12th Biology Graduate Student Symposium

April 8th 2019

Biology Graduate Student Association

MEMORIAL UNIVERSITY

Schedule at a Glance

8:15-9:50	**Registration** Science Lobby
8:50-9:00	**Opening remarks (Juliana Balluffi-Fry)** Arts 1045
9:00-10:15	**Oral Presentations** Arts 1045 & 1049
10:15-10:45	**Coffee Break** Science lobby
10:45-12:15	**Oral Presentations** Arts 1045 & 1049
12:15-13:00	**Lunch** Science Lobby
13:00-14:45	**Oral Presentations** Arts 1045 & 1049
14:45-15:45	**Coffee Break** Poster Session (Science lobby)
16:00 – 17:00	**Keynote Presentation** SN 2109
17:00-19:00	**Reception** Quintanas

Symposium Planning Committee 2019

Juliana Balluffi-Fry
Symposium Chair
BGSA Professional
Development Coordinator

Matteo Rizzuto
External Funding/Sponsors
BGSA Chair

Michel Laforge
Photo Contest Coordinator
BGSA Communications
Officer

Quinn Webber
Judging Coordinator
BGSA GSU and Faculty
Student Representative

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BGSS Committee Member

Maggie Folkins
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Meal Coordinator
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Elizabeth Moore
BGSS MI communications
BGSS Committee Member

Isabella Richmond
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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 acid profiles 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!

Dean of Science

Dr. Mark Abrahams

On behalf of the Faculty of Science, I am very pleased to welcome you to the Biology Graduate Student Symposium (BGSS) for 2019. This annual event features the enthusiasm and creative energy of our graduate students as they present the ideas and results of their research. It is a great opportunity to see the next generation of scientists in action as they both present and discuss their research before it appears in our journals and textbooks. As usual, this symposium is a highlight of the academic year and I am very pleased that the graduate students are maintaining this excellent tradition.

Head of the Department of Biology

Tom Chapman

The Biology Graduate Student Symposium was conceived by students for students. There were two prominent graduate student voices that were part of the development of this event, Drs. Peter Wesley and Robyn Auld. They felt that an in-house conference would bring the department together (breaking down tribalism) and would give senior graduate students an opportunity to practice presenting conference-style lectures. Their first BGSS special speaker invite was to me, so this event has come a long way from its humble beginnings.

On behalf of the Department of Biology I welcome all participants. And I am thankful to the BGSA for continuing the tradition of making the BGSS a significant feature in the life of our department.

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

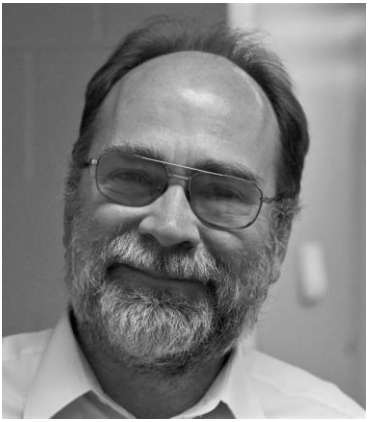
Juliana Balluffi-Fry

On behalf of the 2019 Biology Graduate Student Association and Symposium Planning Committee, I would like to welcome all students, faculty, audience members and our keynote speaker, Dr. Joel Brown, to the 12th 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 to our exhibitors SAEN, WWF, MI/CFER, OSC touch tank, ThermoFisher Scientific, CPAWS-NL, the St. John’s Fermentary, and the NL Department of Wildlife. I would also like to thank Dr. Joel Brown for travelling all the way to Newfoundland to deliver our keynote presentation, and tomorrow’s public talk at the Geo Center. Lastly, I would like to thank all the amazing BGSA members and volunteers who have helped plan the symposium and make today run smoothly; without you the BGSS would not be possible!

Keynote Speaker

Dr. Joel S Brown

Professor emeritus, University of Illinois at Chicago; Senior Member Moffitt Cancer Center



Joel Brown is a Senior Member of Integrated Mathematical Oncology at the Moffitt Cancer Center, and Distinguished Professor of Biology Emeritus at the University of Illinois at Chicago. He is a wildlife biologist, evolutionary ecologist, and cancer researcher. Childhood experiences in Zimbabwe created a love of nature and animals that grew into an academic career. For 30 years, his laboratory and graduate students have worked from A to Z with aardvarks in South Africa and zebra at the Brookfield Zoo, Chicago. Joel now currently uses game theory to provide a conceptual framework for modeling and understanding the onset and progression of metastatic cancers for developing “evolutionarily enlightened” treatment strategies. Joel completed his bachelor’s degree in zoology at Pomona College (1980, Prof. William Wirtz, advisor), and his Ph.D. degree in ecology and evolutionary biology at the University of Arizona (1986, Prof. Michael Rosenzweig, advisor).

Keynote Summary: Dr. Joel S Brown

The evolution of an evolutionary ecologist: from desert rodents to cancer

Over the course of my life and career, my interests, experiences, and passions have come together (slowly!) into a worldview that sees nature as the complex manifestation of simple mechanisms. From molecules to ecosystems, natural selection gives a rationality to nature. Adaptive foraging behaviors of animals (and plants!) provide indicators of food-safety tradeoffs, habitat quality, population characteristics, species coexistence and ecosystem processes. Fox squirrels and grey squirrels tell how a simple fear gradient of being near or away from a tree can explain species coexistence, biogeographical gradients and even the recovery of deciduous forests after the ice ages. Snow leopards in Nepal reveal the links between feeding behaviors, game theory and conservation. And now, cancer provides my study species, with cancer therapy viewed as a predator-prey game. Perhaps knowing this can improve outcomes – for 18 men in a clinical trial using evolutionary game theory it has. The career that led to these projects did not happen as a grand plan; rather it entailed ups and downs, shifting fields of study, an insatiable curiosity, and a love of adventure. Quoting Kierkegaard; “*Life can only be understood backwards; but it must be lived forwards*”. Advice for graduate students and scientists? Be doing. Don’t take yourself too seriously, but take what you do seriously. And, there are worse things than being wrong, you can be trivial.

Past Keynote Speakers

2018 – Dr. Susan Lingle
University of Winnipeg

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

Alessia Caterina Ciraolo	Cumulative impacts of hypoxia and trawling on the Northeast Pacific benthos
Brandy Biggar	The effect of extreme weather events and refuge availability on green crab abundance and physiology
Caley Ryan	Evaluating the impact of a removal program for the invasive European green crab (*Carcinus maenas*) in Placentia Bay, Newfoundland
Chirathi Wijekulathilake	Predictors of reproductive success
Gustavo A. Diaz Cruz	Characterization of novel virulence factors produced by a plant-pathogenic *Streptomyces* strain isolated in Newfoundland
Jackie Saturno	Investigating the role of fishing gear in the generation of microplastic waste and ingestion by Atlantic cod in Fogo Island, Newfoundland
Logan Zeinert	Maturity of the Caribbean spider crab *Maguimithrax spinosissimus* across three different environments in Eleuthera, The Bahamas
Madison Philipp	Impact of paternal history on honesty of sexual signals and mate quality in anadromous Atlantic salmon (Salmo salar)
My Dang	Susceptibility to *Aeromonas salmonicida* subsp. *salmonicida* in Atlantic salmon (*Salmo salar* L.) of farmed, hybrid and wild type parentage
Rachel Marshall	Distribution and seasonal behavior of Atlantic halibut (*Hippoglossus hippoglossus*) in the Gulf of St. Lawrence based on data from pop-up satellite archival tags
Tegan Padgett	The Newfoundland and Labrador Mosquito Project: a citizen science-based study of mosquito populations and viral pathogens
Tomas Araya-Schmidt	Reducing seabed impact of Northern shrimp and Greenland halibut trawling in the Nunavut offshore fishery through trawl modifications
Elizabeth Moore	Do cod discarded from pots experience behaviour impairment?

PRESENTATION SCHEDULE – Arts 1045

8:50 – 9:00	**OPENING REMARKS**	
9:00 – 9:15	**Juliana Balluffi-Fry**	Foraging for elements: snowshoe hare responses to intraspecific black spruce elemental variation
9:15 – 9:30	**Travis Heckford**	Spatial stoichiometry: multi-species comparisons of elemental traits on the landscape
9:30 – 9:45	**Isabella Richmond**	Temporal variability in boreal plant stoichiometry
9:45 – 10:00	**Patrick Lauriault**	Determining critical habitat for sensitive cyanolichens in Newfoundland
10:00 – 10:15	**Kaushalya Rathnayake**	The relative importance of olfactory signaling to fly-moss spore dispersal network structure of two sympatric moss species in Newfoundland, Canada
10:15 – 10:45	**COFFEE BREAK**	
10:45 – 11:00	**Nicolas Peñafiel**	Population genomics for the conservation of two IUCN endangered Bolivian palms
11:00 – 11:15	**Laura Teed**	Spatial heterogeneity of a Newfoundland rhodolith bed along environmental gradients
11:15 – 11:30	**Danielle Quinn**	The complexity of species complexes: Supervised machine learning to facilitate cryptic skate classification and observer training in real time
11:30 – 11:45	**Jessica Randall**	Occurrence of ichthyoplankton in herring diets of eastern Newfoundland
11:45 – 12:00	**Evelyn MacRobert**	Habitat use by age-0 juvenile Cod and their predators
12:00 – 12:15	**Emilie Geissinger**	Overwinter survival and movement of juvenile Atlantic cod (*Gadus morhua*) in nearshore coastal Newfoundland
12:15 – 13:00	**LUNCH BREAK**	
13:00 – 13:15	**Jaclyn Aubin**	Why should I care? Patterns of allocare in St. Lawrence estuary belugas
13:15 – 13:30	**Kaylee Busniuk**	The pilfering of puffins: kleptoparasitic behaviour by herring gulls
13:30 – 13:45	**Katrina Shwedack**	Dark-eyed juncos adjust song structure in response to traffic noise
13:45 – 14:00	**Levi Neweduik**	Using integrated step selection analysis to distinguish social and spatial influences on habitat selection behaviour
14:00 – 14:15	**Christina Prokopenko**	Trait-mediated functional response: antipredator traits drive prey switching in multi-prey systems
14:15 – 14:30	**Michel Laforge**	Green-up or snow-off? Reconsidering phenological drivers of migration

