11th Biology Graduate Student Symposium

April 12th, 2018



Schedule at a Glance

8:15-9:50	Registration Science Lobby
8:50-9:00	Opening remarks (Emma Cooke) Room 2101
9:00-10:15	Oral Presentations Rooms 2101 & 2098
10:15-10:45	Coffee Break Science lobby
10:45-12:00	Oral Presentations Rooms 2101 & 2098
12:00-13:00	Lunch Science Lobby
13:00-14:30	Oral Presentations Rooms 2101 & 2098
14:45-15:45	Coffee Break Poster Session (Science lobby)
16:00 – 17:00	Keynote Presentation C 2004
17:00-19:00	Reception Quintanas

Symposium Planning Committee 2018

Emma Cooke

Symposium Committee Chair BGSA Professional Development Coordinator

Michael Laforge

Photo Contest Coordinator BGSA Communications Officer

Matteo Rizzuto

Public Talk Organizer External Funding/Sponsors BGSA Seminar Coordinator

Quinn Webber BGSA Seminar Coordinator

Liang Zhu BGSA GSU and Faculty Rep

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Internal/External Funding Science Communication Workshop Coordinator BGSA Chair

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Fundraising BGSA Special Events Coordinator Dean, School of Graduate Studies

Dr. Aimee Surprenant

As Dean of the School of Graduate Studies at Memorial University of Newfoundland it is one of my greatest pleasures to hear about and promote graduate student research. The students in Biology make that very easy for me to do. The varied projects they are involved in are fascinating whether they investigate fundamental contributions in



fruit fly genetics, fieldwork on wolf behaviour, or fatty lipids in Arctic plankton. There is always something for me to crow (or tweet) about. In addition to their innovative research, many of the students are heavily engaged in knowledge mobilization and translation--a buzz-word laden phrase for making research understandable and useful to the public. This step--going from the laboratory to the community--is not part of 'traditional' laboratory work but it is increasingly important for academics to show how their work can contribute to the public good. Thanks to all the Biology graduate students for helping the university showcase the fantastic work that is being done. Keep me up to date on what you are doing! Interim Dean of Science

Dr. Mary Courage

I would like to welcome you to the 2018 *Biology Graduate Student Symposium*. This event is a great opportunity for our students to highlight their research projects in an informal setting, to network among their peers and faculty mentors, and to communicate their findings and ideas for the next steps in their research. The audience will hear the latest findings on a range of



topics and issues of current importance in biology and will no doubt appreciate the creativity, the challenges, and the hard work of our next generation of young scientists. The rapid pace of social, environmental, medical, and technological change today will confer a huge responsibility on them. Nationally and globally there is a high demand for innovation, discovery, and application in all the science fields and biology is at the centre of many of them. The symposium promises to be a stimulating experience for all participants and a great forum for discussion of current and future challenges!

Head of the Department of Biology

Dr. Paul Marino

On Behalf of the Department of Biology I welcome all participants and thank them for continuing the tradition of making the Biology Graduate Student Association (BGSA) annual research symposium a significant feature in the life of the Department of Biology. This research symposium brings together graduate students, not only from the Department of Biology, but



also graduate students from the Centre for Fisheries Ecosystems Research, Cognitive and Behavioural Ecology, Environmental Science and the Department of Ocean Sciences. The symposium breaks the boundaries among units and highlights the multidisciplinary nature of biological research at Memorial University. The efforts of the BGSA and the graduate students in the participating units are very much appreciated. Graduate Officer, Department of Ocean Science

Dr. Chris Parrish

On behalf of the Department of Ocean Sciences, I am pleased to wish you a very productive symposium which will bring together a diverse breadth of exciting research taking place campus-wide. This is a wonderful opportunity for you to inform us (your colleagues, peers, supervisors / mentors, etc.) of the excellent research that you have been doing at



Memorial University, and I am sure this year's BGSS will again be a resounding success.

This symposium is about providing you with a forum to communicate your research interests and progress, and for us (the audience) to acknowledge your accomplishments, and to assist you in your further growth if possible. I am sure there will be many first-rate presentations during the symposium, and interesting discussions, and I am happy to see that the tradition of the BGSS continues. It is a great event, and provides not only an important forum for you to develop as young scientists, but also for the Memorial community to assist you in this transformation. Enjoy the symposium! Biology Graduate Student Association, Symposium Chair

Emma Cooke

On behalf of the 2017-18 Biology Graduate Student Association and Symposium Planning Committee, I would like to welcome all students, faculty, audience members and our keynote speaker, Dr. Susan Lingle, to the 11th annual BGSS! The BGSS was created to enhance student professional development opportunities, provide



students with an opportunity to share their research, and support the research of their peers.

I would like to extend a huge thank you to all our sponsors for helping us keep this event running free for students, and thank you to our exhibitors SubC Imaging, SAEN, WWF, MI/CFER, OSC touch tank and Petty Harbour Mini Aquarium. I would also like to thank Dr. Susan Lingle for travelling all the way to Newfoundland to deliver our keynote presentation, and tomorrow's public seminar. Lastly, I would like to thank all the amazing volunteers who have helped plan the symposium and make today run smoothly; without you the BGSS would not be possible! Keynote Speaker

Dr. Susan Lingle

Susan did a M.E.Des. in Environmental Science at the University of Calgary and a PhD in Zoology at Cambridge University, and is now an Associate Professor in Biology at The University of Winnipeg. She and her students conduct longterm work on mule deer, white-tailed deer and coyotes at a prairie grassland field site in southern Alberta. The



open landscape makes it possible to observe behaviours and events (e.g., predator-prey interactions) that are difficult to observe elsewhere. Students in her lab are currently using direct observations of deer to investigate species differences in courtship behaviour and behavioural mechanisms that may transmit prions associated with Chronic Wasting Disease (CWD). Another facet of research in her lab is animal communication. Susan and her students conduct playback experiments with deer, and more recently with humans, to investigate the evolution of infant cries and other emotional vocalizations. She is excited to visit MUN and Newfoundland. Keynote Summary

Dr. Susan Lingle

Associate Professor, University of Winnipeg

When deer fight back: Prey defences as a window into behaviour, ecology and animal minds

Whether a prey animal flees or fights when a predator approaches can shape the social behaviour, ecology and even the psychology of the prey animal. In this presentation, I will illustrate how the divergent responses of white-tailed and mule deer to predators - fleeing vs. fighting, respectively - influence coyote hunting success and prey survival. I will then summarize research we have done to investigate whether these differences in antipredator behaviour shape other aspects of their behaviour or their population ecology, including seasonal and annual variation in survival patterns and density dependent survival. Last, I will introduce you to our current research into infant cries (distress calls), a type of vocalization that fawns make when attacked by covotes and a form of communication that appears nearly universal across mammals.

Past Keynote Speakers

2017 – Dr. Joe Roman University of Vermont

2016 – Dr. James Sulikowski University of New England

2015 – Dr. Catherine Potvin *McGill University*

2014- Dr. Diane Orihel University of Alberta

2013- Dr. Jean-Michel Weber University of Ottawa

> **2012- Dr. Lisette Waits** University of Idaho

2011- Dr. Stephanie Carlson University of California Berkeley

> **2010- Dr. John Smol** *Queen's University*

2009- Dr. Tom Nudds University of Guelph

2008- Dr. Tom Chapman *Memorial University*



PROGRAM



Poster Session

14:45 – 15:45 Science Lobby

Anne Provencher St-Pierre	Applying remote sensing and landscape metrics to spatiotemporal analysis of kelp distribution in the northern Gulf of St. Lawrence	
Bronwen Hennigar	Effects of anthropogenic light and noise on the vocal behaviour and spatial ecology of birds	
Eugueni Matveev	Examining the intra-individual relationship between bev behaviour and physiology in the green shore crab (<i>Carcinus maenas</i>)	
Jaclyn Aubin	Investigation of allomaternal care in the endangered St. Lawrence estuary beluga (<i>Delphinapterus leucas</i>) population	
Jeffrey Ethier	Using microphone arrays to determine critical habitat and microhabitat for common avian species in decline	
Jingyu Liu	Characterization of a cryptic secondary metabolite in the common scab pathogen <i>Streptomyces scabies</i>	
Juliana Balluffi-Fry	Multi-scale test of moose foraging strategy using quantitative elemental measures for forage quality and quantity	
Julie Jacques	Temperature and reproductive stage modulate consumption, fecal production, and roe yield, in green sea urchin (<i>Strongylocentrotus droebachiensis</i>) fed a new formulated feed	
Katrina Shwedack	Does anthropogenic noise cause a communication breakdown in dark-eyed juncos (<i>Junco hyemalis</i>)?	
Kaylee Busniuk	Kleptoparasitic interactions between Atlantic puffins (<i>Fratercula arctica</i>) and herring gulls (<i>Larus argentatus</i>)	
Leanne Guzzwell	Breeding success at the Northern Gannets' (<i>Morus bassanus</i>) southernmost Colony – Cape St. Mary's, Newfoundland: A comparison of methods	
Luke Bown	Production of coronafacoyl phytotoxins involves a novel biosynthetic pathway in the plant pathogen <i>Streptomyces scabiei</i>	
Sydney London	The interactive mechanisms regulating reproduction and feeding in zebrafish	
Travis Heckford	Constructing the stoichiometric landscape: Spatial correlates of plant elemental composition	

PRESENTATION SCHEDULE - ROOM 2101

8:50 - 9:00		OPENING REMARKS
9:00 - 9:15	Emma Cooke	Assessing the use of coastal seine surveys in detecting recruitment signals of Atlantic cod (<i>Gadus morhua</i>)
9:15 - 9:30	Violaine Shikon	Larval fish community structure along the Northeast coast of Newfoundland
9:30 - 9:45	Heather Penney	Banded killifish on the edge: Potential reproductive issues in a species of concern
9:45 - 10:00	Evelyn MacRobert	Spatial risk: Influence of piscivorous fish on selection of nursery habitat by Age-o juvenile cod
10:00 - 10:15	Emilie Geissinger	Overwinter growth, condition, and survival of juvenile Atlantic cod (<i>Gadus morhua</i>) in coastal Newfoundland
10:15 - 10:45		COFFEE BREAK
10:45 - 11:00	Elena Salogni	How do pups differ in size in the most sexually dimorphic species of seal?
11:00 - 11:15	Quinn Webber	Space-use and social organization in a gregarious ungulate: testing the conspecific attraction and resource dispersion hypotheses
11:15 - 11:30	Michel Laforge	Migration timing of caribou reveals plasticity in movement and forage selection in response to environmental change
11:30 - 11:45	Christina Prokopenko	Killing time: Exploring temporal variation of wolf (<i>Canis lupus</i>) kill rates on multiple prey in Riding Mountain National Park
11:45 - 12:00	Sana Zabihi- Seissan	Gray wolves (<i>Canis lupus</i>) follow the prey habitat and prey catchability hypotheses to track prey in a multi-prey system
12:00 -		LUNCH BREAK
13:00 - 13:15	Rachel Wigle	Drivers of arboreal lichen community diversity and structure
13:15 - 13:30	Meghan Noonan	Modelling forest restoration after moose over browsing
13:30 - 13:45	Lancy Cheng	Finding a needle in the syringe box: Identifying Newfoundland and Labrador's first willow flycatcher (<i>Empidonax traillii</i>)
13:45 - 14:00	Maria Esther Nieto- Blazquez	Evolutionary history of the tropical conifer genus <i>Podocarpus</i> in Hispaniola
14:00 - 14:15	Sander Bennett Boisen	Clade-by-clade analysis of community phylogenetics data reveals multiple levels of structure with possible link to process

