DALHOUSIE UNIVERSITY

37th Annual

Cameron Conference

FOR BIOLOGY & MARINE BIOLOGY HONOURS STUDENT RESEARCH

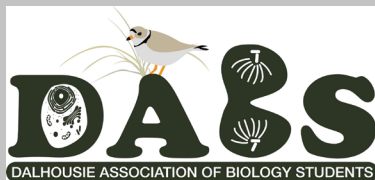### Saturday
11 February 2023
9:00 am - 12:30 pm

Sponsored by the Department of Biology

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Dalhousie Association of
Biology Students

Dalhousie Association of
Marine Biology Students

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DAMS

On the Origin of the Cameron Conference

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

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

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

Thanks to Professor Brian Hall for this synopsis

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

Third Floor Atrium
Life Sciences Centre

9:00 am
Conference Welcome

Professor Sophia Stone
Chair of Biology Department

9:10-10:10 ~ Poster Session 1

1	Hannah Bordin	An assessment of manual and machine learning methods for analyzing seagrass restoration success
2	Maddison Brown	Effect of cage design on growth and shell shape of cultured eastern oysters (*Crassostrea virginica*)
3	Hannah Charness	Juvenile kelp resilience and its role in Nova Scotian kelp bed recovery
4	Ashley Chiasson	Improved inference and analysis of the fungal DNA component within the microbial metagenome of pediatric oncology patients
5	Christopher Corriveau	Estimating age of Atlantic halibut (*Hippoglossus hippoglossus*) using whole genome methyl-sequencing

6   Sofia D'Angelo   Investigating the thermal biology of the orange-footed sea cucumber (*Cucumaria Frondosa*)

7   Matt Durant   Spatial co-occurrence of threatened groundfish in commercial fisheries highlight areas of conservation priority

8   Amelie Frappier   Biogeography of diazotrophs based on the *nifH* gene and genome availability

9   Émilie-Rose McBeath   Do foraging space requirements explain edge habitat associations and perch preferences of the Olive-sided Flycatcher (*Contopus cooperi*) in Nova Scotia?

10   Maclean Rivers   The role of Bcl-2 associated genes (BAGs) during programmed cell death in *Aponogeton Madagascariensis* leaves

11   Sophie Roy   Using biogeochemical markers to determine the colony of origin of Leach's storm petrels (*Hydrobates leucorhoa*) stranded on Atlantic Canadian oil platforms

12   Kylie Santella   Morphological and molecular characterization of Chlorellates isolated from the Gulf of St. Lawrence

13   Kennedy Whelan   Exploring the relationship between PML and YAP in KRAS mutated lung cancer

10:15 – 11:15 - Poster Session 2

14   Jenna Bustin

Effects Of low And high frequency noise on begging calls of nestling tree swallows (*Tachycineta Bicolor*)

15   Mikaela Ermanovics

Assessing the impact of simulated ocean alkalinity enhancement on phytoplankton in natural assemblages

16   Delaney Hicks

Addressing the inconsistencies between the catch and trade data for sharks and rays through updated estimates of conversion factors

17   Jensen Keltie

Investigating the impacts of ocean alkalinization on the composition of the microbial community in the Bedford Basin, NS, Canada

18   Zaina Lamontagne

Determining salinity influences on the growth of juvenile Atlantic whitefish (*Coregonus huntsmani*)

19   Kathleen McVittie

Fine-scale spatial distribution of northern bottlenose whale (*Hyperoodon ampullatus*) calves on the Scotian Shelf between 1988 and 2021.

20   Haran Prasad

Investigating the role of filamin in muscle elasticity and maintenance in *Drosophila melanogaster*

21 Karina Ricker

The effect of sex ratio on female reproductive success in Japanese medaka (*Oryzias latipes*)

22 Greg Santangeli

Environmental DNA detection of Atlantic salmon via the use of novel nuclear repeat-based primers

23 Alexis Savard-Drouin

Resilience of kelp beds to global change

24 Ellie Shaver

Investigating the breeding habitat occupancy of common nighthawks (*Chordeiles minor*) in Kespukwitk

25 Alison Tran

The response of XBAT35.1 in *Arabidopsis thalliana* to abiotic stress
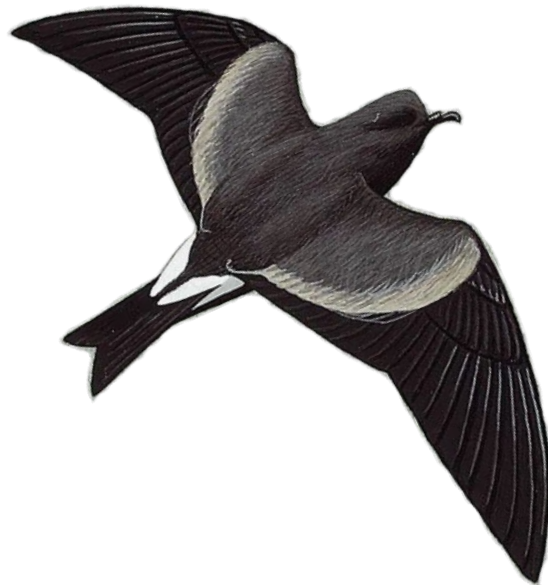
11:30 – 12:30
4-Minute Speed Talks

Session Chair - Dr. Patrice Côté

Aaron Judah	Functional integrity and vulnerability of shark and ray communities across the world's coral reefs
Ada Clarke	Post-mating reproductive isolation across eastern and western populations of *Lobelia cardinalis* (cardinal flower)
Sian Bryson	Predicting the seasonal growth patterns of Atlantic sea scallops (*Placopecten magellanicus*) for improved fishery management
James Simms	Examining the effect of a loss of function mutation on plant drought tolerance in *Arabidopsis thaliana*
Brogan Regier	Kelp distribution along the Atlantic coast of Nova Scotia
Anna Brailey	Effect of physiological condition and migration on breeding in Cassin's auklets and rhinoceros auklets on Triangle Island, British Columbia
Laura Keen	Climate vulnerability in Canadian marine protected areas (MPAs)
Riley Somerville	Noninvasive real time monitoring of liver fat content during ex-vivo machine preservation

Abstracts

LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME

An Assessment Of Manual And Machine Learning Methods For Analyzing Seagrass Restoration Success

Author: Hannah Bordin

Programme: Biology

Supervisor(s):   Derek Tittensor, Biology Department, Dalhousie University

Abstract

Seagrasses are submerged marine flowering plants that form large meadows in soft-sedimented and shallow coastal areas. There are over 70 species worldwide, living in both temperate and tropical bioregions. Seagrass meadows are both highly productive and biodiverse and perform important ecosystem functions including the provision of biogenic habitat, sequestering carbon, and protecting against coastal erosion. Despite their widespread importance, seagrass ecosystems have been experiencing rapid declines in recent decades due to a variety of human activities. The seagrass *Zostera marina*, commonly known as eelgrass, is both widespread and abundant in Atlantic Canada, and has been designated an Ecologically Significant Species (ESS). Eelgrass beds experience anthropogenic risk from coastal development, nitrogen runoff, invasive species, and climate change, among others. Given the ecological benefits of seagrass beds and their high rates of decline, active restoration efforts are essential in maintaining the long-term viability of these ecosystems. These methods need to be accurately monitored and analyzed to ensure their success, such as through analyzing field images of restoration sites and calculating the change in seagrass cover over time. My thesis examines a pilot seagrass restoration effort in Nova Scotia and compares trade-offs in methods for assessing restoration success. I evaluate three methods of manual image analysis and one machine learning approach (feature-extraction transfer learning) to assess machine learning for this type of study, and to determine the consistency and feasibility of these approaches. I find that estimates of cover are not significantly different among the three manual image analysis approaches. Ultimately, this project will compare the accuracy and effort of the machine learning approach to the manual image analysis approach.