PRESENTATION SCHEDULE – Arts 1049

9:00 – 9:15	**Marta Miatta**	Sea pens fields as key biogenic habitats in deep-sea soft sediments: The case of the proposed Laurentian Channel Marine Protected Areas
9:15 – 9:30	**Charlotte Wilson**	Health, stress, and longevity of crabs in laboratory conditions
9:30 – 9:45	**Shahinur Islam**	Behavioural traits variation among divergent North American and European farm and wild Atlantic salmon populations
9:45 – 10:00	**Julie Jacques**	Aggregation, feed consumption, and roe yield of *Strongylocentrotus droebachiensis* (Green sea urchin) fed at different stocking densities in a tiered raceway system
10:00 – 10:15	**Zoe Zrini**	Using data storage tags to study the effects of hydrostatic pressure on the heart rate of lumpfish (*Cyclopterus lumpus*)
10:15 – 10:45		**COFFEE BREAK**
10:45 – 11:00	**Tyler Lantiegne**	Female post mating pre-zygotic barriers to hybridization in salmonids
11:00 – 11:15	**Manuel Soto-Dávila**	*Aeromonas salmonicida* subsp. *salmonicida* early infection and immune response of Atlantic cod (*Gadus morhua* L.) primary macrophages
11:15 – 11:30	**Jose Ignacio Vasquez**	Genomics analysis of *Vibrio anguillarum* J360 isolated from an outbreak in cultured Lumpfish (*Cyclopterus lumpus*)
11:30 – 11:45	**Md. Ahmed Hossain**	Cold shock proteins of *Aeromonas salmonicida*
11:45 – 12:00	**Setu Chakraborty**	*Aeromonas salmonicida* iron-regulated outer membrane proteins provide protection to *Cyclopterus lumpus* against furunculosis
12:00 – 12:15	**Joy Chukwu-Osazuwa**	Characterization and selection of potential vaccine candidates against *Piscirickettsia salmonis* using reverse vaccinology approach
12:15 – 13:00		**LUNCH BREAK**
13:00 – 13:15	**Hajarooba Gnanagobal**	In-silico characterization of riboflavin supply pathways in *Aeromonas salmonicida*
13:15 – 13:30	**Arshad A. Shaikh**	Deciphering cellular signaling pathways of *Streptomyces clavuligerus* for antibiotic production
13:30 – 13:45	**Trung Cao**	Vaccine evaluation against *Vibrio anguillarum* in Lumpfish (*Cyclopterus lumpus* L)
13:45 – 14:00	**Jordan Wight**	Antibiotic resistance patterns in environmental *E. coli* found in St. John's, Newfoundland
14:00 – 14:15	**Jayamini Jayawardhane**	Nitric Oxide and reactive oxygen species mediated metabolic changes in barley and rice seed embryo during germination
14:15 – 14:30	**Purvikalyan Pallegar**	Cyclic-di-GMP signaling and the gene transfer agents (GTAs) production in *Rhodobacter capsulatus*
14:30-14:45	**Phoebe (Yuting) Li**	TxtH is a key component of the thaxtomin biosynthetic machinery in the potato common scab pathogen

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

2018 – Evolution and Ecology – Ethan Armstrong

2018 – Cellular and Molecular Biology – Jordan Wight

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

2018 - Evolution and Ecology – Quinn Webber

2018 – Cellular and Molecular Biology – Joost Verhoeven and Sabrina Inkpen

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

2018 – Juliana Balluffi-Fry

2017 – Anne Provencher St. Pierre

2016 – Brittany Palm-Flawd

2015 – Carley Schacter and Katherine Robbins (co-authors)

2014 – Sarah Adcock and Barbara de Moura Neves

2013 – Laura Wheeland

2012 – Andrew Murphy

2011 – Michelle Fitzsimmons

Joe Brown Award

2018 – Lancy Cheng

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

Cumulative impacts of hypoxia and trawling on Northeast Pacific benthos

Alessia C. Ciraolo* & P. V. R. Snelgrove

Department of Ocean Sciences, Memorial University of Newfoundland

Natural variation and human activities both impact British Columbia (BC) continental slope benthos, where recent studies demonstrate impingement of the Oxygen Minimum Zone (OMZ), a natural disturbance, on the continental slope between 600 and 1200 m depth. Bottom trawling, an anthropogenic disturbance, has also targeted this area since 1994 from 150 m depths on the outer shelf through slope depths to 2000 m. The individual and cumulative impacts of these activities on benthic diversity and functioning remain largely unknown. Improved scientific knowledge on cumulative impacts could help in developing strategies for monitoring and protecting diversity and ecosystem functioning of vulnerable environments. Our study will examine the co-varying effects of depth and dissolved oxygen trends through short-term (<24 h) shipboard incubations of sediments collected by multicoring and successive lab work to evaluate the separate and synergistic effects of impacts on: 1) how seabed macrofaunal and microbial diversity interact with O_2 gradients and historical trawling intensity; 2) how they interact in recycling organic matter and regenerating nutrients. We hypothesize that cumulative effects of increasing hypoxia and trawling exceed their individual effects in terms of biodiversity loss and decreased ecosystem functioning.

The effect of extreme local weather events and refuge availability on green crab abundance and physiology at a global scale

Brandy Biggar* & A. Bates

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

Climate change associated warming is expected to shift species' distributions and facilitate invasions, but little is known about how extreme weather events will confound these expectations. *Carcinus maenas* is a formidable competitor that has invaded nearly every continent, making it a compelling model species to examine how extreme weather events impact abundances in its native, naturalized, and invasive geographic ranges. Using time-series abundance data from both sides of North America and Europe, we quantify how *C. maenas* has responded to cold spells and heat waves. We predict that crab populations at the edges of their temperature tolerances will be most sensitive to extremes in environmental temperature. We further predict that abundance changes will be related to the availability of thermal refugia. Soft substrates which allow crabs to burrow, and access deeper water, which is cooler in the summer and warmer in the winter, may allow crabs to avoid temperature exposure. Preliminary analyses support a strong role of temperature in predicting abundance change in the green crab, where lack of access to thermal refugia during cold winter months leads to marked declines.

Evaluating the impact of a removal program for the invasive European green crab (*Carcinus maenas*) in Placentia Bay, Newfoundland

Caley Ryan[1]*; Le Bris, A.[1]; Best, K.[1]; & McKenzie, C.H.[2]

[1] Centre for Fisheries Ecosystem Research, Fisheries and Marine Institute of Memorial University
[2] Northwest Atlantic Fishery Centre, Fisheries and Oceans Canada, St. John's, NL A1C 5X1

Populations of invasive green crab have become established on much of North America's east coast. By competing and predating on native species, green crabs significantly impact local biodiversity and habitats, including bivalve and eelgrass beds. Green crabs were first observed in Newfoundland in North Harbor in 2007 and have since spread throughout Placentia Bay, damaging eelgrass beds and subsequently reducing local fish densities. A five-year removal program is aiming to reduce abundance of green crab in Placentia Bay. More than 150 metric tons of crabs were removed in the first two years and the average catch per unit of effort (CPUE) decreased from 2 to 1.09 kg/trap between 2017 and 2018. However, CPUE can be a biased measure of abundance trends due to being influenced by factors other than abundance. The objective of this research is to develop a generalized linear mixed model to standardize the CPUE of green crab in Placentia Bay. Temperature, depth, and salinity sensors were placed on traps to record environmental factors. This model will help inform on the efficacy of the green crab control fishery in Placentia Bay and the capacity of large efforts to control established populations of aquatic invasive species.

Factors that shape the reproductive success in Dark-eyed Juncos (*Junco hyemalis*)

Chirathi Wijekulathilake* & D. Wilson

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

The fitness of an organism involves its ability to survive and reproduce and is usually measured by the number of offspring that an organism can contribute to the next generation. Mating success is one major factor that contributes to the total fitness of an individual which results from male-male competition and female mate choice. Previous research work emphasizes how male competition and female mate choice involves sexual selection. However, the importance of these processes on the reproductive success of free-living birds has been poorly studied. Therefore, we investigate the morphological, behavioural, and ecological predictors of reproductive success in dark-eyed juncos (*Junco hyemalis*). By obtaining multiple measures of reproductive success, including the number of eggs laid, number of eggs that hatch, and number of nestlings that fledge, and by correlating them with morphology, song performance, dominance and territory, and nest site selection, we will be able to identify the factors that shape reproductive success in wild Dark-eyed Juncos. These findings, in turn, will help us to understand the population declines of the songbirds in general.

Do cod discarded from pots experience behaviour impairment?

Elizabeth Moore* & Favaro, B.

Centre for Sustainable Aquatic Resources, School of Fisheries, Fisheries and Marine Institute of Memorial University of Newfoundland

Increasing evidence shows that sublethal effects of fishing have serious consequences that receive comparatively less attention than direct fishing mortality in the scientific literature. The northern cod (Gadus morhua) stock remains under a moratorium, and alternative gear types are being investigated as a way to reduce impacts on cod. However, even these gear types may have unintended consequences by negatively altering cod behaviour. In Newfoundland, there is interest in using cod pots to discard cod alive. An initial study will examine if barotrauma (injuries related to pressure changes) negatively influences the behaviour of cod caught in pots. The study is designed to fish cod pots from a control depth and one experimental depth (a large pressure change). Cod will be tagged and tracked using acoustic telemetry to measure vertical and horizontal swimming behaviour over several weeks. It is expected that cod fished from deeper depths will experience a longer recovery period, during which time normal behaviours are impaired. Behaviour impairment may be an issue in a population context. The fisheries for northern cod occur during the summer and fall when cod are feeding; long disruptions in feeding may impact developing gonads and energy stores for overwintering.

