Dalhousie University Halifax, NS on March 8, 9, and 10 2024.

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The Science Atlantic Biology and Applied Aquatic Science (BAAS) joint conference is hosted by Dalhousie University Halifax, NS on March 8, 9, and 10 2024.

The Science Biology and Applied Aquatic Science (BAAS) Conference is an annual event that brings together students from across Atlantic Canada to share their research, and network with other students and faculty. We are very excited to welcome everyone to our beautiful city.

The Organizing Committee

Dr. Lois Murray, Biology Conference Co-Chair

Dr. Nicanor González, Biology Conference Co-Chair

Dr. Anne Dalziel, Aquaculture & Fisheries Chair

Dr. Stevan Springer, Biology Chair

Plenary Speakers

We are happy to have two plenary speakers this year.

Erin Bertrand is an Associate Professor in the Department of Biology at Dalhousie University. Her group employs physiological, biochemical, and bioanalytical approaches to improve our understanding of controls on marine microbial activity and how microbes influence major biogeochemical processes in the ocean.

Photo Credit: Maya Bhatia

Chuck Bangley is a marine biologist broadly interested in fisheries interactions, trophic ecology, and habitat selection in marine predators, with a particular interest in elasmobranchs. His research includes delineation of potential shark habitat, acoustic telemetry of highly migratory elasmobranchs, and characterization of diet and trophic relationships with economically important fish species.

Molecular windows into ocean productivity

Erin Bertrand

Department of Biology at Dalhousie University

Marine phytoplankton are responsible for nearly half of the primary productivity on Earth. This talk will describe the molecular underpinnings of how these tiny photosynthesizers grow, support marine ecosystems, and respond to change. Using examples from the Southern Ocean and the Scotian Shelf, I'll show you that phytoplankton need their vitamins, too, and discuss what that means for ocean productivity. Then we'll move North and, using examples from the Arctic, I will show you how we can use measurements of proteins to understand how these plankton are likely to respond to melting glaciers and other aspects of global change. I will share stories of what its like to do molecular research at sea and in remote environments, including with indigenous communities, and how my views on this work evolved as I became a mother and a field researcher on the frontlines of climate change.

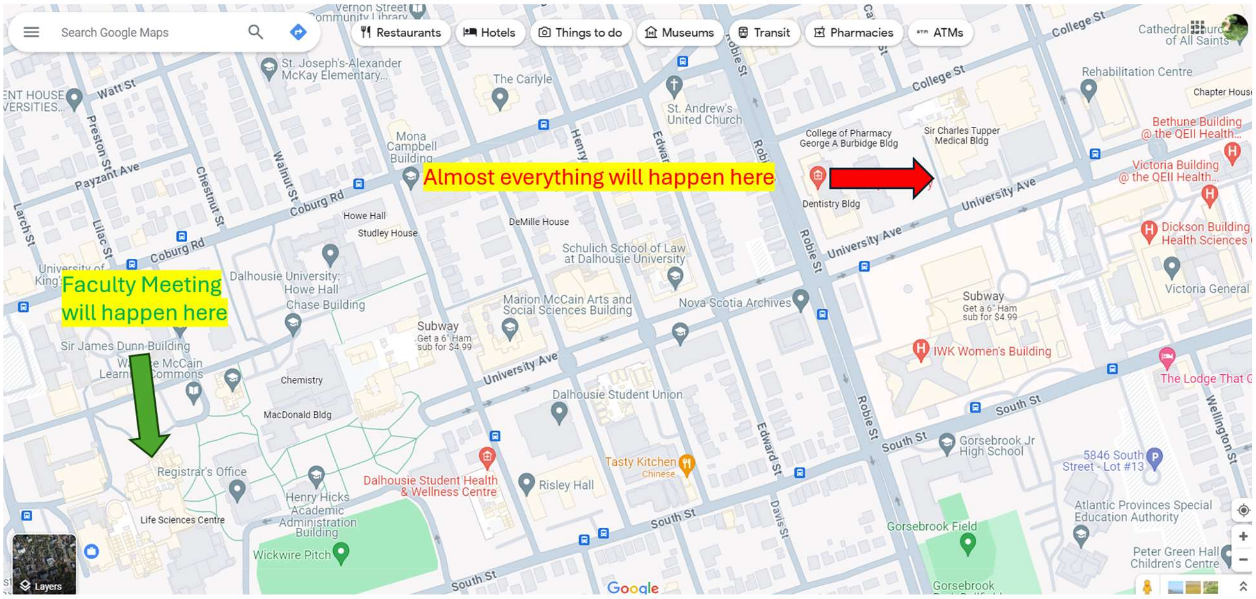
Sharks as Indicators of Ecosystem Change

Chuck Bangley

Department of Biology at Dalhousie University

Climate change is already altering ecosystems in ways that are directly observable, and one of the most rapidly-changing ecosystems is the Northwest Atlantic Ocean. For large, highly migratory marine predators such as sharks, movement into new areas is not constrained by physical barriers but by their own environmental tolerances. When environmental conditions change to become more favorable, these species are likely to be among the first to shift into newly-available habitat. This situation has already moved beyond the hypothetical, as several shark species have already been documented expanding their distribution and becoming more common where once they were considered rare or unheard of. Here I will review findings from my own work and others' to demonstrate that sharks and other highly migratory marine predators can serve as early indicators of marine ecosystem change.