Effect Of Physiological Condition And Migration On Breeding In Cassin's Auklets And Rhinoceros Auklets On Triangle Island, British Columbia

Author: Anna Brailey
Programme: Biology
Supervisor(s):   Dr. Glenn Crossin, Biology Department, Dalhousie University

Abstract

In migratory animals, experiences during one stage of the annual cycle can influence performance in subsequent stages via carry-over effects. Previous studies on seabirds have examined the physiological and nutritional factors related to breeding phenology, and whether these are subject to environmental variation and aspects of migration biology. In theory, individuals can modulate their behaviour and physiology in unpredictable environments to minimise migratory and phenological delays. However, studies regarding the association of physiology and carry-over effects in a range of seabird species have provided mixed results in terms of their significance and effects on breeding parameters. In this thesis, I use a large geolocation (GLS) tracking database to examine how individual variation in migration timing and speed, as well as physiological condition, affects the breeding phenology in two North Pacific seabird species, the Cassin's auklet (*Ptychoramphus aleuticus*) and rhinoceros auklet (*Cerorhinca monocerata*), breeding sympatrically on Triangle Island (50.86° N, 129.08° W) in British Columbia, Canada. Upon returning to the breeding colony, GLS loggers and feathers were collected from 27 Cassin's auklets and 27 rhinoceros auklets after 1 year, from 2014 to 2017. Feathers were assayed for corticosterone levels (fCort) and stable carbon (δ13C) and nitrogen (δ15N) isotope ratio measurements. Analysis of GLS tracks revealed a high degree of differential migration by the individuals of both species, with non-breeding migrations ranging from 100 km to 2 500 km away from the breeding colony. Preliminary analyses of rhinoceros auklet GLS data showed that the speed of return migration was greater in birds that over- wintered in areas further from Triangle Island. However, migration speed and distance had no detectable correlation with the physiological metrics. Positive associations were found between laying date and fCort, δ13C, and δ15N, suggesting that physiological condition directly affected phenology regardless of overwintering location. More extensive linear models, using several predictor variables and AIC model selection will be used to examine the effects of these variables on individual breeding fitness. Data for the Cassin's auklet will be forthcoming. This thesis strengthens our understanding of how processes in the migratory, non-breeding period can affect future fitness and reproductive success in migratory seabirds.

Effect Of Gear Type On Growth And Shell Shape Of Cultured Eastern Oysters (*Crassostrea virginica*)

Author: Maddison Brown

Programme: Marine Biology Co-op

Supervisor(s):   Dr. James Duston, Department of Animal Science and Aquacutlture, Dalhousie University

Abstract

Optimizing shell shape for commercial oysters has received little attention, although the value of uniformly shaped oysters can be up to 60% more per oyster compared to irregularly shaped. This study looks at the creation of optimal shell shape of Eastern oysters (*Crassostrea virginica*) for commercial use using BOBRs and traditional OysterGro gear. BOBR (benefit of being round), produced by Dockport LTD, is a new off bottom gear with a cylindrical shape for natural tumbling. Five BOBRs were filled with four litres of small oysters, and five with large oysters. Four litres of control oysters were placed in two OysterGro bags. The cages were held in the Robinson's Cove lease of Shandaph Oysters on Big Island Nova Scotia from June 29th until October 24th. Measurements of length, width, and depth were taken on June 29th, August 22nd, and October 24th. The Galtstoff index and a width/length index were calculated to assess shell shape . Hurricane effects caused the loss of data of OysterGro for October 24th measurements with potential effects on final measurements. Preliminary results show a mean Galtstoff index decrease of 0.09 for small sized, 0.05 for large sized, and 0.20 for control, indicating better shape in OysterGro cages. Further analysis of results is needed for statistical significance. These results could supply valuable information to maritime commercial farms about optimal gear usage for economic success.

Predicting The Seasonal Growth Patterns Of Atlantic Sea Scallops (*Placopecten magellanicus*) For Improved Fishery Management

Author: Sian Bryson

Programme: Marine Biology

Supervisor(s): David Keith, DFO, Bedford Institute of Oceanography

Nancy Shackell, DFO, Bedford Institute of Oceanography

Abstract

The Atlantic sea scallop (*Placopecten magellanicus*) fishery is one of the most significant fisheries in the Canadian Maritimes, accounting for a tenth of all seafood landings in the Maritimes Region by value. Over 75% of these scallops are harvested offshore on Georges Bank. Scallop growth varies with temperature, food availability, and depth; this contributes to significant seasonal and spatial variability in productivity. It is expected that condition factor (the relationship between meat weight and shell height) also varies seasonally, with low condition in the fall after spawning and high condition in the spring when food is abundant. When scallop condition is low, a larger number of scallops must be harvested to reach the weight-based fishery quotas. The increased effort required to land more scallop may also lead fishers to spend longer at sea, dredging the ocean bottom more often and increasing the impact on the benthic ecosystem.

Developing a better understanding of seasonal patterns in condition could lead to the development of novel management strategies that reduce these impacts and increase the efficiency of the scallop fishery. Using samples from commercial vessels collected by DFO from 1982-2009, we created monthly and annual models to predict scallop condition. A generalized additive model was used to model the relationship between meat weight and shell height for each month and for each year. These models were then used to extract a prediction of meat weight for a shell height of 100 mm (i.e., scallop condition).

We found that scallop condition is highest in the late spring and early summer (peaking in June) and lowest in October. These results are similar to findings for Atlantic sea scallop in other regions. Atlantic sea scallop spawn in the fall. During this time, energy is expended on reproduction instead of muscle growth, so the adductor muscle (the harvested "meat") atrophies. In the following spring, plankton in the North Atlantic typically experience a period of rapid population growth (referred to as the spring bloom). This bloom provides the nutrients scallop need to recover from spawning. Understanding these patterns can help improve the management of the fishery, both reducing environmental impacts and fishing effort.

Effects Of Low And High Frequency Noise On Begging Calls Of Nestling Tree Swallows (*Tachycineta bicolor*)

Author:	Jenna Bustin
Programme:	Marine Biology
Supervisor(s):	Dr. Andrew Horn, Biology Department, Dalhousie University

Abstract

Recent escalation of anthropogenic noise has led to increased research on how animal signals are affected by this disturbance. A frequent finding is that birds shift the frequency of their calls or songs to higher frequencies that might avoid the low frequencies found in most noise. Nestling tree swallows raise the frequency of their begging calls above low frequency noise, but whether they, or any passerines, can both raise and lower the frequency of their begging calls in response to higher or lower frequency noise has not been studied. In this study, a low frequency noise, high frequency noise, or a control treatment was played at tree swallow (*Tachycineta bicolor*) nest boxes, from when nestlings were 3 days old until they were 14 days old. The low frequency noise treatment overlapped with the bottom portion of the nestlings natural begging calls, and the high frequency noise overlapped with the upper portion of their calls, to determine whether the nestlings can actively adjust their calls to avoid certain frequencies of noise. Nestlings were recorded at day 7 and day 14, and the structure of individual begging calls were analyzed using Raven Pro software. Measured call parameters included average power density, bandwidth, duration at 90%, peak frequency, number of inflection points in the peak frequency contour (PFC), maximum and minimum frequencies in the PFC, and overall minimum and maximum frequency. At both nestling ages, no variables showed statistically significant differences across treatments, except for call duration in older nestlings at day 14, where call duration was significantly higher for nestlings raised in the high frequency treatment. Despite previous research findings showing changes in the frequency of begging calls when broad band white noise was played, our study showed no significant change in call frequency in either noise treatment. More generally, the shifts in call or song frequency that passerines often show in elevated noise are not necessarily adaptive responses to the frequency structure of the noise.

Juvenile Kelp Resilience And Its Role In Nova Scotian Kelp Bed Recovery

Author: Hannah Charness
Programme: Marine Biology
Supervisor(s):   Dr. Anna Metaxas, Oceanography Department, Dalhousie University

Abstract

The global decline of kelp ecosystems has resulted in the widespread loss of coastal ocean productivity and biodiversity. The deterioration of Nova Scotian kelp beds due to warming ocean temperatures and invasive encrusting bryozoan colonization has caused the collapse of Southwestern Shore (SWS) ecosystems, however, the Eastern Shore Islands (ESI) maintain functional kelp beds despite experiencing these pressures. Without a clear mechanism for their persistence, juvenile resilience and connectivity of beds through recruitment may be driving ESI kelp bed survival. We investigated the response of juvenile kelp from two dominant species after transplantation to sites in the ESI and SWS of Nova Scotia. Three resultant juvenile treatment types were studied: *Saccharina latissima* juveniles seeded from spores collected at the ESI (1) and from the SWS (2), and *Laminaria digitata* juveniles seeded from spores collected at the SWS (3). These treatment types were compared against unseeded substrates (Oceanite blocks) measuring natural recruitment and growth rates at the ESI. Growth rates and survivorship of all treatment types were lower at the SWS compared to the ESI. *S. latissima* kelp showed consistently higher growth rates and mean kelp lengths, while *L. digitata* exhibited higher survival rates. Treatment type influenced juvenile success, as kelp seeded from the ESI showed higher growth rates and lengths than those seeded from SWS. Unseeded blocks experienced lower growth rates and mean kelp length than *S. latissima* treatments, but showed high survival rates, similar to *L. digitata* treatments. These results suggest the presence of environmentally-driven, intra-specific genotypic and phenotypic variation in kelp populations along Nova Scotian coastlines. Studying patterns in juvenile kelp phenotypic deviation in response to environmental stressors furthers our understanding of how kelp are adapting to climate pressures. This data can be used to predict the potential resilience of kelp beds based on the state of juvenile populations, and indicates that juveniles seeded from healthy kelp beds are more likely to succeed when transplanted into stressed ecosystems compared to those seeded from collapsed beds. From these results, we can determine how the introduction of new juvenile populations can influence kelp bed connectivity and resilience.