Characterization of a novel virulence factor produced by a plant-pathogenic *Streptomyces* strain isolated in Newfoundland

Gustavo A. Díaz-Cruz* & D.R.D. Bignell

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

Common scab (CS) is a very important disease of potato. It is characterized by the presence of superficial, pitted and/or raised lesions on the tuber surface, negatively affecting the quality and market value of the potatoes. CS is mainly caused by *Streptomyces scabies*, which uses a virulence factor called thaxtomin A for disease development. However, some pathogenic *Streptomyces* strains do not produce thaxtomin A, and instead use other phytotoxins to cause disease. This is the case for *Streptomyces* sp. strain 11-1-2, which was isolated from CS-infected tubers in Newfoundland. Preliminary studies showed that culture extracts of this strain are highly toxic to plants, but the phytotoxin(s) responsible is yet to be identified. Here, we propose to characterize the phytotoxin(s) produced by this strain. The strain will be cultured under conditions that promote the production of the phytotoxin(s), after which the phytotoxin(s) will be purified and its chemical structure determined. The genome of the pathogen will then be analyzed for the biosynthetic genes involved in the production of the phytotoxin(s). To confirm the role of the phytotoxin(s) in the plant pathogenic phenotype of *Streptomyces* sp. 11-1-2, mutant strains will be created that are no longer able to produce the phytotoxin, and the pathogenicity of the mutants will be assessed using plant bioassays. Ultimately, this study will enhance our knowledge on the virulence mechanisms of plant pathogenic *Streptomyces* spp., and will assist in the development of better management strategies and breeding programs to reduce the impact of CS disease on potato production.

Comparing various plastic polymer fishing rope to determine the amount of plastic fragmentation under environmental contact

Jacquelyn Saturno*[1]; Max Liboiron[2]; & Brett Favaro[1]

[1] Centre for Sustainable Aquatic Resources, School of Fisheries, Fisheries and Marine Institute of Memorial University of Newfoundland
[2] Department of Geography, Memorial University of Newfoundland

Although plastic pollution is the most abundant form of contamination in coastal regions and marine ecosystems, little is known of how much active fishing produces plastic waste. Studies conducted in fishing communities around the world, including Newfoundland, have confirmed microplastics (< 5 mm) resembling fishing rope threads in the digestive tract of fish, including Atlantic cod (*Gadus morhua*). Currently, it is not known if these microplastics could also be attributed to active fishing as fishing gear does undergo wearing and abrasion. In this particular study, we compared four different types of plastic polymer ropes that are commonly used in the fishing industry (polyethylene, polypropylene, polyethylene-polypropylene blend, and nylon) to determine if fragmentation occurs at different rates depending on plastic polymer composition. This was done by rigorously wearing them down against an artificial seabed. Trials were standardized into 5 minute increments and ended when ropes reached a 50% loss in diameter. An initial finding has shown that all ropes, regardless of plastic polymer composition degraded within 2 hours of abrasion, despite the ropes being abrasion resistant. This study aims to establish an understanding of how abrasive wear on rope being used in fishing communities may directly cause the generation of microplastic pollution.

Population structure and size at maturity of the Caribbean spider crab *Maguimithrax spinosissimus* in Eleuthera, The Bahamas

Logan R Zeinert* & I. J. McGaw

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

The Caribbean spider crab (*Maguimithrax spinosissimus*) is the largest crab in the western Atlantic, reaching 3 kg in weight and 170 mm carapace width (CW). At present there is no established fishery for *Maguimithrax spinosissimus*, in addition its short larval stage and herbivorous nature could make this species a potential candidate for aquaculture. The present study investigated the size ranges at patch reefs, blue holes and anchialine ponds in Eleuthera, The Bahamas (January and June 2018). A total of 354 individuals were collected; males comprised 42.1 % of the population with a mean CW of 107.7 ± 1.48 mm, while the mean CW of females was 94.3 ± 0.87 mm. Principal Component analysis and linear discriminant analysis were used to determine size at maturity: males reached maturity at 86.3 mm, whilst female maturity was reached at 79 mm. On average the meat yield of the wet mass of the crab was 12.43 ± 0.68 %, which is comparable to other decapods. We also used the gastric mills to determine the age of crabs by sectioning the ossicles and looking for rings of seasonal growth. The data gathered for this species could be used to establish management plans for an artisanal fishery in the Bahamian archipelago.

Impact of paternal history on honesty of sexual signals and mate quality in anadromous Atlantic salmon (*Salmo salar)*

Madison Philipp* & C. Purchase

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

Sexual signaling theory posits that the advertising mate, typically the male, produces a phenotypic trait that is preferred by the choosing mate to signal reproductive readiness and mate quality. The energetic cost to produce these signals creates a differential in signal production between males that are considered high or low 'quality'. Successful reproduction depends on the ability of a male to attract a female, as well as the ability of his spermatozoa to successfully fertilize an egg. Once activated, spermatozoa survive for only a short time making swimming velocity crucial for fertilization. Spermatozoa velocity can be inhibited through damage caused by reactive oxygen species (ROS). Antioxidants, such as carotenoids, act as neutralizers to the ROS induced toxicity, helping to protect spermatozoa against biological damage. Carotenoids also produce bright red and orange hues used in sexual signals. Carotenoids can only be obtained through the diet, making carotenoids limiting based on an individual's ability to acquire and assimilate carotenoids. Anadromous Atlantic salmon (*Salmo salar*) populations consist of males with different reproductive histories. Virgin and repeat spawners compete for mating opportunities with the same females. Repeat spawners have different migration pathways and therefore different diets than virgin spawners. We hypothesize that due to this difference, repeat spawners have a duller sexual colouration and lower quality spermatozoa. Analyses are still ongoing, however, preliminary observations suggest a distinct difference in colouration, and therefore carotenoids, between virgin and repeat spawning Atlantic salmon.

Susceptibility to *Aeromonas salmonicida* subsp. *salmonicida in* Atlantic salmon (*Salmo salar* L.) of farmed, wild type and hybrid crosses

My Dang[1*]; S. Dove[2]; T. Cao[1]; A. Hossein[1]; H. Gnanagobal[1]; M. Soto-Dávila[1]; I. Vasquez[1]; S. Chakraborty[1]; M.L. Rise[2]; I. Fleming[2]; J. Westcott[3]; & J. Santander[1]

[1]Marine Microbial Pathogenesis and Vaccinology Laboratory, Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL, Canada;
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Aeromonas salmonicida subspecies *salmonicida* is the causative agent of furunculosis in several fish species including Atlantic salmon (*Salmo salar*). Although genetic susceptibility and resistance to *A. salmonicida* has been documented in salmon, the mechanisms are still not well understood. Here, we compared naïve and immunized Atlantic salmon from farmed (North American [NA] and European [EO]), wild (Northeast Placentia R.) and hybrid crosses (NA farmed female by wild male, and EO farmed by wild reciprocal crosses) to *A. salmonicida* susceptibility. The smoltified Atlantic salmon were intraperitoneally (IP) immunized with formalin-killed *A. salmonicida* and boosted 4 weeks post-primary immunization. The control consisted of fish IP injected with phosphate buffered saline (PBS). The fish were challenged at 10 weeks post-primary immunization. Naïve fish were IP challenged with 2.5×10^4 CFU/100 g. The immunized fish were challenged with 4×10^6 CFU/100g. We found that wild Atlantic salmon were significantly more susceptible to *A. salmonicida* than the farmed and hybrid crosses ($p < 0.001$). Colonization of lymphoid tissues by *A. salmonicida* correlated with fish susceptibility. In contrast to naïve fish, no differences in susceptibility were found between vaccinated farmed, wild, and hybrid crosses challenged with a high dose of *A. salmonicida*. These results indicate that wild fish are more susceptible than farmed and hybrid crosses to *A. salmonicida* infection. Additionally, formalin-killed *A. salmonicida* triggered similar immune protection in all Atlantic salmon strains evaluated. This study provides new insights into immune response to *A. salmonicida* infection and immunization in Atlantic salmon.

Distribution and Seasonal Behavior of Atlantic halibut (*Hippoglossus hippoglossus*) in the Gulf of St. Lawrence based on data from Pop-up Satellite Archival Tags

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Atlantic halibut supports the most valuable groundfish fishery per unit weight in Atlantic Canada, and the total landed value has increased from $16M CAD in 2006 to $57M in 2016. The fishery is currently managed as two separate stocks, the Gulf of St. Lawrence (GSL) stock, and the Scotian shelf and Southern Grand Banks stock. However, precise knowledge of population structure remains elusive, partly because seasonal distributions, migration routes, and feeding and spawning areas remain largely unknown. To gain knowledge of stock structure, spawning, and feeding behaviors, more than 100 Atlantic halibut were equipped with pop-up satellite archival tags (PSATs) since 2013 in the GSL. Data returned by the PSATs was used in a geolocation model to reconstruct migration tracks. Results suggest that Atlantic halibut complete their annual migration cycle within the GSL, supporting the current management of Atlantic halibut as two separate stocks. Furthermore, putative winter spawning and summer feeding behaviors were observed in relatively deep waters (300 - 450 m) and shallow inshore waters (< 100 m) respectively. However, further work is required to characterize these putative spawning and feeding behaviors with electronic tag data and inform the spatial management of this important fishery resource.

The Newfoundland and Labrador Mosquito Project: a citizen science-based study of mosquito populations and viral pathogens

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Mosquitoes are one of the most important vectors for infectious diseases and pose a threat to public health. Pathogens such as West Nile virus are a recent introduction to Canada (2002), and to date, Newfoundland and Labrador is the only province that has not detected this virus. With climate change occurring, the ranges of mosquitoes are changing, and new species are colonizing different areas. Newfoundland and Labrador has limited information regarding what mosquito species are present and what viral-pathogens they carry. The aim of this project is to use citizen scientists to collect mosquito samples from across the province for 1) understanding mosquito species distribution, 2) exploring the existence and distribution of viral-pathogens detected in the mosquitoes, and 3) comparing existing climate data to find out how climate change is affecting the mosquitoes and their viruses. In 2018, we distributed mosquito collection packages to citizens across the province. The participants collected mosquitoes and mailed the samples back to MUN. Each sample was identified to species and screened for select viruses. Mosquito identification results have confirmed the presence of *Aedes japonicus* which is a previously detected invasive mosquito to the province and *Aedes vexans* which is a native species previously detected in Labrador but has now been detected in St. John's. Screening results showed no detectable presence of West Nile virus or Bunyamwera and California serogroup viruses. This study will be repeated in 2019 and the outcomes will lead to a better understanding of the mosquito population and related public health risks in Newfoundland and Labrador.