PRESENTATION SCHEDULE - ROOM 2098

9:00 - 9:15	Maggie Folkins	Using underwater video to conduct resource assessments for new emerging fisheries in Kimmirut, Nunavut	
9:15 - 9:30	Ethan Armstrong	Investigating single-beam sonar as a tool to detect the benthic footprint of aquaculture in Newfoundland	
9:30 - 9:45	Liang Zhu	Characterization of diet and growth for a marine species currently undergoing distribution shifts	
9:45 - 10:00	Khalil Eslamloo	Discovery of microRNAs associated with antiviral immune responses of Atlantic cod macrophages	
10:00 - 10:15	Sabrina Inkpen	Effects of varying dietary Omega-6 and Omega-3 Fatty Acid levels and immune stimulation (Viral Mimic versus LPS) on the transcriptome of Atlantic Salmon macrophages	
10:15 - 10:45		COFFEE BREAK	
10:45 - 11:00	Joost Verhoeven	The microbiome of deep sea carnivorous sponges	
11:00 - 11:15	Brandon Piercey	The role of xenobiotic response element family transcriptional regulators and DUF397-containing proteins during antibiotic production in <i>Streptomyces</i> <i>clavuligerus</i>	
11:15 - 11:30	Nader AbuSara	Examination of clavulanic acid biosynthesis using a comparative genomics approach	
11:30 - 11:45	Yuting (Phoebe) Li	Investigate the role of TxtH in the biosynthesis of the thaxtomin A in the common scab pathogen <i>Streptomyces scabies</i>	
11:45 - 12:00	Jordan Wight	Detection and characterization of antibiotic resistant coliforms: What's found in the lakes and ponds around us	
12:00 - 13:00		LUNCH BREAK	
13:00 - 13:15	Devin Cochrane	Differential expression of alternative oxidase modulates the normoxic and hypoxic metabolism of amino acids, organic acids, and reactive oxygen and nitrogen species	
13:15 - 13:30	Jayamini Jayawardhane	Nitric oxide production by plants under anoxia	
13:30 - 13:45	Amrita Ghosh	Effect of cytokinins on the somatic embryogenesis of lowbush blueberry plants	
13:45 - 14:00	Victor Valdez	Nitrogen cycling genes in a long-term land-use converted boreal land in Newfoundland, Canada	
14:00 - 14:15	Sean Hacker Teper	What's for dinner? Building a Newfoundland rhodolith community food web	
14:15 - 14:30	Laura Teed	Influence of bioturbators on annual growth rate of southeast Newfoundland rhodoliths, <i>Lithothamnium glaciale</i>	

Awards to be presented:

Best M.Sc. talk in Evolution and Ecology Best M.Sc. talk in Cellular and Molecular Biology Best PhD talk in Evolution and Ecology Best PhD talk in Cellular and Molecular Biology Joe Brown Award for Excellence in Science Communication Best Poster

Past Award Winners:

Best M.Sc. Talk

2017 – Evolution and Ecology – Sana Zabihi-Seissan

2017 – Cellular and Molecular Biology – Kelcey King

2016 – Evolution and Ecology – Kyle Millar

2016 – Cellular and Molecular Biology – Kelcey King and Luke Bown

2015 – Evolution and Ecology – Kyle Millar

- 2015 Cellular and Molecular Biology – Andrew Chaulk
- 2014 Chris Hammill
- 2013 Morag Ryan
- 2012 Margie Wilkes
- 2011 Becky Graham

2010 – Kevin Ma 2009 – Rachel Buxton 2008 – Alain Lusignan

Best PhD Talk

2017 – Evolution and Ecology – Brittany Palm-Flawd

2017 – Cellular and Molecular Biology – Marc Gruell

2016 – Evolution and Ecology – Emilie Novaczek

2016 – Cellular and Molecular Biology – Linda Lait

2015 – Evolution and Ecology – Holly Caravan

2015 – Cellular and Molecular Biology – Lancey Cheng

2014 – Renauld Belley

2013 – Barbara de Moura Neves and Paul Regular 2012 – Arnault Lebris 2011 – Amy-Lee Kowenberg 2010 – Peter Westley 2009 – Alex Bond 2008 – Susan Squires

Best Poster

- 2017 Anne Provencher St. Pierre
- 2016 Brittany Palm-Flawd
- 2015 Carley Schacter and Katherine Robbins (coauthors)
- 2014 Sarah Adcock and Barbara de Moura Neves
- 2013 Laura Wheeland

2012 – Andrew Murphy 2011 – Michelle Fitzsimmons

Joe Brown Award

- 2017 Emilie Novaczek
- 2016 Miguel Meijas
- 2015 Greg Furey and Emilie Novaczek
- 2014 Margie Wilkes
- 2013 Chris Hammill
- 2012 Jill Robinson
- 2011 Margie Wilkes
- 2010 Kevin Ma
- 2009 Julia Wheeler
- 2008 Sempath Seneviratne



ABSTRACTS



Effect of cytokinins on the somatic embryogenesis of lowbush blueberry plants

Amrita Ghosh^{1,2*}; A.U. Igamberdiev¹; & S.C. Debnath²

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²St. John's Research and Development Centre, Agriculture and Agri-Food Canada, St. John's, NL

An efficient protocol has been developed for somatic embryogenesis from leaf explants of two lowbush blueberry (*V. angustifolium* Ait.) wild clones using two cytokinins, 6-benzyl amino purine (BAP) and thidiazuron (TDZ). At the low concentration of BAP and TDZ (1 µM) in the basal medium (BM), no morphogenesis was observed. BAP induced callus and adventitious shoots thereafter when added in the media at a concentration of $2.5 - 10 \mu$ M. The highest number of adventitious shoots was induced when BM was supplemented with 10 µM BAP (35.5/explant). BM containing only TDZ gave rise to somatic embryos after 6 weeks of culture. The highest number of somatic embryos per explant (40.67/explant) was recorded at the high concentration of TDZ (10 µM). Somatic embryos germinated when they were transferred to the BM containing relatively low concentration of TDZ $(2.5 \,\mu\text{M})$ after 4 weeks of embryo induction. Plantlets of 4 – 5 cm height were removed from tissue culture system and 100% survival rate was acquired following the acclimatization process when transferred to the ProMix BX in small plastic pots $(25 \times$ 18×6 cm). Thus, it is evident from the current study that somatic embryogenesis in lowbush blueberry plants requires high concentrations of TDZ.

Applying remote sensing and landscape metrics to spatiotemporal analysis of kelp distribution in the northern Gulf of St. Lawrence

Anne Provencher St-Pierre*; & P. Gagnon

Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

Kelps are important drivers of productivity in cold-water systems. Quantifying distribution of kelp beds at broad spatial (km) and temporal (10s of years) scales is key to assessing structural and functional stability of these biologically diverse communities, yet is inherently difficult to achieve both logistically and conceptually. Changes in kelp distribution in the Mingan Archipelago (northern Gulf of St. Lawrence) were quantified from aerial images of 3 km2 of shallow (<7 m) seabed around six islands acquired in the summers of six years from 1983 to 2016. Each of the 10,308 spatial units (15 x 15 m each) on the imagery was visually assigned one of two cover types in each year: kelp and non-kelp. Kelp coverage generally increased over time, from 44% in 1983, to 62% in 2016. Landscape metrics showed that the mean surface area of kelp patches increased from 10,710 m2 in 1988, to 32,130 m2 in 2016. This increase was caused mainly by the expansion of the largest kelp patch, from 10-15% of the entire study area from 1983 to 1999, to 22-32% from 1999 to 2016. Clumpiness index and mean distance between nearest patches of a same cover type were consistent, from 0.50 to 0.66 and 36 to 44 m, respectively, across all years and cover types, indicating that both cover types were highly aggregated. Relationships between landscape metrics, kelp bed stability, and environmental variability (e.g. ice cover, water temperature, exposure to waves, bathymetry) are discussed.

The role of xenobiotic response element family transcriptional regulators and DUF397-containing proteins during antibiotic production in *Streptomyces clavuligerus*

Brandon Piercey*; & K. Tahlan

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Streptomyces clavuligerus is a known producer of many bioactive natural products (NP), including clavulanic acid (CA). CA is an atypical β-lactam, as it lacks intrinsic antimicrobial activity. Rather, CA has the ability to inhibit β-lactamases; enzymes that confer resistance to 6-lactams such as penicillin and cephalosporin. CA production requires industrial scale fermentation of S. clavuligerus. As a result, there is considerable interest in further understanding CA regulation. In addition to genes encoding for CA, more than 40 cryptic biosynthetic gene clusters have been identified in S. clavuligerus. Further understanding antibiotic regulation may allow for the activation of these cryptic gene clusters. The Xenobiotic Response Element (XRE) family of transcriptional regulators have been shown to be differentially expressed in *S. clavuligerus* mutants defective in development and/or NP biosynthesis. This suggests XREs may be involved in regulating development and specialized metabolism. Previous studies have shown that the XRE regulator WhiJ functions in inhibiting NP biosynthesis, while its association with a DUF397containing protein abolishes this negative regulation. Thus, XRE/DUF397 pairs may be pivotal in regulating NP biosynthesis in S. *clavuligerus*. By creating mutants defective in genes encoding for XREs and DUF397-containing proteins, as well as double mutants defective in XRE/DUF397-pairs the role of these regulators may be elucidated. The mutants will be assessed for their ability to produce NP, including CA as well as novel products. Understanding the complex regulatory mechanisms involved in controlling NP biosynthesis is essential to in allowing complete exploitation of the biosynthetic capabilities of the Streptomyces.

