbial communities colonizing SMFCs. Samples were analyzed following the IMR protocols and pipelines - downstream analyses were performed in QIIME2 and Anvi'o. Microbial communities colonizing the SMFC anode were distinct from those sampled in the background sediment and open circuit control. Diversity and evenness were lowest in SMFCs, suggesting the presence of a selective pressure. Deltaprotteobacteria Desulfobulbus and Nanoarchaeota Woesearchaeota genera were identified as SMFCs-selected taxa. This data seeks to further understand SMFCs such that their design might be optimized and tailored for the remediation of marine contaminants.

Examining The Role Of The *ARI11* Gene On Plant Growth, Development And Drought Stress Tolerance.

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

Abstract

The Ubiquitin Proteasome System (UPS) is an important mechanism for degradation of eukaryotic proteins. The UPS controls protein abundance by attaching ubiquitin, a highly conserved protein, to selected substrates, which are then targeted by the 26s proteasome for degradation. Within the UPS system, E3s play a critical role as the final step in attaching the ubiquitin molecule to the target protein, thereby defining the specificity of the system. One of the important roles of the UPS is its involvement in the stress response pathway, which allows plants to adapt to various stressors such as drought, salinity, high temperatures, pathogens, etc. This project investigates the role and impact of the *ARIADNE11* (*ARI11*) gene, which encodes for an E3 ligase, on plant growth, development, and stress tolerance. While there is limited knowledge about its function, *ARI11* seems to be central to plant development and tolerance as indicated by previous lab studies that has observed significant differences in mutant survivability and morphology. To further understand *ARI11*'s function, a mutant analysis was conducted using *Arabidopsis thaliana* (Arabidopsis) with normal and decreased expression of this gene to assess morphology, and drought survivability rates. Growth parameters, such as height, number of siliques (seed pods), rosette shape and size, seed shape and size and biomass, were analyzed to compare wild-type plants. A drought stress assay was used to determine the survivability rates. By comparing the post-drought recovery rates of plants with normal expression of *ARI11* and decreased expression of *ARI11*, the gene's impact on stress tolerance was evaluated. As the detrimental effects of climate change, such as recurring droughts, become increasingly apparent, this project aims to enhance our understanding of plant stress responses. This knowledge may translate into helping us develop effective strategies for mitigating the impact of climate change on crop production and yield.

The Phylogeny And Taxonomic Position Of Gem-Kin, A Culture Representing The Evolutionarily Pivotal Kinetoplastid Taxon Allobodonidae

Author: Julia Packer
Programme: Biology
Supervisor(s): Dr. Alastair Simpson, Biology Department, Dalhousie University

Abstract

Many branches on the eukaryotic tree of life have undetermined placements. Ongoing sampling and genetic analysis efforts aim to help solve these issues and structure the tree. The kinetoplastids are an important and diverse group of protists, with some members being parasitic and used in biomedical research, while others are free-living and may be ecologically important in the environments they are a part of. Isolate 'GEM-kin' represents a novel 'undescribed' free-living kinetoplastid which may help in determining the branching order of the sub-groups within Kinetoplastidea. Preliminary DNA sequence data from GEM-kin place it in the kinetoplastid subgroup Allobodonidae. Allobodonids have an uncertain placement within Kinetoplastidea due to a lack of molecular data, gathering data on GEM-kin may help solve this issue. I aim to confirm GEM-kin's placement within Allobodonidae and assess where Allobodonids sit within Kinetoplastidea. Morphological data from scanning electron microscopy (SEM) and differential interference contrast (DIC) light microscopy imaging shows that GEM-kin is broadly similar to several other kinetoplastid taxa, including its hypothesized relative Allobodo chlorophagus (the only described species in Allobodonidae). GEM-kin has two flagella, a shorter anterior and a longer posterior, which arise from a flagellar pocket, and the flagellar pocket is perpendicular to its feeding apparatus. Using PCR, the SSU rRNA gene of GEM-kin was amplified for sequencing. Phylogenetic analyses of the SSU rRNA sequence will test the placement of GEM-kin within Allobodonidae, and help establish whether GEM-kin should be assigned to the genus Allobodo, or alternatively, represents a new genus. A protocol for high-density growth of GEM-kin was established, and RNA extracted from mass cultures. This will be sequenced using Illumina technology to obtain the first transcriptome sequence of an allobodonid. Future phylogenomic analyses of these data will help resolve where allobodonids branch off in the kinetoplastid tree.