Reducing seabed impact of Northern Shrimp and Greenland Halibut trawling in the Nunavut offshore fishery through trawl modifications

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Bottom trawls used in the Nunavut offshore Northern Shrimp and Greenland Halibut fishery currently use rolling rockhopper footgear, which is known to roll in the bosom section, when facing the towing direction, but not on the quarters and wings, where the towing direction is not perpendicular to the footgear axis, increasing seabed impact and species mortality. This project will develop an aligned rolling footgear to reduce the seabed impacts associated with bottom trawling in the Nunavut offshore fishery. First, we will document and evaluate the existing fishing gear technology used in the fishery (through software simulation, physical models in the flume tank and observations at sea), secondly we will design physical models of the new aligned rolling footgear for evaluation in the flume tank, and finally we will construct a real scale experimental footgear for at-sea evaluation (compare catch rates and performance of experimental and traditional footgear). This new technology will reduce penetration depth of the footgear components (i.e. rockhoppers) into the seabed, along with a reduction in contact area, due to its rolling and aligned capacities, lessening seabed physical impact and species mortality without compromising catch of target species or increasing bycatch. We expect to reduce the frictional force of the footgear with the seabed, which will potentially reduce drag and increase wing-end spread. This project will help industry meet eco-certification conditions as well as increase its social license to operate.

Foraging for elements: snowshoe hare responses to intraspecific black spruce elemental variation

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Herbivores must consume carbon dense primary producer matter and transform it into their relatively more nitrogenous (N) and phosphorous (P) body tissues. Therefore, herbivores have evolved strategies to select plants of higher nutrient (i.e., N and P) contents. While the plant species preferences are known for many herbivore species, questions still remain regarding selection for intraspecific variation in nutritional contents. Herbivores may selectively browse within a plant species, particularly in systems of low plant diversity and nutrient availability, like the boreal forest. Here, we tested for snowshoe hare selection of nitrogen and phosphorus content in black spruce, a low-quality, but abundant browse species. We first measured black spruce N and P contents in 36 sites across a 500 m x 500 m snowshoe hare live-trapping grid on the island of Newfoundland. Black spruce N and P content are correlated ($r = 0.66$), suggesting that there is natural spatial variation in growing conditions and nutrient availability across the sample grid. We then presented individual hares from the study grid with two choices of spruce, from areas with highest (~1.4 %N; ~0.19 %P) and lowest (~0.8 %N; ~0.10 %P) nutrient composition in 24-hour cafeteria-style experiments ($n = 22$). The preliminary cafeteria experiments demonstrated that hares have a non-significant preference for spruce of higher N and P content ($t = 1.73$; $p = 0.09$). This provides early evidence that snowshoe hares may detect and choose naturally occurring higher nutritional contents within a low-quality browse species, as defined by elemental compositions.

Spatial co-occurrence and the foliar stoichiometric niche of a coniferous and deciduous tree

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A species' ecological niche can be assessed by the response of indicator traits to changes in resource availability and community competition. The stoichiometry of plant foliage, notably the concentration of common elements (Carbon, Nitrogen, and Phosphorus), represent key ecological indicator traits. Here, we construct stoichiometric niche hypervolumes from the foliar C, N, P of two juvenile stage species with different tactics of resource acquisition and use, a slow-growing coniferous (balsam fir, *Abies balsamea*) and a fast-growing deciduous (white birch, *Betula papyrifera*) tree. Using relative measures of niche size (i.e., volume) and position (i.e., location in data space), we explored how the stoichiometric niche of our species differed when they spatially occur alone and co-occur at different extents. At the local extent we assessed spatial co-occurrence by comparing between two biogeographically distinct populations, and at the regional extent by combining populations and comparing across all individuals. At the local extent, for one population of white birch and both balsam fir populations, niche size did not appreciably vary, however, in each case niche position did differ. In comparison, one population of white birch exhibited a 0.2 – 54 % increase in niche size in response to spatial co-occurrence. At the regional extent, in response to spatial co-occurrence balsam fir niche size did not vary; however, niche position did differ. In comparison, white birch exhibited 19 – 75 % increase in niche size in response to spatial co-occurrence. Our results provide evidence that biogeographic constraints are an important factor to consider when niche modelling foliar stoichiometry across different spatial extents.

Temporal variation in boreal plant stoichiometry

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All organisms are composed of three major elements, carbon, nitrogen, and phosphorus. It is currently unknown how species' elemental composition varies interannually in terrestrial environments, specifically in the boreal forest. Temporal variation in the stoichiometry of plants is a key factor in understanding how terrestrial ecosystems function. If plant stoichiometry varies inconsistently between years, the habitat and resources available for consumers may be changing on an annual basis. My objective was to determine if there is evidence for temporal variation in plant stoichiometry and if so, what is driving it. We collected plant samples from four sites on the island of Newfoundland in 2016 and 2017 to obtain the stoichiometry (carbon, nitrogen, and phosphorus) of four boreal plant species (*Abies balsamea, Acer rubrum, Betula papyrifea,* and *Vaccinium angustifolium*). We then used model selection with Akaike Information Criterion to evaluate interannual variation in plant elemental composition. We found evidence for interannual variation in carbon in all plants and nitrogen and phosphorus in *Abies balsamea*. Next, we investigated four potential factors responsible for driving the majority of interannual variation: site, enhanced vegetation index, number of growing degree days, and height of the individual sampled. Understanding the stoichiometry of an ecosystem and how stoichiometric composition varies spatially and temporally allows us to predict how it will change over time and provides a deeper understanding of the boreal forest.

Determining critical habitat for two sensitive cyanolichens in the Central Avalon Forest Ecoregion of Newfoundland, Canada

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Boreal Felt lichen (*Erioderma pedicellatum*) and Vole Ears Lichen *(Erioderma mollissimum*) are sensitive lichens that face threats of both air pollution and habitat destruction, as demonstrated by their response to widespread deforestation in Scandinavia and Nova Scotia. However, the habitat for these lichens in Newfoundland is largely intact. This presents the opportunity to provide empirical evidence of what constitutes critical habitat for these species. The goal of this study is to help ensure the persistence of these two lichens, which are either globally endangered (*E. pedicellatum*) or classified as endangered under the Species at Risk Act of Canada (*E. mollissimum*). This study considers habitat characteristics at the stand level, as well as tree level characteristics to aid in future sampling measures as these species are cryptic and rare on the landscape, making them difficult to find. We collected the stand level measurements on paired presence/absence plots of 5 m in radius. The tree level habitat measurements took place on five trees within each plot in a point-quarter survey arrangement. Preliminary analysis have shown that, contrary to popular opinion, these cyanolichens are not sensitive to natural or anthropogenic gaps. Other early findings suggest that the distribution of these lichens are driven by tree level (microscale) differences in habitat rather than tree stand level parameters. Furthermore, we report 1 new occurrence of *E. mollissimum* and 124 new *E. pedicellatum* found in the summer field season of 2018.

Unraveling the role of olfactory signals in fly mediated spore dispersal system in two sympatric moss species

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Nearly half of the species of the globally distributed moss family Splachnaceae use brood-site deception as a strategy of spore dispersal. Brood-site deceptive species grow on feces and on carrion and other animal matter. Their spores are dispersed to these substrates by flies that are attracted by visual and olfactory signals to their mature sporophytes.

We focus on two species, *Splachnum ampullaceum* and *S. pensylvanicum*. that coexists on the summer dung of moose (*Alces alces* L.) either as mixed-species populations or single populations in peatlands on the island of Newfoundland, Canada. The sporophytes of each species have relatively distinct olfactory signals and very distinct visual signals. The odor chemistry of *S. ampullaceum* mimics herbivore/moose dung whereas that of *S. pensylvanicum* mimics omnivore dung. We manipulated the odor signals in each moss species by adding carnivore-mimicking scent to *S. ampullaceum* and herbivore mimicking scent to *S. pensylvanicum* populations and observing the changes in spore-disperser fly communities associated with manipulated and non-manipulated moss populations.

Preliminary data analysis shows that altering olfactory signals shifts the composition of the fly assemblage attracted to each moss species such that scent manipulation converged each moss species' fly fauna closer to that associated with the other (unmanipulated) moss species. This result confirms that of an earlier study focusing on visual signals that suggested that olfactory, not visual signals promote visitor specificity whereas visual signals primarily act to magnify the degree of attractiveness of mature moss populations to potential spore-dispersing flies.

Population genomics for the conservation of two IUCN endangered Bolivian palms

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The Tropical Andes of South America are home to an astounding number of plant species. Among them, several palm lineages have found in this hotspot opportunities for dispersal and/or speciation. Palms of the genus *Parajubaea*, however, represent a special Andean case of low diversification, with only three species recognized, despite the genus’ origin at 22 Mya. Two of them, *P. torallyi* and *P. sunkha*, are endemic to Bolivia and are listed as endangered by the IUCN, since they show restricted ranges, where they face rapid habitat degradation and limited regeneration. Contrastingly to several other Neotropical palm genera, research on any aspect of the biology of *Parajubaea* is scant, including its genetics. The goal of the present study is to understand the genetic diversity and genetic structure of *P. torallyi* and *P. sunkha* populations in order to inform future conservation actions. A total of 168 individuals from three populations of *P. sunkha* and four populations of *P. torallyi* were genotyped using Genotyping by Sequencing. After filtering, we obtained 272 million reads which we assembled de novo into loci using STACKs. We recovered 1432 single nucleotide polymorphisms within 531 loci across all samples. Preliminary analyses suggest that individuals belong to seven genetic clusters, which show discrepancies between the sampled sites. *P. sunkha* shows higher indices of genetic diversity than *P. torallyi*. Pairwise comparisons between populations showed overall low genetic differentiation. No apparent correspondence between geographic distance and genetic differentiation between populations was found. Assessing the genetic diversity within species and populations will guide future conservation efforts.

Spatial heterogeneity of a Newfoundland rhodolith (*Lithothamnion glaciale*) bed along environmental gradients

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Coralline red algae can form extensive aggregations referred to as rhodolith beds. Rhodolith abundance within a bed is thought to be driven by moderate hydrodynamic forces, and bioturbators that clear rhodoliths of sediment and cause them to roll, giving thalli access to light energy. To gain knowledge about factors that control the distribution and abundance of rhodoliths in, and spatial limits of, rhodolith beds in cold-temperate regions, we quantified with a drop camera system, rhodolith (*Lithothamnion glaciale*) abundance, dominant bioturbator presence (green sea urchin, *Strongylocentrotus droebachiensis*, and common sea star, *Asterias rubens*), and bottom type every 20 to 60 m at depths of 5 to 114 m over 3432 m^2 of seabed in St. Phillip's, southeastern Newfoundland. Sensors attached to the camera frame or at various locations on the seabed recorded light intensity, water temperature, and water flow acceleration. Rhodolith abundance increased with light and temperature, being highest on bottoms composed of a mixture of coarse sand, gravel, and dead rhodolith fragments. Flow acceleration did not vary significantly along a depth gradient between the shallowest (7 m) and deepest (21 m) portions of the bed over which water flow was recorded, yet increased along a 610 m transect traversing the bed longitudinally at a depth of ~15 m, where rhodolith abundance increased with flow acceleration. Bioturbator abundance was generally low throughout the bed and unrelated to rhodolith abundance. Results challenge the long-standing paradigm that water motion is the main factor determining the spatial limits of rhodolith beds.