Effects of anthropogenic light and noise on the vocal behaviour and spatial ecology of birds

Bronwen Hennigar1*; & D. Wilson1,2

¹Department of Psychology Memorial University of Newfoundland, St. John's, NL ²Department of Biology, Memorial University of Newfoundland, St. John's, NL

Understanding the direct effects of how anthropogenic disturbance influences animal behaviour is challenging as varying forms often occur simultaneously. Consequently, observational studies tend to rely on measuring the combined effects of multiple disturbances, such as traffic noise, artificial lighting, and habitat alteration in conjunction with observing the effects of roadways on animal behaviour. Experiments can indicate whether the effects of multiple disturbances are redundant, additive, or synergistic, but most experiments conducted to date have either focused on a single type of disturbance, such as noise, or on captive animals housed in artificial environments that may not be necessarily representative of their wild counterparts. We tested the effects of light and noise on the singing and spatial ecology of birds during the avian breeding season in 2016 (May-July) and 2017 (May-June), in Labrador, Canada. We manipulated noise and light treatments within 110 40x40m area using a 4-unit, 8 channel microphone arrays within a relatively pristine boreal forest habitat. Arrays recorded avian vocalizations produced before, during, and after manipulations, which allowed us to localize singing birds as they respond to treatments. Analysis shows the independent and combined effects of anthropogenic light and noise on the vocal behaviour and fine-scale spatial movements of birds. Our 'living laboratory' experiments seek to provide greater insight into the mechanisms underlying previously reported declines in avian populations affected by anthropogenic disturbance in order to help manage and offset the effects of light and noise on avian populations.

Killing time: Exploring temporal variation of wolf (*Canis lupus*) kill rates on multiple prey in Riding Mountain National Park

Christina Prokopenko*; S. Zabihi-Seissan; & E. Vander Wal Department of Biology, Memorial University of Newfoundland, St. John's, NL

Predator-prey interactions can change in animal abundance and distribution. For example, predators and prey each vary their space use to maximize or minimize their encounter rates. This tension is often quantified spatially, but important variation in space use behaviour, and its consequences exists over time. Wolves in Riding Mountain National Park, Canada, feed on multiple prey species (moose, white-tailed deer, and elk). We evaluated temporal variation in kill rates by wolves responding to a diverse prey source using the ideal gas law. Kill rates were determined from the GPS data of wolves and related to wolf speed and prey GPS data, and covariates that influence detectability (e.g. light levels). Wolf speeds were much greater than that of their prey, thus governing the effective speed of the system. Yet overall kill rates, winter kill rates, prey specific kill rates of moose (primary prey, 43.7% of diet) and white-tailed deer (22.4%) were not related to speed but increased with total light. Only summer kill rates increased with speed, possibly due to the restricted movements and ability to track prey from denning and pup rearing. My work indicates a decoupling between wolf movement and hunting success, challenging behavioural underpinnings in predator-multiprey dynamics.

Differential expression of alternative oxidase modulates the normoxic and hypoxic metabolism of amino acids, organic acids, and reactive oxygen and nitrogen species

Devin Cochrane^{1*}; P. Vyas¹; G. Vanlerberghe²; & A. Igamberdiev¹

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Department of Biological Sciences, University of Toronto, Toronto, ON

The alternative oxidase (AOX) has a lower affinity for oxygen than cytochrome c oxidase (COX). However, unlike COX, AOX is not inhibited by nitric oxide (NO) and thus could act to maintain respiration under stress conditions such as hypoxia, when the amount of NO can increase. In the present study, transgenic Nicotiana tabacum plants with modified AOX expression were used to examine the role of AOX under both normoxic and hypoxic conditions. AOX amount was found to affect the amount of NO measured under hypoxia. NO was significantly lower in AOX knockdown plants compared to wild type or AOX overexpression plants. AOX amount strongly influenced the activity of the mitochondrial, but not cytosolic isoform of aconitase under hypoxia, which is known to be inhibited in the presence of NO and superoxide. Knockdown of AOX increased the amount of superoxide, malondialdehyde and total antioxidant reducing power, both in normoxia and during reoxygenation after hypoxia. There were also complex changes in production of amino and organic acids due to AOX amount under both normoxic and hypoxic conditions. It is concluded that AOX has pervasive and oxygen concentration-dependent effects on respiratory carbon flow, as well as on the metabolism of reactive oxygen and nitrogen species.

How do pups differ in size in the most sexually dimorphic species of seal?

Elena Salogni1*; S. Sanvito2; F. Galimberti2; & E.H. Miller1

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Elephant Seal Research Group, Sea Lion Island, Falkland Islands

Sexual-size dimorphism (SSD) is commonly investigated in studies of mating systems, sexual selection, and parental investment. In pinnipeds, SSD has been studied widely in adults, in relation to male competition and breeding success. Adult elephant seals (Mirounga) show extreme SSD, which presumably reflects sexual selection favouring large size in males. Presumably, SSD is expressed early in life; This has been investigated little in the northern species (M. *angustirostris*), and most information comes from a single colony at Año Nuevo Island, California, at the northern edge of the species' range. Here, we present information on SSD at birth and weaning at the southernmost colony of the species, the San Benito Islands (Mexico). In 2006 and 2007, we measured 208 newborn pups and 251 pups at weaning. At birth, males were heavier (means 41 vs. 37 kg) and longer (means 128 vs. 126 cm) than females, while sexes did not differ in body mass or length at weaning. We found no evidence of sexrelated differences in growth rate or suckling duration, but SSD differed between different islands. Our results contrast with those from the northern colonies, where pups are generally heavier and show sexual differences in body mass at weaning. We recommend further studies to investigate both spatial and temporal variation within colonies and geographic variation across colonies.

Overwinter growth, condition, and survival of juvenile Atlantic cod (*Gadus morhua*) in coastal Newfoundland

Emilie Geissinger1*; R. Gregory1,2; P. Snelgrove3; & B. Laurel4

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²DFO, Ecological Science Section, St. John's, NL ³Department of Ocean Sciences and Biology, Memorial University of Newfoundland, St. John's, NL ⁴NOAA Alaska Fisheries Science Center, Newport, OR

Atlantic cod (Gadus morhua) typically experience high mortality rates during their first year of life. In subarctic Newfoundland, cod settle into coastal habitats in several recruitment pulses throughout summer and fall, resulting in a broad length-frequency distribution prior to their first winter. The first winter likely represents a critical period in cod survival, ultimately determining cohort strength. Overwinter survival is investigated through a laboratory experiment studying the effect of size and food availability on overwinter growth and condition of age-o cod, and a mark-recapture experiment was conducted to determine overwinter growth and survival rates. Experiment results show that large and small juvenile cod grow and increase condition on low rations, and food availability increases survival and strongly influences overwinter growth and condition. Large cod will survive on low rations better than small cod, indicating that early settlement is better for overwinter survival. Preliminary results of the markrecapture study indicate that size is an important factor for overwinter survival of age-o cod. Our results have significant implications for the survival of juvenile cod in coastal nurseries in a changing climate. Bigger is better when food is not available, but small fish can grow and survive on some productivity.

Assessing the use of coastal seine surveys in detecting recruitment signals of Atlantic cod (*Gadus morhua*)

Emma Cooke1*; R. Gregory1,2; D. Cote2,3; & P.V.R. Snelgrove1,3

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²DFO, Ecological Science Section, St. John's, NL ³Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

The collapse of the Newfoundland Atlantic cod (Gadus morhua) fishery in 1992 motivated studies on the factors influencing population stability and the ability to forecast future cod abundance. This study investigates the potential for using coastal seine surveys of juveniles to predict offshore adult Atlantic cod recruitment at multiple spatial (individual bay to offshore regions), and the factors influencing recruitment signal strength. Access to several multi-year (22+) datasets on juvenile and adult cod population components makes this objective feasible for the first time in Newfoundland. Generalized linear models reveal significant positive relationships between juvenile (age 0 and 1) and adult (age 3) abundance (p<0.05). However, the strength of these relationships varies with distance from nursery habitats and between fisheries management zones. Additionally, water temperature, predator abundance, and chlorophyll-a levels during early life stages appear to influence predictions of adult abundance. Studies evaluating year-class strength often overlook the value of coastal juvenile surveys. However, the potential to forecast adult abundance from juvenile populations could aid in planning for socioeconomic costs of low recruitment years, and enable inference on the response of future populations to climate change and habitat degradation.

Investigating single-beam sonar as a tool to detect the benthic footprint of aquaculture in Newfoundland

Ethan Armstrong^{1,2*}; S. Dufour¹; D. Hamoutene²; & F. Salvo²

¹Department of Biology, Memorial University of Newfoundland, St John's, NL ²Department of Fisheries and Oceans Canada, St. John's, NL, Canada

In Newfoundland, finfish aquaculture has grown substantially in the last decade, and production is expected to double by 2020. Intensive aquaculture production is associated with organic enrichment, which occurs as uneaten feed and animal excretions settle on the seafloor and form a layer of flocculent matter. Sustained deposition alters seafloor conditions, with high organic loading resulting in changes in benthic communities. Aquaculture-linked organic enrichment can be monitored through diver surveys, grab sampling and substrate imaging along defined transects. In Newfoundland, deep water and the predominately hard-bottom seafloor largely preclude the use of divers and grab sampling; instead, monitoring is performed using drop camera imaging, which is time intensive and limited in scale. Singlebeam sonar is an attractive alternative to benthic imaging due to its ability to survey larger areas of the seafloor at lower cost. Here, we examine whether single-beam sonar could be used to detect flocculent matter deposition in our region. Data collected from four single-beam surveys around aquaculture sites were overlain with drop camera images that serve as substrate type ground-truthing. With ensemble methods, algorithms will be constructed using feature data from the single-beam sonar to create and refine predictive models. From these candidate models, we will test whether machine learning can discriminate and identify the footprint of aquaculture production.