Map



Almost everything will happen here

Faculty Meeting will happen here

BAAS 2024 Full Schedule

			Biology speakers	AAS Speakers
Date	Time	Event	Biology speakers	AAS Speakers
Friday	5:30 – 7:30 pm	Ice Breaker/Registration		
Mar 8th				
	7:00 – 8:00 pm	Biology & AAS Committee Dinner		
		(Faculty rep members only)		
	8:00 – 9:00 pm	Biology Committee Meeting (Faculty rep members only)		
		AAS Committee Meeting (Faculty rep members only)		
Saturday	8:15 – 8:45 am	Registration and put up posters		
Mar 9th		*Tupper Link & Registration desk outside Theatre B&C*		
	8:45 – 9 am	Welcome address		
		Theatre B		
	9 – 10 am	Keynote Speaker - Biology. Dr. Erin Bertrand, Dalhousie		
		Theatre B		
	10 – 10:30 am	Break and Poster Viewing		
		Tupper Link & Registration desk outside Theatre B&C		
	10:30 am – 12:00 pm	Oral Presentations – Session 1	1 Abigail Chafe (MUN)	1 Maya Chouinard (Acadia)
		Theatre B- Biology (6 talks)	*2 Emma Simmonds (UNB)*	*2 Anna Gleason (Dal)*
		Theatre C – AAS (6 talks)	*3 Maggie Kelly (SMU)*	*3 Clarissa Lalla (UNB)*
			4 Kate Pennyfather (DAL)	*4 Rebecca Ralph (MUN)*
			5 Eliana Seburn (UPEI)	*5 Subash raj Nataranjan (St. FX)*
			6 Meg Smith (DAL)	*6 Angus Kennedy (St. FX)*
	12:00 – 1:00 pm	Lunch		
		Tupper CHEB C170		
	1:00 - 2:00 pm	AAS Keynote Speaker - Dr. Chuck Bangley, Dalhousie		
		Theatre B		
	2:00 – 3:45 pm (1 hour, 45 min)	Oral Presentations – Session 2	7 Christelinda Laureijs (MTA)	7 Kat Kabanova (Dal)
		Theatre B- Biology (7 talks)	*8 Lauren Burton (DAL)*	*8 Alex Day (MUN)*
		Theatre C – AAS (7 talks)	*9 Olivia Kirkegaard (DAL)*	*9 Brian Conrad (Dal)*
			10 Roman Javorek (ACD)	*10 Emil Senathirajah (UNB)*
			11 Tanner Clow (STFX)	*11 Evan Berthelot (UNB)*
			12 Shann Cox (CBU)	*12 Hannah MacIntosh (MtA)*
			13 Reilly Sullivan (UPEI)	*13 Radka Sevcik (MtA)*
	3:45 – 4:00 pm	Break and Poster Viewing		
	4:00 – 5:00 pm	Poster Viewing (Posters will be judged at this time)		
		Tupper Link		
	6:30 – 8:30 pm (2 hours)	Banquet		
		Tupper CHEB C170		
Sunday	10:00 – 11:30 am (1.5 hours)	Oral Presentations – Session 3	14 Georgia Christie (MTA)	14 Ainhoa Fournier (Dal)
Mar 10th		*Theatre B- Biology (6 talks)*	*15 Katie Burt (MUN)*	*15 Ashley Lansley*
		Theatre C – AAS (6 talks)	*16 April Sharpe (ACD)*	*16 Gavin Hiltz (St. FX)*
			17 Courtney Trask (CBU)	*17 Marco Turner (Acadia)*
			18 Shannon Wallace (STFX)	
			19 Samuel Sequeira (SMU)	
	11:30 – 12:00	Break and Poster Viewing		
	12:00 – 1:00 am	Lunch		
		Tupper CHEB C170		
	1:00 – 2:00 pm	Awards Ceremony + Closing		
		Theatre B		

Section 1 – Biology

Talks

Phylogenetic Relationships in the Andean Genus of Palms Parajubaea

Abigail Chafe[1], Julissa Roncal[1]

[1]Department of Biology, Memorial University of Newfoundland, St. John's, Canada

Contrary to many lineages in the Andean biodiversity hotspot that exhibit high diversification, the palm genus *Parajubaea* (Arecaceae) has only three species despite the genus' origin 22 million years ago. *Parajubaea torallyi and P. sunkha* are IUCN endangered and endemic species of the Andes of Bolivia. *Parajubaea cocoides* is a cultigen, found in Ecuador, Colombia, and Peru. Given that *Parajubaea* is only a recently described genus in the family Arecaceae, information regarding its systematics is incomplete. The goal of my research is to examine the phylogenetic relationships among *Parajubaea* species and to test two hypotheses: (1) Both Bolivian endemic species are sister to each other, and (2) *P. cocoides* evolved from a wild Bolivian *Parajubaea* species. To test these hypotheses, I sequenced five low-copy nuclear genes in the WRKY family for 26 palm individuals and used two phylogenetic reconstruction methods. *Parajubaea cocoides* was sister to a clade formed by *P. torallyi and P. sunkha*, but each of these two Bolivian wild species were not recovered monophyletic. Thus, the hypothesis that *P. cocoides* originated from Bolivian wild *Parajubaea* was not supported. Future studies could use next generation DNA sequencing to further resolve the evolution of Bolivian *Parajubaea* populations since I found low support within this clade.

Seasonal and Temporal Variations in the Underwater Vocalization Behaviours of Weddell Seals (Leptonychotes weddellii) near Davis, Antarctica: Insights from Passive Acoustic Monitoring

Emma Simmonds[1], John M. Terhune[1]

[1]University of New Brunswick - Saint John

Within the Antarctic environment, marine mammals rely heavily on sound for communication. This study investigated the underwater vocal behaviours of Weddell seals (*Leptonychotes weddellii*) using passive acoustic monitoring of calls recorded under landfast ice near Davis, Antarctica (68°34’S, 77°58’E), provided by the Australian Antarctic Division (AAD). Seasonal and daily patterns were examined throughout the austral winter and summer in order to identify if Weddell seals exhibit dawn and dusk choruses—as seen in many songbirds—and to discern seasonal variations in vocalization rates. Using Raven 1.6 software, we analyzed hourly data sampled every ten days from July 24th, 2021, to December 31st, 2021. For each sound file, the calls over eight minutes were counted, and the species was identified. Statistical analyses, including generalized linear effect models and non-parametric tests, assessed the temporal and seasonal trends in underwater vocalizations. Results suggest that the underwater vocalizations increase just before dawn and immediately after sunset until 24 hours of sunlight when calling rates become very low. Furthermore, underwater vocalizations varied across seasons; with the highest calling rates during winter, lower calling rates during the breeding season, and a sharp decline in mid-November as land fast-ice breaks up and predators such as leopard seals (*Hydrurga* leptonyx) enter the area. These findings produce valuable insights to the seasonal and temporal trends in the acoustic behaviour of Weddell seals and will be utilized by the AAD for environmental impact assessments associated with the construction of an airport and ship service centre.

The influence of novel mates and competitors on the courtship and aggression behaviour of Japanese medaka (Oryzias latipes)

Maggie Kelly[1], Laura Weir[1]

[1]Saint Mary's University

For males to mate successfully, they must appropriately allocate their limited mating energy towards courtship (intersexual) and aggression (intrasexual) behaviour. In male Japanese medaka (*Oryzias latipes*), previous research has shown that sex ratio influences how males prioritize inter/intrasexual behaviour. However, there remains a research gap in how the identity of the surrounding individuals affects this balance. The goal of this study is to measure the effects of mate and competitor novelty on the ratio of inter- and intrasexual behaviour of male Japanese medaka. Male behaviour was quantified by observing each male on two different days for two minutes each and the frequency of inter- and intrasexual behaviour was recorded. These observations were collected for all four sex ratios in three scenarios. In all scenarios, males experienced the same sex ratio, but mate and competitor novelty differed. First, male behaviour was quantified across different sex ratios with familiar mates. Second, groups of males from the same tank were placed with novel female mates. Finally, males were placed in situations where both male competitors and female mates were previously unknown to them. We found that in response to both novel mates, and novel mates and competitors, males prioritized intersexual interactions. However, males exposed to novel mates and competitors spent more time on intrasexual interactions compared to males exposed to only novel mates.