Improved Inference And Analysis Of The Fungal Dna Component Within The Microbial Metagenome Of Pediatric Oncology Patients

Author: Ashley Chiasson

Programme: BSc Major in Biology (Honours), Minor in Psychology

Supervisor(s): Dr. Joseph Bielawski, Biology Department, Dalhousie University

Abstract

The human gut microbiome is composed of bacteria, archaea, eukaryotes, and viruses. A healthy gut microbiome is important for several processes, including metabolic functions and in regulating the immune system. The bacterial community and the effects of antibiotics on the microbiome have been studied in depth, however there is far less known about the fungal community and the effects of antifungal compounds. Understanding the fungal community within immune-compromised patients is critical, as fungal infections can be life-threatening in these patients. In addition, this population is subjected to frequent and repeated use of antifungals, which are known to impact the microbiome, and seem to increase the chances of secondary infection by other opportunistic pathogens. The greatest limitation to addressing this problem is the inability to identify and analyze fungal gene sequences within a patient's microbiome, largely because the reference genetic databases are less well developed for fungal microbes. This research is primarily investigating the hypothesis that the fungal component of cancer patient microbiomes differs significantly from healthy individuals and changes in response to patient clinical care. This will be tested by analyzing the relative frequency of fungal genes in metagenomes sampled from cancer patients before and during treatment compared to data sampled from healthy controls. The data used in this study include 283 stool samples collected from 101 pediatric patients being treated for acute lymphoblastic leukemia (ALL) or lymphoma at the IWK Health Centre, and were sequenced and processed in previous studies. To improve the classification of fungal DNA sequences within these data, analyses will be run using new DNA sequence classification software (Kraken2) to assign taxonomic labels to the metagenomic DNA sequences. The output of this will be analyzed with a goal of identifying sequences of fungal origin and improve the ability to make inferences about the fungal component of these patient microbiomes.

Post-mating reproductive isolation across Eastern and Western populations of *Lobelia cardinalis* (cardinal flower)

Author: Ada Clarke

Programme: Biology, Minor in Sociology & Social Anthropology

Supervisor(s): Dr. Mark Johnston, Department of Biology, Dalhousie University

Abstract

Reproductive isolation is one of the methods used by organisms to restrict the interbreeding of incompatible species. In crosses between incompatible plant species, there are a variety of outcomes that can indicate reproductive isolation: a seed is not produced, doesn't germinate, the early seedling dies, or the resulting plant is apomictic and unable to reproduce. Reproductive isolation is an important evolutionary indicator of speciation when observed in previously interbreeding populations.

The species *Lobelia cardinalis* is a geographically widespread herbaceous plant. Populations occur on both the eastern and western coasts of North America as well as northern Central and South America. The eastern and western populations are geographically isolated from each other, in addition to having different pollinators. *L. cardinalis* has previously been considered one species, however their genetic distance from each other has not yet been analyzed. This study examines reproductive crosses between and within the eastern and western populations in order to determine if reproductive isolation is occurring, and if so to what extent it affects individuals produced from these crosses.

Seeds from eleven different *L. cardinalis* populations and 44 different cross types (2816 total individuals) were measured and planted in a common garden experiment. Seed size (mm^2), germination time, early growth rate, and early fitness were measured to determine viability of offspring from different regional cross types within and between the eastern and western populations. Overall, this research will facilitate deeper understanding of reproductive isolation in *L. cardinalis*. Investigating the degree of reproductive isolation between populations will provide evidence for speciation between eastern and western populations.

Estimating Age Of Atlantic Halibut (*Hippoglossus hippoglossus*) Using Whole Genome Methyl-Sequencing

Author: Christopher Corriveau

Programme: Marine Biology

Supervisor(s):   Dr. Daniel Ruzzante, Biology Department, Dalhousie University

Abstract

Estimating the age of fish is a fundamental component of fisheries stock assessment models. Traditional methods in aging fish requires considerable time, expertise, and often employs lethal sampling. Epigenetic methods have emerged as a viable alternative, correlating chronological age and rates of methylation to produce an epigenetic clock. Methylation is the addition of a methyl group to the 5-Carbon of DNA base cytosine. Differentially methylated regions have been shown to have developmental and aging implications, with hypermethylated regions serving to suppress gene expression. This research is the first attempt to produce an epigenetic clock for Atlantic Halibut, an important commercially exploited groundfish. Tissue samples were collected from the caudal fin of 18 captive reared fish 4, 8, and 23 years old, for whole genome enzymatic methyl sequencing (EM-seq). Sequeing was performed on Illumina NovaSeq, paired-end 150-base pairs at 35x depth. An elastic net regression model will be used to identify the minimum number of methylated sites required to estimate the chronological age of Atlantic Halibut. In doing so, we hope to test the viability of existing epigenetic clock models on Atlantic Halibut, and provide a comparatively less invasive technique for aging. These data can be used to inform age structure dynamics in the fisheries stock assessment and conservation of Atlantic Halibut.

Investigating The Thermal Biology
Of The Orange-Footed Sea Cucumber (*Cucumaria frondosa*)

Author: Sofia D'Angelo

Programme: Marine Biology, Minor in French

Supervisor(s):   Dr. Ramon Filgueira, Marine Affairs Department, Dalhousie University

Shelby Clarke, Biology Department, Dalhousie University

Abstract

The orange-footed sea cucumber (*Cucumaria frondosa*) is the most common species of epibenthic sea cucumber in the North Atlantic. These animals are commonly consumed in luxury cuisine, however, rising market demands have led to the overharvesting of many species. Despite an emerging commercial fishery in the North Atlantic, many uncertainties concerning the growth rate and physiology of *C. frondosa* persist, particularly in regard to the effects of elevated temperatures. The objective of this study was therefore to determine the thermal biology of *C. frondosa* under current and future seawater temperatures. To accomplish this goal, the thermal response was studied by analyzing metabolic rates to determine the acclimated and acute response to rising temperatures. The acute response was examined by increasing water temperature from 4 to 16°C by 2°C per hour and metabolic rates were recorded every hour as temperature rose. To investigate the acclimated response, temperature was increased by 2°C per day to until the desired temperature was reached for four treatment groups (4, 8, 12 and 16°C). Upon reaching treatment temperatures, conditions were held for 14 days, and metabolic rates were subsequently recorded every hour for 24 hours. Together these experiments provide a detailed account of the thermal physiology of *C. frondosa* under elevated temperatures. This information can aid in the development of bioenergetic models and can assist in understanding the effect of temperature on the bioenergetics and growth in this species. This project fulfills the growing need to determine growth rates in response to changing environmental conditions to ensure the sustainable management of holothurian fisheries in the North Atlantic.

Title Of Talk Or Poster - Spatial Co-Occurrence Of Threatened Groundfish In Commercial Fisheries Highlight Areas Of Conservation Priority

Author: Matthew Durant

Programme: Marine Biology Co-op, Statistics Minor

Supervisor(s):   Dr. Nancy Shackell, Bedford Instutue of Oceanography

Dr. David Keith, Bedford Instutue of Oceanography

Abstract

Following significant collapses in the early 1990s, several groundfish stocks on the Scotian Shelf have continued to decline, with unintended bycatch in commercial fisheries raising pressing conservation concerns for now threatened species. To mitigate these concerns, new ecosystem-based management tools and a deeper understanding of the spatiotemporal relationships among species at-risk, their environment, and commercial fisheries is required. In this study, a generalized linear mixed model framework incorporating spatiotemporal random effects, was developed to model density patterns for three at-risk groundfish caught as bycatch in commercial fisheries (Atlantic cod *Gadus morhua*, American plaice *Hippoglossoides platessoides*, and White hake *Urophycis tenuis*), as well as two high value fisheries targets (Haddock *Melanogrammus aeglefinus* and Pollock *Pollachius virens*) across the Scotian Shelf, NW Atlantic. Spatiotemporal density predictions for at-risk groundfish between the years 2011-2020 were modelled using fisheries independent research vessel survey data, and overlaid with target species density predictions, to identify areas of high co-occurrence. Pre-collapse density estimates for at-risk groundfish (1983-1992) were also generated, to identify areas of historically important habitat, and compared to current estimates. Historically dense areas for all at-risk groundfish species were identified widely throughout the Scotian Shelf, while current spatial patterns were found to be more restricted around core habitats, most notably George's Bank, the Jordan Basin, and the Laurentian Channel. Areas of high co-occurrence between at-risk species and commercial targets were found to be concentrated across the western region of the Scotian Shelf, most notably on Emerald, George's, and Brown's Banks, suggesting an increased risk of bycatch in these areas. Discussed is the spatial relationship between bycatch and target species, as well as the limitations of current bycatch management efforts using at-sea observer programs. This framework was developed with the intention of broader use, and to provide fisheries management an additional tool to identify areas of potential conservation concern and improve fisheries regulation.