Examining the intra-individual relationship between behaviour and physiology in the green shore crab (*Carcinus maenas*)

Eugueni Matveev*; & I.J. McGaw

Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

An increasing body of research suggests that individual animals have distinct and consistent personalities. Animal personalities are usually defined in terms of 'behavioural syndromes', meaning a cohort of coexpressed behaviours; for example, an animal that is active is also more likely to be more aggressive. If and how behavioural syndromes relate to underlying physiological processes is not fully understood, but recent research suggests that animals with a higher metabolic rate are likely to be more competitive and aggressive. The green shore crab, Carcinus maenas, is an ecologically important invasive species in North America. This species is very tolerant of environmental change and several distinct physiotypes exist. The aim of the current study was to define behavioural syndromes by analyzing the relationship between locomotor activity, boldness, and aggression, and to determine how these may be related to metabolic rate and scope as well as general physiological condition (hemolymph protein index). Initial results suggest that crabs with higher resting metabolic rates are more aggressive and bold and have a competitive advantage in obtaining food when interacting with their less active counterparts. The findings shed light on the relationship between behaviour and physiology and how these affect responses at the individual animal level.

Spatial risk: Influence of piscivorous fish on selection of nursery habitat by Age-o juvenile cod

Evelyn MacRobert1*; R. Gregory1,2; & P.V.R. Snelgrove1

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Fisheries and Oceans Canada, St. John's, NL

Fish experience elevated levels of predation during their early life history stages. Upon reaching the juvenile stage, Atlantic (Gadus morhua) and Greenland (G. ogac) cod reduce their predation risk by settling into coastal eelgrass nursery beds. Although these nursery habitats restrict predator movements, predation mortality nonetheless remains high. This pattern suggests that habitat adjacent to eelgrass beds may hold a greater predation risk than eelgrass beds. Juveniles must balance their need for food with predation avoidance, and movement of predators may therefore influence the distribution of juveniles. We characterized habitat and the distribution of Age-o cod among habitat types through video transects. To determine how predators shaped habitat use by Age-o juvenile cod we tagged a total of 37 predators (Age-1+ G. morhua, G. ogac, cunner Tautogolabrus adspersus and shorthorn sculpin Myoxocephalus scorpius), and used acoustic telemetry to determine their habitat use. Age-o juvenile cod utilized shallow-water eelgrass beds less than 7-m deep, whereas predators predominantly occupied the habitat surrounding eelgrass. From these results we infer that eelgrass habitat indeed provides protective habitat for Age-o cod, but predators may still exert a reduced predation effect by focusing on the periphery of protective habitat and limited availability of juvenile prev.

Banded killifish on the edge: Potential reproductive issues in a species of concern

Heather Penney1*; M. Aline Litt1,2; & C.F. Purchase1

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Department of Biology, Carleton University, Ottawa, ON

Reproduction at the edges of a species' range presents extra challenges because conditions are often sub-optimal. In general, embryos and juveniles are more vulnerable to differences in environmental conditions, which makes early growth and survival particularly challenging in peripheral regions. Banded killifish (Fundulus *diaphanus*) are small, freshwater fish that have a wide but patchy distribution in Newfoundland which is the northern and eastern edge of their range. Subsequently, Newfoundland populations are considered to be of concern. The objective was to determine how low temperatures and conductivities interact to affect embryonic development, which we measured as developmental stage reached, hatch success, hatch time and hatch size. A 4x2 common garden experiment was conducted, where individual embryos were evenly sorted into four temperature (10, 16, 22, 28°C) and two conductivity (0.6, 1.2 mS/cm) treatments. Temperature was an important factor, where warmer temperatures lead to more developed embryos, a higher hatch success and faster hatch time. Embryos had very low hatch success in the 10 and 16°C treatments. Additionally, conductivity and temperature interacted to affect hatch size. The banded killifish are likely challenged by lower than optimal temperature and conductivity conditions in Newfoundland which may result in reproductive declines, and perhaps complete cohort failures in cooler years.

Investigation of allomaternal care in the endangered St. Lawrence estuary beluga (*Delphinapterus leucas*) population.

Jaclyn Aubin^{1*}; E. Vander Wal¹; & R. Michaud²

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Groupe de Recherche et d'Éducation sur les Mammifères Marins. Tadoussac, QC

Allomaternal care, a reproductive strategy by which offspring are cared for by multiple female group members, is common among odontocetes, but has not been described in wild belugas (Delphinapterus leucas). Despite this, in the endangered St. Lawrence Estuary beluga population, conservationists often encourage allomaternal adoption by releasing orphaned calves into groups of females with young. However, the outcomes of these rescues are unknown, and the effectiveness of this protocol has recently been questioned. During the summer of 2017, we collected footage of female belugas with young in the Saguenay-St. Lawrence Marine Park using an unmanned aerial vehicle, and conducted continuous focal behavioural sampling of calves, yearlings, and juveniles to determine whether allomaternal care occurs in this population. Mother-offspring pairs typically swim in echelon formation, a behaviour similar to infant carrying. We predicted that echelon swimming would not be restricted to mother-offspring pairs, but that offspring would echelon swim with multiple females. Preliminary analysis shows that, as predicted, focal calves, yearlings, and juveniles were observed echelon swimming with multiple females. Interestingly, calves were most likely to echelon swim with more than one female. These findings offer empirical support to the practice of rescuing and releasing orphaned calves in this endangered population.

Nitric oxide production by plants under anoxia

Jayamini Jayawardhane^{*}; A. Ghosh; P. Vyas; A.U. Igamberdiev Department of Biology, Memorial University of Newfoundland, St. John's, NL

Under the hypoxic stress, the cycle of nitrite-dependent respiration or the phytoglobin /nitric oxide (Pgb/ NO) cycle in plants has been shown to produce small amounts of ATP by mitochondria using nitrite (NO₂⁻) which substitutes oxygen as a terminal electron acceptor. The produced NO, which escapes mitochondria, can be scavenged but a part of it escapes the cell and can be detected. In this study, we have analyzed the NO production and aconitase enzyme activity by the hypoxia-sensitive plants barley (Hordeum vulgare L.) moderately tolerant to hypoxia maize (Zea mays L.) and hypoxia-resistant plant rice (Oryza sativa L.) under low-oxygen stress. The profiles of NO accumulation by the 14-days-old plant species fed by 50 mM sodium nitrate in the nitrogen atmosphere were measured via the Chemiluminescent Detector CLD 88p (Eco-Physics, Dürnten, Switzerland). Total NO accumulation was averaged every 30 min for individual plants. Another set of plants was subjected to anoxic stress for 3 h in a steady inflow of nitrogen gas at 120 mL min⁻¹to measure the activity of aconitase (EC 4.2.1.3). Aconitase, which is sensitive to NO, was evaluated spectrophotometrically in the mitochondrial and cytosolic compartments of leaf cells of the anoxically incubated seedling species. The results demonstrate the species-specific rates of production of NO and the differences in aconitase inhibition in the anoxic atmosphere by the four economically valuable crop species differing by the resistance to hypoxia and by their survival under lowoxygen stress.

Using microphone arrays to determine critical habitat and microhabitat for common avian species in decline

Jeffrey Ethier1*; W. Balsom2; & D. Wilson3

¹Cognitive and Behavioural Ecology, Memorial University of Newfoundland, St. John's, NL ²Lockheed Martin, Halifax, NS ³Department of Psychology, Memorial University of Newfoundland, St. John's, NL

The decline among North American landbirds has significant economic and ecological impacts. While legislation provides a framework for conservation, data are lacking for many species. Traditionally, these aspects are measured using methods that are limited by cost and human resources. I used a novel microphone array technology in Labrador to localize avian species at risk and characterize the habitat and microhabitat in which they occur. My objectives are to (1) demonstrate the practicality of using microphone arrays to monitor avian communities, (2) develop explanatory models for determining the relationships between habitat characteristics and species richness, occupancy, and vocal density, and (3) demonstrate the microhabitat preferences of two common species in steep decline, Boreal Chickadee and Cape May Warbler.

Characterization of a cryptic secondary metabolite in the common scab pathogen *Streptomyces scabies*

Jingyu Liu*; & D.R.D. Bignell

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Streptomyces scabies is the causative agent of potato common scab (CS) disease, which causes significant economic losses to potato growers worldwide. CS is characterized by the formation of lesions on the potato tuber surface that range from superficial to deep-pitted, and these lesions negatively impact the market value of table stock and processing potatoes, while seed potatoes can be rejected based on the presence of CS lesions. The ability of *S. scabies* to cause CS is primarily based on the production of a phytotoxic secondary metabolite (SM) called thaxtomin A, which is an essential virulence factor for the organism. In addition, S. scabies has the genetic potential to produce other SMs that might contribute to CS disease development; however, most of the genes predicted to be involved in production of these SMs are silent under laboratory conditions, and thus there is little known regarding the nature of these metabolites and their role in CS disease. The aim of this research is to characterize one cryptic (unknown) SM that is thought to resemble phenazine metabolites produced by various bacteria. The putative biosynthetic genes that produce this cryptic metabolite are expressed at low level or not at all under laboratory conditions, and therefore different strategies are being employed in order to activate or enhance expression of these genes in S. scabies. This presentation will discuss the strategies being used as well as our preliminary results of the bioassays being utilized to detect various bioactivities that might be associated with the cryptic metabolite.

The microbiome of deep sea carnivorous sponges

Joost Verhoeven*; & S. Dufour

Department of Biology, Memorial University of Newfoundland, St John's, NL

The *Cladorhizidae* is a unique family of carnivorous marine sponges characterized by the absence of a fully formed aquiferous system and instead has specialized structures to trap and feed on mesoplanktonic prey. While sponges are known to host a wide range of microbial associates, the composition and specificity of the microbial communities in carnivorous sponges is poorly understood. Here, we used 16S-rRNA gene data to examine and compare the bacterial communities associated with distinct anatomical regions of two carnivorous sponge species, Chondrocladia grandis and Cladorhiza oxeata, sampled from the deep sea with remotely operated underwater vehicles, in both Baffin Bay and the Gulf of Maine (*C. grandis* only). The two sponge species hosted distinct bacterial communities, with taxonomic diversity being greater in C. grandis. Some bacterial taxa were consistently recovered in multiple host individuals from geographically distant sites, suggesting these sponges actively retain specific bacterial communities. Within C. grandis, certain bacterial taxa were enriched in particular anatomical regions, suggesting functional roles in carnivorous sponge metabolism or other biological processes. Stable isotope analysis provided no evidence for methanotrophy in the sponges examined, but Gulf of Maine C. grandis might incorporate 13C-depleted carbon via the bacteria-mediated heterotrophic degradation of other hydrocarbons. Overall, our results demonstrate that the carnivorous sponge microbiome appears hostspecies specific and stable, even over large geographical areas. The observed differences in bacterial community composition and diversity between *C. grandis* and *C. oxeata* may reflect differences in trophic adaptability, specialization and overall reliance on associated bacteria.
Detection and characterization of antibiotic resistant coliforms: What's found in the lakes and ponds around us

Jordan Wight*; A. Lang; & K. Tahlan

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Antimicrobial resistance is an ever-increasing threat in the fight against infectious disease. Prevalence of resistance has emerged significantly in recent decades as antimicrobials have increasingly been used and abused for plant, animal, and human uses. Detection and monitoring of antibiotic resistant bacteria in the environment is therefore critical in understanding the prevalence of resistance outside of the clinical setting, as detection in the environment indicates that resistance is likely already widespread. In this presentation, I will outline my findings to date of a small-scale study in the city of St. John's, surveying antibiotic resistant coliforms in three diverse bodies of water over a period of several months. Various culture-based methods have been adapted to allow initial direct antibiotic susceptibility testing as well as differentiation in only 2 days from environmental samples. From these results, resistance rates from the initial screening, examination of multidrug resistance, as well as characterization of genetic resistance determinants will be investigated. Findings will then be related back to the larger NSERC Lake Pulse Network and these methods will be implemented over the course of 3 years for the study of a panel of lakes from across Canada.