Evolution of genome size and repetitive DNA in *Lobelia cardinalis*

Author: Kate Pennyfather
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Supervisor(s): Dr. Mark Johnston, Biology Department, Dalhousie University

Abstract

Eukaryotes display immense variation in genome size, with an estimated 60,000-fold variation from the smallest to largest genomes. Despite the magnitude of this variation, the causes and consequences remain largely unknown. Many scientists argue that this variation can be attributed to repetitive DNA, which does not code for proteins and is capable of autonomously replicating in the genome. This argument is supported by the minute effect of gene number on genome size among Eukaryotes and the much stronger correlation between genome size and the amount of repetitive DNA. Additionally, multiple studies have compared genome size and repetitive DNA content between closely related species, allowing for the identification of specific repetitive DNA classes that have driven genome size increases in individual species or groups. The angiosperm species *Lobelia cardinalis* (cardinal flower, Campanulaceae) provides an excellent opportunity to perform similar research across populations of a single species, as it has an expansive geographic range with isolated populations displaying variation in genome size, morphology, and pollinator species. As such, this study was performed to test the hypothesis that genome size variation across *L. cardinalis* populations can be attributed to repetitive DNA. As well, we aimed to determine the specific repetitive DNA classes that have driven genome size increases in individual populations, to identify any phylogenetic or geographic patterns of repetitive DNA evolution. To perform this research, 658 plants from 33 *L. cardinalis* populations were grown in the Dalhousie greenhouse. Using leaf tissue, genome size estimates were obtained through flow cytometry, and repetitive DNA content was estimated through DNA sequencing and the use of RepeatExplorer2. Genome size results show a 1.3-fold variation across populations, as well as a negative correlation between genome size and longitude, indicating a tendency for larger genomes in the western portion of the *L. cardinalis* range. Once analyzed, data on repetitive DNA content will supplement these findings to provide information on the relationship between genome size and repetitive DNA in *L. cardinalis*. The understanding of this relationship will allow us to contribute to the heavily debated discourse surrounding Eukaryotic genome size.

Shifting Intersexual Dynamics And Sexual Conflict Of Japanese Medaka (*Oryzias latipes*) Amongst Inverse Sex Ratios.

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Programme: Biology & Psychology
Supervisor(s): Dr. Laura Weir, Biology Department, Saint Mary's University

Abstract

Sexual conflict theory— the concept that males and females have conflicting evolutionary interests— has been an established spin-off of Darwin's theory of sexual selection. Despite sexual conflict being a long-standing hot topic within behavioural ecology, there remains a gap in the understanding of sexual conflict in fish. It has been shown in various other vertebrate classes that the number of males to females in a community greatly moderates the severity of sexual conflict and influences intersexual dynamics. Generally, as the mating population becomes more male-biased, males become more aggressive towards both males and females as males become more competitive. Further, as males become more in excess, females can generally afford to be more choosy about their mates and will be more selective in their matings. Therefore, sexual conflict often becomes more tense in male-biased populations. Using Japanese medaka (*Oryzias latipes*) as a model, the current study seeks to understand and analyze male-female interactions in inverse sex ratios for evidence of sexual conflict. I predict that sexual conflict between medaka will become more tense in male-biased sex ratios, aligning with the general trend amongst other vertebrates. After mating, females cannot mate again until the next day and therefore I also predict that females will experience less male courtship behaviours and will respond with more courtship resistance after mating that day. In this study, interactions between males and females in sex ratios of 4:8 males to females and 8:4 males to females were observed and recorded via JWatcher. Whether females had mated that day was recorded based on her presence of or lack of external eggs. Five behaviours happening to and perpetrated by the observed female were selected to represent courtship and aggression. Courtship behaviours included males following females, male courtship dances, and refusal signalling from females. Aggression behaviours included chasing, categorized into two groups based on the individuals involved. Sixty-seven females were observed for 2-minute intervals on four different occasions. The occurrences of these behaviours will then be statistically analyzed, with specific interest in female responses to male behaviours, for significant evidence of sexual conflict across inverse sex ratios. Understanding Japanese medaka sexual conflict may deepen knowledge of medaka behaviour within shifting sex ratios in the wild.