Evolution of genome size and repetitive DNA in Lobelia cardinalis

Kate Pennyfather[1]

[1]Dalhousie University

Eukaryotes display immense variation in genome size. However, the causes and consequences of this variation remain largely unknown. Many scientists argue that genome size variation can be attributed to repetitive DNA, which does not code for proteins, and is capable of autonomously replicating in the genome. The angiosperm species *Lobelia cardinalis* (cardinal flower, Campanulaceae) provides an excellent opportunity to study genome size variation and repetitive DNA, as it has an expansive geographic range with isolated populations displaying variation in genome size, morphology, and pollinator species. As such, this study was performed to test the hypothesis that genome size variation across *L. cardinalis* populations can be attributed to repetitive DNA. As well, we aimed to determine the specific repetitive DNA classes that have driven genome size increases in individual populations, to identify any phylogenetic or geographic patterns of repetitive DNA evolution. To perform this research, 33 *L. cardinalis* populations were grown in the Dalhousie greenhouse. Using leaf tissue, genome size estimates were obtained through flow cytometry, and repetitive DNA content was estimated through DNA sequencing and the use of RepeatExplorer2. Genome size results show a 1.3-fold variation across populations, and a tendency for larger genomes in the western portion of the *L. cardinalis* range. Once analyzed, data on repetitive DNA content will supplement these findings to provide information on the relationship between genome size and repetitive DNA in *L. cardinalis*. The understanding of this relationship will allow us to contribute to the heavily debated discourse surrounding Eukaryotic genome size.

Experimental Validation of a Statistical Test of Adaptation in Whale Myoglobin

Eliana Seburn[1], Marcus Gauthier[1], Stevan Springer[1]

[1]University of Prince Edward Island

Whales can dive for long periods by holding oxygen-binding myoglobin in their muscles at high concentrations. In the lineage leading to whales, six adaptive amino acid changes increase myoglobin's charge and folding stability, presumably to prevent precipitation at high concentrations. Higher charge increases repulsion between myoglobin molecules, and increased folding stability reduces protein aggregation. Both traits could reduce the precipitation of myoglobin, so which trait did selection target? We aim to determine the target of selection by verifying computational estimates of folding stability and charge with empirical measurements. Computational estimates indicate that charge evolved in an unusual direction; the six amino acid substitutions in whales are rare in the space of possible mutations. This suggests that charge is the target of selection and that folding stability may have evolved as a byproduct of selection on charge. We have expressed both the ancestral and derived alleles in E. coli, both of which can be isolated using His-tag purification. An assay to measure protein folding stability has been developed and optimized using isolated horse myoglobin. We have also developed a recombination method to generate the 64 intermediate alleles between the ancestor and derived alleles. The empirical estimates these methods generate will support a novel statistical method to verify targets of selection during adaptation. The potential applications are broad, and knowing which traits are targets of selection is critical.

Identifying the glacial lineage of North Mountain Brook Trout (Salvelinus fontinalis): A mtDNA whole-genome analysis

Meg Smith[1], Daniel Ruzzante[1], Lisette Delgado[1], Cait Nemeczek[1]

[1]Dalhousie University

Brook Trout (*Salvelinus fontinalis),* a salmonoid native to northeastern North America, is among the most popular species for recreational angling in the Canadian Maritime provinces. A recent study examining the nuclear genome of nine Brook Trout populations in North Mountain, Nova Scotia revealed the presence of several potential chromosomal inversions in the three westernmost populations. This project aims to determine whether the restricted occurrence of these putative inversions may be explained by post-glacial dispersal; specifically, that two or more glacial lineages recolonized the region with one supplying the putative inversions. To this end, whole mitogenome sequences from 192 Brook Trout representing the nine North Mountain populations were analyzed. Thirty unique mtDNA haplotypes were identified. Five of these haplotypes contained individuals with putative inversions as well as individuals without the inversions, suggesting the inversions did not significantly affect haplotype divergence. A neighbour-joining dendrogram and a haplotype network were constructed. Both showed all by one haplotype diverging from a single node, suggesting a single lineage origin. The outlying haplotype was the same in both cases, a rare (N=2) haplotype from the easternmost stream, and as such is unrelated to the putative inversions in the west. These findings support the conclusions made by other phylogeographic studies which suggest a single lineage of Brook Trout likely recolonized most of the Canadian Maritimes. We further conclude that the putative inversions previously identified are unrelated to refugial lineage and more research will be necessary to determine their age and origin.

Examining the relationship between insulin and neuronal activity in the rat dorsomedial hypothalamus

Christelinda Laureijs[1], Karen Crosby[1]

[1]Mount Allison University

Although insulin plays a key role in energy metabolism, relatively little is known about its function as a satiety hormone in the brain. The dorsomedial hypothalamus (DMH) is associated with appetite regulation, and it is also a major site of insulin receptors. Since neurons in the DMH stimulate appetite, we hypothesized that insulin inhibits excitatory synaptic transmission (glutamate signalling) at DMH neurons. We used whole-cell patch clamp recordings to compare excitatory postsynaptic current amplitudes in DMH neurons before and after applying 500 nM insulin. We also applied insulin in the presence of an insulin receptor inhibitor (Hydroxy-2-naphthalenylmethylphosphonic acid; HNMPA) and insulin-like growth factor 1 receptor (IGF1-R) blocker picropodophyllotoxin (PPP) to explore insulin binding mechanisms. All brain slices used in the recordings were from young male and female Sprague-Dawley rats. Insulin decreased excitatory synaptic transmission in the DMH neurons of both sexes. Insulin continued to decrease glutamate signalling with HNMPA present, which implies that insulin does not require insulin receptors to bind to DMH neurons and alter intracellular pathways. Recordings taken in the presence of PPP show no change in glutamate signalling with insulin, suggesting that insulin may bind to insulin-like growth factor 1 receptors on DMH neurons. Together, our results suggest that insulin decreases neuronal activity in the DMH, possibly by binding to insulin-like growth factor 1 receptors. This research contributes to our understanding of how insulin acts in the brain to potentially influence appetite, with direct applications to research on the physiological effects of obesity and diabetes.

