DALHOUSIE
UNIVERSITY

33rd Annual

Cameron Conference

FOR BIOLOGY & MARINE BIOLOGY HONOURS STUDENT RESEARCH

Saturday
9 February 2019
9:30 am - 4:00 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

Third Floor Atrium
Life Sciences Centre

9:30 am
Conference Welcome

Professor Paul Bentzen
Chair of Biology Department

9:40-11:00 Poster Session 1

1	Meagan Adams	Comparative Genomics Of The Bloom-Forming Alga *Aureococcus anophagefferens*
2	Emily Blacklock	Detection Of Paralytic Shellfish Toxins In *Homarus americanus* Through Alternative Non-Invasive Spectral Methods
3	Justin Brown	Exploration Of HlyU DNA Binding And Virulence Gene Regulation In *Vibrio parahaemolyticus*
4	Tovah Kashetsky	Does Performing A Cognitively Challenging Task Promote Neuron Survival And Neural Gene Activity In Zebra Finches (*Taeniopygia guttata*)?
5	Emily Kraemer	LAMP As A Tool For Rapid Detection Of *S. parasitica* In Salmonid Farms
6	Marco Lee	Waiting For What? Explaining Variation In The Timing Of Female Reproduction

7	Sara MacPhee	Transovarial Transmission Of Human Pathogenic Bacteria Between Mothers And Eggs In *Ixodes scapularis* And *Dermacentor variabilis*
8	Meghan Martin	Developmental Timeline Of Mitral Valve Chordae Tendineae Differentiation Using Anatomical And Thermal Analysis
9	Dayna Mikkelsen	Identifying Antimicrobial Resistance Genes In Uncultivated Bacteria And Archaeal Metagenome-Assembled Genomes
10	Keaton Sinclair	Low Pass Whole Genome Sequencing (LPWGS) For Structural Variant Detection In Multiple Myeloma Samples
11	Michael Williams	Optic Nerve Conductivity In A Mouse Model Of MS With Reduced Levels Of The Voltage-Gated Sodium Channel Nav1.6

11:05 - 12:05

Oral Presentations Session 1 - LSC 242

Session Chair - Dr. Patrice Côté

Zachary Ford	Developing A Novel Protocol For The Anaesthesia Of Zebrafish (*Danio rerio*)
Renata Serio	Expression Of *Arabidopsis thaliana* XBAT35, An E3 Ubiquitin Ligase, During Response To Abiotic Stress
Keryn Winterburn	*Crassostrea virginica* Mortality under Anoxic Conditions: Influence of Temperature and Secondary Bacterial Source
Cailyn Zamora	Determination Of Genome Size, Chromosome Number And Ploidy Level In *Aponogeton madagascariensis*

12:05 - 13:25

Steele Ocean Sciences Building Atrium
Potluck Lunch!

13:25-14:40 Poster Session 2

1	Thomas Baker	Testing And Refining Species Distribution Models For Three Landbird Species-At-Risk In Nova Scotia, Canada

2	Amanda Belanger	Habitat preference and use in Peruvian Amazon river dolphins: Boto (*Inia geoffrensis*) and Tucuxi (*Sotalia fluviatilis*)
3	Gabrielle Deveau	Acoustic Tagging To Document Atlantic Coast Residency Patterns And Inter-Year Site Fidelity Of Atlantic Torpedo Rays
4	Rhyl Frith	Mixotrophic Growth Of Commercially Valuable Phytoplankton Through Nutrient Remediation Of A Food-Grade Source
5	Alison Gladwell	Acoustic Monitoring Of Leach's Storm-Petrels (*Oceanodrama leucohora*) As An Index Of Nesting Density
6	Lauren Jackson	Determining If Non-Genetic Environmental Effects On *Avena barata* Individuals Result In Significant Spatial Patterns
7	Rebecca Jardine	Factors Impacting Nest-Site Selection In The Barn Swallow (*Hirundo rustica*)
8	Charity Justrabo	Assessing Impacts Of Tag Burden On Energy Storage Of Female Grey Seals Through Analysis Of Body Condition And Reproductive Output
9	Katherine King	Genetic Identification Of *Eubalaena glacialis* Prey Species In The Gulf Of St. Lawrence Using Fecal Analysis
10	Tor Kitching	A New Protein Mass Spectrometry-Based Method For Phytoplankton Abundance Assessments Applied On The Scotian Shelf

11	David Krug	Species Cover And Distribution Of Aquatic Invasive Species In Atlantic Canada Before And After An Extreme Temperature Event
12	Amy McAllister	Acoustic Click Patterns In Northern Bottlenose Whales (*Hyperoodon ampullatus*) Off Eastern Canada
13	Daniela Notte	Estimating Abundance Of Brook Trout (*Salvelinus fontinalis*) Populations In The North Mountain, NS Using Parent-Offspring Relationships
14	Heather Perry	Examining The Prevalence Of Alternative Reproductive Strategies In Male *Salmo salar* From Two Norwegian Rivers
15	Gabrielle Persad	Genetic Relationships Of The White And Common Forms Of The Threespine Stickleback In Nova Scotia
16	Alex Setchell	Assessing Anthropogenic Impacts on Plant and Lichen Communities in Nova Scotia's Forested Wetlands
17	Zacharye Simai	Characteristics Of Forested Wetland Habitat For Three Landbird Species At Risk In Nova Scotia
18	Annie Simons	Genetic Differentiation In *Percichthys trucha* Among Drainages In Patagonia
19	Anna Williams	Does Anthropogenic Noise Decrease Immune Response In Tree Swallow (*Tachycineta bicolor*) Nestlings?

20	Liz Woolaver	Maternal-Paternal Conflict In Cardinal Flower Populations
21	Jasmine Yeung	Photographic Sex Analysis Of Northern Bottlenose Whale (*Hyperoodon ampullatus*) Populations On The Eastern Canadian Continental Shelf

14:45 - 15:45

Oral Presentations Session 2 - LSC 242

Session Chair - Dr. Alan Pinder

Catalina Albury	Effect Of Vitamin B_{12} Starvation On Heat Resistance In *Fragilariopsis cylindrus*
Kyle d'Entremont	Estimated Changes In The Breeding Population Of Leach's Storm Petrels On Kent Island, New Brunswick And Factors Affecting Nest Site Selection
Andrea Gigeroff	Molecular Phylogeny Of Colponemids, An Evolutionary Significant Group Of Alveolates
Nicole Ure	Mark Density Of Cape Breton Long-Finned Pilot Whales (*Globicephala melas*) Using Drone Photography

15:45

Closing Remarks - Dr. Alan Pinder

Group Photo

16:00 to Late

Social Mixer!
Fifth Floor Lounge
Life Sciences Centre

Abstracts

LISTED ALPHABETICALLY

BY

AUTHOR'S LAST NAME

Comparative Genomics Of The Bloom-Forming Alga *Aureococcus anophagefferens*

Author: Meagan Adams
Programme: Biology
Supervisor(s): Dr. John Archibald, Biochem and Molecular Biology, Dalhousie University

Abstract

Aureococcus anophagefferens is a single-celled marine alga that causes detrimental algal blooms along the eastern coast of the United States as well as China. These blooms have resulted in the destruction of the coastal sea beds, causing the loss of much of the local ecology, leading to economic crashes due to its effect on the seafood industry. Despite its ecological significance, little is known about the biology and evolution of *Aureococcus* species. To better understand the genomic organization and evolutionary forces such as lateral gene transfer (LGT) that may be acting upon the species, the genome of *A. anophagefferens* strain CCMP 3368 was sequenced using short and long read technologies. The genome is being compared to the reference genome of strain CCMP 1998 to determine the differences in gene content among them and the underlying reasons. The goal of this project is to build a stronger foundation for further research of the evolution and presence of LGT of this species, as more genomes of *A. anophagefferens* become available in the future.

Effect Of Vitamin B_{12} Starvation On Heat Resistance In *Fragilariopsis cylindrus*

Author: Catalina Albury
Programme: Biology
Supervisor(s): Dr. Erin Bertrand, Biology Department, Dalhousie University

Abstract

Marine microbes play an integral role in global biogeochemical cycles, notably carbon fixation and export. Shifts in temperature and micronutrient concentration have been known to alter the rates of these processes. An improved understanding of microbial nutrient dynamics and their effect on primary productivity is essential for accurate predictions of ocean biogeochemistry in the face of a changing global climate. Past observations of the green temperate algae *Chlamydomonas* have demonstrated increased heat tolerance under high availability of vitamin B_{12}, which is used to catalyze the production of methionine, an essential amino acid. The purpose of this study was to determine how increased temperatures and B_{12} limitation affect the growth of *Fragilariopsis cylindus*, a psychrophilic diatom and key species in polar microbial assemblages. In the experiment, *F. cylindrus* cultures were exposed to B_{12} limitation and increased temperatures. Cultures were monitored for heat stress which was characterized by chlorosis, decreased F_v/F_m, and decreased growth rate. These markers of heat stress were observed in cultures exposed to elevated temperatures, regardless of the availability of B_{12}. The results of this study suggest that B_{12} availability may not result in increased temperature tolerance in *F. cylindrus*, raising questions concerning the differences in the role of methionine in heat tolerance amongst chomophytes and chlorophytes.