Assessing The Impact Of Simulated Ocean Alkalinity Enhancement On Phytoplankton In Natural Assemblages

Author: Mikaela Ermanovics

Programme: Biology & Ocean Sciences, Co-op

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

Abstract

I tested the potential impacts of Ocean Alkalinity Enhancement (OAE) on phytoplankton in the Bedford Basin in a mesocosm study. Ocean Alkalinity Enhancement is a process whereby an alkaline substance is added to the surface ocean to capture and store CO_2 as bicarbonate for thousands of years. According to the IPCC, we must not rely on carbon dioxide removal strategies such as OAE to restrict warming to the 1.5°C target set out by the 2015 Paris Agreement (IPCC 2022). Planetary Technologies, the industrial partner on this project, plans to use the Bedford Basin as the pilot site for this innovative technology. I deployed six mesocosms in the Bedford Basin with three duplicated treatments: a control, and alkaline treatments with 50 µM and 500 µM magnesium hydroxide additions. These correspond to target and 10x target concentrations for OAE and resulted in changes of 0.3 and 0.8 pH units, respectively. Incubations lasted only 24 hours because exposure to high concentrations of magnesium hydroxide in OAE will be transient as it is diluted by water flow. Mesocosms were sampled before and after the addition of magnesium hydroxide and again 24 hours later. Physicochemical parameters, including particulate and dissolved carbon pools, were measured; phytoplankton community composition and abundance were assessed by flow cytometry and chlorophyll-a content. Flow cytometric data was classified using a 5-dimensional matrix, after removing data bins influenced by magnesium hydroxide. Statistical tests for treatment effects on population structure (flow cytometric data) and chlorophyll-specific growth rates were tested using analysis of similarity (ANOSIM) and analysis of variance (ANOVA), respectively. At harvest, there was no significant difference in community composition between treatments ($p = 0.13$) nor between chlorophyll-specific growth rates ($p = 0.26$). There were significant differences ($p < 0.05$) in both community composition and growth rates between the start and end of the experiment. The phytoplankton populations grew rapidly but there was no detectable effect of alkalization on composition or growth rate. This study is an important first step in assessing the potential impact of OAE and demonstrates that it can be undetectable.

Biogeography Of The Dominant Diazotrophs Based On The *nifH* Gene And Genome Availability

Author: Amelie Frappier
Programme: Marine Biology
Supervisor(s):   Dr. Julie Laroche, Biology Department, Dalhousie University

Abstract

Nitrogen is often a limiting factor of ocean primary productivity. The synthesis of many bioorganic molecules essential for life, such as proteins and nucleic acids, requires nitrogen. One of the major processes controlling the inventory of bioavailable nitrogen in the ocean is nitrogen-fixation, which introduces new nitrogen into the food web of marine ecosystems. Nitrogen-fixation is performed by specialized bacteria and archaea referred to as diazotrophs. Diazotrophs are key microorganisms in the global nitrogen cycle because of their ability to fix atmospheric nitrogen into ammonia. Nitrogenase (*nifH*) genes are essential for nitrogen fixation and have historically been used to inform the biogeography of diazotrophs. Biogeographical studies of diazotrophs using *nifH* data have been conducted in the past, but with sparser datasets. Here, we re-examined the biogeography of diazotrophs in the ocean by creating one of the largest available *nifH* amplicon sequence variant (ASV) databases for marine environments. A total of 2822 globally collected water samples from past research expeditions supplemented with data from the scientific literature were used to create the database. The *nifH* ASVs were generated using PCR and Illumina sequencing, resulting in a total of 5 589 806 ASVs. To identify the ASVs, they were inserted in a reference *nifH* gene tree. The taxonomic identification by the reference *nifH* gene tree was tested by placing ASVs with known identifications in the tree. Preforming this test allowed us to identify the ASVs incorrectly identified or unable to be identified by this method and to ultimately improve our taxonomic identification by using GTDB to identify these ASVs. To identify the dominant diazotrophs, the database was reduced to contain only ASVs with a minimum number of reads and present in a minimum number of samples. Using this *nifH* ASV database, the biogeographical patterns and the temporal distribution of the dominant diazotrophs will be analyzed. The shared metabolisms amongst diazotrophs in specific areas will also be identified to investigate what other functions diazotrophs have in the environment. Through this research, we aim to better understand the distribution patterns and the roles of dominant diazotrophs in marine environments.

Addressing the inconsistencies between the catch and trade data for sharks and rays through updated estimates of conversion factors

Author: Delaney Hicks

Programme: Marine Biology, Honours

Supervisor(s): Dr. Aaron MacNeil, Biology Department, Dalhousie University

Dr. Chris Mull, Biology Department, Dalhousie University

Dr. Ana Martins, Biology Department, Dalhousie University

Abstract

Sharks and rays have been an important fishery resource for centuries; however, the demand and trade for shark and ray meat has increased globally over the past few decades. Despite some sustainable fishing, increased fishing pressure has driven the overexploitation of many shark and ray species. This overexploitation is concerning as sharks and rays are characterized by slow life histories meaning they are long lived, slow growing, and mature late, and once their populations are overfished recovery can take decades. With the increasing number of overfished sharks and rays, proper monitoring of global fisheries and trade is needed. Accurate estimates of individuals landed with reliable species identification are a key component of effective management. Landings are typically reported in live weight while trade data is reported in dressed or processed weight, making direct comparisons challenging. To alleviate discrepancies between the catch and trade databases, accurate conversion factors that can account for the differences between the live and various dressed weights are crucial. To date, there are only a limited number of conversion factors for sharks and rays, but with covariates such as depth, body length, weight, body plan and taxonomy, generalized conversion factors can be applied to other species that lack data. The goal of this project is to compile and review conversion factors for shark and ray species through a literature review and develop a statistical model to predict species and commodity specific conversion factors that can unify the catch and trade databases. Having conversion factors in place for individual species and their products will directly address inconsistencies between the landing and trade databases. Harmonizing these databases will allow for more accurate estimates of the number of individuals being fished and traded worldwide, providing important information to guide the management and conservation of sharks and rays. This project will provide managers with critical information for managing shark and ray populations globally.

Functional Integrity And Vulnerability Of Shark And Ray Communities Across The World's Coral Reefs

Author: Aaron Benjamin Judah

Programme: Marine Biology

Supervisor(s):   Dr. Aaron MacNeil, Department of Biology, Dalhousie University

Dr. Matthew McLean, Department of Biology and Marine Biology, University of North Carolina Wilmington

Dr. Christopher Mull, Department of Biology, Dalhousie University

Dr. Ana Barbosa Martins, Department of Biology, Dalhousie University and Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University

Abstract

Sharks and rays support many ecological roles in coastal marine ecosystems, however widespread overfishing and habitat loss have resulted in population declines, with over 59% of coral reef sharks and rays threatened with extinction. Despite the intrinsic vulnerability of shark and ray populations due to their life-history characteristics, such as slow growth, low fecundity and late reproductive maturity, shark and ray community structure from a trait-based approach has rarely been quantified. Here, we provide a global assessment of shark and ray functional community structure among 352 tropical coral reefs in 53 nations and regions across the world's oceans. We find that socio-economic and environmental conditions mediate shark and ray functional diversity, functional originality (the uniqueness of the community based on their traits) and functional specialization (the degree of representation of specialist trait combinations). Higher human population impacts drove changes in trait structure, favoring invertivores and benthic sharks and rays. Large-bodied, pelagic and benthopelagic, deep diving, piscivorous and higher order carnivorous species are also less abundant under increased human impacts. Biogeographically, Atlantic assemblages are more functionally original and diverse likely due to the high degree of isolation of oceanic islands across the tropical Pacific. Pacific assemblages are more represented by traits indicative of reef sharks rather than rays, such as fusiform morphology and pelagic or benthopelagic lifestyles. We uncover novel benefits from marine protected areas and restrictions as well as delineate priority taxa for conservation based on unique trait combinations and elevated extinction risk. Our findings illustrate the large-scale functional degradation of shark communities on coral reefs and identify management tools as powerful avenues for protecting shark and ray functional integrity.

Climate Vulnerability in Canadian Marine Protected Areas (MPAs)

Author: Laura Keen

Programme: Marine Biology

Supervisor(s): Dr. Ryan Stanley, Department of Fisheries and Oceans Canada and Bedford Institute of Oceanography
Dr. Christine Stortini, Department of Fisheries and Oceans Canada
Dr. Daniel Boyce, Department of Fisheries and Oceans Canada and Biology Department, Dalhousie University

Abstract

Anthropogenic actions are driving rapid climate changes in ocean ecosystems. While mitigating greenhouse gas emissions can slow the associated rate of change in global climate, ocean warming will likely continue for decades to come. Targeted adaptation and mitigation efforts enacted by governments offer some support to ecosystems and the functions they provide in a dynamic ocean. Marine Protected Areas (MPAs) are one management tool that can support these adaptation and mitigation efforts. MPAs, and networks of MPAs, offer spatial protections from harmful human activities, may promote resilience to climate change, and create carbon-sequestering biogenic habitats. Despite these applications, there remains no clear climate change objective for the Canadian MPA Network.