Multi-scale test of moose foraging strategy using quantitative elemental measures for forage quality and quantity

Juliana Balluffi-Fry*; E. Vander Wal; S.J. Leroux; Y. Wiersma; T.R. Heckford; & M. Rizzuto

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Foraging ecology, in the context of herbivory, often investigates an herbivore's selection tradeoff between guality (nutritional content and digestibility) and quantity (biomass). However, patterns of herbivore selection between these two measures is thought to depend on the scale of observation. While this idea needs more testing across taxa, we first must define a quantitative measure for forage quality and quantity that we can apply at many spatial scales. Stoichiometric distribution models (StDM's) can predict elemental quantities for understory plant forage quality (% nitrogen), as well as quantity (grams of carbon per m₂), across a landscape. In this study, we apply this method to the white birch-moose system of Newfoundland, and with moose GPS collar data, measure moose selection for birch quantity and quality at both the home range scale and patch scale using a resource selection function and integrated step selection function respectively. We expect to detect a decrease in selection for birch quantity and an increase in selection for birch quality as we change the scale of foraging observation from home range to patch. In this poster, I will present preliminary results as well as further discuss the foraging theory and the significance of StDM's.

Temperature and reproductive stage modulate consumption, fecal production, and roe yield, in green sea urchin (*Strongylocentrotus droebachiensis*) fed a new formulated feed

Julie Jacques*; & P. Gagnon

Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

The green sea urchin, Strongylocentrotus droebachiensis, is interesting for aquaculture purposes because its roe (gonads) has a high commercial value on international markets. Numerous feeds have been developed to enhance roe yield with mixed results. Two laboratory experiments were carried out to assess consumption, fecal production, and roe yield in *S. droebachiensis* collected in an urchin barren in southeastern Newfoundland and fed a new formulated feed at three water temperatures representative of winter-spring lows: ~1 [ambient], 3, and 6°C. The first experiment lasted four weeks and was carried out with pre-spawned urchins. The second experiment lasted eight weeks with post-spawned urchins. Urchins were fed the feed ad *libitum* in flow-through tanks (20 urchins per tank, n=30). Mean feed consumption was higher in post-spawned than pre-spawned urchins for all temperature treatments, peaking at 6°C in both pre- (40.6 g feed kg urchin⁻¹) and post-spawned (60.1) individuals. Fecal production was higher in post-spawned urchins, with 31.6, 46.7, and 97.1 g feces kg urchin⁻¹ at 1, 3, and 6°C, respectively, and was positively correlated to feed consumption ($R^2 = 0.88$). Gonad index (GI, an indicator of roe yield) was highest at 6°C in both pre- (9.6%) and postspawned (19.2%) urchins, increasing by 141.6% and 142.2% from initial GI, respectively. Findings indicate green sea urchin roe yield meeting international markets' demand are achievable with the new formulated feed in about six weeks in relatively cold-water aquaculture settings.

Does anthropogenic noise cause a communication breakdown in dark-eyed juncos (*Junco hyemalis*)?

Katrina Shwedack*; & D. Wilson

Department of Psychology, Memorial University of Newfoundland, St. John's, NL

In recent years, increasing noise pollution (Slabbekoorn & Ripmeester 2008) can overlap with birdsong (Francis et al. 2009) and disrupt vocal communication and sexual selection. I am investigating the impact of noise on acoustic communication in dark-eyed juncos (Junco hyemalis). Although the effects of noise on song structure are wellknown, it remains unclear how receivers perceive songs that have been altered by noise, and whether noise-induced changes in song structure are adaptive (e.g. Cardoso & Atwell 2010, Proppe et al. 2013). To test this, I recorded songs in quiet and noisy environments, and replaced territorial males with speakers simulating a singing male patrolling his territory. The playbacks were from one of five treatments: junco songs recorded in noisy conditions played back in a noisy environment (noisy X noisy), quiet X noisy, noisy X quiet, quiet X quiet, or a heterospecific song used as a control (in noisy or quiet environments). Each territory was surrounded with a microphone array, capable of localizing vocalizing birds in 3-dimensional space. I used the array to monitor intrusion rates of neighbouring males. Success of the broadcasted songs was determined by how well they deterred neighbouring males from intruding; this provided a natural measure of song success. I will conduct 12 trials per treatment. I expect the playback recorded in quiet conditions to be more successful in quiet environments, and playback from noisy conditions to be more successful in noisy environments. This would indicate that dark-eyed juncos adaptively alter their song in the presence of noise.

Kleptoparasitic interactions between Atlantic puffins (Fratercula arctica) and herring gulls (Larus argentatus)

Kaylee Busniuk*; & D. Wilson

Department of Psychology, Memorial University of Newfoundland, St. John's, NL

Kleptoparasitism refers to an individual stealing a procured food item from another individual (Rothschild and Clay 1952). Herring gull (Larus argentatus) kleptoparasitism has been shown to impact the breeding success of Atlantic puffins (Fratercula arctica) by interrupting food deliveries to chicks in burrows (Nettleship 1972). Studies have suggested that puffins adapt their behaviour to mitigate risk of kleptoparasitism (Rice 1987, Pierotti 1983, Merkle et al. 1998), but such studies have not considered the behaviour of and impact on individuals. Using videos recorded from Gull Island, Newfoundland, I am investigating the behavioural strategies that puffins use to avoid kleptoparasitism. I am observing individually marked puffins and relating their behaviour to the presence and number of gulls. Additionally, I am exploring how individual gulls respond to the provisioning behaviour of puffins, and which strategies are the most effective for successful kleptoparasitism. I expect that, with an increasing number of gulls, puffins landing with food will enter their burrow more quickly, display more aborted landing attempts, and clump together temporally as they approach the burrows, as compared to puffins landing without food. I expect that puffins adopting these strategies will be less likely to be kleptoparasitized. I predict that gulls engaging in kleptoparasitism will be more successful when they move down-slope versus up-slope during attacks, when they physically attack puffins versus when they startle them by lunging, when they initiate attacks on closer versus more distant puffins, and when they attack on their own versus when they attack in a group of gulls.

Discovery of microRNAs associated with antiviral immune responses of Atlantic cod macrophages

Khalil Eslamloo1*; S.M. Inkpen1; R. Andreassen2; & M.L. Rise1

'Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

²Department of Pharmacy and Biomedical Laboratory Sciences, Oslo and Akershus University College of Applied Sciences

This study aimed to profile microRNAs (miRNAs) responsive to the viral mimic, polyriboinosinic-polyribocytidylic acid (pIC), in Atlantic cod (Gadus morhua) macrophages. Macrophages were isolated from individuals and exposed to pIC or phosphate-buffered saline (control) for different time points (i.e. 12, 24, 48, 72 h post-stimulation; HPS). Following sequencing of 12 RNAseq libraries, DESeq2 analyses determined four (i.e. miR-731-3p, miR-125b-3-3p, miR-150-3p and miR-462-3p) and two (i.e. miR-2188-3p and miR-462-3p) significantly differentially expressed miRNAs at 24 (n=3) and 72 HPS (n=3), respectively. RNAseq-identified miRNAs were subjected to qPCR assays using samples at all time points (n=6). The results of miR-731-3p, miR-462-3p and miR-2188-3p were validated by gPCR, and these miRNAs showed a time-dependent up-regulation by pIC. Also, qPCR and in silico analyses showed a co-up-regulation for miR-731-3p and miR-462-3p as well as putative interferon-sensitive response element motifs in the promoter region of the miR-731/miR-462 cluster. Additional Atlantic cod miRNAs, previously identified as immune responsive in higher vertebrates, were analysed by gPCR. As shown by qPCR assays at 48 or 72 HPS, miR-128-3-5p, miR-214-1-5p and miR-451-3p were up-regulated by pIC, whereas miR-30b-3p expression was down-regulated in response to pIC stimulation. This was the first report of pIC-responsive miRNAs in Atlantic cod, and the miRNAs identified herein are suggested to play roles in antiviral responses of this species.

Finding a needle in the syringe box: Identifying Newfoundland and Labrador's first willow flycatcher (*Empidonax traillii*)

Lancy Cheng*

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Empidonax is a genus of flycatchers which are renowned for the difficulty to identify. These small sized insect eaters are very similar in plumage and some are best to distinguish by vocalizations. Fifteen species of Empidonax flycatchers have been recognized in this genus, 11 of which are distributed in North America. Three Empidonax species had been recorded in Newfoundland and Labrador (NL), including Yellow-bellied, Alder and Least Flycatchers. An Empidonax flycatcher was sighted on November 08, 2017, in St. John's, NL, Canada, which was an obviously late record. Wing/tail morphology and other plumage characteristics identified it as Trail's Flycatcher, a supposed species now considered to be two distinct but closely related species, Alder Flycatcher and Willow Flycatcher. Bioacoustic analysis excluded the possibility of Alder Flycatcher, leaving the only possibility of being Willow Flycatcher. This is the first record of Willow Flycatcher in the province of NL, adding its total bird species to 404. This is also the first and the only confirmed November record of this species in Canada.