Testing And Refining Species Distribution Models For Three Landbird Species-At-Risk In Nova Scotia, Canada

Author: Thomas Baker
Programme: Biology Co-op
Supervisor(s): Dr. Cindy Staicer, Biology Department, Dalhousie University

Abstract

The Canada Warbler (*Cardellina canadensis*), Olive-sided Flycatcher (*Contopus cooperi*) and Rusty Blackbird (*Euphagus carolinus*) are three migratory landbird species that have experienced severe declines. During their breeding season in Nova Scotia, they are often found in wet, poor-nutrient sites, especially forested wetlands. Habitat protection is an important tool to provide breeding refuges for these species, yet locations of their critical habitat in Nova Scotia are unknown. Species distribution models (SDM's) can be used to identify critical habitat and project it geographically. SDM's for all three species were created in 2017 by Shannon Bale using occurrence data primarily from 2006-2010. These models cannot be used to identify critical habitat as they did not incorporate breeding evidence. This past summer I used point count and playback surveys to collect occurrence data for these three species. Building on surveys undertaken in 2017, I focused on the Eastern Shore region and Cape Breton, both areas with poor coverage in previous surveys. Playback surveys broadcast 30 s recordings of songs and calls of the respective species, which can often provoke a reaction from a bird that had previously been undetectable. Additionally, the behavior of the bird reacting to the playback was recorded for 5 min as this response can differ depending upon pairing status and breeding stage. Densities can be calculated from the point count surveys. Volunteer birders aided in collection of occurrence data by sending in their observations of the three species. Altogether 100 sites with Canada Warbler occurrences, 55 sites with Olive-sided Flycatcher occurrences and 17 sites with Rusty Blackbird occurrences were obtained in 2018. I have tested Shannon Bale's models by determining the probability of species presence that they predict for each of these occurrence points. Additionally, I am using the combined 2017 and 2018 occurrence data to create SDM's using Maxent software and reverse step-wise elimination. Maxent software estimates the relative probability of species presence by comparing environmental variables at occurrence points to those at 10,000 randomly selected background points. To test the models, I am using the Area under the Receiving Operator Curve (AUC) method. These new SDM's should better reflect the current status of these species, contribute to the identification of critical habitat, and identify important areas to protect.

Habitat preference and use in Peruvian Amazon river dolphins: Boto (*Inia geoffrensis*) and Tucuxi (*Sotalia fluviatilis*)

Author: Amanda Bélanger
Programme: Biology & Psychology
Supervisor(s): Dr. Andrew Wright, Bedford Institute of Oceanography

Abstract

The Peruvian Pacaya-Samiria National Reserve is a low-land tropical forest within the Amazon Basin inhabited by two sympatric cetaceans, the Pink River Dolphin / Boto (*Inia geoffrensis*) and Tucuxi (*Sotalia fluviatilis*). These animals are respectively considered endangered and data deficient by the IUCN. There is still debate about the ecology of these animals, particularly regarding their habitat preference and use. To determine in which habitats these animals were most abundant, as well as which habitats they preferred for feeding, 5 km line transects were conducted in the lakes, rivers, and channels of the Samiria River. The surveys were conducted over an approximately six-week period during the transition from the high to low water season, each year from 2015-2018. Generally, the pink dolphins appeared to prefer the channels over lakes and rivers. Tucuxi on the other hand did not appear to have any preference, although this may be due to the lower overall rate of occurrence in the area. These results appear to be consistent over the years of study, within the reserve. As top predators, the presence of these dolphins can be used as indicator species for the health of the river system. While the Pacaya-Samiria National Reserve is often considered a refuge from anthropogenic threats, climate change still impacts the ecosystem through an increasing number of floods and droughts. The results of this study contribute to a better understanding of these animals and their ecology (i.e. habitat use), making them a more effective indicator of changes in their environment.

Detection Of Paralytic Shellfish Toxins In *Homarus americanus* Through Alternative Non-Invasive Spectral Methods

Author: Emily Blacklock
Programme: Marine Biology Co-op
Supervisor(s): Dr. John Garland, Clearwater Seafoods
Dr. Alan Pinder, Biology Department, Dalhousie University

Abstract

The hepatopancreas of the American lobster, *Homarus americanus*, is known to sequester many natural toxins, including saxitoxins which can result in paralytic shellfish poisoning if consumed. These saxitoxins are a concern for human health at high concentrations. As a result of this concern, import regulations have been set for American lobster shipped to Japan, where the maximum suggested limit for the consumption of these saxitoxins has been set to 80µg/100g STXeq.

The standard method for the detection and quantification of paralytic shellfish toxins (PST) include methods which are both costly, time consuming and destructive in nature. Hyperspectral imaging and raman spectroscopy are two methods which utilize various wavelengths of light to detect the presence of different compounds within tissues. The use of spectral imaging techniques would allow for a method which is cost effective, time efficient and less invasive.

Lobster which contained various amounts of PST were examined with hyperspectral imaging and raman spectroscopy. Images of the lobster as a whole animal, hemolymph and hepatopancreas were taken with an infrared hyperspectral camera. Samples of the hepatopancreas and hemolymph were examined with a near infrared FT-Raman spectrometer. Data were analyzed with various software programs and compared to the lobster PST concentrations as determined by the standard enzyme-linked immunosorbent assay method.

The methods examined are not yet determined to be suitable for quantification of PST concentrations in *Homarus americanus*. Preliminary PLS-DA classification of the external carapace hyperspectral data suggests low correlation with the categorized PST concentrations into positive and negative values (R^2=0.22624). From this analysis, predictions of the classification of the external carapace into positive and negative values have higher false negative rate (65.0%) and a false positive rate (4.17%). Further analysis with both methods is required to determine whether the classification and quantification models can be improved. Preliminary results suggest hyperspectral imaging of the external carapace of the lobster could potentially be used to categorize individuals into positive or negative PST concentrations based on the importation limit.

Exploration Of HlyU DNA Binding And Virulence Gene Regulation In *Vibrio parahaemolyticus*

Author: Justin Brown
Programme: Biology
Supervisor(s): Dr. Nikhil Thomas, Department of Microbiology and Immunology; Division of Infectious Diseases, Dalhousie University

Abstract

Vibrio parahaemolyticus (*Vp*) is a Gram-negative marine bacterium that exists in a free-living state or in commensal or pathogenic relationships with marine organisms, particularly bivalve molluscs. *Vp* is globally recognized as the leading cause of seafood-borne gastroenteritis, presenting a significant threat to human health. Bacterial type-III secretion systems are needle-like multi-protein complexes that facilitate the direct translocation of effector proteins into eukaryotic host cells, establishing infection. *Vp* possesses two type-III secretion systems, representing critical virulence factors. T3SS-1 is associated with cytotoxicity while T3SS-2 is linked to enterotoxicity. The *Vp* T3SS-1 is comprised of protein products of various genes within corresponding genetic operons whose expression are under the control of the ExsA master transcriptional regulator. Two regulatory proteins, HlyU and H-NS form a genetic switch that regulates *exsA* expression and therefore T3SS-1 in *Vp*. H-NS is involved in the repression of *exsA* transcription, while HlyU is a positive transcriptional virulence gene regulator and essential mediator of *Vp* pathogenesis. A 56-bp protected region exists within the *exsA* promoter containing an inverted repeat sequence, representing the likely HlyU binding site. We hypothesize that the HlyU homodimer binds inverted repeats within the *exsA* promoter leading to a novel cruciform structure that supports *exsA* transcription, and biogenesis of T3SS-1. Our experimental design involves the genetic engineering of DNA plasmid deletion constructs targeting specific regions of the *exsA* promoter. The resulting constructs will be used to measure promoter activity in a bioluminescence assay. We hypothesize that deletions within the *exsA* promoter will result in unstable cruciform formation, obstructing HlyU binding, thus preventing *exsA* transcription and T3SS-1 activity. Additionally, an experiment involving the incorporation of an inverted repeat containing a fluorophore-quencher pair into a plasmid is planned for real-time observation of cruciform formation. The identification and characterization of *Vp* infection mechanisms is imperative in our understanding of the illnesses caused by these bacteria.

Estimated Changes In The Breeding Population Of Leach's Storm Petrels On Kent Island, New Brunswick And Factors Affecting Nest Site Selection

Author: Kyle d'Entremont
Programme: Biology
Supervisor(s): Dr. Robert A. Ronconi, Canadian Wildlife Service, Environment Canada

Abstract

Declines in seabird populations serve as an indicator for the health of marine ecosystems. Leach's Storm Petrel's (*Oceanodroma leucorhoa*) are a burrow-nesting seabird that breed on coastal islands throughout much of the North Atlantic, with the majority of the world's population in Atlantic Canada. Colonies throughout Atlantic Canada have experienced population declines of 10-30% in the past 20 years which resulted in them being up-listed to "Vulnerable" by the IUCN in 2016. One of the most well studied colonies is located on Kent Island, New Brunswick in the Bay of Fundy and has not been censused since 2000/2001. Since the last census, the population of predatory Herring Gulls (*Larus argentatus*) on the island has declined by 36% and a dramatic change in habitat types has also occurred due to the eradication of invasive Snowshoe Hares (*Lepus americanus*), which has allowed young forest to replace areas that were predominantly fern/raspberry bramble. In order to determine if this population of petrels has faced similar declines as other major colonies, a census of the colony was conducted from June to July 2018. 56 transects were established every 50m along the length of the island and 10 m^2 plots were searched for petrel burrows and their occupancy every other 10 m along each transect. Population estimates were calculated by extrapolating the number of burrows found in the area surveyed over the area of the entire island. Additionally, habitat characteristics and predator presence were recorded for each plot in order to examine correlations with burrow density and occupancy rates. Classification and regression tree analysis was used to determine which environmental factors affected burrow densities and occupancy rate. The estimated number of breeding pairs on Kent Island in 2018 was 21,260 (CI 14,349-28,171), which represents a 16% decline since the most recent survey in 2000/2001. This population decline could have broader implications for the state of the Bay of Fundy marine ecosystem and may also be contributed to changing habitat characteristics and predator-prey dynamics on the island.