Characterization of immune modulation by protease IV in Pseudomonas aeruginosa acute murine lung infection

Lauren Burton[1], Rhea Nickerson[1], Xiyang Zhang[2], Ashley Stueck[3], Zhenyu Cheng[1]

[1]Department of Microbiology and Immunology, Dalhousie University, Halifax, NS, Canada, [2]Department of Anesthesia, Pain Management & Perioperative Medicine, Dalhousie University, Halifax, NS, Canada, [3]Department of Pathology, Dalhousie University, Halifax, NS, Canada

Pseudomonas aeruginosa is an opportunistic pathogen capable of causing a variety of infections in a wide range of hosts, including both acute and chronic lung infections. A key *P. aeruginosa* virulence factor, protease IV (PrpL), has been shown to exacerbate the inflammatory response to lipopolysaccharide in murine macrophage cells *in vitro*, but this immune modulation has yet to be investigated *in vivo.* In this project, I further investigated the role of protease IV in *P. aeruginosa* acute lung infection using mice intratracheally infected with either *P. aeruginosa* PA14 or a mutant strain with a deletion of the *prpL* gene, PA14/Δ*prpL* (Δ*prpL*). Mice were assessed for morbidity and weight loss over the 24-hour course of infection, and lung bacterial burden post-infection was quantified. Modulation of the inflammatory response was assessed by comparing the expression of key inflammatory cytokines and mitogen-activated protein kinase activation, as well as immune profiling by flow cytometry and histological analysis. I hypothesized that the Δ*prpL* mutant would have reduced virulence compared to PA14. Overall, there were no significant differences in weight loss, morbidity, and lung bacterial burden between the two *P. aeruginosa* strains, suggesting that there were minimal differences in virulence between PA14 and Δ*prpL.* The similarity in virulence between strains may be due to the many other proteases secreted by *P. aeruginosa* compensating for the lack of PrpL activity in the Δ*prpL* mutant strain, and it is possible that using a higher infectious dose of bacteria could help to reveal subtle differences between the strains.

Characterization of Antibiotic Tolerance and Protein Synthesis of Pseudomonas aeruginosa Ribosomal Transposon Mutants.

Olivia Kirkegaard[1], Renee Raudonis[1], Zhenyu Cheng[1]

[1]Department of Microbiology and Immunology, Dalhousie University

Pseudomonas aeruginosa is an opportunistic pathogen known for its rapid development of antibiotic resistance. As one of the most frequent causes of nosocomial infections, research regarding *P. aeruginosa* and its resistance mechanisms remains critical. In this study, I characterized *P. aeruginosa* ribosomal transposon mutants by testing their tolerance to several classes of antibiotics as well as their protein synthesis capabilities. It was hypothesized that the ribosomal mutants would show increased antibiotic resistance and decreased protein synthesis compared to wild-type. The mutants were observed to have similar or increased resistance to the antibiotics tested compared to wild-type, with some exceptions. These exceptions primarily occurred in mutant strains with slower growth rates compared to wild-type. These results suggest a relationship between ribosomal mutations of *P. aeruginosa* and antibiotic resistance, in which fitness costs of the mutations may be associated with decreased antibiotic resistance. Notably, all of the mutants were found to have increased tolerance in the presence of Tobramycin compared to wild-type when treated at the minimum inhibitory concentration. The protein synthesis of the mutant strains was variable with no apparent trends. A better understanding of ribosomal mutants of *P. aeruginosa* may provide further insight into its resistance mechanisms, which could be beneficial in the prevention of antibiotic resistance and in the development of novel therapies against *P. aeruginosa* infection.

Exploration of the Expression of MMP and TIMP Genes Congruent with Onset of Sea Star Wasting Syndrome

Roman Javorek[1]

[1]Acadia University

Sea stars are a keystone predator species, filling an essential niche in ecosystems across the globe. Sea Star Wasting Syndrome (SSWS)- a suite of loosely defined characteristics which lead to changes in behaviour, followed by the development of a ‘melting’ phenotype has been documented in numerous populations and species of the echinoderms since its 2013 onset, decimating sub-tidal and benthic sea star populations in the North American Pacific coast. The causative agent of SSWS is unknown, as are the future implications of SSWS on marine ecosystems. In an overview paper of the current knowledge about SSWS, Oulhen and colleagues suggest that the disease could potentially be intrinsically derived. This paper proposes a potential mechanism by which sea stars may be self-digesting their collagenous Mutable collagenous tissue (MCT) via matrix metalloproteinase (MMP) activity. In this study, sixteen sea stars of *A. rubens* were collected and housed in saltwater aquaria, where they were exposed to a shock event, where salinity was drastically dropped below their preferred salinity. Endpoint PCR was used to determine the presence/absence of MMPs and their inhibitors (TIMPs) within the coelomic fluid before and after the stressful event. Results indicate differential expression of MMP and TIMP genes in concert with the emergence of the wasting phenotype.

Gill morphology of Kryptolebias marmoratus in response to multiple stressors

Tanner Clow[1], Tammy Rodela[1]

[1]St. Francis Xavier University

The gills act as a physical boundary between fish and their environment. The amphibious mangrove rivulus (*Kryptolebias marmoratus*) can modify the structure of their gills in response to environmental changes. These morphological alterations change the surface area of the gills through modifications of interlamellar cell masses (ILCMs). In their natural mangrove habitats, these fish are often exposed to low oxygen (hypoxia) and high environmental ammonia (HEA). While an increase in gill surface (reduction in ILCM) improves oxygen uptake, the thinner barrier may lead to an influx of ammonia that can be lethal. However, little is known about how these two environmental stressors, with opposing physical pressures impact gill morphology. I hypothesized that when exposed to combined hypoxia and HEA, *K. marmoratus* remodel their gills to prioritize oxygen uptake. To test this hypothesis, lineages from Belize and Honduras were acclimated to control, hypoxia, HEA, or combined treatments for 7 days. Fish were euthanized, processed for paraffin sectioning, and stained using Hematoxylin and Eosin. Lamellar length, lamellar width, and ILCM were quantified. In response to all stressor exposures, the Belize lineage decreased their ILCM. However, the Honduras lineage only remodelled their gills under the combined exposure by increasing the length of their lamellae and reducing their ILCM. These findings suggest that while there is a convergent response with both lineages to the combined exposure, the Belize lineage appears to be more sensitive to individual stressors. Further examination of these isogenic lineages will help us tease out morphological difference due to habitat differences.