The complexity of species complexes: Supervised machine learning to facilitate cryptic skate classification and observer training in real time

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The inability to differentiate accurately and confidently among morphologically similar species that overlap spatially (cryptic species) constrains effective conservation and management strategies. Traditional modeling approaches may reveal differences in morphological characteristics among such species without providing a practical means of classifying individual specimens. Cryptic Winter Skate (Leucoraja ocellata) and Little Skate (L. erinacea) populations in the Bay of Fundy, Nova Scotia, Canada illustrate this challenge. Machine learning offers a promising alternative to statistical inference techniques by detecting otherwise "hidden" patterns without the need for explicit indication of pattern location. By applying supervised machine learning to decipher this classification problem, we generated predictions of species' classification with equal or higher accuracy than alternative methods. We will present a case study of the strengths, limitations, and potential application of these routines for retroactive and on-the-ground differentiation of Winter and Little Skate, explaining its broader application for a wide range of classification challenges.

Occurrence of ichthyoplankton in autumn herring diets of Eastern Newfoundland

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Capelin is the keystone forage fish in the Northwest Atlantic ecosystem where it is a conduit of energy from lower to higher trophic levels. The capelin population collapsed in the early 1990s with minimal recovery in the subsequent three decades. Atlantic herring, an inshore forage fish in the region, is a known predator of the early life stages of fishes. In the Barents Sea, herring predation is a major driver of capelin recruitment dynamics. Atlantic herring diet in eastern Newfoundland has not been assessed since the 1940s. The objective of this study is to describe the diet of herring in autumn, a period of potential temporal and spatial overlap with capelin larvae, by pairing stomach content and stable isotope analyses. Adult herring were sampled weekly from August to November of 2017 and 2018 in Trinity Bay, Newfoundland. Stomach contents were identified to the lowest possible taxonomic level. Muscle samples were analyzed for stable isotopes and the results compared with signatures from neighboring bays, collected between 2012 and 2017. Preliminary results from the 2017 stomach samples (n=340) indicated that the most frequently consumed prey items included copepods (primarily *Temora* spp.), decapod larvae, cladocerans and the early life stages of fishes (eggs, larvae and juveniles). Of the fish larvae found in the stomachs, the majority were identified as capelin while loose otoliths were primarily from gadids. We anticipate that the results from 2018 will generally reflect similar prey composition as 2017 but possibly with a smaller contribution of larval capelin due to low larval numbers observed in the fall ichthyoplankton surveys. As 2018 data becomes available, we will compare the results between years and neighboring bays, as well as distinguish the long-term contribution of pelagic and benthic prey to herring diets.

Spatial risk: Influence of piscivorous fish on selection of nursery habitat by Age-0 juvenile cod

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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-0 cod among habitat types through video transects. To determine how predators shaped habitat use by Age-0 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-0 juvenile cod utilized shallow-water eelgrass beds less than 7 m deep. While predator habitat use varied across season and diel period, predators predominantly occupied the habitat surrounding eelgrass. From these results we infer that eelgrass habitat indeed provides protective habitat for Age-0 cod, but predators may still exert a reduced predation effect by focusing on the periphery of protective habitat and limited availability of juvenile prey.

Winter is not that rough: capture-recapture study shows high overwinter survival in juvenile Atlantic cod

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Atlantic cod (*Gadus morhua*) experience high mortality rates during their first year. In subarctic Newfoundland, cod settle into coastal habitats in several pulses through summer and fall, producing a broad length-frequency distribution prior to their first winter. The first winter, likely a critical period in cod survival, ultimately determines cohort strength. We evaluated juvenile size-structured overwinter survival and movement using mark-recapture techniques. Juvenile cod were marked with the fluorescent dyes, Calcein and alizarin red-S, in two batches in October 2016. Fluorescent dyes mark otoliths, potentially producing two distinct marks in each fish. Fish were recaptured in May 2017 from the release site and two neighboring coves to determine overwinter movement and survival, where we estimated survival using Cormack-Jolly-Seber models. Although recaptures include 3 marked fish from a neighboring cove approximately 1.2 km from the release site, none were recaptured from the second cove (1.8 km away). Higher apparent survival overwinter (59.4 %) than in fall (55.5 %) defies our expectation that survival of young-of-year juvenile cod would decrease overwinter, and that fish would not move to new sites post-winter. Our results have important implications for determinations of survival in the first year of life in subarctic juvenile fishes.

Why should I care? Patterns of allocare in St. Lawrence estuary belugas

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Allocare, investment in offspring from non-parents, is widespread among social odontocetes, suggesting that these group-living whales could provide insight into the mechanisms underlying the evolution of allocare. Variations across taxa suggest that the evolutionary pressures driving allocare vary across odontocete populations. Among bottlenose dolphins, allocare is driven by the need for subadult females to acquire parenting skills (“learning-to-parent”), and an indiscriminate attraction towards neonates (“natal attraction”), while allocare in sperm whales is best explained by kin selection and reciprocal altruism. Among belugas (*Delphinapterus leucas),* allocare has been anecdotally reported in wild populations. Through a sustained observational effort targeting groups of females with offspring in the endangered St. Lawrence Estuary beluga population, we quantified allomaternal associations to identify which of these four hypotheses for the evolution of allocare (kin-selected care, reciprocation, learning-to-parent, and natal attraction) are consistent with patterns of allocare in this population. Given that we observed significantly more adult than subadult allomothers ($p < 0.001$), and that allomaternal investment, particularly the duration of allomaternal associations, increased significantly with offspring age ($p < 0.001$), we found no support for the learning-to-parent and natal attraction hypotheses, and were unable to exclude the kin-selected care and reciprocation hypotheses.

The pilfering of puffins: kleptoparasitic behaviour by herring gulls

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Herring gulls (*Larus argentatus*) steal prey items from Atlantic puffins (*Fratercula arctica*) returning to their burrows to provision their chicks; this potentially imposes a significant waste of energy on adult puffins and reduces food available to chicks. Many studies have described kleptoparasitism in this system, but few have explored the behaviour from the gull's perspective. Using video recordings and first-person dictation, we observed and described 1532 approaches by puffins, and all kleptoparasitic behaviour of gulls that ensued. Gulls never attacked a puffin without conspicuous prey, but attacked 18.2 % of puffins that landed with prey and 7.2 % of approaching puffins that had prey but that aborted their landing attempt. Preliminary results suggest that gulls were more likely to attack puffins that landed versus aborted their landing, held larger versus smaller prey, and landed closer to versus farther from the gull. Gulls were more likely to obtain prey items if they made physical contact with the puffin and if they attacked a landing puffin. Gulls were never successful in stealing prey items from a puffin that aborted its landing. Our results indicate that gulls use distinct behaviours to obtain a puffin's prey.

Dark-eyed juncos adjust song structure in response to traffic noise

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Anthropogenic noise has been linked to reduced biodiversity and reproductive success in animals, possibly because noise disrupts acoustic signaling that is critical for survival and reproduction. Previous correlational studies show that some animals mitigate the disruption by shifting signal production to quieter times or by changing the structure of their signals in ways that minimize acoustic masking. However, there have been few experimental studies, making it unclear whether these changes are due to noise or to potentially confounding factors, such as the habitat alteration that often accompanies noise. Here, we broadcasted experimental traffic noise or silence through a loudspeaker in an otherwise undisturbed boreal forest during the avian breeding season, and recorded the vocal responses of nearby resident dark-eyed juncos (*Junco hyemalis*) using a microphone array. Experimental traffic noise caused juncos to produce shorter songs with decreased frequency bandwidth and increased minimum frequency and syllable rate. These changes may facilitate communication in noisy environments by reducing acoustic masking, and may thus help to explain why juncos thrive in noisy environments

Using integrated step selection analysis to distinguish social and spatial influences on habitat selection behaviour

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Movement is the mediator of spatially explicit trade-offs in animals and the means by which animals shape their social and spatial environments. Through integration of movement and habitat we can understand the processes underlying fine-scaled habitat selection behaviour. For social animals, density constrains home range size and negatively influences selection of preferred habitats, but underlying habitat selection decisions are likely made at finer patch scales as individuals move through their home ranges. We use integrated step selection analysis to incorporate movement and resource selection by elk (*Cervus canadensis*) in Riding Mountain National Park, allowing us to understand how the influence of conspecific density on elk movement produces habitat selection patterns at the patch scale. Our results shed light on how fine-scaled individual movement produces the emergent patterns predicted by optimal foraging theory.

Trait-mediated functional response: antipredator traits drive prey switching in multi-prey systems

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The eco-evolutionary tension between responsive prey and receptive predator underlies the dynamics of physiology, behaviour, populations, and communities. We advance the well-established link between resource-consumption rates and (a) resource density and (b) resource antipredator traits with a mechanistic and quantitative framework applicable to multi-prey systems. Here we create a 'trait-mediated functional response' model for a single predator and two prey, where prey antipredator traits exert variable influence on the stages of the predation sequence: searching, chasing, or handling. We illustrate how dissimilarity in traits that increase time invested by the predator influence both prey and predator. Stabilizing negative density-dependent predation (Type III functional response) was only observed in a select few contexts. Our results indicate that prey-specific consumption rates and overall energetic gains are sensitive to relative and absolute density of prey. Specifically, predators become more discerning with more prey on the landscape, leading to a 'meta-functional response'. Our model represents a synergy of foundational and contemporary predator-prey theory with trait-based ecology, providing a new paradigm to guide future research through the reality of diverse predator-prey systems.