Influence of bioturbators on annual growth rate of southeast Newfoundland rhodoliths, *Lithothamnium glaciale*

Laura Teed1*; D. Belanger1; P. Gagnon2; & E. Edinger1,3,4

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL

³Department of Geography, Memorial University of Newfoundland, St. John's, NL ⁴Department of Earth Sciences, Memorial University of Newfoundland, St. John's, NL

Coralline red algae can form extensive aggregations referred to as rhodolith beds. These beds offer complex habitats to several ecologically and economically important species. For example, colonizing echinoderms use rhodolith beds as spawning and settlement grounds while acting as bioturbators that clear rhodoliths of sediment. Discovery of beds in coastal Newfoundland, namely the St. Phillip's rhodolith bed (>500 m2), has stimulated research on the effects of bioturbators on rhodolith growth. The present study quantified apical growth of Newfoundland rhodoliths (Lithothamnion *glaciale*), with and without bioturbators. Thirty-six rhodoliths collected from the centre of the St. Phillip's rhodolith bed were weighed after rhodoliths were stained with Alzarian red. Three rhodoliths were placed into one of 12 mesh cages installed 5 m apart in the centre of the bed (~15 m depth). Six cages were placed ~50 cm above the seabed to deter bioturbators (raised), while remaining cages were attached directly to the seabed (bottom) and deployed for one year. Rhodolith branch tips were sanded and imaged with Nikon Coolpix 4500 connected to a stereomicroscope. Photos were analyzed using ImageJ to measure maximum growth from the stain to the branch tip. Growth rates did not significantly differ in the presence of bioturbators (p=0.730). Mean apical growth rate across bottom and raised rhodoliths was 0.552 mm yr-1 (±0.067, SD) and 0.565 mm yr-1 (± 0.056) , respectively. Overall growth rate, regardless of position was 0.558 mm yr-1 (±0.072). Apical growth of Newfoundland rhodoliths is slower than warm-water rhodoliths (~1.5-2.5 mm yr-1).

Breeding success at the Northern Gannets' (*Morus bassanus*) southernmost Colony – Cape St. Mary's, Newfoundland: A comparison of methods

Leanne Guzzwell1*; W. Montevecchi2; S. Wilhelm3; D. Fifield4; & J.F. Rail5

1. Department of Cognitive and Applied Behavioural Ecology, Memorial University of Newfoundland, St. John's, NL

2. Department of Psychology, Memorial University of Newfoundland, St. John's, NL

3. Canadian Wildlife Service, Environment and Climate Change Canada, Mt. Pearl, NL

4. Science and Technology, Environment and Climate Change Canada, Mt. Pearl, NL

5. Canadian Wildlife Service, Environment and Climate Change Canada, Quebec, QC

Northern Gannets (Morus bassanus) have been well studied in Newfoundland, and much is known about their prey consumption, chick growth and their foraging and migratory behavior (e.g. Montevecchi et al. 1984, 2009; Fifield et al. 2014). However, there is no published information on their annual breeding success. Data were collected from 2009-2017, through combined efforts of Cape St. Mary's staff, Canadian Wildlife Service (CWS) and Memorial University of Newfoundland. Cape St. Mary's staff collected data between 2009-2010, in 2011-2015, nest attendance data were collected by the CWS and in 2016-2017, I collected data from May to September. Breeding success was determined using a continuous method, by dividing the number of chicks on September 1 by the number of apparently active nests during May to September. For comparisons with previous short-term assessments of breeding success, 1-day and 2-day methods were also used. The 1-day method divided chick presence by active nest sites on September 1, whereas the 2-day method divided chick presence on September 1 by active nests mid season. In 2016, there was no detectable difference [F2,12= 0.49, p = 0.62], continuous (0.49 ± 0.11) , 2-day method (0.52 \pm 0.09) and 1-day method (0.57 \pm 0.17). In 2017, there was no detectable difference $[F_{2,12} = 0.16, p = 0.85]$, continuous (0.33 ± 0.13) , 2-day method (0.38 ± 0.12) and 1-day method (0.34 ± 0.12) 0.14). From 2009-2017 breeding success at Cape St. Mary's showed significant inter-annual variation [F 8, 50 = 7.4, p = 0.000] with a mean of (0.49 + 0.19) (range; 0.35 - 0.81).

Characterization of diet and growth for a marine species currently undergoing distribution shifts

Liang Zhu1*; J.A.D. Fisher1; & D. Robert2

'Center for Fisheries Ecosystem Research, Marine Institute, Memorial University of Newfoundland, St. John's, NL ²Institut des sciences de la mer de Rimouski, Universite de Quebec a Rimouski, Rimouski, OC

Increases in ocean temperatures are driving the polewards distribution shift of marine species worldwide. Incursions by species into regions that had previously been unsuitable for their establishment may result in ecological consequences for native species such as altered predatorprey interactions. An example of such a species in the Northwest Atlantic is silver hake (Merluccius bilinearis), a small gadoid species that is primarily distributed from the Georges Bank to the Scotian Shelf. Following the occurrence of exceptionally warm temperatures in the Gulf of St. Lawrence since 2010, large abundances of silver hake have been encountered in surveys of the northern Gulf. Lower ocean temperatures in the Gulf of St. Lawrence have been thought to act as a biogeographic barrier for silver hake in the past, but this event may represent a dramatic expansion of this species' northern range. Silver hake is of interest because it matures rapidly and is known to be an important predator of both invertebrates and fish. Using silver hake samples caught during survey trawls from 2015-2017, stomach content analysis was undertaken to investigate the trophic role of this species in its new habitat. The ageing and measurement of otoliths from the same samples were used to determine the rate of growth of these fish. Our study aims to provide new insights on shifting marine species distributions and interactions at the northern edge of a geographic range.

Production of coronafacoyl phytotoxins involves a novel biosynthetic pathway in the plant pathogen *Streptomyces scabiei*

Luke Bown^{1*}; M. Altowairish¹; Y. Li¹; F. Berrue²; & D. Bignell¹

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Aquatic and Crop Resource Development, National Research Council of Canada, Halifax, NS

Phytotoxic natural products have been shown to play an important role in the ability of phytopathogenic microorganisms to cause disease. They can allow the producing organism to evade plant defense responses during host colonization and infection. The coronafacovl phytotoxins are a family of natural products that are biosynthesized by phylogenetically distinct plant pathogenic bacteria and which function as virulence factors for these organisms. One of the most studied coronafacoyl phytotoxins is coronatine (COR), which is produced by the phytopathogenic bacterium Pseudomonas syringae. COR functions as a phytohormone mimic and allows manipulation of host defence signalling pathways during infection. COR and other coronafacoyl phytotoxins consist of the polyketide compound coronafacic acid (CFA) linked via an amide bond to different amino acid or amino acid analogs. Recent studies from our lab have demonstrated that the potato common scab pathogen *Streptomyces* scabiei produces the coronafacoyl phytotoxin N-coronafacoyl-Lisoleucine, and gene deletion analyses have shown that production of the CFA moiety in this organism involves a novel biosynthetic pathway as compared to *P. syringae*. In addition, we provide evidence that this novel pathway is conserved in other Actinobacteria that are predicted to produce coronafacoyl phytotoxins but not in other phytotoxin - producing organisms. We additionally reveal that production of coronafacoyl phytotoxins may occur in both plant pathogenic and non-pathogenic bacteria based on genomic analyses. This suggests that production of these natural products may be more prevalent than previously realized and that their role for the producing organism may not be limited to host-pathogen interactions.

Using underwater video to conduct resource assessments for new emerging fisheries in Kimmirut, Nunavut

Maggie Folkins*; S.M. Grant; & P. Walsh

Fisheries and Marine Institute of Memorial University of Newfoundland, St. John's, NL

Food security in small northern communities such as Kimmirut, Nunavut is in a constant fragile state. Very little is known of the benthic marine species that may be present and harvestable either at a small scale (subsistence fishery) or large scale (commercial fishery) near this community. Guidelines for establishing a new emerging fishery are in place to ensure an integrated approach involving science, business principles and effective involvement of government is achieved. Primary feasibility involves determining which species present in the area are harvestable in commercial quantities. In August 2017, we conducted preliminary surveying in areas around the community using four types of sampling pots design to target whelk and shrimp which are known to be present in the Hudson strait, south of the community. Here we try and gain an understanding of what species are present through fisheries assessments, multi-beam surveys, underwater camera assessments and local traditional knowledge. By catch data analyses and through the use of underwater video of the seafloor species density and abundance estimates can be achieved. This research will contribute to our understanding of the benthic marine species found in northern regions of the Hudson strait. This will give insight to whether these species are present in harvestable quantities and could eventually help increase food security in the community of Kimmirut.

Evolutionary history of the tropical conifer genus *Podocarpus* in Hispaniola

Maria Esther Nieto-Blazquez*; & J. Roncal

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Hispaniola is the second largest island in the Caribbean and a biodiversity hotspot. The island was formed as a result of the fusion of 2 palaeo-islands (north and south) around the Mid-Miocene around 15 million years ago. The complex topography of modern Hispaniola includes mountain ranges that run from east-to-west separated by deep arid valleys. This makes the island a good system to evaluate the effects of geological events and dispersal barrier formation on the geographical distribution of species genetic diversity and their historical demography. The tropical-subtropical conifer genus Podocarpus is confined to mountainous regions in Hispaniola, where we find two endemic species: *P. hispaniolensis* and *P. buchii*. The former occurs in Cordillera Septentrional (north of the island), while the latter is found in Sierra Baoruco and Sierra de Neiba (south of the island). Both species grow in sympatry in the Central Cordillera, the oldest mountain range in Hispaniola located in the central portion of the island. We used single nucleotide polymorphisms (SNPs) to test whether Central Cordillera is a zone of secondary contact or origin for *Podocarpus* species. We hypothesized that populations from Central Cordillera are ancestral, based on the assumption that the older systems would sustain older populations and genetically more diverse. Preliminary results show that Podocarpus in Hispaniola followed a stepping-stone colonization pattern from the North towards South of the island with multiple bottlenecks in each mountain colonization event, rejecting the hypothesis of Central Cordillera being the ancestral region for Podocarpus in Hispaniola. However, although marginally, Central Cordillera populations are genetically more diverse that south and north populations.

Modelling forest restoration after moose over browsing

Meghan Noonan*; S. Leroux; & L. Hermanutz

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Globally over browsing by herbivores has resulted in severely degraded forests, with areas failing to naturally regenerate after herbivore disturbance. This failed regeneration leads to an overall reduction in plant biomass, reduced biodiversity and altered forest regeneration trajectories. In Newfoundland, invasive moose (Alces alces) selectively browse palatable species including balsam fir (Abies balsamea), the foundation tree for island coastal forests, resulting in the loss of the advanced regeneration of fir saplings. This has led to the development of spruce moose savannahs in severely degraded forest patches. Mathematical modelling will be used to identify high priority sites for forest restoration and develop effective restoration protocols for balsam fir dominant boreal forests. Modified Markov models will be used to predict effective restoration protocols. Different restoration scenarios will be tested to assess restoration potential for sites with varying canopy gap sizes and browsing intensities. Models will be parameterized with field data and aerial photos from the NCC Salmonier property located on the Avalon Peninsula. This work will aid forest management by informing decision-making processes and providing a suite of effective restoration protocols to restore forests. The results on this study will be of interest to ENGO's, provincial forestry, industrial forestry and Parks Canada.