Circadian regulation of gene expression in the electric organ of the gymnotiform fish Brachyhypopomus gauderio

Shann Cox[1], Vielka Salazar[1]

[1]Cape Breton University

Endogenous cellular circadian clocks have been shown to be major regulators of metabolic functions. The nocturnal gymnotiform fish *Brachyhypopomus gauderio* has emerged as a good candidate animal system to study the cellular and molecular mechanisms underlying the circadian regulation of energy metabolism. *B. gauderio* produce a weakly electric signal, referred to as an electric organ discharge (EOD), for habitat navigation and communication with conspecifics. The EOD displays sexual dimorphism, circadian regulation, and high energetic demands. While both sexes of *B. gauderio* exhibit larger signals in the nighttime compared to the daytime, males exhibit a much larger signal increase in the nighttime. This enhanced nighttime EOD requires a large portion of a male's energy budget to EOD production. In addition, the EOD circadian change is mediated at the cellular level by changes in the number of melanocortin receptors, androgen receptors, and sodium-potassium ATPases. However, genes associated with the link between the circadian rhythm and energy regulation has yet to be fully characterized in the electric organ of *B. gauderio.* For my project, I have used direct RNA sequencing to characterize the expression of genes in the electric organ from male (n=4) and female (n=4) *B. gauderio* sampled during day and night. I will also conduct a comparative study to look at the different expression of genes between sexes and day-night cycles. The results of this study will give further insight into the molecular mechanism underlying the circadian regulation of the electric signal and its energetic cost in *B. gauderio*.

Analyzing Kynurenine Pathway Metabolites in Breast Cancer Tumors

Reilly Sullivan[1], Munkhtuul Enkhbat[1], Tayah Sommer[1], Mukhayyo Sultonova[1], J. Patrick Murphy[1]

[1]University of Prince Edward Island

Breast cancer (BC) is a leading cause of cancer-related death in women, demanding new treatment approaches such as targeting metabolic alterations of tumors. Among metabolic pathways, the kynurenine pathway (KP) is known to be differentially regulated across breast cancer tumors. KP metabolites are known to have bioactive effects that may influence anti-tumorigenic roles and immunosuppression. This study involves analyzing the metabolic profiles of tumors, specifically KP-metabolites, in subsets of patients defined by their expression of KP-enzymes, IDO1 and KYNU. Using public datasets, I have identified that subsets defined by high expression of IDO1 (IDO1-high) have increased survival, while KYNU-high patients show decreased survival. Using metabolomics data, I have identified several metabolites that are differentially abundant between high and low IDO1 and KYNU breast tumors. Together, these data suggest that some KP metabolites produced by IDO1-high tumors possess antitumor properties, while the those produced by KYNU may have tumor promoting properties. It is also unclear which cell-types are producing KP-metabolites. Using scRNA-seq data, we are investigating KYNU and IDO1 high cell-types across the tumor environment and are working towards identifying the spatial arrangement of these cells. Identifying the roles of KP metabolites, and the cell-types that produce them may point to new therapeutic targets that improve BC patient prognosis.

The Effects of Urbanisation on Salamander Health in New Brunswick and Nova Scotia

Georgia Christie[1], Julia L. Riley[1]

[1]Mount Allison University

With a growing need for urban spaces, forests in New Brunswick and Nova Scotia are increasingly being encroached upon by expanding cities. These forests, which account for about 80% of the region's land area, are home to seven salamander species. The most abundant salamander in this region is the Eastern Red-backed Salamander (*Plethodon cinereus*), which is a bioindicator species of Acadian Forest ecosystem health. Previous studies show that urbanization can affect abundance, diversity, and body condition of amphibians, however the direction and magnitude of these impacts vary between species. To investigate how urbanization impacts environmental quality, species richness, abundance, and body condition for salamanders, we completed surveys in 13 natural forests and 12 urban parks during the salamander active season. These surveys involved flipping cover objects in a standardized 30 m^2 circular area and collecting microclimatic data. We found that urban parks and natural forests were not substantially different in environment or salamander species richness. Urban parks exhibited greater salamander abundance than natural forests by more than four times on average. Contrary to previous research that suggested that increased population density reduces body condition, we find that body condition does not vary between the two treatment groups despite the difference in abundance. These findings will contribute to our understanding of the impacts of urbanization on Eastern North American amphibians.

Clicking with Cats: Assessing socialization methods on Domestic Cat (Felis catus) welfare in the animal shelter environment

Katie Burt[1], Carolyn Walsh[1], Paul Marino[1], Julie Posluns[2]

[1]Department of Biology, Memorial University of Newfoundland, St. John's, Canada, [2]ACAAB

Large numbers of domestic cats (*Felis catus*) pass through animal shelters each year. The shelter environment can challenge a cat's wellbeing and overall health, with negative effects that are exacerbated with increased length of stay (LOS). Decreased welfare can manifest as undesirable behaviours, such as hiding or aggression, lowering a cat's chance of adoption and increasing LOS. There is growing interest in studying strategies designed to improve shelter cat wellbeing and promote timely adoptions, although very few studies have considered "clicker training" (CT), a form of operant conditioning, as a method of social enrichment. Here, I address this prominent gap in the literature and compare the effects of CT on shelter cat wellbeing against other socialization techniques that may be easier than CT to implement, including structured play sessions and "treatment-as-usual", which includes gentle interactions between staff/volunteers and cats. Cats (N=15) were quasi-randomly assigned to one of the three conditions and received standardized behavioural evaluations prior to, during, and after treatment, including the Fear, Anxiety, and Stress scale, and the Human Approach, Response to Petting, and Participation in Play tests. Changes in individual cats' test scores over time were evaluated and group scores were compared to assess for differences in treatment condition effectiveness, which suggested potential ceiling effects to be addressed in future studies. The outcomes of this study will provide evidence regarding the differential effects, if any, of the socialization treatments to inform shelter practices in the implementation of strategies that may optimize benefits for cat welfare and adoptability.

The microplastic invasion: examining the effects of the ingestion of polystyrene microplastic spheres on mosquito cold tolerance

April Sharpe[1], Laura Ferguson[1]

[1]Acadia University

The ability to withstand low temperatures, in part, determines the geographic range of ectotherms, such as mosquitoes; however, stress can modify thermal tolerance and potentially impact the ability of a species to live or establish in cold environments. Microplastics may act as a stressor for mosquito larvae, who readily ingest plastic microparticles. Further, microplastics can act as ice nucleators in the environment, and thus could also accelerate freezing processes in mosquitoes. To determine if microplastic pollution will increase susceptibility to cold injury, we exposed first instar larvae of the species *Aedes aegypti, Culex pipiens,* and *Culex territans* to a 20 000 microplastic/mL solution (3 μm diameter) dark red polystyrene beads. We maintained larvae in simulated autumn temperatures and photoperiod to allow for cold acclimation. Once the larvae reached the 4th instar, we measured the supercooling point and chill coma recovery time. We further maintained larvae of an additional species, *Culiseta melanura, for a prolonged winter exposure, as this species overwinters in the larval stage.* There was no significant effect of microplastic exposure on the supercooling point in *Aedes aegypti, Culex pipiens,* or *Culex territans*, nor initial movements in chill coma recovery time; however, microplastics reduced the time for *Aedes aegypti* to return to the surface of the water. Plastic exposure also slowed the ability for *Culiseta melanura* to recover from chill coma. Overall, this suggests that high microplastic exposures may cause sublethal tissue injury that reduces the ability for mosquitoes to recover from cold stress.