Green-up or snow-off? Considering phenological drivers of herbivore migration

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Migration is considered a behaviour used to optimize an animal's exposure to favourable environmental conditions. Spring is an energetically costly time for reproducing herbivores, as they must meet heightened energy demands not only of long-distance displacement but also of gestating and rearing young. Spring in northern climates is also a time of rapid environmental change. Melting snow provides easier access to forage and ease of travel, and newly emergent vegetation represents a valuable new nutritional resource. These processes are spatio-temporally variable, and as a result, habitat selection for herbivores in spring is a complex dynamic process. Individuals must optimize both the timing of important life-history events such as migration and parturition while also adopting habitat selection strategies that maximise use of locally available resources. We used remotely-sensed data to examine the timing of female caribou (*Rangifer tarandus*, n = 128) migration and parturition as a function of the availability of two important measures of environmental change—snow melt and green-up. We generated resource selection functions to test whether caribou were selecting for areas associated with these environmental changes during both migration and afterwards during the calving season. Our results show that caribou migration typically occurs during the peak of snow melt, with parturition and the subsequent energetic costs associated with lactation occurring during the peak of green-up. Resource selection functions revealed interactions between animals selecting for areas of snow-off and green-up. Our results have important implications for understanding trade-offs in herbivore resource selection strategies in variable landscapes.

Sea pen fields as key biogenic habitats in deep-sea soft sediments: The proposed Laurentian Channel Marine Protected Area example

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Sea pens are soft corals (order Pennatulacea) that live on soft sediments at virtually all depths. In the Laurentian Channel Area of Interest (AOI), off the southwest coast of Newfoundland and Labrador, sea pens were a primary reason for the creation of the AOI. Sea pens create important biogenic habitats and nurseries for many species of groundfish and invertebrates, including commercially important taxa. This study was the first to assess their role as habitat providers for macroinfaunal communities. We evaluated abundance, biodiversity, and community and functional structure of macroinfauna, with a focus on polychaetes, across different habitats within the AOI. Sediment samples were collected in summer 2017 and 2018 using an ROV or multicorer, respectively, whereas sea pen densities were estimated from video transects. We also considered several environmental parameters (e.g., depth, temperature, grain size, sediment organic content) as potential drivers of macrofaunal patterns. Preliminary results suggest that sea pens, particularly *Pennatula* spp., play a key role in enhancing local biodiversity and functional diversity of macrofauna. Our study confirmed the importance of these biogenic habitats and the need to protect them from anthropogenic impacts and stressors. These results will also help in evaluating the conservation objectives proposed for the Laurentian Channel MPA and in developing adequate monitoring protocols.

Long and short term laboratory stressors on decapod crustacean health and longevity

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Decapod crustaceans are frequently held in aquaria and are an important research animal for ecological and physiological studies. With increasing awareness of crustacean 'pain' and stress, it is becoming important to understand the factors influencing overall health, and ultimately survival of crustaceans in a laboratory environment. Knowledge of these issues could influence decisions to include decapod crustaceans in animal care guidelines, similar to those currently in place for vertebrates and cephalopods. There are a number of articles that detail short term stress, but little is known about longer term health and survival of decapods in a laboratory setting, and the impact of shorter term experimental procedures on recovery times. We used the green crab (*Carcinus maenas*) to investigate 1) the effect of animal density and environmental enrichment on physiological condition, and survival and 2) the recovery times following short term handling stress. These results will provide important baseline information on long and short term laboratory stressors in crustaceans for use in future research and animal care protocols.

Do behavioural traits vary among divergent North American and European wild and farm Atlantic salmon (*Salmo salar*) populations?

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In animals, individuals often display consistent differences in behaviours across situations and contexts (e.g., animal personality). However, little is known about how such behavioural traits might vary in a context-dependent manner, with selection favouring correlated behaviours only in particular types of environments. For example, farm salmon often escape into the wild and may produce hybrids and feral offspring that interact with wild conspecifics. The outcomes of this interaction may reflect differences in the selective environment having affected behavioural traits associations. In Newfoundland, Canada, there is an interest in farming European origin (EO) salmon in addition to the current North American (NA) Saint John River strain. However, as these two farmed populations are genetically diverse, we need to know whether the behavioural trait differences of EO farm strain will be greater than more local NA farm strains. We thus designed a common-garden experiment to measure how individual fish from NA and EO farm populations behaved relative to their wild conspecifics and hybrids in four different contexts (exploration, exposure to a novel object, boldness under predation risk and aggression). Our findings indicate that NA and EO farm fish were similarly more explorative, bold, and aggressive than wild fish and related hybrids. We also found the presence of the behavioural correlation in some circumstances suggests that behavioural syndrome covary consistently with aspects of the selective environment. Overall, these results suggest that the variation of the behavioural trait among divergent NA and EO farmed and wild populations depend on the degree of selective pressure in the domestication process, and the geographic and ancestral relationships.

Aggregation, feed consumption, and roe yield in green sea urchin (*Strongylocentrotus droebachiensis)* fed at different stocking densities in a tiered raceway system

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Green sea urchin (*Strongylocentrotus droebachiensis*) produces one of the finest and most consumed roe in Asia's top seafood markets. Accordingly, methods are continuously devised to quickly produce high volumes of high-quality green sea urchin roe. Green sea urchins form 2-dimensional aggregations at a pace that increases with urchin density, which suggests that clustering at a high stocking density may reduce feed consumption and roe yield in containment systems. We carried out a roe enhancement experiment in a tiered raceway system during which ~1400 sexually mature green sea urchins were fed bi-weekly during seven weeks with advanced aquaculture feed. Urchins were grouped at low (50 individuals m^{-2}), intermediate (130 individuals m^{-2}), and high (209 individuals m^{-2}) stocking densities in 0.38 m^2 compartments through which seawater at 6 °C flowed at a moderate rate of 75 L min^{-1}. We used generalized linear mixed models to analyze aggregation, and general linear mixed models to analyze feed consumption and gonadosomatic index (GSI), as a function of density. Urchins aggregated mainly in downstream portions of the compartments. Among the three stocking densities, feed consumption and GSI did not differ, averaging respectively 6.8 g feed per kg urchins per day (± 0.1 g) and 20.8 % (± 0.2 %). The high GSI and low variability achieved, together with low urchin mortality (0.4 %), showed the tiered raceway system can quickly produce high volumes of urchin roe regardless of stocking density, which is a major operational advantage for roe producers.

Using data storage tags to study the effects of hydrostatic pressure on the heart rate of lumpfish (*Cyclopterus lumpus*).

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Data storage tags (DSTs) allow for the continuous recording of several physiological parameters in free-living animals, and could be an effective tool for studying fundamental questions in biology such as how hydrostatic pressure affects fish physiology. Available literature on this topic is limited to a narrow range of species, and rarely considers the interactive effects of hydrostatic pressure and other environmental variables. Lumpfish are an interesting model species for this research as DSTs and pelagic trawl records show that they are found at depths up to 1000 m. In my research, lumpfish (~ 200 to 400 g) were recovered for ~ 6 days after surgically implanting them with Star-Oddi HR DSTs, and their heart rate (HR) response was measured when exposed to increasing hydrostatic pressure (to 80 bar; 800 m in depth) alone; or increasing temperature (12 to 20 °C), decreasing temperature (12 to 4 °C) or decreasing oxygen levels (to 50 % air saturation) in the absence and presence of 80 bar pressure. In addition, I determined their HR response to increasing temperature up to their critical thermal maximum (CT_{max}, ~ 22 °C) at atmospheric pressure, and after a brief chase (exhaustive exercise). Hydrostatic pressure resulted in an increase in HR from ~ 48 to 61 bpm, but did not affect effect the HR responses to either temperature or hypoxia. The chasing stressor and increasing temperature to CT_{max} only resulted in a maximum HR of 76 and 78 bpm, respectively. My research provides the first evidence that lumpfish have a limited capacity to increase HR.

Conspecific sperm preference in the context of hybridization

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Through sexual selection, a female seeks to father offspring with the best quality male to maximize her reproductive fitness. To ensure maximum exposure to high quality males, females can utilize a polyandrous mating system. This is important because the female has higher costs to reproduction due to limited and energetically expensive gametes. While internally fertilizing females have a large degree of pre- and post- mating control (cryptic female choice), external fertilizers are limited in the mechanisms with which they can bias paternity. In salmonids, this cryptic female choice is mediated through the ovarian fluid, a viscous ion-rich solution released with the eggs. Ovarian fluid has been linked to strong conspecific sperm preference, or upregulation in sperm swimming velocity in Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*). This implies that ovarian fluid could inhibit hybridization, particularly when sperm from conspecific males and non-conspecific males are in competition. We hypothesize that all sperm swimming velocity is upregulated in ovarian fluid compared to water, but conspecific ovarian fluid upregulates sperm swimming velocity more. We conducted a novel study comparing the degree of sperm upregulation by ovarian fluid compared to a control of water with three species, Atlantic salmon, brown trout, and brook char (*Salvelinus fontinalis*). Comparing upregulation from water allows for the determination of conspecific sperm preference while accounting for variation in male quality. Samples were collected from 70 fish in November. Analysis of sperm swimming performance is ongoing. Preliminary data and conclusions will be presented.

Aeromonas salmonicida subsp. *salmonicida* early infection and immune response of Atlantic cod (*Gadus morhua* L.) primary macrophages

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Atlantic cod has an expanded repertoire of MHC-I and TLR components, but lacks the MHC-II, the invariant chain/CD74, and $CD4^+$ T cell response, essential for production of antibodies and prevention of bacterial infectious diseases. The mechanisms by which *G. morhua* fight bacterial infections are not well understood. *Aeromonas salmonicida* subsp. *salmonicida* is a recurrent pathogen in cultured and wild fish, and has been reported in Atlantic cod. Macrophages are some of the first responders to bacterial infection and the link between innate and adaptive immune response. Here, we evaluated the viability, reactive oxygen species (ROS) production, cell morphology, and gene expression of cod primary macrophages in response to *A. salmonicida*. We found that *A. salmonicida* infects cod primary macrophages without killing the cells. Likewise, infected Atlantic cod macrophages up-regulated key genes involved in the inflammatory response (e.g. *IL-1β* and *IL-8*) and bacterial recognition (e.g. *BPI/LBP*). Nevertheless, our results showed a down-regulation of genes related to antimicrobial peptide and ROS production, suggesting that *A. salmonicida* utilizes its virulence mechanisms to control and prevent macrophage anti-bacterial activity. Our results also indicate that Atlantic cod has a basal ROS production in non-infected cells, and this was not increased after contact with *A. salmonicida*. Electron microscopy results showed that *A. salmonicida* was able to infect the macrophages in high number, and release outer membrane vesicles during intracellular infection. These results suggest that Atlantic cod macrophage innate immunity is able to detect *A. salmonicida* and trigger an anti-inflammatory response, however, *A. salmonicida* controls the cell immune response to prevent bacterial digestion during early infection.