Acoustic Tagging To Document Atlantic Coast Residency Patterns And Inter-Year Site Fidelity Of Atlantic Torpedo Rays

Author: Gabrielle S. Deveau
Programme: Marine Biology Co-op
Supervisor(s): Dr. Fred Whoriskey, Ocean Tracking Network, Dalhousie University
Dr. Chris Harvey-Clark, University Veterinarian, Dalhousie University

Abstract

The Atlantic Torpedo Ray (*Tetronarce nobiliana*), the largest known species of electric ray, periodically inhabits the coastal waters of Nova Scotia, however, their temporal and spatial distribution along the coast has not been thoroughly investigated. To study the residency and distribution of Atlantic Torpedo Rays in the Northwest Atlantic Ocean, 27 individuals were dart tagged with 69 Hz acoustic transmitters over multiple years starting in 2016. These fish were subsequently tracked primarily on two acoustic receiver arrays: the Halifax Line (spanning the continental shelf off Halifax) and the NSTR array (3 receivers near Halifax). Rays occupied inshore areas in autumn (September and October; within < 22 km from shore), moving offshore during winter months (> 153 km from shore). The absence of detections between mid-December and late February suggests the animals moved off the shelf for extended periods of the year. Ten rays were detected over multiple years, with three individuals returning to the NSTR site over two consecutive years between July and November. Receiver site Residence Index (RI) analysis revealed the rays display a strong site fidelity to the inshore waters. The results suggest that the Atlantic Torpedo Ray undergoes yearly movements, possibly linked to water temperatures. Evidence of inter-year site fidelity demonstrates that the Nova Scotian shelf may serve as a vital habitat for the Atlantic Torpedo Ray.

Developing A Novel Protocol For The Anaesthesia Of Zebrafish (*Danio rerio*)

Author: R Zachary Ford
Programme: Biology
Supervisor(s): Dr. Michael Schmidt, Dept of Anaesthesia, Dalhousie University

Abstract

With current widespread use of zebrafish (*Danio rerio*) as an animal model in translational studies, anaesthesia must be used to ensure safety in translational protocols. The current standard for this anaesthetic care is tricaine methanesulfonate. Notwithstanding its intended clinical effects, tricaine can increase risk of acidosis and cause detrimental changes to zebrafish cardiac and pulmonary systems at high doses. These setbacks limit the translational practicality of studies necessitating surgical resection. Substantiated by its extensive use in clinical anaesthesia, there are few adverse effects associated with administration of the agent sevoflurane. This study aims to develop a novel protocol for the anaesthesia of zebrafish using sevoflurane in order to mediate adverse effects associated with use of tricaine.

Baseline physiological and behavioural changes were observed in zebrafish treated with increasing concentrations of tricaine (TRIC), indicating expected behaviours at each stage and plane of anaesthesia. These changes were then compared to subjects treated with sevoflurane (SEV), as well as the combinatory effects of each tricaine and sevoflurane when co-administered with the inert gas, argon [as 20.9% O_2; 79.1% Ar] (Ar). Through video analysis of zebrafish physiology and behaviours, dosing curves for each protocol (TRIC, SEV, TRIC + Ar, SEV + Ar) were generated. The concentrations of anaesthetic agent required to reach each subsequent stage and plane of anaesthesia were determined and compared across protocols. This allowed for determination of the efficacy of each protocol, and observation of any adverse physiological and behavioural traits associated with administration of each agent.

Mixotrophic Growth Of Commercially Valuable Phytoplankton Through Nutrient Remediation Of A Food-Grade Source

Author: Rhyl Frith
Programme: Marine Biology Co-op
Co-op Supervisor: Dr. Hugh MacIntyre, Department of Oceanography, Dalhousie University

Abstract

Microalgae are capable of efficiently remediating wastewater streams through the uptake of nitrogen and phosphorous, which are known to cause eutrophication in water bodies. Though many studies have investigated the treatment of domestic and industrial wastewaters, few have focused on using microalgae to remediate food-grade wastewater streams. This study explores the possibility of large-scale mixotrophic phytoplankton cultivation using distillate tails, a plant-based, nutrient-rich by-product of distillation, to develop food-grade products and augment growth rate and/or biomass yield. At a one-percent dilution, the tails supply 190 µM phosphate, 5 µM nitrate and 8 µM ammonium. Based on a published molar N:P ratio of 16:1, the dissolved organic nitrogen content may be as high as 3 mM. Ten commercially-exploited species were screened at low and high light to test for augmented growth rate and/or biomass yield with the addition of the tails. Of all the screened species, *Tetraselmis suecica* showed the highest rate of increase in growth rate, as determined by increases in chlorophyll a fluorescence. Preliminary results from particulate carbon and nitrogen analysis show elevated biomass yields as particulate carbon and nitrogen across tail-amended cultures, suggesting that the tails supplied available C and N. Analyses on preserved samples will determine whether or not the phytoplankton could out-compete co-occurring bacteria to utilize the nutrients in the tails. If so, distillate tails would be a valuable resource for commercial production of phytoplankton biomass and food-grade natural products.

Molecular Phylogeny Of Colponemids, An Evolutionary Significant Group Of Alveolates

Author: Andrea Gigeroff
Programme: Biology
Supervisor(s): Dr. Alastair Simpson, Biology Department, Dalhousie University
Yana Eglit, Biology Department, Dalhousie University

Abstract

Alveolates are a clade of protists (eukaryotes which are not animals, plants, or fungi) that includes ecologically and medically important microbes such as ciliates, dinoflagellates, and apicomplexan parasites. Colponemids are a poorly understood assemblage of alveolates that consume other eukaryotic microbes. The current understanding of the biodiversity and phylogeny of colponemids is based on the ribosomal small subunit RNA (SSU rRNA) gene from just four species, which are placed in three phylum-level clades. “Colponemids” are currently inferred to be paraphyletic, and more closely related to apicomplexans and dinoflagellates than to ciliates. However, due to insufficient data available, both of these inferences are poorly supported.

For this study, four strains of predatory organism were identified as possible colponemids by cell morphology: GEM-Colp, LRS2-L, F2-L, and PSL3-Colp. These were cultured and the SSU rRNA gene was sequenced and analyzed with the objective of clarifying whether colponemids are truly paraphyletic and more closely related to dinoflagellates and ciliates.

To culture these organisms, I first isolated an appropriate prey species for each. I then picked single predator cells from crude enrichments into pure prey cultures to establish lines containing only two eukaryotes: predator and prey.

Once stable predator-prey cultures were established, I extracted DNA and amplified the SSU rRNA gene via PCR with universal eukaryote primers. The full SSU rRNA gene for GEM-Colp has been sequenced thus far. The obtained SSU rRNA gene sequence was aligned to a selection of other eukaryote sequences, weighted towards alveolates, and a maximum likelihood phylogeny inferred using RAxML. Preliminary analysis placed GEM-Colp within the alveolates and closer to dinoflagellates and apicomplexans than to ciliates. The analysis did not place GEM-Colp with any of the three existing colponemid clades with high statistical support. GEM-Colp may represent a fourth major “colponemid” clade.

Understanding the phylogenetic placements of alveolates other than the major groups – dinoflagellate algae, ciliate predators, and apicomplexan parasites – may be able to illuminate the early evolution of these disparate groups. Because “colponemids” appear more closely related to dinoflagellates and apicomplexans, presence or absence of morphological characters, such as plastids or apical complexes, can be investigated.

Acoustic Monitoring Of Leach's Storm-Petrels (*Oceanodrama leucohora*) As An Index Of Nesting Density

Author: Alison Gladwell
Programme: Marine Biology Co-op
Supervisor(s): Dr. Rob Ronconi, Canadian Wildlife Service
Dr. Andrew Horn, Biology Department, Dalhousie University

Abstract

Population monitoring of burrowing, nocturnal seabirds is challenging, as species spend limited time on remote oceanic islands to breed. To attempt to mitigate this challenge, acoustic monitoring has been used to assess diurnal activity patterns in seabird populations, but rarely to assess whether acoustic recordings can be used to relate the call activity to the nesting density or population size. From June-July, 2018, we distributed passive acoustic recorders across 21 sites throughout a colony of Leach's Storm-petrels (*Oceanodrama leucohora*) on Kent Island, New Brunswick. Recording sites varied in habitat types, nesting densities and exposure to predators. The nesting density was measured within the 7853.98 m^2 area centred on each acoustic meter. Recordings were analyzed using Raven acoustic software to estimate the average calls/hour of petrels and Herring Gulls (*Larus argentatus*), the petrels' main predator. Preliminary results suggest that call activity has the strongest relationship to local nesting density 6 hours after sunset ($R^2 = 0.898$, $p = 0.048$). Call rates indicate the first calls occur ~2 hours after sunset, and the last calls occurring ~1 hour before sunrise, typically peaking 4-7 hours after sunset. As the analysis continues, a general linear mixed model will be applied to assess if various environmental and phenological factors affect the relationship between call activity and nesting density. Exploratory results may identify conditions that affect the diurnal patterns of storm-petrels, such as wind patterns and light exposure. Call activity can be used to estimate nesting density, so acoustic monitoring may be an effective tool for assessing populations of Leach's Storm-petrels on remote breeding islands.

Determining If Non-Genetic Environmental Effects On *Avena barata* Individuals Result In Significant Spatial Patterns

Author: Lauren Jackson
Programme: Biology
Supervisor(s): Dr. Robert Latta, Dalhousie Department of Biology

Abstract

This thesis project aimed to answer the question of if, and how much, the local environment of *Avena barata* effects the fitness of each individual. *Avena barbata* is a species of wild oat that is native to the Mediterranean, but has been particularly successful as a colonizer in Californian grassland areas. Historical data collected by Latta et al. from two plots in California between the years of 2003 and 2007 was used in this experiment. The genotype families of the individuals planted were randomized and three markers of fitness were measured from each individual. The non-genetic environmental effect of the local environment on each individual was determined by calculating the deviation of each individual from the mean estimation of fitness performance of the individual's genotype. Several methods have and will be used to determine how the environmental effects vary spatially within the local environment. The effects were mapped to compare them and there were some visible trends where the positive or negative environmental effects were congregated in an area of a couple of individuals. However, we do not yet know if these spatial patterns are significant. To do so, we need to perform the next steps, which include creating correlograms and variograms on Rstudio. Furthermore, the spatial patterns will be compared year to year to determine if there are any consistent patterns over time.