The Cost Of Fishing To Extinction: How The Price Of Sharks And Rays Drive Global Fisheries

Author: Madeleine Platt
Programme: Marine Biology Co-op
Supervisor(s): Dr. Aaron MacNeil, Biology Department, Dalhousie University
Dr. Christopher Mull, Biology Department, Dalhousie University

Abstract

The decline of sharks and rays (elasmobranchs) has become a global concern, with 36% of species threatened with extinction due to deteriorating ocean ecosystems and overexploitation. Sharks and rays are susceptible to overexploitation due to their slow life history traits, coupled with increasing demand and the economic globalization of the shark and ray meat industry. This study investigates the dynamics of global elasmobranch fisheries, focusing on understanding the influence of prices, including variability across countries and species, temporal shifts in species-specific prices reflective of market demand trends, and the influence of commodity types on overall price dynamics within these fisheries. This project utilizes the Sea Around Us dataset containing reported and reconstructed catch data, analyzing 68 countries comprising 95% of global landings and trade of sharks and rays, spanning from 1950 to 2019. I use a Bayesian hierarchical modelling framework to determine the key predictors of price within the dataset, considering various covariates such as species, commodity types, fishing sector, continent, country, economic class, and year. Preliminary findings highlight the variability in ex-vessel prices across continents and species, for example ex-vessel price of blue shark, which is the most heavily landed species globally, varies between the Americas, where, in 2019, fishermen only received an average of 644USD/tonne and Europe where, in the same year they received upwards of 1000USD/tonne . Overall, a global increase in elasmobranch prices is observed over time, highlighting the possible role of increasing demand on fisheries. This research contributes to the understanding of the complex dynamics governing global elasmobranch fisheries, offering insights crucial for the development of effective conservation strategies and sustainable management practices in the face of escalating demand and threats to these vulnerable species. This project hopes to provide insights for managers and conservationists to focus their efforts towards areas more susceptible to overexploitation and contribute valuable research to the ongoing Global Shark Meat Project at Dalhousie.

Using Trail Cameras Help To Evaluate The Source And Impact Of Predation On Leach's Storm Petrels (*Hydrobates leucorhous*)

Author: Isabel Ross
Programme: Marine Biology Co-op
Supervisor(s): Dr. Sarah Gutowsky, Biology Department, Dalhousie University

Abstract

Leach's Storm Petrels (*Hydrobates leucorhous*) are a small threatened seabird found across the North Atlantic. This study examined a nesting colony on Country Island in Nova Scotia, which is home to several other species of seabird, including endangered Roseate Terns (*Sterna dougallii*). Country Island was managed for predators from 1998-2019 due to severe impacts of both avian and mammalian predators on nesting seabirds in the 1990s, and there has been an active research camp monitoring the seabird populations in most years, including 2023. Currently, suspected predators of petrels include American Herring Gulls (*Larus argentatus*), two species of corvid (American Crow *Corvus brachyrhynchos* and Common Raven *Corvus corax*), North American River Otters (*Lontra canadiensis*), and Eastern Meadow Voles (*Microtus pennsylvanicus*). In 2023, 16 motion-triggered trail cameras monitored petrel burrows across the island, collecting information on species presence and behaviour. Camelot, a trail camera image management program, was used to organize and annotate 47,524 images, 74% of which were not false triggers (i.e., contained wildlife or researchers). In order to better understand predator occurrence in relation to petrel and research activity, predator species presence and behaviour were evaluated relative to the intensity of petrel activity, the phase of the petrel breeding season, researcher presence, and distance from the research camp. Otters, corvids, and voles were present throughout the petrel breeding season while gulls were only detected from late June until early August, and only hatch-year gulls which are unlikely to pose a threat. Vole activity peaked around mid-August coinciding with the end of the hatching phase of the petrel breeding season, suggesting that small petrel chicks may be especially vulnerable to vole predation. While distance from the research camp did not appear to impact petrel presence, there was evidence that predator presence increased with distance from the camp, suggesting that research activity may be a deterrent to predators. Corvids, otters, and voles were all directly observed predating or destroying petrel burrows. My findings indicate that trail cameras are an effective method for monitoring predation at seabird colonies, and could be used to inform future approaches to protecting the petrel population at Country Island and other colonies in Atlantic Canada.