My project addresses this deficit by assessing vulnerability within Canadian MPAs. A literature review of global climate change policies in marine planning was conducted to evaluate Canada's progress in relation to other nations. This review revealed that while there were mentions of climate change in Canada's MPA plans, management actions did not directly address it; however this trend was indicative of a wider phenomenon whereby climate change is superficially addressed in MPA management. Next, data from an ecosystem vulnerability analysis was overlaid with Canadian MPA boundaries to assess representativity, specifically quantifying whether Canadian MPAs include the full spectrum of climate vulnerability within Canada's Exclusive Economic Zone. This assessment was conducted hierarchically within ocean basins, bioregions, and at the smallest scale within a draft network of conservation on the Scotian Shelf-Bay of Fundy bioregion. Distributional analyses indicate that MPAs tend to be placed in areas of lower vulnerabilities (ranging 0.25 to 0.4 on a 0-1 scale), particularly in the Arctic and Atlantic oceans and Arctic bioregions (Western Arctic, Eastern Arctic, and the Arctic Basin). Deepwater MPAs further from human impacts are overrepresented in the network which may contribute to this pattern. These findings suggest that the addition of MPAs where climate vulnerabilities are higher, particularly in shallower waters and the Arctic, would improve the overall representativity of climate and therefore should help to support greater climate resilience.

Investigating The Impacts Of Ocean Alkalinization On The Composition Of The Microbial Community In The Bedford Basin, NS, Canada

Author: Jensen Keltie

Programme: Marine Biology Co-op

Supervisor(s):   Dr. Julie LaRoche, Biology Department, Dalhousie University

Abstract

Ocean alkalinization is a negative emissions strategy that proposes the addition of alkaline substances to the ocean's surface to enhance its ability to sequester carbon dioxide from the atmosphere. Ocean alkalinization is a promising strategy for mitigating global warming, but its impact on the marine microbial community, especially prokaryotes, is poorly understood. Furthermore, the development and implementation of large-scale ocean alkalinization technology will take years to bring to fruition, during which the oceans will continue to warm, possibly by up to 4 °C at the end of the 21st century. To investigate the effects of simulated ocean alkalinization and warming on the composition and relative abundance of the marine microbial community, incubation experiments were performed on a monthly basis using water sampled from the Bedford Basin, NS, Canada. Seawater was sampled from the Bedford Basin at a 1 m depth, dosed with magnesium hydroxide at concentrations of 0, 100, 500 uM to increase its alkalinity, and incubated for 48 hours at either the ambient temperature of the Bedford Basin or the ambient temperature plus an additional 4 °C to simulate future warming. Samples were collected at 0 and 48 hours for DNA sequencing, pH and dissolved inorganic carbon (DIC) analysis. The preliminary results for changes in the relative abundance of microbial species between magnesium hydroxide concentrations and temperatures will be presented.

Determining Salinity Influences On The Growth Of Juvenile Atlantic Whitefish (*Coregonus huntsmani*)

Author: Zaina Lamontagne

Programme: Marine Biology Co-op; International Development Minor

Supervisor(s): Dr. Paul Bentzen, Biology Department, Dalhousie University

John Batt, Aquatron Laboratory, Dalhousie University

Abstract

The Atlantic Whitefish (*Coregonus huntsmani*) is a critically endangered anadromous salmonid endemic to Nova Scotia. As a basal representative of the *Coregonus* genus, its extinction would mean a loss of genetic diversity. The only surviving population of the species was confined by an unpassable dam to three lakes in the Petite Rivière watershed for 100 years, but even following the addition of fish passages in 2012, there is little evidence of use by Atlantic Whitefish. One recovery goal under the Species at Risk Act is restoring anadromy, but there has been little research on anadromy in Atlantic Whitefish. The limited knowledge that exists of wild anadromous Atlantic Whitefish comes from a population in the Tusket-Annis River watershed, now extirpated. Captive Atlantic Whitefish, however, have been shown to tolerate full seawater as larvae and prefer it as juveniles. Anadromy may result in larger individuals, as seen in the Tusket-Annis population, and this is consistent with some but not all anadromous salmonids. Before attempting to restore anadromy, understanding how migration into seawater may affect their growth is important. To determine if salinity affects the growth of juvenile Atlantic Whitefish, 90 captive-born fish were grown in marine, brackish, or fresh water. Lengths and weights of the fish were recorded over nine weeks after a week-long acclimation period. Data were analyzed using one-way ANOVA tests to compare treatments, and when necessary, Kruskal-Wallis post-hoc tests were used to determine which comparisons were significant. If salinity has no effect or a negative effect on growth in juvenile Atlantic Whitefish, this may indicate there are other factors impacting Atlantic Whitefish's preference for seawater. If salinity has a positive effect on growth, this could provide a possible explanation for their preference for full seawater and more evidence that anadromy is favourable for the species. The data from this study, independent of the result, will provide more information for recovery projects, like restoring anadromy for the species.

Do Foraging Space Requirements Explain Edge Habitat Associations And Perch Preferences Of The Olive-Sided Flycatcher (*Contopus cooperi*) In Nova Scotia

Author: Émilie-Rose McBeath
Programme: Biology
Supervisor(s):   Dr. Cindy Staicer, Biology Department, Dalhousie University

Abstract

The Olive-sided Flycatcher (OSFL; *Contopus cooperi*) is a landbird species at risk that, in Nova Scotia, breeds mainly in managed forests. Tools for species at risk conservation include Beneficial Management Practices (BMPs), such as recommendations to conserve specific habitat features during forestry operations. However, BMPs for this species are currently lacking important details. We need quantitative data to determine the heights, density, and spatial patterns of live and dead trees (snags) that should be left on site when harvesting forests in Nova Scotia. The spatial structure of trees, snags and open spaces in OSFL territories have not yet been quantified, but likely reflect the requirement for foraging space. OSFLs are aerial insectivores, feeding solely on flying insects by sallying from exposed perches at treetops. To forage for insect prey, OSFL appear to need a certain amount of open space, as well as tall coniferous or dead perches along the edges of these open areas. The purpose of this study is two-fold: to assess whether OSFL foraging space requirements explain their edge habitat association and perch preferences, and to specify residual tree structure, composition and spacing, and snag retention in the forestry BMPs for OSFL in Nova Scotia. Behavioural observations of birds (n = 14) collected across Nova Scotia were used to quantify perch preferences. Results showed that 91% of the time OSFL perched at the top of trees, 82% of which were adjacent to clearings. Of the chosen perch trees, 28% were snags; of the live trees used as perches, 70% had dominant crowns (i.e., taller than surrounding canopy) and 19% had broken or dead tops. Average perch heights were 16.3 m. Vegetation transects were collected in 16 OSFL territories to summarize habitat characteristics. Results showed that the forest was spruce-dominated, and that 31% of standing trees were snags. The spatial arrangement of trees and snags along the transects will be quantified using Spatial Point Pattern Analysis. Available foraging space will be quantified from the 3D structure of the transect data.

Fine-Scale Spatial Distribution Of Northern Bottlenose Whale (*Hyperoodon ampullatus*) Calves On The Scotian Shelf Between 1988 And 2021.

Author: Kathleen McVittie

Programme: Marine Biology

Supervisor(s):   Dr. Hal Whitehead, Biology Department, Dalhousie University

                     Sam Walmsley - PhD Candidate, Dalhousie University

Abstract

Healthy offspring are key for population growth but require a large energetic cost for the mother across a wide range of taxa. One possible strategy a mother could implement to reduce energetic expenditure when raising their offspring is to move to preferable habitats, away from individuals without offspring. Studying movement behaviour, however, can be challenging as some animals cover 1,000s of kilometers when migrating and, like cetaceans, are unable to be tagged and tracked for long periods of time. While spatial segregation and habitat preference in parent-offspring (calf) pairs is seen in a selection of cetaceans -whales, dolphins, and porpoises- in frequented locations, we are missing information in most whale species as to mother-calf spatial behaviour. Beaked whales (Family Ziphiidae) are arguably the least studied mammal group due to evasive behaviour patterns, but the endangered Northern Bottlenose whale (*Hyperoodon ampullatus*) display permenant site fidelity off the coast of eastern Canada on the Scotian Shelf, allowing for consistent data collection. This paper looks to understand if calf presence in a group influences spatial behaviour of Northern Bottlenose whales and address if groups with calves have a preferred habitat and if groups with calves are spatially distanced from groups without. Data was collected across 22 field seasons spanning 1988-2021 off the Scotian Shelf in three submarine canyons; the Gully, Shortland, and Haldimand. Sightings of Northern Bottlenose whales (n=2144) with group composition - number of calves, males, and adults- were recorded along with latitude and longitude. Preliminary results of generalized linear mixed models found calf sightings were highest in the Gully ($p < 0.001$) while Shortland ($p < 0.01$) had more no-calf sightings. These results suggest evidence of groups with calves displaying canyon preference across the Scotian Shelf. With better understanding of inter-canyon movement, fine-scale statistical analyses are being conducted from data gathered in the Gully using kernel density estimates and distribution overlap indices. Increasing our knowledge of spatial patterns in Northern Bottlenose whale calves not only aids in the protection of the endangered species, but also furthers our understanding of how population success and fitness are influenced through parent-offspring pair movement.