Factors Impacting Nest-Site Selection In The Barn Swallow (*Hirundo rustica*)

Author: Rebecca Jardine
Programme: Biology
Supervisor(s): Dr. Marty Leonard, Biology Department, Dalhousie University
Dr. Andy Horn, Biology Department, Dalhousie University

Abstract

Humans are known for negatively affecting the environment of other species. However, in some cases, humans may make changes that potentially benefit species. For example, many avian species, including the threatened Barn Swallow (*Hirundo rustica*), use human infrastructure as nesting habitat. While historical breeding data on this species are limited, records show that Barn Swallows have shifted from breeding mostly solitarily in natural habitats to breeding in loose colonies in human infrastructures, such as barns. Little is known about whether this change affects the behaviour and reproductive success of these birds. Previous studies have shown that the costs of nesting colonially may outweigh the benefits. In particular, colonial nesting may increase competition between nesting pairs for nest sites, increase the number of ectoparasites and make nest sites more obvious to predators. Therefore, the objective of my study was to determine whether Barn Swallows are choosing nest sites that will allow them to reduce the negative effects of coloniality. I predicted that if Barn Swallows were attempting to reduce these costs, they should nest as far from conspecifics as possible and in locations that are away from access points (e.g. doors) for predators. I also predicted that reproductive success would be higher in colonies where nests were more dispersed and further from access points. To test these predictions, I monitored four Barn Swallow colonies in New Brunswick from May-August 2018, where I mapped the location of all nests relative to each other and to access points and noted the clutch size and success of each nest. My preliminary results showed that nests were evenly distributed within structures, suggesting that individuals could be maximizing distance between nests as an attempt to reduce some of the costs associated with coloniality. Next steps for analysis include determining whether the distribution of active nests and characteristics of buildings, such as access points, impact reproductive success within a colony. This study may contribute to Barn Swallow conservation by clarifying the costs and benefits of nesting in human infrastructure and by identifying design features for alternative nesting sites that might increase the Barn Swallow population.

Assessing Impacts Of Tag Burden On Energy Storage Of Female Grey Seals Through Analysis Of Body Condition And Reproductive Output

Author: Charity Justrabo
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Supervisor(s): Dr. Don Bowen, Bedford Instutue of Oceanography; Biology, Dalhousie University
Dr. Damian Lidgard, Biology Department, Dalhousie University

Abstract

The deployment of data-logging instruments and satellite telemetry devices (tags) on marine mammals has increased the amount of data that exists about their at-sea behaviour. Despite this rapid increase in biologging studies on marine mammals, there are few studies of the potential negative impacts of these instruments. This is particularly relevant for highly-streamlined marine mammals, such as the grey seal, because a tag may increase drag and thus energy expenditure of the animal. The goal of this study was to investigate the possible reproductive impacts of different size instruments (n = 17) adhered to the pelage of female grey seals. Instrument models were divided into eight treatment groups based on the frontal areas of each instrument, drag force, and multi-instrument deployments on the animal. This analysis was conducted using data from 179 females (and a similar size control group) collected from 1992-2017 by Fisheries and Oceans Canada on Sable Island, Nova Scotia. Body condition (i.e. maternal mass) and reproductive performance (i.e. pup body mass at weaning), proxies for energy storage of females, were analyzed using a general linear model to assess if there were any deleterious effects on the seals compared to a control group of non-instrumented females. Age of the seal was included to account for differences in reproductive performance related to life stage. Understanding tagging impacts is crucial to recognizing adverse physiological effects that may lead to reduced reproductive output or survival probability in a marine mammal.

Does Performing A Cognitively Challenging Task Promote Neuron Survival And Neural Gene Activity In Zebra Finches (*Taeniopygia guttata*)?

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Abstract

Environmental enrichment can affect neurogenesis, specifically the rate of proliferation of new neurons and cell survival. One form of environmental enrichment is cognitive enrichment, in which the subject performs a task that requires exercising their cognitive abilities. The purpose of this study was to investigate the effect of cognitive enrichment on neurogenesis and neural gene activity in zebra finches (*Taeniopygia guttata*), a songbird species known for its auditory discrimination abilities and vocal learning. To do this, 8 birds were trained to use a Go/No-Go operant discrimination apparatus, then they were divided into three groups: the discrimination task group (birds earn all food from correctly performing the acoustic discrimination task), the yoked group (birds' chambers were connected to the chamber of a discrimination task bird and heard all stimuli presented to the discrimination bird in real time, but food was ad libitum), and the control group (had food ad libitum and heard nothing). After three weeks birds were sacrificed and brains harvested. Through immunohistochemsitry, the cell birth marker bromodeoxyuridine (BrdU) was labeled to measure cell survival, while the immediate-early gene ZENK was used to measure neuronal activity in neural regions examined are involved in auditory or spatial perception and singing (caudomedial mesopallium, caudomedial nidopallium, hippocampus, and HVC). I hypothesized that there would be more neuron survival and more neural activity in the brain areas of interest in birds that had to perform the learning task (discrimination task group) compared to birds that did not perform the learning task (yoked and control groups). I also predicted birds in the yoked group would have intermediate levels of surviving cells and active neurons, and control birds would have the lowest levels of surviving cells and active cells. If results support this, it would suggest that performing this cognitive enrichment task increased neural gene activity and survival of neurons in brain regions involved in auditory or spatial perception and singing for birds that learned the discrimination task compared to birds that did not.

Genetic Identification Of *Eubalaena glacialis* Prey Species In The Gulf Of St. Lawrence Using Fecal Analysis

Author: Katherine King
Programme: Marine Biology Co-op
Supervisor(s): Dr. Timothy Frasier, Biology Department, Saint Mary's University

Abstract

Historically, North Atlantic right whales (*Eubalaena glacialis*) have primarily spent the summer months feeding in the Bay of Fundy and Roseway Basin, which are known to contain high concentrations of their preferred prey, *Calanus finmarchicus*. In the past few years, however, there has been a distribution shift and they have abandoned these feeding areas and instead large numbers have shifted their distribution into the Gulf of St. Lawrence during the summer. It has been hypothesized that this is due to a shift in prey distribution. My thesis focuses on testing this hypothesis by developing a molecular method of copepod species identification, and then applying this technique to determine the prey species found in North Atlantic right whale fecal samples collected in the Gulf of St. Lawrence. To do this, a protocol was first developed and validated using copepod samples of known species. Specifically, five different primer pairs were tested across these species to identify which primer pairs amplify most consistently across copepod species, while also providing enough resolution for species identification. Once validated, these protocols were used to identify the relative contribution of different copepod species in right whale fecal samples. The results of this study, in addition to what has been found by other researchers, will help in identifying what the North Atlantic right whales are eating in the Gulf of St. Lawrence, and thus aid our understanding of why the whales have shifted their distribution. This work will therefore shed more light on why right whales have shifted their distribution, and what this could mean for the future conservation efforts for this species.

A New Protein Mass Spectrometry-Based Method For Phytoplankton Abundance Assessments Applied On The Scotian Shelf

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Abstract

Marine microbes are dominant marine primary producers and are directly relevant to the nutrient cycling and carbon fixation and export ability of the global oceans. The ability to determine primary producer abundance and community structure allows for improved estimates of carbon transfer, in addition to estimates for biomass, health and diversity. Community structure is integral to understanding impacts to the trophic dynamics in the context of climate change. Given the currently rapid pace of global change, there is a need for biomass abundance data in order to increase carbon cycling prediction accuracy and precision.

The methods commonly used for assessing phytoplankton community structure include 16S sequencing and High Performance Liquid Chromatography (HPLC) pigment analysis. 16S chloroplast sequencing provides relative abundance information with high taxonomic resolution. HPLC pigment data utilizes measured pigment ratios to chlorophyll a (chl a) to evaluate the highest likelihood of taxon concentration and provides information at a level of broader taxonomic groupings. These methods could be complimented by an approach able to reach similar resolution as 16S and also provide absolute measures of abundance. The objective of this study is to evaluate the method of assessing community structure and abundance through protein-based HPLC Mass-Spectrometry (MS) on the Scotian Shelf, Canada (2015-2017). We hypothesize that the spatial and temporal trends from the protein MS data-set will match and be correlated to those that were described using 16S sequencing and HPLC pigment analysis.

Here we compare datasets via correlation of observed MS-based protein concentrations to taxa concentration from the pigment data and NMDS-partial mantel tests between 16S relative abundance and environmental parameters including MS-protein concentrations. Current preliminary results indicate that seasonal trends revealed via pigment and 16S analysis are also reflected in the protein-MS data. These data suggests that protein MS measurements hold the potential to be a quantitative, high throughput method for assessing phytoplankton abundance and community composition that can be included in future oceanographic and ecosystem studies, including the ongoing AZMP monitoring program.

LAMP As A Tool For Rapid Detection Of *S. parasitica* In Salmonid Farms

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Dr. Nasif Sarowar, Animal Sci & Aquaculture, Dalhousie University

Abstract

One of the challenges of salmonid aquaculture is the management of devastating fungal disease outbreaks caused by the freshwater pathogen *Saprolegnia parasitica*. The existing technique to diagnose the disease involves PCR and sequencing of the internal transcribed spacer (ITS) region of rDNA of fungal mycelia from infected fish, which can be time consuming and expensive. To develop an environmental DNA detection technique that is simpler, faster and much more specific, Loop-Mediated Isothermal Amplification (LAMP) may be a useful tool. Unlike conventional PCR, six different primers were designed using PrimerExplorer V5 from the ITS region of *Saprolegnia parasitica*. DNA from a number of *Saprolegnia spp.* was also tested to evaluate specificity of the primers. Successful amplification was run at a constant 71°C. Amplification was detected by turbidity change and visualization by gel electrophoresis, colour change using the dye hydroxynaphthol blue (HNB), and/or by fluorescence detection under UV light using green fluorescent dye. The designed primers were able to specifically probe different *S. parasitica* strains and resulted in turbid end products in 30 minutes, with a detection limit of 10 fg/µl DNA. Purity of primers was found to be crucial to successful amplification. The LAMP eDNA detection method is straightforward and rapid for detection of *Saprolegnia parasitica* in salmonid farms sites and may prove to be a useful tool for the diagnostics of the disease.