Using eDNA Metabarcoding to Assess Invertebrate Biodiversity in Eelgrass (Zostera marina) Beds Across Nova Scotia

Courtney Trask[1]

[1]Cape Breton University

Eelgrass (*Zostera marina*) beds are a common feature of Atlantic coastlines and represent diverse, productive marine communities that are highly valued for their ecosystem services. As nearshore environments vulnerable to human impacts, and as sentinels of environmental change, eelgrass beds require regular monitoring to measure biodiversity levels and to detect changes with time. Environmental DNA (eDNA) metabarcoding provides a relatively new approach for monitoring aquatic biodiversity, yet its ability to provide a comprehensive assessment of eelgrass communities relative to more traditional methods (e.g., visual surveys) remains to be determined. In this study, eDNA COI metabarcoding was used to characterize invertebrate biodiversity in 17 eelgrass beds spanning the breadth of Nova Scotia, from Chebogue to Aspy Bay. Three 1L water samples and one field control collected at each site underwent eDNA extraction, PCR amplification, clean-up, and multiplexing before being sequenced for taxonomic assignment. Across the 17 sites, 170 invertebrate species were identified with a taxonomic probability assignment of >95%. Of the species reported, only 57 (34%) were detected in traditional surveys. Conversely, 76 taxa recorded using traditional methods were not found in eDNA analyses. eDNA was successful, however, in detecting 18 of the 23 most common invertebrate taxa based on published species records from 11 Nova Scotian eelgrass beds. While eDNA clearly represents an exciting new monitoring tool for eelgrass ecosystems, further work is needed to establish the limitations of this approach in documenting species' presence based on factors such as taxonomic affiliation, ecology (infaunal/epifaunal), body size, and abundance.

From waste to wonder: the effects of insect frass on plant growth and bacterial symbioses

Shannon Wallace[1], Cory Bishop[1]

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Black Soldier Fly, *Hermetia illucens,* larvae can be reared on organic waste to produce high-protein livestock, fish, or pet food products. This process contributes to a circular economy, a system that prioritizes the recycling of resources. A waste product of this process is frass, a mixture of exoskeletons, excrement, and organic matter that holds promise as a plant growth-promoting agent. The objective of my research was to understand how frass enhances plant growth, and whether the bacterial community of frass can form associations with plant roots. Lettuce seedlings were planted in a potting medium amended with autoclaved, pasteurized, and untreated frass. Once grown, plant growth endpoints were recorded. DNA was extracted from root tissue for high-throughput amplicon sequencing of the 16S rRNA gene to gain insight into the root-associated bacterial community. Average wet shoot masses for the autoclaved, pasteurized, and untreated frass, and potting medium control were 5.48 ± 2.10g, 5.81 ± 2.41g, 5.63 ± 2.36g, and 1.09 ± 0.46g, respectively. Average water loss after drying for the autoclaved, pasteurized, and untreated frass, and control were 4.86 ± 1.77g, 5.12 ± 2.05g, 5.15 ± 2.15g, and 0.92 ± 0.42g, respectively. For both measures, an ANOVA test revealed significant differences between treatment groups (mass: p = 2.92E-14, df = 3; water loss: p = 1.03E-14, df = 3). A PERMANOVA test performed on a PCoA plot showed significant differences in the root-associated bacterial community between treatments (p = 0.001). Therefore, I conclude that frass increases lettuce seedling growth and the occurrence of identified plant growth-enhancing taxa in the roots of lettuce seedlings.

Chironomus dilutus larvae exposure to treated vs untreated contaminated wetland sediment

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Wetlands in Nova Scotia (NS) have been contaminated by mercury (Hg) and geogenic arsenic (As), the waste products of gold mining during the 1800s. These elements have since remained in the environment, bioaccumulating in benthic species and transferring through higher trophic levels. Here, we evaluated using a reactive amendment (R) composed of zero-valent iron (ZVI), supported by a protective capping (PCR) of silica sand, ZVI, bentonite, and zeolite as a risk management strategy for impacted wetlands. We examined the treatment's ability to reduce toxicity to the freshwater larval invertebrate *Chironomus dilutus* in a laboratory experiment. Additionally, in preparation for a field mesocosm test assessing the *in situ* success of the treatment at Muddy Pond in NS, a pilot cage test was conducted to assess potential cage effect and identify an appropriate cage mesh size among 200 µm, 243 µm, 300 µm that would allow chironomids with the most sediment exposure while preventing them from escaping. Results showed that being placed in cages had no impact on chironomid survival, with the highest survival in contaminated sediment for cages with 243 µm mesh. The toxicity test confirmed that total water Hg and As concentrations overlying the contaminated sediment were reduced by at least 71% and 99% respectively, when treated with both R and PCR. Survival increased from 45% in the contaminated sediment to 90% when treated, while growth increased by 36.5% and Hg bioaccumulation decreased by 42%. Our study indicates that this risk management strategy can successfully reduce sediment toxicity to chironomids.

Section 2 – Applied Aquatic Science

Talks

A correlational assessment of the effects of ship noise on sperm whale click counts in Baffin Bay

Maya Chouinard[1, 2]

[1]Acadia University, [2]Dalhousie University

More than a decade of research has revealed that underwater sources of anthropogenic noise have adverse effects on cetaceans, interfering with whale communication, foraging efforts, and socialization; in severe cases, leading to injury or death. Ship noise is a widespread source of acoustic disturbance, consequently it has negative impacts on many marine ecosystems. However, little research has been done on ship noise effects on Arctic ecosystems. It is concerning because humans and other species are increasing their presence in Arctic waters due to changing sea ice conditions. We studied sperm whales *Physeter macrocephalus* in Baffin Bay to assess their response to ship noise exposure. Acoustic recordings were collected using an autonomous glider equipped with a hydrophone. Ship passes were identified in the data using ship tracking (AIS) data and the number of sperm whale clicks occurring before, during and after ship noise were manually counted. A negative binomial model was fitted, where click variation was explained by date of ship pass, distance between the glider and the ship, and whether clicks occurred before, during or after the ship encounter. Preliminary results suggest click counts may increase with distance from ships, and there may be a statistical difference between the number of clicks recorded after and during ship exposure. Changes in clicking may indicate important changes in sperm whale behaviour such as an increase or decrease in foraging efforts. Our study contributes to our understanding of the threats posed by ship noise for both sperm whales and other endemic Arctic cetaceans.