Examining herring gull (*Larus smithsonianus*) diet through noninvasive bolus collection as an index of predation pressure on conspecific nesting seabird species

Author: Katie Ryder
Programme: Biology
Supervisor(s): Dr. Sarah Gutowsky, Biology Department, Dalhousie University

Abstract

In Nova Scotia, anthropogenic food sources support inflated numbers of American herring gulls (*Larus smithsonianus*), whose predation can detrimentally impact other local species. On Country Island, NS, a predator management plan was implemented in 1998 to protect co-nesting seabird species-at-risk from significant predation by gulls and other predators. Gulls were prohibited from nesting on the island from 1998-2019, but the program has been suspended since 2020. With the return of gulls on Country Island, we are now reassessing the efficacy and necessity of the predator management program by evaluating impacts of gulls in the absence of management intervention. My research evaluates the prevalence of at-risk seabirds in gull diet via non-invasive bolus collection. Boluses represent the indigestible, regurgitated portion of a gull's diet and were collected on Country Island from May-July 2023. I examined the frequency of occurrence of different prey items in boluses, and how this varied with location (coastal, near gull nests, within the tern colony, etc.) and time (before or after gull chick hatch), using GLMMs with a binomial response for prey-type occurrence. Boluses indicate that adult gulls on Country Island are primarily foraging on marine invertebrates (64.8% of samples), with birds occurring in their diet relatively infrequently (19.3% of samples). Boluses containing marine invertebrates were more likely to be found on the coast while boluses containing birds and mammals were more likely to occur inland, near the tern, gull, and storm-petrel colonies. The likelihood of bird and mammal prey occurring in boluses decreased after gull chick hatch while the likelihood of marine invertebrate, fish, and insect prey increased. Prey types occurring near their respective source habitats suggests that gulls rest and produce boluses near their preferred foraging sites. Decreasing occurrence of bird and mammal prey after gull chick hatch suggests that adult gulls may be feeding these prey types to their chicks; so while these species may still be experiencing predation, they are not represented in adult boluses. This suggests that breeding gulls may shift their diet to provide chicks with prey of higher nutritional quality. My findings will aid in the conservation of Country Island's at-risk seabird species and will help inform future predator management strategies.

Optimizing Nutrient Delivery Methods And Sterilization Techniques For Sugar Kelp (*Saccharina latissima*) In Dalhousie's Aquatron

Author: Tessa Schaeffer
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Supervisor(s): Dr. Carolyn Buchwald, Oceanography Department, Dalhousie University

Abstract

Sugar kelp (*Saccharina latissima*) is a brown algae of the class Phaeophyceae and is farmed for seafood, bioremediation, and bioethanol. Kelp aquaculture is on the rise in Nova Scotia and thus it is essential to optimize all elements of the farming process in order to obtain a successful at-sea yield. My research focuses on the indoor nursery stage, where microscopic spores grow into macroscopic juvenile sporophytes. Contamination by biological organisms such as diatoms, ectoprocts, and other algae are a notable problem during the nursery stage, as young sporophytes are easily outcompeted. Further, it is not yet known how different nutrient delivery methods will affect contamination and sporophyte growth. In my project, I aim to optimize nutrient delivery methods and water sterilization techniques for sugar kelp seedlings growing in Dalhousie’s Aquatron. Two nutrient delivery methods (bulk addition and low-level addition) were tested against three water sterilization techniques (coarse sand filtration, 0.35-µm filtration, and addition of germanium dioxide) over a 6-week period to determine the effects on sporophyte length, density, and contamination of spools. There were 6 treatments with n=3 replicates. The seawater used in this experiment was pumped directly from the Atlantic Ocean. Preliminary results showed that tanks treated with 0.35-µm filtration showed the highest sporophyte density (247 sporophytes/cm of twine for low-level nutrient addition and 172 sporophytes/cm for bulk nutrient addition). Further, tanks treated with germanium dioxide showed the lowest sporophyte density (110 sporophytes/cm for low-level nutrients and 78 sporophytes/cm for bulk nutrients). Tanks with low-level nutrient addition also consistently showed a higher density of sporophytes/cm than tanks with bulk nutrient addition. Two-way ANOVA tests will be performed to determine if these results are significant. Interestingly, none of the spools themselves showed notable growth of contaminating organisms, which might be attributed to the large density of sporophytes each spool had, which were able to outcompete any potential contaminants. My research will optimize the Aquatron as a viable, ongoing kelp nursery, as well as contribute to the growing sustainable aquaculture industry in Nova Scotia.