Migration timing of caribou reveals plasticity in movement and forage selection in response to environmental change

Michel Laforge^{1*}; Q. Webber²; & E. Vander Wal¹

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL ²Cognitive and Behavioural Ecology, Memorial University of Newfoundland, St. John's, NL

Plasticity in behaviour allows individuals to acclimate to fluctuating environmental conditions. The ability to cope with change is often variable among individuals, and understanding how individuals modulate behaviour across contexts is vital to understand populationlevel responses to environmental gradients. The phenological mismatch hypothesis posits that climate change decouples consumer phenology from that of their resources as trophic levels are unlikely to respond to environmental warming equally. Despite indirect evidence that mismatch negatively affects fitness in ungulates, individual-level analyses of plasticity in forage acquisition and migratory behaviour are lacking. We quantified migration timing and selection for newly emergent forage resources in caribou (Rangifer tarandus). We quantified migration date and used resource selection functions to calculate individual-level selection for emergent forage. We used behavioural reaction norms to test how these behaviours changed as a function of date of green-up at the individual-level to examine personality and plasticity in migration. We found that timing of migration was highly plastic and that individuals responded to earlier springs by migrating earlier ($\beta [\pm 95\% \text{ CI}] = 1.165 [0.986, 1.342]$). Migratory plasticity was correlated with selection for newly emergent forage, suggesting that animals are able to adapt speed and timing of migration to between-year variation in forage availability, suggesting that plasticity in migration timing may be adaptive. We conclude that caribou are plastic in their response to changing environmental conditions and may therefore have some behavioural ability to cope with climate change.

Examination of clavulanic acid biosynthesis using a comparative genomics approach

Nader AbuSara*; M. Moore; B. Piercey; S. Srivastava; N. Furgason; C. McIsaac; & K. Tahlan

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Clavulanic acid (CA), a potent β -lactamase inhibitor, was initially discovered as a metabolic product of *Streptomyces clavuligerus*. However, recent genome-sequencing projects suggest that CA biosynthetic capability exists in a wider range of bacteria. Here, we determined the complete genome sequence of two CA producers, S. jumonjinensis and S. katsurahamanus. The genome of S. jumonjinensis was found to consist of an 8.47 Mb linear chromosome with 7423 predicted coding sequences and 48 predicted secondary metabolite biosynthetic gene clusters, while the S. katsurahamanus genome was found to consist of a 7.25 Mb linear chromosome with 6123 predicted coding sequences and 39 predicted secondary metabolite biosynthetic gene clusters. A comparison of the CA biosynthetic gene cluster in the known CA producers (S. clavuligerus, S. jumonjinensis, S. katsurahamanus) and in CA non-producers (Streptomyces pratensis, Saccharomonospora viridis) revealed a higher degree of similarity in genetic composition and organization in the CA producers as compared to the non-producers. Of particular note is the presence of large gene, nocE, which is located in the middle of the CA biosynthetic gene cluster in the CA non-producers, while the same gene is located elsewhere on the chromosome in the CA producing organisms. Deletion of *nocE* in *S. clavuligerus* significantly decreased the growth rate of the mutants as compare to the wild-type strain, without affecting the production of CA or another secondary metabolite, cephamycin C. Overall, our results demonstrate how comparative genomic studies may help us to understand why some cryptic gene clusters are silent in some Streptomyces species but are highly active in others.

Space-use and social organization in a gregarious ungulate: testing the conspecific attraction and resource dispersion hypotheses

Quinn Webber^{1*}; M. Peignier; E.L. Koen²; M.P. Laforge²; A.L. Robitaille²; & E. Vander Wal²

¹Cognitive and Behavioural Ecology Interdisciplinary Program, Memorial University of Newfoundland, St. John's, NL ²Department of Biology, Memorial University of Newfoundland, St. John's, NL

Animals use a variety of proximate cues to assess habitat quality when resources vary spatiotemporally. Two non-mutually exclusive strategies involve direct assessment of landscape features and observation of social cues from conspecifics as a form of information transfer about forage resource quality. The resource dispersion hypothesis (RDH) proposes that animal space-use and social organization are driven by the abundance and distribution patterns of resources, whereas the conspecific attraction hypothesis (CAH) proposes that animal space-use varies based on the distribution of conspecifics rather than the location of resource patches. We tested the RDH and the CAH as non-mutually exclusive explanations for the spatial and social organization of caribou (Rangifer tarandus). We estimated inter-annual site fidelity and constructed networks representing home-range overlap and social associations among caribou. We found that home-range overlap and social associations were related to the distribution of resources in summer and conspecific attraction in winter. In summer, when resources are relatively homogeneously distributed, inter-annual site fidelity was high and home-range overlap and social associations were low. Conversely, in winter when resources are relatively patchily distributed, inter-annual site fidelity was relatively low and homerange overlap and social associations were high. Our results have implications for our understanding of caribou socioecology, suggesting that caribou use season-specific strategies to locate forage. Caribou populations are declining globally, and our finding that conspecific attraction affects access to forage suggests that further disturbance and fragmentation of caribou habitat could limit social association among caribou, particularly in winter when access to resources may be inhibited.

Drivers of arboreal lichen community diversity and structure

Rachel Wigle*

Department of Biology, Memorial University of Newfoundland, St. John's, NL

Lichens are present in virtually all terrestrial ecosystems, contributing to the diversity of ecological communities through species interactions and inter-dependencies. However, how lichen communities are structured through space (e.g., similarities and differences in lichen communities between host trees within a stand and between host trees of the same species across stands) is less well-studied. To better understand the variables affecting community structure of arboreal lichens, I will describe the mechanisms driving patterns of lichen communities on vellow birch (Betula alleghaniensis) and balsam fir (Abies balsamea) in the Avalon Forest Ecoregion in Newfoundland, Canada. I will use tree-level (bark pH, texture, tree age, size, and canopy cover) and stand level (ground cover, slope, aspect, canopy cover, and position on slope) variables, and the interactions between them, to explain lichen community composition between trees of the same species, and between different tree species within the same stand. I aim to improve our predictions of how spatial drivers shape lichen community patterns. These results will also be able to direct management efforts in identifying areas of high conservation value and they will help to inform illegal timber harvesters about the greater impacts of their actions.

Effects of varying dietary Omega-6 and Omega-3 Fatty Acid levels and immune stimulation (Viral Mimic versus LPS) on the transcriptome of Atlantic Salmon macrophages

Sabrina Inkpen^{1*}; N.C. Smith¹; K. Eslamloo¹; X. Xue¹; A. Caballero-Solares¹; R.G. Taylor²; & M.L. Rise¹

¹Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL ²Cargill Innovation Center, 4335, Dirdal, Norway

Diet composition and fish health maintenance are important factors in maximizing quality and cost-effectiveness in the aquaculture industry. In this study, we isolated head kidney leukocytes from Atlantic salmon fed two diets for 12 weeks – one higher in omega-6 (ω 6) and one higher in ω 3 fatty acids. To investigate the effect of dietary $\omega_{6:\omega_{3}}$ on cellular responses to immune stimulation, adherent macrophages were incubated for 24 h with the viral mimic polyriboinosinic-polyribocytidylic acid (pIC), lipopolysaccharide (LPS), or phosphate-buffered saline (PBS). A microarray study indicated that 40 transcripts were more highly expressed in high ω3fed fish, and 76 transcripts were more highly expressed in high ω 6-fed fish, in at least one treatment group [Rank Products (RP) analysis, p<0.05]. Additionally, the study indicated differences in the transcriptomic response to immune stimulation: in high ω_3 -fed fish, 690 and 305 transcripts were dysregulated by pIC and LPS stimulation, respectively; while in high ω 6-fed fish 989 (pIC) and 470 (LPS) transcripts were dysregulated [overlapped RP and significance analysis of microarrays (SAM), p<0.05]. Notable overlap was also observed between LPS- and pIC-responsive transcripts, with 130 transcripts dysregulated by both treatments in one or both diet groups, suggesting potential shared pathways between macrophage antiviral and antibacterial responses.

Gray wolves (*Canis lupus*) follow the prey habitat and prey catchability hypotheses to track prey in a multi-prey system

Sana Zabihi-Seissan*; C. M. Prokopenko; & E. Vander Wal Department of Biology, Memorial University of Newfoundland, St. John's, NL

Predators have more than one means by which they can track the distribution of their prey on the landscape. These alternative tactics are described by the prey abundance hypothesis for prey that are aggregated in space, the prey habitat hypothesis for uniformly distributed prey, or the prey catchability hypothesis for prey that are more difficult to capture. The gray wolf, a generalist predator, likely employs multiple tactics when diverse prey with distinct distributions and behaviour are available. We conducted a study on 9 GPS collared wolves in three packs in Riding Mountain National Park, Manitoba, where wolves prey on moose (Alces alces) and elk (Cervus canadensis). We evaluated wolf selection for prey density, habitat selection and vulnerability on the landscape through Resource Selection Analysis, Wolves selected for moose and elk vulnerability, and moose habitat selection, supporting the prey catchability and prey habitat hypotheses. Surprisingly, wolves avoided moose and elk density, which highlights the ongoing space race between predator and prey. Therefore, wolf space-use is driven by the resources of their primary prey, thereby increasing encounters, and areas on the landscape which improve attack success of their large bodied prey. This work illustrates the role landscape variation plays in predator-prey dynamics.

Clade-by-clade analysis of community phylogenetics data reveals multiple levels of structure with possible link to process

Sander Bennett Boisen^{1*}; J. Roncal¹; & M. Bursinzky

¹Department of Biology, Memorial University of Newfoundland, St. John's, NL

Phylogenetic community ecology is a growing field with increasingly complex methodology. The original prospect of inferring community assembly process from phylogenetic patterns has proven to be difficult. Phylogenetic clustering - the tendency for species in a community to be phylogenetically closer than expected by chance has been linked to environmental filtering, while phylogenetic evenness - the tendency for species in a community to be less related than by chance - is the expected result of competitive exclusion. As multiple assembly processes occur at the same time the predicted phylogenetic pattern becomes one of noise or randomness and inference about the underlying assembly process is challenging. In response to this we have taken a clade-by-clade approach to community phylogenetics and show how this can alleviate some of the challenges. We applied this clade-by-clade methodology on two spatial scales: a regional scale for 7 distinct plant habitats across Newfoundland and a local scale for 25 plots in 2 different plant communities in Gros Morne National Park. Our results show that phylogenetic community structure is lineage specific and can be found on many levels within the phylogeny. This highlights the weakness of inferring assembly processes based on phylogenetic patterns at deep phylogenetic nodes only. Phylogenetic clustering in bogs suggest that environmental filtering played a major role in the assembly of this community.