Metabolomic insights into cobalamin deprivation in the Scotian Shelf diatom Bacterosira constricta

Anna Gleason[1], Catherine Bannon[1], Erin Bertrand[1]

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Cobalamin, or vitamin B_{12}, is required by half of all surveyed phytoplankton (auxotrophs) but is produced only by select bacteria and archaea. Cobalamin has been shown to be a critical currency for microbial interactions and cobalamin availability has important implications for community composition and primary productivity in various regions of the ocean. Pseudocobalamin is a B_{12} analog made by cyanobacteria that can be remodeled into cobalamin by some organisms when sufficient DMB is present. However, the sources of DMB as well as the identity of remodeling organisms remain largely unknown. Here, we isolated and cultivated the Scotian Shelf diatom, *Bacterosira constricta*. We grew *B. constricta* over a range of different cobalamin concentrations. Then, using mass spectrometry, we quantified cobalamin quotas and cobalamin in spent media to confirm that *B. constricta* is a non-auxotroph. We found that despite being non-auxotrophic for cobalamin, there were significant changes in the production of key metabolites. Specifically, we observed the first culture measurements of DMB for a eukaryote and observed that this measurement appears to be influenced by cobalamin availability. This work suggests that diatoms may play an important role in remodeling dynamics. The influence of cobalamin deprivation goes beyond auxotrophy and can significantly impact the production of key metabolites, such as DMB which may have important consequences for microbial community composition.

Exploring Estuarine Protist Dynamics: A Case Study on Salt Marsh Restoration in the Musquash Estuary

Clarissa Lalla[1]

[1]University of New Brunswick

Salt marshes, wetlands found in estuaries are highly dynamic and productive coastal ecosystems with rich biodiversity. Anthropogenic disturbances such as historic diking for agriculture, habitat degradation from coastal development, and climate change have damaged these ecosystems which provide essential services such as shoreline protection and long-term carbon sequestration. Due to their ecological importance, the preservation and restoration of these ecosystems are of grave importance. The Musquash Estuary (Marine Protected Area) is an ideal model for studying the role of microorganisms in salt marsh restoration. It is composed of several established salt marshes, and **a chronosequence of salt marsh** sites at various stages of restoration. In our work we will apply environmental DNA (eDNA) metabarcoding towards (1) establishing a baseline inventory, (2) quantifying spatial and seasonal variability, and (3) assessing the predictability of protist taxonomic and functional diversity in the Musquash Estuary based on physico-chemical properties. We will first examine the planktonic protist diversity along the estuarine gradient at high tide to provide a foundational understanding of species availability in the estuary. Next, we will examine the microplankton and microbenthos diversity of salt marsh pools and creeks at low tide, along a chronosequence of salt marsh restorations to compare them to those found in established salt marshes. Our research will contribute to our understanding of estuarine protist dynamics, explore the utility of protist eDNA metabarcoding for the ecosurveillance of salt marsh restoration, and provide meaningful considerations during the development of monitoring systems and management plans for salt marsh restoration.

Development of machine learning methods to estimate local fluid flow environments surrounding marine pelagic organisms

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Many marine organisms exhibit behavioral and physiological responses to their physical surroundings, including characteristics of their local fluid environment, such as turbulence. In the laboratory study of pelagic life, it is therefore crucial to have a method to characterize the fluid environment surrounding organisms. Particle image velocimetry (PIV) is a technique that characterizes a fluid velocity field using tracer particles dispersed in the fluid. These tracer particles are imaged twice in rapid succession with a high-speed camera, and correlation analysis of the two images is used to estimate the velocity field. Although PIV is widely used to study organism-fluid interactions, it suffers from inaccuracy when images are of poor quality (e.g., low contrast) or when the fluid velocity field has very small-scale structure. Furthermore, PIV does not incorporate the laws of fluid mechanics. Recent developments in machine learning have raised the possibility that neural network techniques may be able to resolve these problems. In this approach, a neural network can be trained to learn the optimal mapping between experimental particle images and the associated velocity field. In this talk, I will present our preliminary results learned from developing a proof-of-concept simulated 1D PIV setup to be used as a benchmark for neural network methods currently under development. This work has the potential to provide improved velocity estimates by implicitly incorporating the laws of fluid mechanics into the flow measurement algorithms.

Effect of environmental estrogen EE2 on spermatogenesis of marine medaka Oryzias melastigma

Subash raj Natarajan[1], Arkadiy A. Reunov[2], Doris W. T. Au[3], Yana N. Alexandrova[3], Michael W.L. Chiang[3], Miles T. Wan[3], Konstantin V. Yakovlev[3], Yulia A. Reunova[3], Alina V. Komkova[3], Napo K. M. Cheung[3], Drew R Peterson[3]

[1]stfx, [2]supervisor, [3]co author

Ethinylestradiol (EE2) is a synthetic hormone that is a derivative of the natural hormone estradiol. It was the first orally active synthetic estrogen, synthesized in 1938 by Hans Herloff Inhoffen and Walter Hohlweg at ‘Schering AG’ in Berlin. Currently, EE2 is used in almost all modern forms of combined oral contraceptives along with treatment for several deficiency conditions. For many years, due to environmental pollution by human society, uncontrolled accumulation of EE2 has occurred in various regions of the world. Environmental EE2 is capable of mimicking natural estrogen and, when ingested through water and food, can have detrimental effects on vertebrates and humans. It is known that although both sexes are susceptible to the disease, the greatest extent and number of harmful effects are observed in males. Despite known adverse effects of EE2 on male fertility, the specific mechanisms remain unidentified. EE2 is known to reduce offspring survival in fish, but gonadal morphological changes and gametogenesis do not necessarily accompany this. To identify changes that may occur in gonads and reproductive cells, it is necessary to conduct studies with microscopy and statistical analysis. In this study, we use the marine medaka *Oryzias melastigma* to analyze the effects of environmental estrogen EE2 on male reproductive cells through spermatogenesis. Conclusively, through this study we predict to find specific changes in the spermatogenesis process caused by environmental estrogen EE2, thereby providing a clearer understanding of its mechanisms and impacts on male reproductive health.