Predicting Habitat Suitability For The Basking Shark (*Cetorhinus maximus*) In The Northwest Atlantic

Author: Vanessa Schiliro
Programme: BSc Marine Biology
Supervisor(s): Dr. Boris Worm, Biology Department, Dalhousie University

Abstract

The basking shark (*Cetorhinus maximus*) is a globally endangered filter-feeding elasmobranch, observed seasonally throughout the Atlantic continental shelf in Canada. The Atlantic population is currently considered of "Special Concern" by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), however recent trends in this species' abundance and distribution remain poorly understood as the last assessment was performed over 16 years ago. Gaps in data, seasonal changes and interannual variability in the regional distribution of basking sharks further complicate effective management and conservation efforts. Here, I present an analysis of over 9,000 opportunistic basking shark sightings in Atlantic Canada, these data informed species distribution models that included suspected environmental drivers of basking shark distribution and predict current and near-future habitat suitability under a business-as-usual climate scenario. Results suggest that areas of high current and future habitat suitability are strongly driven by sea surface salinity, temperature, and net primary productivity and that areas of high habitat suitability will be primarily restricted to the Gulf of Maine, and less towards the northern range of the Northwest Atlantic in the future. This research improves our ability to forecast changes in habitat quality and provides an opportunity to design dynamic spatial protections that reduce overlap with known threats such as vessel collisions and bycatch.

Development Of Fibronectin-Based Protein Fibers For Promoting Cell Adhesion To Biomaterial Textiles

Author: Jana Sewidan
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Supervisor(s): Dr. John Frampton, School of Biomedical engineering, Dalhousie University

Abstract

Promoting cell adhesion to biomaterial textiles is imperative for advancing biomedical research. Fibronectin (FN)-based fibers are promising candidates for such applications due to their fibrous nature. FN, a highly abundant self-assembling structural protein, is crucial for ECM formation and stability. Its importance encompasses roles in wound healing, cell development, adhesion and differentiation, thereby affecting cellular communication and regulation, processes crucial for tissue maintenance. This study investigates the development and use of fibronectin-based protein fibers for biomaterial functionalization using a single-pin contact-drawing and a FN-Poly(ethylene oxide)(PEO) solution. Initial findings reveal the potential of FN to produce protein fibers with an average diameter of 4um when using a FN-PEO solution with a ratio of ~5.5:1 PEO relative to FN. However, the stability of the fibers under aqueous conditions is currently undergoing testing through a graded hydration process. Various washing protocols are used involving 1% glutaraldehyde, an incubator, 1x phosphate buffered saline (PBS), and graded concentrations of PEO in both 1x and 10x PBS. The use of a UVC crosslinker demonstrated increased stability of the fibers during hydration, leaving behind a trace of the fibronectin fiber after dissolving the PEO. The application of a heparin treatment is anticipated to increase the FN self-interactions, further enhancing the fibers stability during hydration protocols. Once the fibers successfully survive the hydration process, the study proposes the creation of multiple fibers using a multi-pin contact drawing method. This approach aims to produce an unwoven scaffolding material for cell culture testing. This methodology creates opportunities for integrating fibronectin protein fibers into scaffolding materials with potential in advancing tissue enginerring and regenerative medicine applications.

Movement Behaviour Of Young-Of-The-Year Porbeagle Sharks (*Lamna nasus*) In Comparison With Older Animals In Northwest Atlantic

Author: Wendy Shue
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Supervisor(s): Dr. Heather Bowlby, Bedford Institute of Oceanography, DFO