Cultural and temporal variation in abundance of fluke markings across four decades for sperm whales (*Physeter macrocephalus*) found off the Galápagos Islands

Author: Andreanne Paul-Chowdhury

Programme: Marine Biology

Supervisor(s):   Dr. Hal Whitehead, Biology Department, Dalhousie University

Ana Eguiguren and Elizabeth Zwamborn, PhD Candidates Whitehead Lab

Abstract

Sperm whales (*Physeter macrocephalus)* are a matrilineal species, in which stable "social units" of females and their offspring interact with conspecifics with their culturally and vocally distinctive clan. For research purposes, individuals are identified by the unique set of markings found along the trailing edge of their flukes, which are thought to be the result of social interactions with other sperm whales as well as other cetacean species and predators. However, it is unknown whether there is any variation in the type or abundance of markings between different clans or within clans over time. Four decades of photo-identification data was used to identify individual sperm whales and their respective markings off the Galápagos – from the 1980s-90s consisting of the Regular and Plus-one clans (n=1967) and the 2010s-20s consisting of the Short and Four-Plus clans (n= 915). We used a contingency table to compare mark rates and types between clans. A Chi-square test was then used to test if differences observed were statistically significant. For comparing mark rates across years, we used a generalized linear model (GLM) with a Gaussian distribution in which rates for each mark type were modelled as a function of year and clan. If whales are subjected to differences in mark-contributing social behaviours or predation pressures across clans, then we would expect to find a significant difference in marking types and rates between clans. In terms of temporal variation, if these markings are from interspecific interactions between sperm whales or predators and whales do not face significant changes in type or frequency of these events across time, then there should be no significant difference in marking over time. This research contributes to our understanding of the differences in culture between sperm whale clans, particularly as related to social interactions and predation pressures.

Investigating The Role Of Filamin In Muscle Elasticity And Maintenance In *Drosophila melanogaster*

Author: Haran Prasad

Programme: Biology

Supervisor(s): Dr. Nicanor Gonzalez-Morales, Biology Department, Dalhousie University

Abstract

The current study aimed to investigate the mechanistic role of Filamin, a protein encoded by the cheerio (Cher) gene, in muscle elasticity and maintenance in *Drosophila melanogaster* (fruit flies) which are widely accepted as a model organism in scientific research. Cheerio tends to be the only active gene that encodes for this protein. Our study employed the use of *D. melanogaster* as an experimental model, as it is inexpensive, has a short life cycle, fast generation times and are amenable to genetic manipulation. The genome of *D. melanogaster* shares a significant degree of homology with human genes, making it a suitable model organism to study muscle elasticity and maintenance. The primary focus of this study was to examine the function of Filamin, a member of the highly conserved scaffolding protein family, in muscle development. To test the role of Filamin in muscle elasticity and maintenance, thoracic muscles were obtained from 14 filamin mutants and a control group of fruit flies. The samples were then analyzed using Atomic Force Microscopy (AFM) to understand the mechanical properties and structure of the myofibrils. Furthermore, each Filamin mutant and the control were placed in a custom 3D printing tool for wing beat analysis. The results of the study indicate that Filamin plays a crucial role in the elasticity and maintenance of the muscles. The wing beat frequency analyses revealed a correlation between Filamin and muscle elasticity and maintenance. The analyses shows a higher correlation value between the two wings for the control fruit fly, and shows lower correlation values as the Ig-domain deletion size increases from Filamin[ΔIg22] to Filamin[ΔIg14-21] . These are supported by the AFM data which indicate high elasticity values for the control, and decreases as the Ig-domain deletion size increases. These results have implications in understanding human muscle disorders such as Muscular dystrophy and Myasthenia gravis and could potentially benefit from the enhancement of muscle reconstruction properties.

Kelp Distribution Along The Atlantic Coast Of Nova Scotia

Author: Brogan Regier

Programme: Marine Biology

Supervisor(s): Dr. Anna Metaxas, Oceanography Department, Dalhousie University

Dr. Craig Brown, Oceanography Department, Dalhousie University

Abstract

Over the past three decades, warming ocean temperatures have threatened kelp beds around the world. This has resulted in a decline in kelp biomass off the coast of Nova Scotia and a shift from productive kelp beds to turf-covered barrens. Since kelp ecosystems provide a variety of benefits, such as coastal protection and serving as important habitats for many species, it is crucial to understand the current state of their distribution and abundance. The Metaxas lab has developed a model for the Atlantic coast of Nova Scotia to predict where kelp is likely to occur based on a variety of habitat suitability factors, such as substrate type, depth, and relative exposure. The output of this model is a map that displays areas of the ocean or "patches" with the necessary conditions for kelp growth and survival. In order to validate the model, I used a drop camera system to collect underwater video footage at a variety of locations throughout the model's range. These videos were then processed with percent cover analysis and the data was used to designate each model-derived patch as either occupied or unoccupied by kelp. Each occupied patch was also assigned a confidence level of either high, medium, or low based on the quality and type of data that was used. This will allow me to map the current state of kelp beds along Nova Scotia's coast as well as compare the current distribution to historical data. Gaining insight into kelp bed distribution is vital, since it has the potential to inform the placement of marine protected areas that not only protect the kelp ecosystems themselves, but also the socioeconomic and ecological benefits that they provide.

The Effect Of Sex Ratio On Female Reproductive Success In Japanese Medaka (*Oryzias latipes*)

Author: Karina Ricker

Programme: Biology

Supervisor(s):   Dr. Laura Weir, Biology Department, Dalhousie University

Abstract

Behavioural interactions during mating are often influenced by the social environment and may ultimately impact survival and reproduction of individuals in a population. In Japanese Medaka (*Oryzias latipes*), mating behaviour varies predictably based on the relative number of males and females during mating (measured as the operational sex ratio (OSR)). Higher OSRs tend to be associated with higher levels of aggression and competition between males, and a decrease in male courtship behaviours. Female medaka also display more competitive behaviours and aggression towards other females in female-biased OSRs, along with an increase in courtship displays. However, these patterns of increasing aggression corresponding to increased male or female bias do not hold at highly male-biased sex ratios. Instead, in situations where males vastly outnumber females, males often resort to alternative mating tactics like scramble competition, as aggression becomes uneconomical many competitors. Female resistance behaviour also increases at high male densities, suggesting possible conflict between the sexes during mating. However, the extent to which these behavioral changes may affect female reproduction remains unknown. In this study, I investigate the possibility that operational sex ratios have an impact on female reproductive success as a factor influencing clutch size and frequency. To test this, fish were placed in sex ratios of 0.5, 1, 2, and 3, with 6 replicates of each sex ratio. Over the course of 2 months, tanks were checked for egg-bearing females who were identified by unique subcutaneous tags. For each female, the date and number of eggs produced was recorded. Fish were also measured before and after the experiment to investigate the potential effects of growth and size on fecundity. Preliminary data suggests little difference among female clutch sizes and frequencies for varying sex ratios, but more in-depth analysis is ongoing. The results of this study will help improve our understanding of reproductive strategies as well as how environment-dependent behaviours may influence female reproductive success.

The Role Of Bcl-2-Associated Genes (Bags) During Programmed Cell Death In *Aponogeton madagascariensis* Leaves

Author: Maclean Rivers

Programme: Biology

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

                       Nathan Rowarth (PhD Candidate)

Abstract

Programmed cell death (PCD) is a form of cell-mediated destruction that plays an essential role in developing plants and metazoans. PCD is well conserved across different lineages, but the molecular components of plant PCD are not as well understood. *Aponogeton madagascariensis*, commonly known as the lace plant, is a potential model for studying PCD in plants because of the highly predictable way it forms perforations during leaf morphogenesis. The Bcl-2-associated athanogene (BAG) family of proteins performs a wide variety of modulating functions for both plants and animals and have demonstrated some capacity to both positively and negatively regulate programmed cell death. The presence of suspected BAG protein transcripts in the lace plant was revealed via an RNA-seq analysis done by Rowarth et al. Analysis of transcriptomic data revealed the presence of several BAG gene homologs. Little is known about the role of BAG genes in plant developmental PCD. Of these homologs, BAG4 and BAG5 genes were chosen for this study because there is evidence that they may have pro-PCD and anti-PCD functions, respectively. This research has three main objectives: alignment of lace plant BAG genes to other eukaryotic BAG sequences and characterization of predicted peptide sequences based on domains/homology, probing for BAG4 and BAG5 genes by leaf stage using reverse transcription polymerase chain reaction (RT-PCR), and measuring chosen BAG gene mRNA accumulation in chosen leaf stages via quantitative polymerase chain reaction (qPCR). Our working hypothesis was that BAG4 would be more highly expressed in leaf stages that are not undergoing developmental PCD, while BAG5 would be more highly expressed in leaf stages that are undergoing developmental PCD. Partial and full-length primers were designed for BAG4 and BAG5 genes. Current results reveal the predicted domains and homology of the BAG4 and BAG5 genes, as well as the presence and predicted size of the BAG 4 genes. Ongoing work is focused on the quantification of gene expression by leaf stage. This research is important to elucidate the genetic processes underpinning plant PCD.