Species Cover And Distribution Of Aquatic Invasive Species In Atlantic Canada Before And After An Extreme Temperature Event

Author: David Krug
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Co-op Supervisor: Dr. Claudio DiBacco, Bedford Institute of Oceanography

Abstract

Aquatic Invasive Species (AIS) have negative overall effects on native species biodiversity and native ecosystem function. A special concern for AIS in Canada is their biofouling impact on shellfish and other aquaculture operations. This analysis sought to better understanding AIS cover-abundance across different regions and in response to an extreme temperature event. AIS collector plates deployed August and October 2017 were assessed for percent cover and species richness in October 2018. Along with assessment data from October and December 2017 and June 2018, the percent cover and distribution of AIS was compared across 4 geographical regions throughout Nova Scotia and New Brunswick and between sampling dates. Collector plates deployed in June 2017 had higher AIS cover than those deployed later in October 2017. Compared to plates with higher native species cover pre-winter, plates with higher AIS cover pre-winter saw a greater increase in empty space on the plates post-winter. The general trend was a decrease in AIS after over-wintering when water temperatures were at their lowest, with an resurgence once water temperature increased. South West New Brunswick (SWNB) and South West Nova Scotia (SWNS), both on the Bay of Fundy, generally showed higher levels of AIS than other regions. Water temperatures in SWNB and SWNS show similar patterns and experience the smallest temperature range, possibly contributing to the prevalence of AIS in these regions. Temperature, along with other abiotic and biotic factors, play a role in the survival and distribution of AIS. Native species that are more cold adapted fare better over winter while AIS experience increased die off caused by low temperatures. An understanding of AIS dynamics in relation to water temperatures can help scientist predict the spread and distribution of these species as ocean temperatures rise.

Waiting For What? Explaining Variation In The Timing Of Female Reproduction

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Abstract

Natural selection favors individuals that maximize fitness, which should result in minimal variation in fitness-related traits. However, female crickets (*Gryllus texensis*) vary in reproductive timing and investment; some start laying eggs (oviposition) early in adult life (early ovipositors; EO), but others lay their eggs closer to the end of their life (late ovipositor; LO). Eggs are valuable assets, and hatching success varies depending on the oviposition substrate. I hypothesized that LO crickets are following a strategy in which they postpone egg-laying when the substrate is suboptimal. Instead of risking the loss of eggs due to poor conditions, they store their eggs in their lateral oviducts. Only once they are nearing the end of their life do they risk laying their eggs in less optimal substrate. To test this hypothesis, I categorized individuals into subpopulations of EO and LO crickets and assigned them to having either suboptimal (cotton) or preferred (sand) substrate. I then monitored oviposition. I predicted that LO crickets would increase reproductive output when given sand and they would begin to lay eggs earlier. I found that both EO and LO crickets laid more of their produced eggs in sand. However, LO crickets did not change their reproductive output and still postponed egg-laying until late in life. Reproduction in crickets has also been shown to negatively correlate with flight ability. Flight muscles are needed for dispersal flights. Females consume/histolyze these muscles to help fuel reproduction. I found that LO crickets were more likely to have functional flight muscle than EO crickets. LO crickets maintained flight muscles until late in life, while EO crickets histolyzed these muscles as young adults. This pattern did not differ between sand and cotton conditions. LO crickets may be waiting until after their dispersal flights (i.e. signifying a more optimal environment) before starting to produce and lay eggs. I am now testing whether giving females an opportunity to make a dispersal flight will induce LO females to lay eggs earlier. Understanding the adaptive significance behind variations in the timing of female reproduction will provide insight into the evolution of diversity in fitness-related traits.

Transovarial Transmission Of Human Pathogenic Bacteria Between Mothers And Eggs In *Ixodes scapularis* And *Dermacentor variabilis*

Author: Sara MacPhee
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Supervisor(s): Dr. Tatiana Rossolimo, Biology Department, Dalhousie University

Abstract

The two primary species of ticks found in Nova Scotia, *Ixodes scapularis* and *Dermacentor variabilis*, carry a variety of pathogenic bacteria. In order to understand how to control and minimize the damage caused by these bacteria, it is important to understand how the bacteria spreads. These bacteria pass between ticks in a variety of different ways, including transovarially, where the bacteria proliferates in the ovaries of an adult female tick and is subsequently passed on to their offspring when that female lays eggs. In this research, adult female ticks who had taken a blood meal were collected from Nova Scotian veterinarians and various animals in the Halifax Regional Municipality. They were kept in a lab environment until they laid eggs, then the 28 *Ixodes scapularis* and 20 *Dermacentor variabilis* which laid eggs were tested along with their offspring for markers indicating infection with *Babesia* spp., *Bartonella* spp., *Rickettsia* spp., *Anaplasma phagocytophilium, Borrelia burgdorferi*, and *Francisella tularensis*. Sequences of interest were amplified via polymerase chain reaction (PCR) and then imaged using gel electrophoresis. Primers were designed to test to the level of the genera for *Babesia* spp., *Bartonella* spp., and *Rickettsia* spp., and to test to the level of species for *A. phagocytophilium, B. burgdorferi*, and *F. tularensis*. Previous research had indicated that *A. Phagocytophilium* would transmit transovarially in *D. variabilis* but not in *I. scapularis*, while *Rickettsia* spp. and *Babesia* spp. would transmit transovarially in both *I. scapularis* and *D. variabilus*, and *B. burgdorferi, F. tularensis* and *Bartonella* spp. would not transmit transovarially in either. Preliminary results indicate that of the ticks tested, transovarial transmission of *F. tularensis* was indicated to occur in all of the *D. variabilis* mothers who were infected with the bacteria and in 40% of the *I. scapularis* mothers who were infected. *Rickettsia* spp. was not detected in any of the specimens, so its transmission status could not be determined. *Bartonella* spp. was detected in 5 of the *I. scapularis* mothers, and in none of their respective offspring, indicating that it is likely not transovarially transmitted. It is not known as of yet if *B. burgdorferi, Babesia* spp., or *A. phagocytophilium* transmit transovarially.

Developmental Timeline Of Mitral Valve Chordae Tendineae Differentiation Using Anatomical And Thermal Analysis

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Supervisor(s): Dr. Sarah Wells, School of Biomedical Engineering, Dalhousie University

Abstract

There are lots of ways to mend a broken heart, but how do the heart and its valves form and change over time? Previous work done in our lab has shown – for the first time – that heart valves undergo adaptive remodeling. From this research, we hypothesized that this may be a recapitulation of fetal developmental mechanisms. What is missing is a detailed study of the structural-mechanical changes in mitral valve chordae during fetal development.

The chordae tendineae are tendon-like structures that attach from the basal end of the leaflets and attach to the papillary muscles. The chordae are made up of an exterior of endothelial cells with an interior comprised of mostly collagen with small amounts of elastin. There are three anatomically and functionally different types of chordae in the mitral valve: strut, basal, and marginal chordae. These chordae are distinct in their mechanical and anatomical properties.

Whole heart samples were collected from fetal bovine calves from Reid's Meats Abbatoir in Wolfville, Nova Scotia. Gestational age was calculated from the fetal crown to rump length. Samples measured to date had a crown to rump length between 60-70cm, having a gestational age of 202-226 days. Each leaflet was photographed and examined using Image J software. To examine thermal properties chordae samples of were subject to Differential Scanning Calorimetry (DSC).

So far, it has been seen that chordae tendineae in these samples have differentiated into the three anatomically different structures. The leaflet is thin at the coaptation zone but thickens in the atrial zone. The average peak temperature for the strut chordae was 60.6°C (±1.03) and the average enthalpy was 2.07 J/g (±0.46). The average onset temperature was 59.3°C (±1.10) for the same samples. This is the first look at fetal mitral valve structures anatomically and thermally, giving an insight into how early these structures form and differentiate. These results are preliminary, giving a look into the development in the third trimester of pregnancy. Future work will be done to examine mitral valves from the first and second trimester and to examine periostin protein expression in these valves. Furthermore, parameters measured here will be compared to adult bovine maternal remodelling.

Acoustic Click Patterns In Northern Bottlenose Whales (*Hyperoodon ampullatus*) Off Eastern Canada

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Abstract

Cetaceans often rely on acoustics to carry out important life functions such as navigation, foraging, and communication. Beaked whales, of the family Ziphiidae, use acoustic clicks to locate prey during foraging dives, however, little is known about how acoustic signals may be used in non-foraging contexts, including that of social communication between conspecifics. Compared to other beaked whales, the use of sound in northern bottlenose whales (*Hyperoodon ampullatus*) has been relatively well described, and they are known to produce several types of broadband impulsive vocalizations, ranging from 0.5 to >50 kHz in frequency. These vocalizations include upswept frequency modulated pulses, buzz clicks, and more variable surface clicks. From acoustic recordings of northern bottlenose whales encountered off the Scotian shelf, two major click types have been found. The first type is generated at depth, likely while the whales are foraging, and the second type is generated while whales are at the surface, often in a social context. These click types have been observed to differ in peak frequency and in the variability of click duration and inter-click interval (ICI). This suggests that surface clicks may serve a function other than foraging, such as echo-locating of companions or social communication. Recordings were made using a hydrophone array towed behind the sailing vessel Balaena between 1988-2017 in the presence of northern bottlenose whales belonging to the Scotian Shelf population in Nova Scotia, as well as whales in Newfoundland and Labrador. Recordings during 45 surface encounters were assessed for the presence of social clicks and click patterns. Four distinct social click patterns were identified from the Scotian Shelf and Newfoundland, including a quick-click train with ICIs shorter than 0.3 s, and a quick-start train of 4-5 clicks with ICIs that increase with each successive click. The dominant pattern of clicks identified from encounters was the double-click pattern, which is a click train with pairs of clicks with short ICIs of 0.3-0.5 s long, separated by longer ICIs less than 1.0 s. Patterned clicks were characterized in terms of the ICI, frequency, duration, and bandwidth for comparison with regular foraging clicks. This analysis will significantly expand our understanding of the biology and behaviour of northern bottlenose whales, and provide a detailed quantitative description of the nature of social communication among beaked whales.