Genomics Analysis of *Vibrio anguillarum* J360 isolated from an outbreak in Lumpfish (*Cyclopterus lumpus*).

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Vibrio anguillarum also known as *Listonella* is a Gram-negative marine pathogen that causes vibriosis, a fatal hemorrhagic septicemia of fish, crustaceans, and mollusks, in freshwater and seawater. *V. anguillarum* causes negative economic impact on the aquaculture industry worldwide. Here, we describe the phenotypic, virulence, and genomics characteristics of *V. anguillarum* J360 isolated from lumpfish (*Cyclopterups lumpus*). Koch's postulates were determined in naïve lumpfish. Phenotypic, biochemical and enzymatic profiles were completed using classic microbiology tests, API20NE, and API ZYM. PacBio platform (Genome Quebec) was utilized for whole genome sequencing. *V. anguillarum* J360 has two chromosomes, chromosome I (CP034572.1), chromosome II (CP034573.1), and a large plasmid (pVaJ360; CP034572.1). *V. anguillarum* J360 genome has a total length of 4,549,571 bp, and an average of 44.13% of G+C content. Phylogenetic analysis using replication mechanism, stress-associated, and housekeeping genes such as 16S, *ftsZ*, *gapA*, *gyrB*, *mreB*, *pyrH*, *recA*, *rpoA,* and *topA,* indicates that *V. anguillarum* J360 is related to *V. anguillarum* NB10. Pseudogenes, pathogenic islands, mobilome, prophages, and antibiotic resistant genes also were identified. The whole genome sequence of *V. anguillarum* J360 will allow us to understand the pathogenesis evolution of *V. anguillarum,* and to design vaccines against this pathogen to prevent future outbreaks.

Cold Shock Proteins of *Aeromonas salmonicida*.

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First described in the 19th century, *Aeromonas salmonicida* subspecies *salmonicida* is one of the oldest known fish pathogens and the causative agent of furunculosis in marine and freshwater fish. *A. salmonicida* is an important pathogen due to its nearly worldwide distribution, broad host range and potential devastating impacts on wild and farm fish. *A. salmonicida* chromosome and plasmids are susceptible to endogenous mutagenesis caused by thermal inducible insertion sequences (ISs). ISs appeared to maintain the bacterium in a psychrophilic lifestyle in order to conserve their genomic integrity. *A. salmonicida* endogenous mutagenesis is induced at temperatures over 26 ºC, influencing physiology and virulence. Thermal inducible ISs modify the *vapA* gene, which encodes for the A-layer protein array. Regulatory mechanisms of *A. salmonicida* ISs are unknown. We determined that the ISAS3 family mutates the *vapA* gene. Genetic analysis of the ISAS3 promoter showed a conserved Csp binding box. In this study, we evaluated the role of CspB and CspD on the *A. salmonicida* endogenous chromosomal mutagenesis and virulence in lumpfish (*Cyclopterus lumpus*). *A. salmonicida* Δ*cspD* showed a low frequency of *vapA* modification after heat-shock, a reduced growth at 28 ºC, and low virulence in fish host. *A. salmonicida* Δ*cspB* mutant showed a faster growth at 28 ºC and reduced virulence. Also, we found that *A. salmonicida* Δ*cspB* Δ*cspD* has a faster growth at 28 ºC and absence of virulence. In summary, we found that CspD plays a major role in the *A. salmonicida* endogenous mutagenesis and both CspB and CspD influence growth and virulence.

Aeromonas salmonicida Iron-Regulated Outer Membrane Proteins provide protection to *Cyclopterus lumpus* against furunculosis

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The Gram-negative bacterium, *Aeromonas salmonicida*, is the etiological agent of furunculosis in salmon and salmonids, including lumpfish. Lumpfish (*Cyclopterus lumpus*), a native fish in the North Atlantic Ocean, is utilized as cleaner fish to bio-control sea lice infestations. Effective vaccine programs against *A. salmonicida* have been identified as a high priority area for cleaner fish aquaculture. Here, we hypothesized that *A. salmonicida* iron-regulated outer membrane proteins (IROMPs) confer immune protection against furunculosis. Groups of 100 lumpfish (~8 g) were i.p. immunized with total outer membrane proteins (OMPs) purified from *A. salmonicida* grown under iron-rich and iron-limited condition. Formalin-killed commercial vaccine and an in-house bacterin were used as positive controls. Mock vaccinated fish injected with PBS were used as negative control. The fish were boost immunized at four weeks post-primary immunization. Samples of tissues and blood were collected at different time points for histopathological and ELISA analysis. Fish were challenged with 100,000× the LD50 of *A. salmonicida* (10^7 CFU ml^{-1}) at twenty-four weeks post-primary immunization to evaluate vaccine efficacy. Relative percent of survival (RPS) of lumpfish immunized with bacterin (commercial and in-house) and IROMPs was 99 % and 60 %, respectively. Total OMPs from *A. salmonicida* grown under iron-rich condition produced toxic effects to the immunized fish. These results indicate that IROMPs from *A. salmonicida* confers immune protection to *C. lumpus* against furunculosis. This study provide a future guide for lumpfish vaccination programs.

Prediction of novel antigenic peptides for development of vaccines against the marine pathogen *Piscirickettsia salmonis*

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Piscirickettsia salmonis, a Gram-negative pathogen of fish, is the etiological agent of salmonid rickettsial septicemia (SRS) or Piscirickettsiosis. SRS is a prevalent disease in the Canadian Salmon aquaculture industry and recently has been detected in other emergent aquacultures like Lumpfish. Effective vaccines against SRS are currently not available. Here, we utilized the reverse vaccinology approach to predict and characterize potential antigens encoded by chromosomal and plasmids genes of LF-89 and EM AY6492A *P. salmonis* strains. We selected outer membrane proteins (OMPs) with trans-membrane domains that harbor B- and T-cell epitopes. We utilized Vaxign and pbsorbT to predict their subcellular localization. Protter was used to predict OMPs that secreted peptides to the external surfaces. Vaxijen and Vaxign were used to predict their antigenic and adhesin probabilities (with a cut off of 0.5). The B- and T- cell epitopes were predicted using Bepipred linear epitope prediction and Vaxitop (cut-off ~0.5), respectively. A total of 17 LF89 and 18 EM90 proteins were identified based on these characteristics. Eight of these predicted antigens are hypothetical proteins, 6 from LF89 and 2 from EM AY6492A. The 3D structure of the selected proteins was analyzed and the B- and T-cell epitopes were localized. Predicted antigens common to all *P. salmonis* genomes were identified. The result of this study provides data on potential novel antigens against *P.salmonis* that can be used in vaccine development against *P.salmonis.*

In-silico characterization of riboflavin supply pathways in *Aeromonas salmonicida*

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Riboflavin is the precursor of canonical co-factors flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD), essential for intracellular redox reactions and extracellular bacterial physiology. Most bacterial pathogens can either synthesize riboflavin *de novo* or scavenge riboflavin from the host tissues through high-affinity transporters. *Aeromonas salmonicida* is a Gram-negative pathogen of fresh and marine water fish and the etiological agent of furunculosis. Here, we *in silico* characterized the transcriptional organization of riboflavin provision pathways in *A. salmonicida*. We found that the *A. salmonicida* riboflavin biosynthetic pathway (RBP) is encoded by 4 transcriptional units; the main unit consist of an operon of *ribDE1BAH* along with the global regulators *nrdR* and *nusB*, and 3 independent monocistronic units including *ribA*, *ribB* and *ribE*. Additionally, a regulatory FMN riboswitch was identified in the intergenic region of the second *ribB* ortholog which seems to respond to riboflavin availability. We observed that *ribE1* and bifunctional *ribBA* from the main RBP operon have duplicated orthologs outside of the main operon viz; *ribE* (*ribE1*), *ribA* and *ribB* (*ribBA*), which could play a role in *A. salmonicida* virulence and physiology. *ribN* transporter is encoded by a monocistronic unit that could transport riboflavin under limiting conditions. Currently, we have constructed mutants of *ribE1*, *ribE*, *ribBA, ribA, ribB* and *ribN* in order to study the role of gene duplication in RBP, and riboflavin transport in *A. salmonicida*. Additionally, we are experimentally characterizing the transcriptional organization of *A. salmonicida* RBP and riboflavin transport.

Exploiting cellular signaling in *Streptomyces clavuligerus* for antibiotic production

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The discovery of bacterial specialized metabolites and their use as antibacterial, antifungal and anticancer agents established one of the most significant advances in medicine, but the growing threat of antibiotic resistance needs to be addressed. This requires the development of new antimicrobial compounds using new approaches. The *Streptomyces* synthesize a large variety of specialized metabolites and have numerous biosynthetic gene clusters (BGCs) responsible for their production. Based on the numbers of BGCs present in different *Streptomyces* species it has been found that up to 90 % of specialized metabolites are not produced under laboratory conditions and are known as "cryptic" since their identities and functions are unknown. Therefore, it is important to understand cellular signaling pathways which are responsible for the adaptation of bacteria in diverse environmental conditions, to activate such "cryptic" BGCs for specialized metabolites production for exploitation. Our focus is on *Streptomyces clavuligerus*, a producer of clavulanic acid which is a potent β-lactamase inhibitor. Various genes situated in signaling pathways of *S. clavuligerus* are involved in the regulation of clavulanic acid either positively or negatively, making them good candidates for study. Overexpression and mutation of these genes can lead to increased clavulanic acid production, and in the activation of "cryptic" BGCs. Work being conducted by our group on one such pathway will be discussed, and the progress made will also be reported.