Using Biogeochemical Markers To Determine The Colony Of Origin Of Leach's Storm Petrels (*Hydrobates leucorhous*) Stranded On Atlantic Canadian Oil Platforms

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

Abstract

Leach's storm petrels (*Hydrobates leucorhous*) are pelagic seabirds that breed on offshore islands, many of which are located off the coast of Atlantic Canada. These birds play an important role in the marine food web because they spend most of their lives out on the open ocean foraging. This species' ecology is poorly understood, primarily due to its cryptic nature while at sea and its small size, but recent studies show that it undertakes trans-equitorial migrations through the Atlantic Ocean. However, population declines in Canada have led to a status listing of Threatened by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). The marine survival of petrels is presumed to be a main driver of these decreases. There are several potential causes, including natural and anthropogenic impacts. Anthropogenic stressors include exposure to petroleum products, as well as collisions with man-made structures, both of which are involved with offshore gas production in Atlantic Canada. Through monitoring efforts by Environment and Climate Change Canada (ECCC), it is known that hundreds of petrels die each year on oil and gas platforms off of Newfoundland. The 2020 COSEWIC Assessment Report identifies physical impacts with offshore oil production structures and supply vessels as a pervasive threat to juvenile storm petrels. At present, the identity and provenance of these juveniles is unknown. Knowledge on the origin of these birds would be useful for the development of mitigation strategies. Working with collaborators at ECCC, I am analysing the biochemical composition of feathers collected from dead juvenile storm petrels at oil and gas platforms. By comparing the biochemical signatures (trace elements- Al, Mn, Ni, Cu, Zn, Mo, Ag, Ba, Pb, U; stable isotopes- $\delta13C$, $\delta15N$) of feathers from the unknown petrels with those obtained from baselines in feathers collected from juveniles at 6 breeding colonies across Atlantic Canada, I will attempt to identify the provenance of unknown birds via a multivariate quadratic discriminant analysis. Analyses are ongoing, but preliminary exploration of the data are revealing distinct population groupings amongst the 6 colonies (baselines). I anticipate being able to assign a colony of origin to the unknown samples once feather assays are complete. I predict that many of the stranded juveniles will be from the colony at Baccalau Island in Newfoundland, as it is closest in proximity to the offshore oil platforms.

Environmental DNA Detection Of Atlantic Salmon Via The Use Of Novel Nuclear Repeat-Based Primers

Author: Gregory Santangeli

Programme: Marine Biology

Supervisor(s):   Paul Bentzen, Biology Department, Dalhousie University

Ian Bradbury, Department of Fisheries and Oceans Canada

Abstract

Environmental DNA (eDNA) analysis has recently emerged as an effective approach to detecting and monitoring aquatic organisms. However, the effectiveness of current eDNA methods is limited by the ability to detect eDNA in very low concentrations using published DNA primers that target mitochondrial DNA (mtDNA). For species of high importance, such as the Atlantic Salmon (*Salmo salar* L.), developing species specific primers with a high level of sensitivity is vital to ensure that data from eDNA-based conservation surveys is reliable and accurate. Here, we developed novel eDNA primers that target highly repetitive regions of the *S. salar* nuclear genome and determined their efficiency in comparison to conventional mitochondrial primers. We tested the detection limits of our primers using dilution series of genomic *S. salar* DNA samples in a controlled laboratory setting, as well as with samples of eDNA collected from environments containing captive and wild specimens of *S. salar*. Data collected showed that the lower detection limit of newly developed primers was over 100x smaller than that observed with mitochondrial primers. The nuclear repeat-targeting primers were able to reliably detect minute concentrations of *S. salar* DNA from both controlled mesocosms and from wild salmon in field samples. In all instances, nuclear primers were significantly more sensitive than mtDNA primers and retained similar levels of species specificity. Results highlight the increased sensitivity that nuclear repeat primers can offer for eDNA detection and emphasize the possible benefits associated with using nuclear repeat primers in future *S. salar* conservation efforts.

Morphological And Molecular Characterization Of Chlorellates Isolated From The Gulf Of St. Lawrence

Author: Kylie Santella

Programme: Marine Biology Co-op

Supervisor(s):   Dr. Caroline Chénard, National Research Council Canada

Abstract

Phytoplankton are the base of marine food-webs and are particularly sensitive to the effects of climate change. The group Chlorophyta is a taxon of green algae which are often predominant in temperate waters where their seasonal blooms provide bioavailable carbon and other nutrients to the community. Chlorophyta are also frequently used in biotechnology and pharmaceutical industry due to the unique carotenoids, vitamins, and fatty acids produced by their chloroplast. Despite their ecological and biotechnological importance, the Chlorophytes has few classified species and a general lack of knowledge regarding their biology.

Here, we characterized morphologically and genetically three novel species of Chlorophytes recently isolated from the Gulf of St. Lawrence (AGSB-0012, AGSB-0049, and AGSB-0055).

The phytoplankton strains were classified based on morphological assessment, and comparison of 18s ribosomal subunit RNA using Geneious software. The 18s ribosomal subunit and 28s ribosomal subunits were used to generate phylogenetic trees of each of the species. Phylogenetic analysis revealed that species can be clustered on trees with between 98% and 100% probability values, providing strong evidence that these species can be classified as *Nannochloris sp.* (AGSB-0012), *Droopiella spaerkii.* (AGSB-0049), and *Chlamydomonas sp.* (AGSB-0055). These genera are largely unclassified, with *Nannochloris* having only 2 accepted species.

Light microscopy was used to identify distinguishing external features and mean diameter per cell (n=20). AGSB-0012 were coccoid and 2.01μm in diameter, AGSB-0049 were oblong and 3.89μm in diameter, AGSB-0055 featured an eyespot and were 4.93μm in diameter. Morphological assessment classified AGSB-0012 as *Nannochloris sp.*, AGSB-0049 as *Droopiella sp.*, and AGSB-0055 as *Chlamydomonas sp.* based on their size, shape, and external distinguishing features. The isolated cultures were grown at 16°C with light bubbling and 16:8 hour light:dark cycle. Samples were measured using flow cytometry and instantaneous fluorescence readings. All three species achieve the growth peak on day 10.

Evidence suggests a strong relationship between the isolated strains and their respective classifications. The isolation and classification of these strains facilitates a stronger understanding of temperate phytoplankton biology. Further studies may focus on the role of these strains in their communities and how these strains can be used in biotechnology.

Resilience Of Kelp Beds To Global Changes

Author: Alexis Savard-Drouin

Programme: Marine Biology Co-op

Supervisor(s): Dr. Anna Metaxas, Oceanography Department, Dalhousie University

Abstract

Despite the recent worldwide declines in highly productive kelp ecosystems, the Eastern Shore Islands (ESI) in Nova Scotia, a temperate island archipelago characterized by high wave exposure, maintains luscious kelp beds amidst global changes. The goals of this study were to 1) understand if ESI kelp beds are resilient to warming waters and bryozoan invasions, and 2) uncover possible mechanisms behind this resilience for the two dominating kelp species: *Laminaria digitata* and *Saccharina latissima*. We investigated changes in density and canopy cover from October 2018 to November 2022 at six ESI sites with differing levels of wave exposure. Since high wave action coincides with kelp density and canopy cover, we sampled kelp at three sites across a gradient of wave exposures to measure blade tissue mechanical properties and kelp morphological characteristics. We found that although species lose canopy cover during the warmer months due to bryozoan outbreaks, thali density stays consistent every year, and kelp recover canopy cover over the winter. Seasonally, tissue strength increases from July to August for *L. digitata*, but decreases for *S latissima*. This coincides with peaks in bryozoan outbreaks. We also found signs of phenotypic plasticity for both species, indicating that wave action induces tissue elasticity. Overall, this study shows clear signs of resilience, as kelp beds in the ESI are persisting every year. We also uncovered a possible mechanistic explanation for the resilience of ESI kelp beds to current stressors: ESI kelp have stronger tissues than kelp from historical records which collapsed. As temperatures and the duration of bryozoan invasions continue to increase, persistent kelp beds could find refuge in areas of high wave action and species composition may shift to favour *L. digitata*.