Identifying Antimicrobial Resistance Genes In Uncultivated Bacteria And Archaeal Metagenome-Assembled Genomes

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Abstract

Antimicrobial resistance (AMR) is a severe global health crisis. In the United States, it has been estimated at least 23,000 people die each year from antibiotic resistant infections. To better understand AMR, there have been efforts to record molecular determinants of antimicrobial resistance in databases such as the "Comprehensive Antibiotic Resistance Database" (CARD) (Jia et al. 2017). CARD includes a "Resistance Gene Identifier" (RGI) which detects AMR genes in genome sequences. RGI provides "Loose", "Strict" and "Perfect" stringency thresholds for each gene to improve accuracy and sensitivity. RGI also uses two AMR detection models, the protein homolog model which detects homologous AMR protein sequences in the genome and the protein variant model which identifies mutations inferring AMR from reference sequences. A metagenome is a collection of genetic material from a community of microorganisms commonly containing organisms that have never been isolated and cultivated in laboratory conditions. A recent paper (Parks et al. 2017) assembled almost 8,000 genomes from publicly available metagenomes which included a diverse taxonomic distribution of novel uncultivated archaeal and bacterial organisms.

The main objective of this study was to identify antimicrobial resistance genes in metagenome-assembled genomes (MAGs) from the Uncultivated Bacteria and Archaea (UBA) data (Parks et al. 2017). The CARD RGI was used to predict AMR genes in 7,903 MAGs which were then analyzed using Pandas (a Python data analysis library). 871 of 7,903 MAGs contained genes with a high degree of similarity to known AMR genes ("Perfect" or "Strict" stringency matches) (excluding antibiotic efflux genes). Of these 871 MAGs, each had an average of 2.6 AMR genes per MAG for a total of 2,276 AMR genes identified.

To identify more distant AMR gene homologues, CARD's "Loose" algorithm identified several beta-lactamase genes including Klebsiella pneumoniae carbapenemase (KPC), OXA-related genes, New Delhi Metallo-β-Lactamase (NDM) and mobilized colistin resistance (MCR) genes in several genomes. Further phylogenetic analysis was used to identify more accurate NDM and MCR homologues. The MCR phylogenetic analysis identified a potential novel MCR clade and three UBA genomes showing homology to MCR-5 reference sequence. The UBA data contained a diverse set of AMR genes and phylogenetic analysis further characterized the diversity and evolution of NDM and MCR genes.

Estimating Abundance Of Brook Trout (*Salvelinus fontinalis*) Populations In The North Mountain, NS Using Parent-Offspring Relationships

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Abstract

The estimation of population abundance is a central goal in ecology and conservation biology as well as in fisheries management. Traditionally estimated through catch per unit effort (CPUE) trends or mark-recapture studies, abundance estimates are often difficult to ascertain and unreliable especially for widespread and largely inaccessible marine populations. The close-kin mark-recapture (CKMR) method of estimating population abundance employs genetic data to identify parent-offspring pairs (POP). An individual's genotype can be considered a recapture of the genotype of its parents. This method removes the need for physical marking of individuals. I sampled 7 resident brook trout (*Salvelinus fontinalis*) populations inhabiting small streams in the North Mountain area of Nova Scotia. I then estimated abundance using the CKMR method in order to test its feasibility when working with wild fish populations. Samples were obtained via double-pass electrofishing in the summers of 2014 to 2018. Roughly 3700 individuals were genotyped at 31 microsatellite loci to determine the number of POPs. Assuming that parents and offspring are sampled independently and using information on age-specific fecundity and survival rates, this number is then used to estimate population size. Standard mark-recapture population sizes were also estimated to validate the accuracy of the CKMR method.

Examining The Prevalence Of Alternative Reproductive Strategies In Male *Salmo salar* From Two Norwegian Rivers

Author: Heather Perry
Programme: Marine Biology Co-op
Supervisor(s): Jeff Hutchings, Biology Department, Dalhousie University

Abstract

Mature male Atlantic salmon (*Salmo salar*) exhibit one of two alternate mating strategies, based on their size and reproductive investments. Juvenile growth rate influences the age at which maturity is initiated and how energy is distributed among reproductive traits. Those that grow quickly tend to mature earlier in life (1-3 yr) as parr and invest proportionally more energy to gonads but at relatively small sizes (~7-15 cm). Those that grow slowly early in life mature later (4-7 yr), following a migration to and from sea, as 'anadromous' males, and invest in secondary reproductive traits such as a larger body (50-100 cm) and kype (a hook-like secondary sex characteristic used during mate competition).

Mature male parr and anadromous males differ in their reproductive investment and fertilization success. Anadromous males use their secondary reproductive traits to engage in aggressive intrasexual contests to gain primary access to females. As a group, mature parr achieve considerable fertilization success by sneaking into egg nests ('redds') during spawning. Higher ATP content in parr sperm provides the energy required to fertilize eggs from a greater distance, helping them avoid life-threatening attacks from dominant males. Although parr are more likely to survive until reproduction, their average fertilization success is considerably lower than that of anadromous males. It has been hypothesized that alternative strategies co-exist within populations in an evolutionarily stable equilibrium maintained by negative frequency-dependent selection.

Despite extensive studies of alternative reproductive strategies in Atlantic salmon, remarkably little temporal information is available for wild populations. Thus, it is highly fortunate that a collaboration with Norwegian researchers has yielded data on mature male parr from the Os and Flåmselva rivers for 10 and 25 years respectively. Sampling was conducted by annually electrofishing 600m-long stretches of the rivers between 1996 and 2016.

The present study explores how selective pressures act on each reproductive strategy, using statistical analyses of age, maturation and year on length, weight and gonadal somatic indices. Outcomes of the study will contribute to our central understanding of how alternative reproductive strategies are established and maintained in Atlantic salmon, which may have implications for their sustainable management.

Genetic Relationships Of The White And Common Forms Of The Threespine Stickleback In Nova Scotia

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Abstract

Threespine Sticklebacks (*Gasterosteus aculeatus*) are a popular target of microevolutionary and population genetics studies as they display phenotypic and ecological variability across their range. A “white” form of the Threespine Stickleback is endemic to Nova Scotia. This form shows behavioural and morphological differences when compared to the “common” form found in the Maritimes and elsewhere. However, recent genotyping by sequencing (GBS) data indicated an unclear genetic relationship between the white and common sticklebacks as well as sticklebacks from the mainland of Nova Scotia and Cape Breton. This study assessed the genetic relationships of white and common Threespine Sticklebacks across their mainland and Cape Breton range. Individuals sampled from sites across Nova Scotia, New Brunswick and Newfoundland and Labrador were genotyped at 71 microsatellite loci. The multilocus genotype of each individual was inferred by the program MEGASAT. Bayesian clustering using the program STRUCTURE assessed the most plausible number of genetic population clusters that minimized deviations from Hardy Weinberg Equilibrium and linkage equilibrium and assigned individuals to a population. Three population clusters were detected: one corresponding to whites found throughout Nova Scotia, another representing commons from the Bay of Fundy coastline, and a third corresponding to commons from the remainder of Nova Scotia. The fact that all white sticklebacks belonged to a single population cluster, regardless of their geographic location, suggests that all white sticklebacks derive from a single divergence event.

Expression Of *Arabidopsis thaliana* XBAT35, An E3 Ubiquitin Ligase, During Response To Abiotic Stress

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

Abstract

With climate change as a growing concern, understanding the mechanisms by which plants respond to abiotic stress is of increasing importance for agriculture and food security. Plants utilize a number of mechanisms, including the ubiquitin proteasome system (UPS), to regulate plant abiotic stress responses to ensure survival. Cell signaling initiated by the hormone abscisic acid (ABA) plays an important role in responses to abiotic stressors such as high soil salinity and drought. The UPS uses three enzymes, E1, E2 and E3 to attach a chain of ubiquitin molecules to selected substrates, which is then degraded by the 26S proteasome. The cell utilizes the UPS to control the abundance of selected proteins to regulate the onset, intensity and duration of cellular response to environmental stresses.

The focus of this study is to characterize the potential role of ubiquitin ligase XBAT35 in the abiotic stress response. XBAT35 is expressed as two isoforms, nuclear localized XBAT35.1 and Golgi-localized XBAT35.2. Using the model species *Arabidopsis thaliana* and gene expression analysis, the goals of this study are 1) to determine if the expression of one or both XBAT35 isoforms are stress-responsive and 2) to determine if changing the expression of either isoform, XBAT35.1 and XBAT35.2, alter plant response to abiotic stresses. Reverse Transcription quantitative Polymerase Chain Reaction (RT-qPCR) assays were used to evaluate the expression of *XBAT35.1* and *XBAT35.2* along with other abiotic stress-responsive genes (e.g. salt responsive *Bip3*) in wild type and *xbat35-1* mutant seedlings, as well as transgenic seedlings overexpression *XBAT35*.1 or *XBAT35.2*. Seedlings were exposed to abiotic stressors such as cold shock, and high salt and were also treated with ABA. Results suggest that both isoforms of *XBAT35* are involved in the abiotic stress response. Importantly, both isoforms of *XBAT35* were upregulated wild type seedlings in response to a variety of abiotic stressors. The study also found that expression of salt responsive gene *Bip3* was altered in transgenic seedlings compared to wildtype, suggesting a role for the E3s in plant response to high salinity. The findings from this research allow us to further understand how plants respond to and tolerate abiotic stress.