What's for dinner? Building a Newfoundland rhodolith community food web

Sean Hacker Teper*; P. Gagnon; & C.C. Parrish

Department of Ocean Science, Memorial University of Newfoundland, St. John's, NL

Rhodoliths are widespread calcareous, branching algae that typically host a diversity of organisms, such as echinoderms, bivalves, and polychaetes. To identify nutritional patterns and to determine trophic linkages, these organisms were collected in rhodolith samples from two sites, chosen for their proximity to freshwater inputs, before, during, and after the spring phytoplankton bloom. Rhodolith size differed significantly between sites, but overall biomass was nearly identical. Preliminary results from lipid class, fatty acid, and stable isotope analyses suggest essential fatty acids (EFAs) and sterols may be important to health and stability of rhodolith communities. Rhodoliths may be a significant source of cholesterol; chitons (Tonicella spp.) could pass it trophically to sea stars (Asterias rubens). Overall, organisms maintained EFAs (EPA, 20:5ω3; DHA, 22:6ω3; and ARA, 20:4 ω 6) whilst shifting diet in response to seasonal food availability; plankton consumption increased during the bloom. While EPA and ARA were abundant in all organisms, DHA was only a major fatty acid in clams (Hiatella arctica). Diets at both sites were similar with considerable bacterial and terrestrial influences; however, total lipid in sediment underlying rhodoliths varied. Overall, results suggest trophic relationships in rhodolith bed communities can shift over short time scales, while being influenced by water-column productivity processes.

The interactive mechanisms regulating reproduction and feeding in zebrafish

Sydney London*; & H. Volkoff

Departments of Biology and Biochemistry, Memorial University of Newfoundland, St. John's, NL

Reproduction and feeding are two critical life processes, the regulations of which involve a complex network of interactions. These interactions have been well characterized in mammals but remain poorly understood in fish. To better understand this relationship, we examined the effects of nutritional status, gender, and reproductive stage on the brain expression of reproductive hormones (GnRH, kisspeptin, GnIH, and neurokinin B - NKB) and appetite regulators (orexin and NPY) in zebrafish (Danio rerio). In order to compare strains, both wild and Casper zebrafish were used. In wild type zebrafish, fasting increased brain mRNA levels of GnIH, GnRH, NKB, and kisspeptin. Differences in the expression of reproductive hormones were seen between males and females, and between reproductive stages (based on gonadosomatic index, GSI) in females, suggesting gender- and GSI-specific effects of nutritional status on reproduction. Gender and reproductive stage did not affect the expression of appetite regulators, with fasting-induced increases in NPY and orexin in all fish. In Casper zebrafish, fasting decreased orexin expression in males, but had no significant effect on either NPY expression or the expressions of any of the reproductive peptides examined, with the exception of NKB, which was higher in fasted males compared to fed males. Our results suggest the existence of a link between nutritional status and reproduction in zebrafish, and indicate reproductive stage-, strain-, and gender-specific differences in the regulation of feeding and reproduction in zebrafish.

Constructing the stoichiometric landscape: Spatial correlates of plant elemental composition

Travis Heckford*; S.J. Leroux; E. Vander Wal; M. Rizzuto; J. Balluffi-Fry; & Y.F. Wiersma

Department of Biology, Memorial University of Newfoundland, St. John's, NL

In terrestrial ecosystems, plants are an important source of energy and organic material, forming the base of most food webs. Plant species require specific optimal elemental ratios for growth, development, and proper functioning. Deviations from these ratios, specifically nitrogen and phosphorus, have been used to indicate sub-optimal growing conditions (i.e., competitive stress, environmental constraints, limitations in soil nutrients). Ecological stoichiometry studies how the mismatch of elemental ratios between producers and consumers influences their interactions; i.e., explaining how and why herbivores will use different areas to acquire limited resources such as nitrogen and phosphorus on the landscape. Our goal was to generate spatial models of plant stoichiometry (C:N, C:P, N:P) using remotely-sensed land cover data. To accomplish this, we sampled and analyzed the elemental composition of blueberry (Vaccinium angustifolium), white birch (Betula papyrifera), red maple (Acer rubrum), and balsam fir (Abies balsamea), which are commonly browsed by snowshoe hare (Lepus americanus) and moose (Alces alces). We constructed a set of a priori hypotheses for our plant species stoichiometry. We developed general linear models for each, using three classes of landscape covariates, (1) abiotic (elevation, aspect, slope), (2) biotic (forest height, canopy closure, and forest age) and (3) land cover (structural; wetland/forest). Our models explained on average 30-50% of the spatial variation of our plant species stoichiometry (C:N, C:P, N:P). These models provide us with a spatially-explicit projection of plant resources from which we can answer novel research questions about how animals use and select for resources on the stoichiometric landscape.

Nitrogen cycling genes in a long-term land-use converted boreal land in Newfoundland, Canada

Victor Valdez^{1*}; A. Ramasami²; V. Kavanagh³; D. Burton⁴; L. Jewell⁵; D. McKenzie⁵; & A. Unc^{1,2}

¹Environmental Science program, Memorial University of Newfoundland, St. John's NL ²Memorial University of Newfoundland, School of Science and the Environment, Corner Brook, NL

³Newfoundland and Labrador Department of Fisheries and Land Resources, Corner Brook, NL

⁴Dalhousie University, Department of Plant, Food, and Environmental Sciences, Truro, NS

⁵St. John's Research and Development Centre, Agriculture and Agri-Food Canada, St. John's, NL

Productivity of agricultural land converted from boreal forest is sustained by significant mineral and organic fertilization, and use of alkaline amendments for management of acidic pH. Fertilization efficacy is associated to soil's microbial activity. The distribution of ammonia oxidation (Cren-, Arch-, bacterial- amoA) and the denitrification (narG, napA, nirK, nirS, nosZ1) gene chains were evaluated on transects across the field's boundaries along a nonmanaged to managed soil gradient. Triplicate soil sampling was done at 0-10 and 10-20 cm depths along gradients at four sites of a potatoeswheat, 70 years old, farm field in Cormack, Newfoundland. Gradient sample points were outside (-3m, -1m) and inside the farmed plot (1m, 3m, 5m). Results are contextualized by soil pH, moisture, organic matter, available and total phosphorous, total nitrogen, and laboratory assessed ammonification and nitrification. N-cycle genes were quantified by Real-Time PCR. Multidimensional statistics was employed to explore the abiotic or biotic triggers for the diversity of N-cycle genes, while the most informative models were identified via Akaike's Information Criterion. Diversity of abiotic and biotic parameters were linked to site and gradient location. For o-10 cm, models confirmed varying levels of correlation between the abundance of each gene, the spatial variables, and abundance of other genes. For 10-20 cm, the associations between genes were more pronounced, with a lower significance attached to spatial variables. Thus, management effects are less pronounced for the deeper soil layer. Results suggest a role for the management and a relationship between the abundance profiles of soil denitrifiers and nitrifiers.

Larval fish community structure along the Northeast coast of Newfoundland

Violaine Shikon1*; P. Pepin2; M. Castonguay3; & D. Robert4

¹Memorial University of Newfoundland, St. John's, NL, Canada ²Department of Fisheries and Oceans Canada, St. John's, NL, Canada ³Department of Fisheries and Oceans Canada, Mont-Joli, QC, Canada ⁴Université de Québec à Rimouski, Rimouski, QC, Canada

The larval stage in marine fishes is of great importance, as survival during the vulnerable larval stage regulates recruitment and adult population dynamics. Coastal embayments of Newfoundland are spawning and nursery for important areas numerous socioeconomically and ecologically important fishes, including Atlantic cod (*Gadus morhua*), Atlantic herring (*Clupea harengus*), and capelin (*Mallotus villosus*). In this study, we examined spatiotemporal patterns in species diversity and composition in two relatively unstudied northern coastal embayments, comparing these results to those found in Trinity Bay. While interannual and among-bay variability in community structure did exist, differences in community structure were driven primarily by sampling month. These results are similar to those previously found for the southern Placentia Bay in the late 1990s, indicating that seasonal patterns of community structure predominate in the coastal waters of Newfoundland, and that such patterns are interannually and spatially consistent. This comparison of larval community structure dynamics bays of Northeastern Newfoundland will allow for a better understanding of species interactions during early life stages and adult spawning locations. Furthermore, as changes in community structure can potentially allow for early detection of ecosystem shifts, the present study provides a baseline for future community research.

Investigate the role of TxtH in the biosynthesis of the thaxtomin A in the common scab pathogen *Streptomyces scabies*

Yuting (Phoebe) Li*; Y. Li; K. Tahlan; & D.R.D. Bignell Department of Biology, Memorial University of Newfoundland, St. John's, NL

Streptomyces scabies causes common scab disease, which is characterized by superficial or corky-like lesions that form on the surface of root and tuber crops such as potato, radish and carrot. These disease symptoms induced by this organism are largely due to the predominant virulence factor, thaxtomin A, a nonribosomal peptide (NRP) that exhibits phytotoxic activity. Production of thaxtomin A involves the nonribosomal peptide synthetases (NRPS) TxtA and TxtB, which are large, multimodular enzymes that are responsible for producing the thaxtomin A backbone. In addition, other enzymes and proteins are known or predicted to be involved in thaxtomin A biosynthesis, including TxtH, a small protein belonging to the MbtH-like protein (MLP) family. MLPs typically function as chaperones required for the proper folding of the adenvlation (A) domain of NRPS enzymes, and/or they function as activators to stimulate the adenylation reaction catalyzed by the A domain. Biochemical studies of TxtH have shown that the protein is required for promoting the solubility of both the TxtA and TxtB A domains in vitro, suggesting that TxtH functions as a chaperone in *S. scabies*. In addition, amino acid residues that are essential for this activity have been identified by performing site-directed mutagenesis of the TxtH protein. A deletion mutant of TxtH in S. scabies has been constructed in order to examine the role of the protein in thaxtomin A biosynthesis in vivo. Furthermore, overexpression of TxtH in S. scabies was performed to determine whether this can enhance metabolite production levels as reported for another MLP.

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