Investigating the breeding habitat occupancy of Common Nighthawks (*Chordeiles Minor*) in Kespukwitk

Author: Ellie Shaver

Programme: Biology

Supervisor(s): Dr. Cindy Staicer, Biology Department, Dalhousie University

Abstract

Common Nighthawks (*Chordeiles minor*) are threatened landbirds that nest in open areas, including clearcuts and burned stands. No single threat to account for population declines has been identified, and there is no quantitative data on their habitat in Nova Scotia. The objective of the study was to determine what habitat factors best explain Common Nighthawk habitat occupancy in Southwest Nova Scotia. Knowledge obtained through this study can be used to prioritize conservation actions for this species in Nova Scotia.

Sixty-five forest sites harvested 1-15 years ago were sampled in Southwest NS. Autonomous Recording Units (ARUs) were used to detect wing-boom sounds, which are indicative of breeding males. ARUs recorded for every other 10 minutes at dusk and dawn for 14 days between July and August 2022. A wing-boom classifier built in KaleidoscopePro was created using 20 recordings from a control site with known breeding pairs. The number of classifier-detected wing-booms and the true number of wing-booms in recordings was highly correlated (r=0.88). This classifier was used to scan study site recordings to find wing-booms, signifying breeding evidence. The classifier was also used to quantify diurnal and seasonal patterns of wing-booms at the control site to validate the timing of samples at the 65 harvested sites.

To investigate the influence of habitat features on breeding site occupancy, quantitative variables were calculated in ArcGISPro for each site in an area around the ARU at a territory scale (250 m radius) and a landscape scale (1 km radius). Variables included average vegetation height and the proportion of the area comprised of forest, cleared forest, non-forest, wetlands, land with water-table of <0.5 m from the surface, waterbodies and developed areas. 'Distance to' variables were also calculated: distance from the ARU to the nearest waterbody, watercourse, wetlands, and land with water table <0.5 m from the surface. The final habitat variable was years since harvest.

To determine which habitat variables best explain breeding evidence, logistic regression will be used to model breeding evidence based on the presence or absence of wing-boom detections per site and various habitat variable combinations. Akaike's Information Criterion will rank identify the most-supported models for predicting breeding habitat occupancy. Results will be useful for identifying suitable breeding habitat for this species at risk in Southwest NS.

Examining The Effect Of A Loss Of Function Mutation On Plant Drought Tolerance In *Arabidopsis thaliana*

Author: James Simms

Programme: Marine Biology Honors

Supervisor(s):   Dr. Sophia Stone, Chair of Biology Department

Abstract

The ubiquitin proteasome system (UPS) is a conserved regulatory pathway found in eukaryotes that plays a key role in modulating the abundance of numerous proteins in the cell. Ubiquitin molecules in the UPS are used alongside enzymes, called E1s, E2s, and E3s, which facilitate the joining of a chain of ubiquitin molecules to a substrate protein; the chain acts as a flag for the 26s proteasome to degrade the target substrate protein. A multitude of different types of E2 and E3 enzymes allow for a vast number of combinations that can be used to target proteins for degradation, facilitating changes to the proteome that promote tolerance to abiotic stresses such as drought, flooding, cold, salt, or heat. This project is part of a larger study that aims to identify E3s that are involved in promoting tolerance to environmental stresses. The objective is to determine if the *Arabidopsis thaliana* (Arabidopsis) gene ARIADNE 11 (ARI11), which encodes for a RING-type E3, is involved in drought stress tolerance.

Arabidopsis plants with a ARI11 loss of function mutation were compared against a wild type in multiple trials to assess their capacity in tolerating various periods of drought from days to weeks. The growth and development of ari11 plants under standard conditions was also compared to wild type via measuring parameters such as rosette leaf size, number, shape, as well as bolt heights, and biomass. On a global scale drought is a devastating environmental challenge that we must face in fighting global food insecurity, as it is unpredictable and causes significant loss to agricultural production. A potential solution to this problem would be developing crops that are able to withstand drought while maintaining yield. By experimenting with Arabidopsis mutants such as ari11 we hope to better understand how plants can survive periods of drought and show a continuation of growth and subsequent yield. Extrapolating knowledge gained to agricultural crops would prove to be a significant step forward for the global food problem, which is expected to worsen over the next several decades.

Noninvasive Real-Time Monitoring Of Liver Fat Content During Ex-Vivo Machine Preservation

Author: Riley Somerville

Programme: Biology

Supervisor(s):   Dr. Boris Gala-Lopez, Transplant Surgery, Dalhousie University

                      Dr. Kevin Hewitt, Department of Physics, Dalhousie University

Abstract

Liver transplantation is a well-researched and tested treatment for Canadians that are living with end-stage liver disease. However, current liver supply is struggling to keep up with the number of patients that require a liver transplant, and poorer quality organs cannot be used since they are more susceptible to damage and failure post-transplantation. Machine perfusion is a new technology that is allowing livers to function outside of the body, while protecting them from any injury. A new, high-throughput Raman spectroscopy system developed by collaborators at Dalhousie University can quantify the fat in livers without the need of a traditional biospy, which is time consuming. By combining these two experimental technologies, we can non-invasively monitor the fat content of fatty lives that are preserved on machine perfusion, avoiding repeating biopsies that may damage the organ. Results will be validated against tissue and perfusate samples, and if successful, we expect to see that Raman measurements are equal or better to a traditional pathologist's rating of fat content over time. This will hopefully open a major door in being able to increase the number of organs available for transplant, by having an accurate, rapid reading of fat content on the spot, minimizing the subjectivity that exists in current techniques. This combo of medical technology will hopefully become a key metric in the future of liver transplantation and organ care.

The Response Of XBAT35.1 In *Arabidopsis thaliana* To Abiotic Stress

Author: Alison Tran

Programme: Biology

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

Abstract

Climate change has made it harder for plants to adapt to environmental stresses, which results in many societal problems, including the lack of food crops. To resolve the crisis, there is a need to understand how plants cope with these stresses in the first place. The ubiquitin-proteasome system (UPS) in plants has a role in modifying their biological processes according to the change in environment. This is done by degrading a specific ubiquitin-attached substrate by the 26S proteasome complex. This is a multi-stepwise process achieved by three enzymes: E1 (Ubiquitin activating enzyme), E2 (Ubiquitin-conjugating enzyme) and E3 (Ubiquitin ligase). This study investigates the role of the ubiquitin ligase XBAT35.1 in its response to abiotic stresses, heat, and high salinity, in various stages, using the model plant *Arabidopsis thaliana*. XBAT35.1 is an E3-type enzyme that is accompanied by its other isoform, XBAT35.2. Preliminary studies have shown that XBAT35.1 transcriptionally responds to high salinity and heat stresses. However, it has not been confirmed how it responds to these abiotic stresses. This is first done by testing the germination rate of XBAT35.1-Overexpressed seeds compared to the control seeds. Next, the root growth rate of young XBAT35.1-OE seedlings is determined in various environments. The first two are done in MS media while the adult stage is experimented with in soil environment.

Exploring The Relationship Between PML And YAP In KRAS Mutated Lung Cancer

Author: Kennedy Whelan

Programme: Biology

Supervisor(s):   Graham Dellaire, Department of Pathology, Dalhousie University

Abstract

Lung cancer is currently the leading cause of cancer death in Canada with about 30% of lung adenocarcinomas harbouring KRAS mutations. In many lung cancers, expression of the promyelocytic leukaemia (PML) protein, a tumour suppressor, is often down regulated. PML is essential for the formation of PML nuclear bodies (PML NBs) within the nucleus which are involved in many cellular pathways such as gene transcription, cellular senescence, apoptosis, and DNA repair. Using quantitative proteomics in PML knockout (PML KO) Lewis lung carcinoma (LLC) cells we identified a downregulation of several YAP target genes which are involved with cellular proliferation, suppression of cell differentiation, epithelial-to-mesenchymal transition, invasion, metastasis, and cell survival. In addition, it was discovered that YAP localization was defective in PML KO cells and tumours that grew from PML knockout cells grew smaller than wildtype cells in vivo. This was unexpected considering that PML is generally considered to be a tumour suppressor. Based on these observations, the relationship between PML and YAP was assessed and found to have a density dependent relationship with PML being upregulated at low density while YAP is nuclear in LLC, A549 and CMT64 cell lines. To support the current hypothesis that PML NBs positively regulate YAP transcriptional activity in KRAS mutated lung cancer cells, we aimed to characterize the density dependent phenotype in an additional cell line (CMT167), create a stable PML knockout in the CMT167 cell line and validate the density dependent PML phenotype in the CMT64 cell line with gene-edited clover-tagged PML CMT64 cells. Qualitative results of the immunofluorescence microscopy showed that the density dependent PML phenotype in CMT64 clover-PML cell was consistent with what was reported before, however the CMT167 cell line had the opposite result. These results showed that the number of PML bodies at low density in the CMT167 cell line appeared to be much lower than at high density and YAP appeared to be more cytoplasmic than nuclear. These studies will help further our understanding of the relationship between YAP and PML NBs in lung cancer and help us better characterize a novel and potentially oncogenic role for PML in the establishment and progression of lung cancer.