Abstract

Porbeagle sharks (*Lamna nasus*) are a threatened shark species found in the North Atlantic Ocean and circumglobally in the Southern Hemisphere. It was previously hypothesized that the Porbeagles in the Northwest Atlantic migrate to the Goerges Bank and the Grand Banks to mate in the Summer before mature females then migrate to the Sargasso Sea to pup. However, a recent study suggested that a biennial instead of an annual reproductive cycle is more likely, which implies that the Sargasso Sea may not be the pupping ground. To identify other potential pupping grounds and reevaluate the current conservation strategies, understanding the distribution and movements of the young-of-the-year (YOY) sharks is critical. The movement tracks of YOY (N=7) and Age 1+ (N=39) sharks tagged between 2005 and 2021 using pop-up satellite archival tags were analyzed to characterize the movement behaviour, swimming speed, depth temperature association, and diving depth in relation to bathymetric depth. YOY sharks showed non-linear movements and remained close to the Georges Bank, while Age 1+ sharks showed clear seasonal migration. Most mature females migrated to the Sargasso Sea by April, while the exceptions remained off the southern and eastern coast of Nova Scotia respectively. Although the median swimming speeds of YOY (0.786 km/h) and Age 1+ (0.721 km/h) were similar, the speeds were significantly more variable in Age 1+ sharks. Age 1+ sharks also had a much wider diving range (0-1992 m) compared to YOY sharks (0-552 m) and used deeper water more often. The variance in temperature was larger in the Age 1+ group despite a similar median, which was reflected by YOY porbeagles spending 69% of the time in waters at 9-15 ˚C, while Age 1+ porbeagles only spent 52% of the time. Compared to Age 1+ sharks, which were observed within or beyond the 200 m bathymetric contour for the same amount of time, YOY sharks spent 1/2 more time in shallow waters (< 200 m). Overall, YOY differed from older animals in their movement pattern, swimming speed variability, depth range, temperature tolerance, and preference for bathymetric depths. This study will provide a more comprehensive understanding of the behaviour of porbeagles and insights into the possibilities of porbeagle pupping grounds in Canadian waters.

Sperm Whale (*Physeter macrocephalus*) Movement Across Temporal Scales Around The Galápagos Between 2013-2014 And 2022-2023

Author: Davjit Kaur Sidhu
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Ana Eguiguren, PhD Candidate, Dalhousie University

Abstract

Movement plays a critical role in behavioural, trophic, and population ecology. The sperm whale, *Physeter macrocephalus*, is a species for which understanding their movement patterns is critical for comprehending their population structure. Sperm whales are a matrilineal species consisting of stable social units of females and juveniles. The social transmission of information forms culturally distinct, and often sympatric, clans. In 2013, cultural groups experienced a large-scale relocation off the Galápagos where there was an entire replacement of two clans by two different ones that were previously absent from the Galápagos. Although sperm whales are an adaptive species, there are a multitude of conditions that influence their movement, such as prey abundance. Prey abundance and distribution are affected by environmental shifts, such as the El Niño Southern Oscillation (ENSO) cycles. The reduced productivity associated with warm ENSO events decreases the feeding success of species, resulting in sperm whales to conserve their foraging strategies and move to areas where their prey intake is maximized. Here, we investigate sperm whale movement across temporal scales around the Galápagos between 2013-2014 and 2022-2023. Data was collected across four field seasons off the Galápagos from 2013-2023. Sperm whales were visually searched for during the day in which photographs were taken of individuals' flukes during encounters. Unique markings on the trailing edge of each fluke were used for individual identification. We used root-mean-square (RMS) displacements to estimate movement rates across temporal scales around the Galápagos. It is expected that clans will display different movement patterns, supported by preliminary results concluding that the Plus-one clan had greater displacements over all time scales than those of the Regular clan. To investigate the relationship between RMS and local environmental conditions, a generalized linear model was used in which RMS was a function of defecation rate. It is expected that because low defecation rates indicate that whales spend more time traveling to new areas with higher prey abundances, poor oceanographic conditions will result in larger displacements. This research contributes to our understanding of whether Galápagos sperm whales photoidentified during the 2013 cultural turnover are present in the same region during 2022-2023.

Identifying The Glacial Lineage Of North Mountain Brook Trout (*Salvelinus fontinalis*): A Mtdna Study

Author: Meg Smith
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Supervisor(s): Dr. Daniel Ruzzante, Biology Department, Dalhousie University
Dr. Lisette Delgado, Biology Department, Dalhousie University