Vaccine evaluation against *Vibrio anguillarum* in Lumpfish (*Cyclopterus lumpus* L)

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Lumpfish (*Cyclopterus lumpus*), a native fish of the North Atlantic Ocean, is utilized as cleaner fish to biocontrol sea-lice infestations in the Atlantic salmon (*Salmo salar*) aquaculture. However, bacterial infections are affecting cleaner fish performance and increasing potential diseases transmission. *Vibrio anguillarum*, the etiological agent of vibriosis, is one of the most frequent bacterial infection in lumpfish, and effective vaccine programs against this pathogen have been identified as a high priority area for the cleaner fish aquaculture. Here, we evaluate the efficacy of several vaccine preparations against a local *V. anguillarum* isolated form moribund lumpfish. *V. anguillarum* bacterins, purified iron regulated outer membrane proteins mixed with adjuvant were utilized as test vaccines using purified outer membrane proteins (OMPs) and the commercial vaccine AlphaJect-micro-4 as references controls. Duplicated groups of 300 lumpfish (20g) were intraperitoneally (IP) immunized. Independent groups of fish were boost immunized at 4 weeks post-primary immunization. Naïve fish mock immunized with phosphate buffered saline (PBS) or PBS-Adjuvant were utilized as control group. The immunized fish were challenged with 100 LD_{50} (10^7CFU/dose) of *V. anguillarum* at 8 weeks post-primary immunization. The vaccine preparations did not influence fish growth. Adhesion and vaccine residues was observed in all the adjuvant-based vaccine preparations. The vaccine preparation triggered different levels of immune protection and only delay mortality against the *V. anguillarum* challenge. These results indicate that effective vaccines against *V. anguillarum* need to be developed for the emergent lumpfish fish aquaculture industry.

Culturing bacteria during field work: a rugged, highly reliable, and cost-effective method for determining real-time fecal coliform loads in surface waters

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Microbial contamination of surface waters can come from a wide variety of sources and poses a significant health threat. Fecal coliforms and *Escherichia coli* do not survive long outside of the intestinal environment and have long been used as an indicator of potentially dangerous contamination. Unfortunately, water samples must be processed within 24 hours as fecal bacterial loads quickly change and therefore older samples poorly represent actual loads at the time of collection. This type of testing is therefore highly dependent on quick access to a microbiology laboratory and this makes determining accurate bacterial loads in remote environments challenging. A limited number of studies have cultured bacteria during field work, however these studies only ran for a few days and severely lacked basic microbiology principles, reliability, quality control, and quality assurance. We have developed and implemented a rugged, highly reliable, and cost-effective method of culturing fecal bacteria while conducting field work. Petrifilms (3M™) are a ready-to-use culturing system that contains a cold-water-soluble gelling media that allows differentiation and enumeration of coliforms and *E. coli* specifically from water samples in 24 hours. This method requires minimal equipment, can be performed in a non-laboratory environment, and produces highly reliable and reproducible results with approximately five minutes of training. Due to the unavailability of rugged and cost-effective portable incubators, we custom built incubators that were used during field work. During sampling in the summer of 2018, real-time bacterial loads in surface waters were determined by five independent teams for 217 lakes from across Canada using this method.

Barley and rice: A comparison of the development of nitric oxide metabolism in seed embryo during germination

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Barley (*Hordeum vulgare* L.) and rice (*Oryza sativa* L.) are two important cereal species in the family Poaceae, demonstrating different levels of sensitivity to hypoxia. Germination parameters, level of nitric oxide (NO), ATP content, ATP/ADP ratio, *S*-nitrosoglutathione reductase (GSNOR) activity, total soluble proteins and total protein *S*-nitrosylation (RSNO) were studied at 0, 3, 9, 15, 24 and 48 h post-imbibition to investigate the development of NO metabolism in the seed embryo during germination. There was no significant difference between the percentages of germination of the two species (> 90 %), but seed vigor index (VI) and germination rate index (GRI) were significantly higher in barley than rice. NO level was higher in rice than in barley and changed in a nearly similar way. It decreased until 15 h and increased after that. Initially, the ATP content and ATP/ADP ratio were higher in barley until 9 h, but rice showed a higher value until 48 h. These levels decreased in both species until 9 h and increased by 48 h. Total soluble proteins were higher in barley than in rice, which decreased until 48 h. RSNO and GSNOR were higher in rice than in barley. RSNO level increased until 9 h and showed a sudden decrease by 15 h in both species. In barley, GSNOR level decreased until 3 h and then increased after that, while rice showed the opposite pattern. The results showed the difference of the metabolic changes between two cereal species during post-imbibition for barley being a hypoxia sensitive species as compared to rice which is a hypoxia tolerant species.

Cyclic-di-GMP signalling proteins and gene transfer agent production in *Rhodobacter capsulatus*

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Gene transfer agents (GTAs) are bacteriophage-like particles that package small pieces of the producing cells' genomes that can then be transferred to other cells. Different GTAs are produced by assorted prokaryotes, such as RcGTA produced by the α-proteobacterium *Rhodobacter capsulatus*. RcGTA gene expression in *R. capsulatus* is regulated by several cellular regulatory systems, including the response regulator CtrA. Transcription of multiple other regulator-encoding genes is affected by CtrA, including genes encoding putative enzymes involved in synthesis and hydrolysis of bis-(3'-5')-cyclic dimeric guanosine monophosphate (c-di-GMP). Cyclic di-GMP acts as a universal second messenger in bacteria that affects diverse cellular processes. To investigate whether c-di-GMP signaling plays a role in RcGTA production, we disrupted eight genes potentially involved in c-di-GMP synthesis or hydrolysis whose expression was changed in the *ctrA* mutant. We found that disruption of one such gene increased RcGTA production and disruption of three other genes decreased RcGTA production. We performed site-directed mutagenesis of the key catalytic residues in the GGDEF and EAL domains responsible for diguanylate cyclase and c-di-GMP phosphodiesterase activities and analysed the activities of the wild-type and mutant proteins in *Escherichia coli* c-di-GMP reporter strains and in *R. capsulatus*. We also measured RcGTA production in the *R. capsulatus* strains where intracellular levels of c-di-GMP were altered by either a heterologous diguanylate cyclase or a c-di-GMP phosphodiesterase. Based on these experiments we conclude that these four proteins are part of the *R. capsulatus* regulatory network controlling RcGTA and that c-di-GMP inhibits RcGTA production. This is the first report on the involvement of c-di-GMP signaling in gene transfer. Further investigation is required to determine further mechanistic details.

TxtH is a key component of the thaxtomin biosynthetic machinery in the plant pathogen *Streptomyces scabies*

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Streptomyces scabies is an important causative agent of potato common scab disease, and the key pathogenicity factor produced by this organism is a plant toxin called thaxtomin A. The biosynthesis of thaxtomin A involves the megasynthetases TxtA and TxtB, both of which contain an adenylation domain (A-domain) that recruits and activates the appropriate amino acid substrates required for thaxtomin A production. The proper function of A-domains often involves a small protein belonging to the MbtH-like protein (MLP) family. The objective of this study was to investigate the role of an MLP called TxtH in the biosynthesis of thaxtomin A in *S. scabies*. Biochemical studies in *E. coli* showed that TxtH is required for promoting the solubility of both the TxtA and TxtB A-domains, and amino acid residues in TxtH that are required for this activity were identified. Deletion of TxtH in *S. scabies* significantly reduced thaxtomin A production, and deletion of two additional MLP–encoding genes in the *S. scabies* genome completely abolished toxin production. All three cognate MLPs from *S. scabies* could partially restore thaxtomin A production in the triple MLP-deficient strain. Furthermore, the constructed *S. scabies* MLP mutants displayed a reduced virulence phenotype compared to the wild-type strain in a potato tuber assay. The results of our study confirm that TxtH plays a key role in thaxtomin A biosynthesis and plant pathogenicity in *S. scabies,* and they show that other MLPs can functionally replace TxtH in the thaxtomin biosynthetic pathway.

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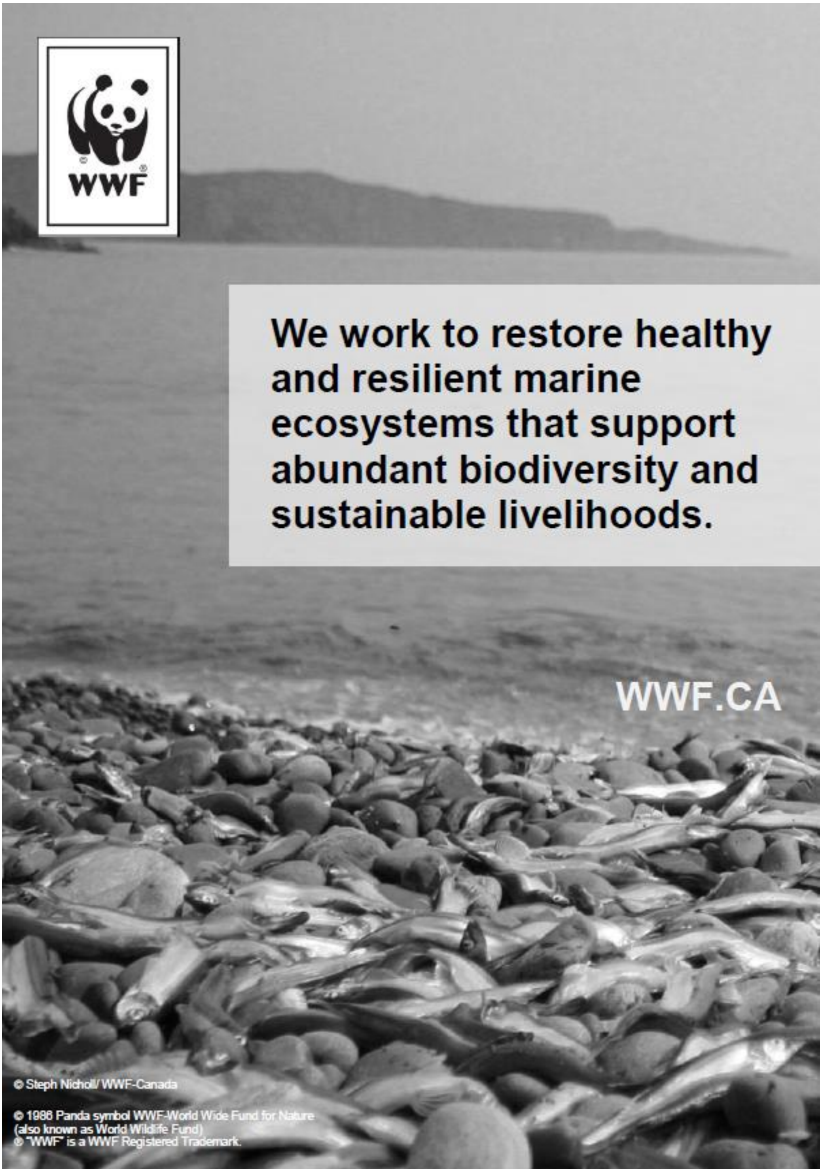

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