Assessing Anthropogenic Impacts on Plant and Lichen Communities in Nova Scotia's Forested Wetlands

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

Abstract

Forested wetlands are understudied ecosystems that provide habitat for a large diversity of species and perform important ecosystem services. Due to the increasing anthropogenic impacts of climate change and direct physical alteration, forested wetlands are declining globally and locally. Despite their importance and vulnerability, forested wetlands lack protection in Nova Scotia. For example, no regulations prevent the harvesting of trees in our wetlands, which are increasingly targets for wood, fibre and biomass as other supplies are exhausted. This study attempted to answer the research question: Are anthropogenic disturbances reducing biodiversity in forested wetlands in Nova Scotia? In order to determine if anthropogenic disturbances, such as forestry activities, have an impact on plant and lichen communities in Nova Scotia's forested wetlands, 30 sites across Nova Scotia were sampled. The abundance of vascular plant species and cyanolichen species on tree boles were sampled along 50 m transect. Predictions were that the diversity would be lower in more impacted sites. Using GIS and Google Earth, the type, extent and intensity of anthropogenic disturbance in and around the study sites was determined. These disturbance measures were then related to species diversity metrics at each site. The species composition was also examined to determine if particular species were more or less likely to occur at sites with more disturbance. The sites were further broken down into different forested wetland types to see if their plant and lichen communities were differentially affected. Should this study find significant support for the hypothesis, these results could suggest that protection of forested wetlands against anthropogenic disturbances is needed.

Characteristics Of Forested Wetland Habitat For Three Landbird Species At Risk In Nova Scotia

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Abstract

Forested wetlands provide numerous ecosystem services, are highly biodiverse, and contain a high concentration of species at risk (SAR). In Nova Scotia, three migratory landbird SAR breed in forested wetlands during the summer: The Canada Warbler (*Cardellina canadensis*), the Olive-sided Flycatcher (*Contopus cooperi*) and the Rusty Blackbird (*Euphagus carolinus*). Habitat data available in Nova Scotia for these three SAR are mainly from the South-Western region of the province. This study examined breeding habitat characteristics for these SAR in the more data deficient Central and Eastern regions of Nova Scotia, including Cape Breton Island. To quantify habitat characteristics, the following were measured along a 50 m transect (n = 35 sites where one or more SAR were present): abundance and composition of the low shrub (0.25-2 m) and tall shrub (2-7m) layers; tree species, height, diameter at breast height (DBH), and health; snag height, DBH and decay class; density of song perches; coarse woody debris volume and decay class; canopy cover; ground cover of sphagnum moss; water feature coverage; and soil saturation level. To determine habitat characteristics important for each species, data for sites with and without particular SAR were analyzed using univariate and multivariate methods. Two-sample tests were used to compare habitat variables at sites where present and absent, Principle Components Analysis was used to reduce the number of variables for further analysis, and Classification And Regression Trees were used to determine the most important variables for distinguishing habitat for each species. Results were compared to those of previous studies for South-West Nova Scotia to assess regional trends. By identifying important breeding habitat characteristics of forested wetlands for these SAR, this study hopes to better inform conservation efforts to conserve these species.

Genetic Differentiation In *Percichthys trucha* Among Drainages In Patagonia

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

Abstract

Biota in the Andes experienced acute shifts in landscape due to the various glacial cycles of the Quaternary. Most species in Patagonia, including the freshwater *Percichthys trucha*, or Creole Perch, would have experienced range contractions and shifts in their distribution due to large ice fields that are known to have covered much of the region during glacial times (Ruzzante et al., 2006). Because of low sea levels much of the continental shelf was exposed, allowing for braided connections facilitating exchange between proglacial lakes that are now geographically separated. Previous studies in *P. trucha* find strong morphological differentiation among and within populations from different drainages, yet no evidence for deep divergence based on mitochondrial DNA (Ruzzante et al., 2011). Here I describe genetic differentiation among *P. trucha* populations from throughout the distribution range of the species in Patagonia on both sides of the Andes.

Tissue (muscle or blood) samples of *P. trucha* from 16 drainages including Pacific and Atlantic drainages in Argentina and Chile were collected beginning in 1998. I then extracted DNA from over 1100 individuals and examined polymorphism at 58 species-specific microsatellite DNA markers. Genetic variation among populations was examined using the program STRUCTURE. Preliminary analysis reveals broad patterns suggestive of isolation by distance both latitudinally and longitudinally, with some evidence of exchange between proglacial lakes, or geographic isolation between populations East and West of the Andes in some populations. A maximum likelihood phylogenetic tree (POPtree) again reveals patterns of isolation by distance, with some outlier populations. Results from a hierarchical AMOVA with populations grouped by drainage, and drainage by basin are discussed, as well as spatial genetic analyses using genGIS.

Low Pass Whole Genome Sequencing (LPWGS) For Structural Variant Detection In Multiple Myeloma Samples

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Abstract

The prognosis and treatment of multiple myeloma is based upon detected copy number variants (CNVs) and chromosomal translocations. The FISH technique is currently the established method for detecting CNVs and translocations. However, in diseases with numerous different chromosomal irregularities, the technique requires many probes be used, contributing to a more laborious, time consuming, and expensive process. A proposed alternative is low-pass whole genome sequencing (LPWGS), a next-generation sequencing method that randomly sequences portions of the genome at resolutions lower than 1.0X to find CNVs and some translocations. Previous work has shown that LPWGS is a cheaper and faster method of detecting CNVs at high-fidelity, but the extent to which it can detect translocations is poorly understood.

The aim of this study was to determine if LPWGS is able to detect translocations indicative of multiple myeloma from purified samples taken from tumours. If LPWGS was able to detect translocations, the various sensitivities of this method would be determined by using computational sub-sampling techniques and by constructing hybrid datasets; this would determine both the minimum number of sequencing reads per sample needed to detect translocations with high precision, and the minimum percentage of tumour DNA in a sample that may be successfully tested.

Six previously-obtained, 95% purified multiple myeloma samples sequenced at ~50 million reads each were analyzed using six different translocation detection algorithms: Manta, SAMBLASTER, Breakdancer, DELLY, LUMPY, and SV-Bay. The limit of detection for each was then determined by analyzing the same dataset at lower read depths: 20, 10, 5, 2, 1, and 0.5 million reads. Following this, their CNV and translocation detection, as well as copy-number calling capability, was tested in synthetic non-purified datasets by mixing the data from 95% pure samples (with subsampling) to produce different purity levels: 50%, 30%, 25%, 20%, 15%, 10%, and 5%. Each of these purities was tested at each of the above-mentioned sequence read depths, for each algorithm.

The implication of LPWGS use in a clinical setting will be discussed, including the potential to significantly reduce wait times and costs of treatment for individuals with diseases involving chromosomal abnormalities.

Mark Density Of Cape Breton Long-Finned Pilot Whales (*Globicephala melas*) Using Drone Photography

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Abstract

Little is known about the intraspecific and anthropogenic interactions of long-finned pilot whales (*Globicephala melas*). However, both the type and density of visible markings on pilot whales can be used to characterize these behavioural interactions. Drone flights from a zodiac were used to collect photographs, at an altitude of approximately 25m, from a population of pilot whales that summers off Cape Breton Island, Nova Scotia, Canada. These aerial images allow for a greater portion of the whale's surface area to be observed in comparison to traditional boat-based photography. Using these photos, I categorized mark types and quantified mark densities for pilot whales (N=110) from different age classes, including adults, juveniles and several different ages of calves ranging from young newborns to older grey calves. Additionally, I divided whales into 6 portions of equal surface area to compare mark densities on specific areas of the body (e.g. melon vs. tail stalk). I then used chi-squared analysis to compare the mark densities on these different areas of the body. I expect there to be a greater overall mark density in mature individuals, especially for mark types known to originate from competitive and sociosexual behaviours (e.g. rake marks). Additionally, I expect that there will be a significant difference in mark densities and types between the different areas of the body. For example, studies of other cetacean species have shown that anthropogenic interactions related to entanglements tend to result in scarring concentrated around the mouth, pectoral fins, and flukes. This is the first time that natural and anthropogenic markings visible in drone photographs have been used to learn more about the behavioural interactions of long-finned pilot whales.

Does Anthropogenic Noise Decrease Immune Response In Tree Swallow (*Tachycineta bicolor*) Nestlings?

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Supervisor(s): Dr. Marty Leonard, Biology Department, Dalhousie University
and Dr. Andrew Horn, Biology Department, Dalhousie University

Abstract

Anthropogenic noise is increasing on a global scale. This noise is having negative effects on both terrestrial and aquatic species, leading to behavioural changes that impact survival. In birds, noise has been shown to affect acoustic communication, but it may also have other effects such as increasing stress levels, which in turn could affect immune responses. Despite these potential effects, there is little known about whether birds experience such physiological changes in response to noise. The goal of my study was to determine if anthropogenic noise decreases immune response in nestling Tree Swallows (*Tachycineta bicolor*). Broods were assigned to either a noise treatment where 65 dB of white noise was played for 24 hours from 2 days post-hatch until 14 days or a control treatment with no added noise. To determine the effect of noise on the immune response, when nestlings were 13 days post-hatch, they were injected with 40 μg of Phytohemagglutinin (PHA) dissolved in 20 μl of PBS in the skin of the left wing-web. After 24 hours, I measured the size of the swelling with electronic calipers at the location of the injection. Smaller swelling indicated a reduced immune response. I found a smaller swelling response in noise compared to control nestlings and in small nestlings compared to large nestlings, although neither comparison was significant. I also found that nestlings in small broods had significantly smaller swellings than nestlings in larger broods. My results suggest that exposure to anthropogenic noise does not dampen the immune response of nestling Tree Swallows but that the competitive environment of the nest may affect the immune response. This information can potentially provide valuable insight on the potential physiological effects of anthropogenic noise.