Abstract

Brook Trout (*Salvelinus fontinalis*), a salmonoid native to northeastern North America, is among the most popular species for recreational angling in the Canadian Maritime provinces. A recent study examining the nuclear genome of nine Brook Trout populations in North Mountain, Nova Scotia revealed the presence of several potential chromosomal inversions in the three westernmost populations. This project aims to determine whether the restricted occurrence of these putative inversions may be due to the presence of two or more glacial lineages among North Mountain Brook Trout, with one supplying the putative inversions to the western streams. To this end, whole mitogenome sequences from 192 Brook Trout representing the nine North Mountain populations were analyzed. Thirty unique mtDNA haplotypes were identified, with 26 being unique to a single population and the remaining four shared only among streams in close geographic proximity. Five of these haplotypes contained individuals with putative inversions as well as individuals without the inversions. A neighbour-joining dendrogram showed all but one haplotype diverging on a single branch that was the sister to the Brook Trout reference mitogenome, suggesting all haplotypes descend from the same lineage. A median-joining haplotype network reiterated the likelihood of a single-lineage origin, having all but one haplotype joined to a single predicted founding haplotype by 1-7 mutational steps. The outlying haplotype, a rare (N=2) haplotype from the easternmost stream, differed from the putative founder by 74 mutational steps. Considering just the CO-I and part of the NADH-I coding regions, this outlying haplotype was found to be identical to another identified in Newfoundland and parts of Labrador. These findings support the conclusions made by other phylogeographic studies on Brook Trout which suggest a single lineage likely colonized most of the Canadian Maritimes, though the nature of the outlying eastern haplotype remains unclear. We further conclude that the putative inversions identified in the western North Mountain populations are unrelated to refugial lineage and more research will be necessary to determine their age and origin.

Presence Of Pathogens In Deer Ticks In Halifax Regional Municipality

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James Kho, PhD candidate. Biology Department, Dalhousie University

Abstract

The deer tick (*Ixodes scapularis*) is known to be a vector for at least 16 human pathogens including *Borrelia burgdorferi* (Lyme disease), *Babesia* spp. (babesiosis), *Anaplasma phagocytophilium* (anaplasmosis), and Powassan virus (*Powassam encephalitis*). The population of *I. scapularis* in Nova Scotia has been increasing in recent years and is expected to continue to rise. Approximately 250 ticks were collected around the Halifax Regional Municipality in Nova Scotia between June and October 2023. Through DNA and RNA extraction, PCR and RT-PCR, and gel electrophoresis, the ticks are each being tested for *B. burgdorferi*, *A. phagocytophilium*, *Babesia* spp., and Powassan virus. Significant correlations between pathogen prevalence, sex, and location will be analyzed using chi-square contingency tests, chi-square goodness of fit tests, and linear regressions. Due to previous data about range expansion and increasing prevalence, it is expected that the prevalence of all pathogens will increase compared to studies performed in previous years. The results from this study will be compared to previous studies in the area and will provide a recent estimate of prevalence of tick-borne pathogens within deer ticks in Nova Scotia.

Investigating The Effect Of Spermidine On Chemotherapy-Induced Oral Mucositis In A 2D Co-Culture Model

Author: Kylie Van Dyke
Programme: Major in Biology (Honours), Minor in Psychology
Supervisor(s): Dr. Brendan Leung, Department of Applied Oral Sciences, Dalhousie University

Abstract

Chemotherapy-induced oral mucositis (CIOM) is a painful and debilitating condition characterized by inflammation and ulceration of the oral mucosa. CIOM can result in compromised nutrient intake, increased hospitalization, and a higher incidence of local and systematic infections. CIOM affects approximately 20-40% of all patients treated with chemotherapy. Despite the prevalence of CIOM, there is still a lack of effective treatment options. Spermidine is a natural polyamine present in all living organisms and an integral component of the human diet. Recent studies have found that spermidine serves as a potential adjunctive therapy for Inflammatory Bowel Disease (IBD) in mice by upregulating the spermidine oxidase (SMOX) enzyme, which promotes the action of inflammatory macrophages of the large intestine. The oral mucosa and the intestinal mucosa share multiple physiological similarities; therefore, I hypothesize that spermidine will mediate the effects of CIOM by increasing cell viability in a dose-dependent manner. An epithelial monolayer of human oral keratinocytes (OKF6/TERT-2) will be treated with doxorubicin chemotherapy to characterize CIOM-like damage and create a standard curve. Different spermidine concentrations will be added to the cell media to observe dose-response and time course effects on the attenuation of CIOM-like damage. Untreated OKF6/TERT-2 cells and OKF6/TERT-2 cells only treated with spermidine will be established as controls. Cell viability will be assessed via alamarBlue assay. If spermidine mediates cell viability, an aqueous two-phase system will be established to compare the effects of spermidine in solution to spermidine-expressing yeast on the attenuation of CIOM-like damage. In previous studies, yeast has demonstrated potential as a sustained biomolecule delivery system with increased residence time and sustained local concentration. Therefore, I expect spermidine-expressing yeast to prolong the viability of OKF6/TERT-2 with CIOM for longer than when treated with spermidine in solution. This research may characterize spermidine as a potential adjunctive therapy for patients with CIOM and demonstrate the use of spermidine-secreting yeast as a prolonged delivery system.

Genomic Analysis Of The Bacterium *Roseibium aggregatum* And Its Role As A Symbiont Of *Oxyrrhis marina*

Author: Shwayam Vinayak
Programme: B.Sc. Biology Honours & Co-op
Supervisor(s): Dr. Claudio Slamovits, Biochemistry Department, Dalhousie University
Alexander Mora Collazos- PhD Candidate, Dalhousie University

Abstract

This research explores the interaction between *Oxyrrhis marina*, a model dinoflagellate extensively researched in the past, and *Roseibium aggregatum*, an unexplored bacterium found within its microbiome. This project firstly aimed to expand the understanding of this model organism and its symbiotic relationships, and secondly to explore the genome and characteristics of *R. aggregatum*. Preliminary conclusions indicate the possibility of a mutualistic symbiotic relationship between *O. marina* and *R. aggregatum*. Further, while analysis is ongoing, the results hint at potential roles of *R. aggregatum* in biogeochemical cycles, and bioremediation. Using tools of genomics and microbiology, nanopore sequencing of *R. aggregatum* was performed to generate an annotated genomic map to explore regions of lateral gene transfer. The bacterium's metabolic pathways were reconstructed and studied to explore interesting features with potential applications in natural and industrial processes. Comparative genomic tools such as pangenome and phylogenetic analysis were used to compare our strain with others that have been previously sequenced worldwide. Following the establishment of its genome and general characteristics, the symbiotic relationship between *R. aggregatum* and *O. marina* was studied. Chemotaxis observations, along with the impact on mutual growth when co-cultured was noted. Lastly, future work in this project will explore specific genes and complementary metabolic pathways involved in symbiosis to better quantify their relationship. Analysis revealed that the *R. aggregatum* genome has 6.5 million bp, and two plasmids, with 57% genes having a known function. Various potential regions of lateral gene transfer were identified, providing an explanation for its characteristics including resistance to 14 antibiotics, and the ability to be resistant to heavy metals including mercury and chromium. The bacterium lacks the Entner-Doudoroff pathway, and 6-phosphofructokinase, making it incapable of metabolizing sugars. It possesses sulfur and nitrogen metabolism indicating potential roles in biogeochemical cycles. Further, it also possesses genes for biosurfactant synthesis. Compared to other strains, 60% of its core genome is shared, while 40% remains distinct (i.e., accessory genome). Observations of interactions of *O. marina* towards *R. aggregatum* reveals positive chemotaxis, and a positive effect on mutual growth when co-cultured.

At-Sea Associations In An Upper-Trophic Level Predator, The Grey Seal (*Halichoerus grypus*)

Author: Monica Wright
Programme: Marine Biology
Supervisor(s): Dr. Damian Lidgard, Fisheries and Oceans Canada

Abstract

The advent of animal-borne telemetry receivers has opened up new avenues for studying species associations and social behaviour among large marine predators, such as pinnipeds. This study will use seven years of acoustic detection and GPS location data, and build upon previous research to examine spatial and temporal patterns of at-sea associations among grey seals on the Eastern Scotian Shelf and in the Gulf of St. Lawrence. From October 2009 and January 2016, 146 adult grey seals from Sable Island, Canada were deployed with Vemco Mobile Transceivers (VMT) and Satellite-GPS transmitters. Of these, 133 were recaptured and their units retrieved in the subsequent breeding season. Between July 2013 and July 2015, 18 grey seals were tagged at Brion Island in the Gulf of St. Lawrence with Bluetooth-linked VMTs and GPS transmitters. This technology allowed for the transmission of data collected by the VMT to the user via the ARGOS satellite system. An association between two individuals was characterized as a series of acoustic detections where the time between detections was >35 min. For every GPS archival point, bathymetry, travel speed, and behavioral state (slow or fast movement) were determined. Behavioural state was estimated using a hidden Markov model. While at sea, 89 seals had been involved in associations with other tagged seals, with a total of 10275 detections recorded in 4846 associations. The median number of detections per association was 2 (range: 1-123) and the median duration of an association was 0.08 h (range: <0.01-9.08 h). Preliminary results indicate that seals formed associations when they displayed slow movement on shallow offshore banks. These findings provide new insights into the social dynamics, foraging strategies, and marine habitat use of this upper-trophic marine predator throughout the year.