Optic Nerve Conductivity In A Mouse Model Of MS With Reduced Levels Of The Voltage-Gated Sodium Channel Nav1.6

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Supervisor(s):	Dr. Patrice Côté, Biology, Dalhousie University Dr. François Tremblay, Opthalmology, Dalhousie University

Abstract

The Atlantic Provinces in Canada is one of the regions with the highest incidence of multiple sclerosis (MS) in the world, with 350 cases per 100,000 population. MS is a progressive neurological disorder that results in demyelination of neurons in the central nervous system. There is circumstantial evidence showing a correlation between the dysregulation of Nav1.6 following demyelination and axonal death. In the experimental autoimmune encephalomyelitis (EAE) mouse model of MS, we used a tissue-specific knockout approach to selectively eliminate Nav1.6 in the optic nerve. Preliminary results reveal improved neuropathology in retinas and optic nerves with reduced Nav1.6 expression relative to tissue with normal levels of Nav1.6 . My project consisted in measuring the conductivity of the optic nerve to determine if the histology translates to improved function. I hypothesized the signal amplitude would increase and the delay would decrease in the acquisition of visual evoked potentials (VEP) at the superior colliculus following a stimulus at the eye with reduced Nav1.6 compared to the control eye. By injecting an adeno-associated virus (AAV) harbouring the CRE recombinase gene in the left eye of mice with a 'floxed' Nav1.6 gene, we selectively reduced Nav1.6 levels in the left eye and used the right eye as a control. During the chronic phase of disease (44 days following EAE induction), we performed electroretinogram (ERG) and VEP recordings on both eyes (C57Bl/6 strain wild-type mice also served as controls). On average, the ERG showed a similar waveform and amplitude for the left and right eyes across treatment groups, indicating both retinas responded similarly to the stimulus. For the VEP, on average there was no significant difference between the left and right eyes for mice with no disease and no CRE. There was also no significant difference between the eye injected with CRE and the control eye for mice with and without EAE, but the data tended to show an increased amplitude for the eye injected with CRE compared to the control. The experiment can be improved by using auditory activity in the inferior colliculus to aid in aligning the left and right electrodes at the same position in the superior colliculus to reduce the error in the measurement and obtain more accurate results than with the current protocol. This study will help to determine how experiment conditions can be improved to accurately assess optic nerve conductivity in the EAE mouse model.

Crassostrea virginica Mortality under Anoxic Conditions: Influence of Temperature and Secondary Bacterial Source

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Supervisor(s): Ramón Filgueira, Marine Affairs, Dalhousie University

Abstract

Low oxygen conditions can result in depressed bivalve defense systems whilst allowing anaerobic bacteria to proliferate, ultimately causing bivalve mortality. Bacteria causing the mortality are assumed to be endogenous to the bivalve. In 2016 there was a high mortality of *Crassostrea virginica* (Eastern Oyster) at Tracadie Bay, New Brunswick. This was ascribed to anoxic water conditions and coincided with an elevated water temperature; however, *C. virginica* mortality occurred at a rate faster than predicted from current literature. The effects of temperature (20˚C and 28˚C) and the introduction of a secondary bacteria source (anoxic farm sediment) was investigated following a fully-crossed factorial design under anoxic conditions to determine oyster survivability. In addition, an experiment was carried out to test if the conventional methodological approach in these types of experiments, i.e. removing dead bivalves from the population, has an impact on survivability. When removing dead oysters, survivability was similar between 28˚C farm sediment (Lt_{50} 9.66 days) and 28˚C sterile sediment (Lt_{50} 10.92 days). Survivability increased for 20˚C farm sediment (Lt_{50} 12.17 days), with the longest survivability in 20˚C sterile sediment (Lt_{50} 17.85 days). The effect of not removing dead oysters resulted on similar survivability between 28˚C farm sediment (Lt_{50} 8.04 days), 28˚C sterile sediment (Lt_{50} 9.29 days) and 20˚C farm sediment (Lt_{50} 9.75 days), and significantly higher value in 20˚C sterile sediment (Lt_{50} 13.67 days). Results demonstrate that at the highest tested temperature (28˚C) the effect of a secondary bacterial source is not significant; however, at lowest temperature (20˚C) it may have an impact. Results also indicate that dead oyster removal increases oyster survivability, which challenges the results obtained with the conventional methods. These results can be used to improve farm management practices as anoxic events become more common due to climate change.

Maternal-Paternal Conflict In Cardinal Flower Populations

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Abstract

During embryogenesis and early development, resources are partitioned from mother to developing offspring. In polyandrous species with multiple offspring per brood, the maternal parent optimally invests equally in each offspring, while each father benefits from garnering higher resource provisioning for its offspring. The result is a tug-of-war between maternal and paternal genes. In angiosperms, embryos are nourished by the endosperm whose size is thought to be facilitated by sex-specific genomic imprinting: growth enhancers in paternal genes and suppressors in maternal genes. These genetic mechanisms co-evolve independently in different populations, so while conflict over resources is matched within populations, it might differ among populations. Hybrid offspring size should be affected when parents are from populations with different levels of conflict due to mismatched levels of growth enhancers/suppressors. Previous work has suggested that hybrids between one eastern and one western population of cardinal flower (*Lobelia cardinalis, Campanulaceae*), a diploid eudicot distributed throughout eastern and southwestern North America, exhibit small seeds when eastern populations are used as dams, suggesting greater levels of conflict in eastern populations. The purpose of the current work is to examine (1) hybrid offspring seed size on a larger scale and (2) the developmental basis of size differences. *L. cardinalis* specimens from 8 populations (5 eastern and 3 western) were grown in a common garden and reciprocally crossed to produce hybrid offspring. Hybrids were also crossed with both parents to produce backcrosses. Seeds were collected at maturity and their size was determined using a scanner and image-analysis software. One eastern and one western population was chosen to investigate seed (embryo and endosperm) development in hybrids and within-population crosses. Ovaries were collected at 3, 6, 9, and 12 days after pollination were examined for 8 traits using confocal laser microscopy. Seed size results indicate that eastern populations exhibit higher levels of conflict over resources. However, results from early development are conflicting: 6 traits indicated no difference in conflict between populations when western plants were used as dams, whereas 7 traits indicated greater conflict in western populations when eastern plants were used as dams. Potential causes of the discrepancy between early development and final seed size are discussed.

Photographic Sex Analysis Of Northern Bottlenose Whale (*Hyperoodon ampullatus*) Populations On The Eastern Canadian Continental Shelf

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Abstract

The northern bottlenose whale (*Hyperoodon ampullatus*), found in the North Atlantic, is sexually dimorphic; when mature, the shape of their foreheads, or melons, can be used to determine the sex of individuals. Several northern bottlenose whale populations reside along the eastern Canadian continental shelf including the Scotian Shelf population which has been the focus of nearly thirty years of research, the Newfoundland population and the Davis Strait-Baffin Bay population. Understanding the sex of individuals and the sex-age ratios of these small populations is important for monitoring the populations' stability and survival. Previously other studies have used photographs to determine the sex of individuals which agreed with genetic data with an error rate of 3.3%. For this project we reviewed and tested a new protocol to see if more specific criteria could improve classification results using an additional 13 years of photographic data and genetic information. For the long term data set collected on the Scotian Shelf, I looked at the development of the melons of male northern bottlenose whales to estimate when they begin to gain dimorphic features and how long this development takes. For each of the three populations I determined the sex ratios, and within the Scotian Shelf population, I determined whether the sex ratios varied spatially or temporally. My preliminary results suggest that a skewed sex ratio is not a concern for northern bottlenose whale population dynamics, and that photographic analysis of melons can provide a confident non-invasive method of identifying individual sex for population monitoring.

Determination Of Genome Size, Chromosome Number And Ploidy Level In *Aponogeton madagascariensis*

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Abstract

Aponogeton madagascariensis, also known as the lace plant, is an aquatic monocot that is native and endemic to Madagascar. Lace plant develops perforations in its leaves through developmentally regulated programmed cell death (PCD). The lace plant has outstanding potential as a model system to study developmentally-regulated PCD in plants due to: the accessibility and predictability of perforation formation, the ability to perform live cell imaging of the thin and semi-transparent leaves, and the availability of an established sterile culture system for propagation. Little to no genetic information is known about the lace plant or members of the Aponogetonaceae family. The importance of the lace plant as a model requires the establishment of genetic information. Therefore, this study aims to determine the genome size, exact chromosome number and ploidy level.

First, sterile mature lace plant leaves were extracted and sent to Benaroya Research Institute to the flow cytometry lab to determine the genome size. To obtain chromosome counts, healthy root tips were removed during sterile propagation and treated in a solution of 8-hydroxyquinoline for 4 hours to halt the active cell division at metaphase. This allows for condensed and stable chromosomes to be fixed in 70% FAA for 2 hours. Roots were rinsed and then either crushed into a fine powder using liquid nitrogen or digested with cellulase and pectinase to isolate root protoplasts. The powder or protoplast solution was spread on a slide in DAPI stain (20µg/ml). Slides were observed using confocal microscopy (100x objective). Micrographs and z-stacks were obtained using the NIS elements program. Stained chromosomes were counted using ImageJ image processing software. The squash procedure was also completed using developing anthers from inflorescences. However, the actively dividing root tips provided better results than attempting to observe a dividing mother pollen cell from the anthers. Preliminary counts from the root squash support a chromosome number of 80 which will be verified through replicates. The flow cytometry revealed a genome size of 1.01pg/C (~995Mbp/C). We will attempt to determine the ploidy level through a combination of flow cytometry with a reference genome of a closely related Aponogeton species and confocal microscopy. If these methodologies are unsuccessful, future research into ploidy level can be performed using Fluorescent In Situ Hybridization (FISH).