Comparing CO2 and CH4 Fluxes in Southern Gulf of Saint Lawrence Salt Marsh Vegetation Zones

Angus Kennedy[1]

[1]St. Francis Xavier University

As we attempt to reduce atmospheric greenhouse gas concentrations to curb global warming driven climate change, there is a need to remove greenhouse gasses (measured in CO_2e) from the atmosphere in addition to stopping their emission. Natural ecosystems remove greenhouse gasses from the atmosphere without the need of human effort. If the net flux of greenhouse gasses from an ecosystem is negative, it is considered a carbon sink. Coastal salt marshes are particularly efficient carbon sinks. However, climate change threatens the function and persistence of salt marshes in the southern Gulf of St. Lawrence. To assess the ability of these salt marshes to remove greenhouse gasses from the atmosphere, I took 114 static gas chamber measurements across five salt marshes in the southern Gulf of St. Lawrence from June to September 2023. I compared the fluxes of CO-$_2$ and CH_4 of healthy and dead *Sporobolus alterniflorus* zones to assess two hypotheses: (1) That all types of dead *S. alterniflorus* zones would have the same CO_2 and CH_4 flux rates, and (2) that healthy *S. alterniflorus* zones would be more efficient carbon sinks than all dead *S. alterniflorus* zones. I found that the different types of dead *S. alterniflorus* zones had different CO_2 and CH_4 flux rates and that healthy *S. alterniflorus* zones were the greatest carbon sinks. As dead *S. alterniflorus* zones become more prominent, regional salt marshes of will have diminished function as carbon sinks.

Effects of temperature and food availability on feeding behaviour and metabolism in the sea cucumber Cucumaria frondosa

Kat Kabanova[1], Ramón Filgueira[1]

[1]Dalhousie University, Department of Biology

Cucumaria frondosa are the largest and most abundant species of sea cucumber in the North Atlantic and Arctic oceans. *C. frondosa* are commercially exploited in Maine and Atlantic Canada and in some areas, catches are declining. Sustainable stock management requires addressing knowledge gaps in their ecophysiology and bioenergetics. While temperature is commonly assumed to be the principal factor affecting the metabolic rates of aquatic ectotherms, food availability determines the feeding ecology and ultimately, growth rates of suspension feeders such as *C. frondosa*. Effects of temperature and food availability on individual feeding rates, metabolism, and population-level feeding activity were investigated in *C. frondosa* held in mesocosms. In the first experiment, temperature was increased from 5°C to 16°C by 1°C every 3 days. Maximum tentacle insertion rates (TIR_{max}; a proxy for food intake) and cloacal opening rates (COR; a proxy for respiration) increased with temperature, while the total proportion of feeding individuals decreased. Beyond 12°C, novel abnormal behaviors - rhythmic openings of the mouth and incomplete TIR - emerged, and became increasingly common at higher temperatures, suggesting thermal stress. In the second experiment, phytoplankton concentration was increased from 2,000 cells ml^{-1} to 50,000 cells ml^{-1} by 10,000 cells ml^{-1} every 3 days. TIR_{max} increased until ~ 30,000 cells ml^{-1}, then plateaued. The proportion of feeding individuals increased with food availability, with all individuals feeding at 40,000 cells ml^{-1}. These findings provide insight into the physiological performance of *C. frondosa* under different environmental conditions and can help inform fisheries management.

Thick-billed Murre Mortality in the Northwest Atlantic Ocean during Spring 2022

Alex Day[1]

[1]Memorial University of Newfoundland and Labrador

Environmental destabilization due to climate change is a major issue for polar animals. Seabirds are one of the most vulnerable groups of vertebrates, and their conservation relies on understanding acute and chronic threats to their survival. During March and April 2022, thousands of thick-billed murres (*Uria lomvia*), deep-diving arctic seabirds with sea ice-associated feeding habits, perished along coasts of southern Labrador and northeastern Newfoundland. Local climate conditions immediately preceding this event compacted sea ice along the southern Labrador coast, changing feeding habitat and decreasing seawater to sub-zero temperatures. Necropsies of murres allowed me to investigate causes of death and to document mortality associations with mass, morphology, age and sex. I will map the spatial and temporal patterns of mortality.

Effect of Gonadotropin Releasing Hormone (Ovaplant-L) Dose on Induced Spawning of Female Striped Bass (Morone saxatilis)

Brian Conrad[1], James Duston[1]

[1]Dalhousie University

The proposed research aims to evaluate the induced spawning of female striped bass (*Morone saxatilis*) using Ovaplant-L, a salmonid gonadotropin releasing hormone analogue. The primary objective is to quantify the spawning response of striped bass to a range of doses: 10 to 75 micrograms per kilogram of body weight. The study design includes three doses with a range of 10 to 75 μg kg^{-1}). An experimental unit consists of one female and three male striped bass, allowing for a dose-response analysis of three replicates. This research is important due to its potential to support the development of land-based striped bass aquaculture in Nova Scotia, providing an alternative to salmonid farming in response to rising water temperatures and public concerns. It offers a path towards a more diversified and sustainable aquaculture industry and allows for a solution to the inability to spawn striped bass in captivity.

Assessing the interactive effects of copper and phenanthrene on ionoregulation in mummichogs.

Emil Senathirajah[1]

[1]University of New Brunswick

Metals and polycyclic aromatic hydrocarbons (PAHs) are pervasive contaminants in aquatic environments and there is currently a limited understanding of their potential synergistic toxic effects in aquatic organisms. To date, the limited number of co-exposure studies suggest the occurrence of more-than-additive toxic effects in some exposure scenarios. Water quality guidelines are currently based on the individual toxicity of metals and PAHs, highlighting a potentially critical knowledge gap. This study conducted 48-hour seawater toxicity tests to assess individual toxic effects of copper (Cu) and phenanthrene (PHE) on iono- and osmo- regulation in mummichog (*Fundulus heteroclitus*). Two separate experiments used distinct methods of PHE dosing, passive dosing and single spiking with 0.01% dimethyl sulfoxide (DMSO) as a co-solvent. In the Cu experiment (nominal 0, 0.5, 1.0, 2.0 mg/L), a decrease in muscle moisture and an increase in tissue sodium and chloride concentrations were observed. Both PHE exposures (nominal 0, 0.25, 0.5, 0.75 mg/L) showed no differences in muscle moisture, or tissue sodium and chloride concentrations. These initial findings suggest that more-than-additive ionoregulatory toxicity is unlikely given the lack of effects of PHE exposure on these parameters. Subsequent experiments will therefore assess the potential of PHE to potentiate the iono-disruptive effects of Cu in mummichog in seawater and freshwater environments using log-logistic modeling to determine EC_{50} and maximal responses for Cu exposure in varying concentrations of PHE. Our goal is that this work will contribute to our understanding of the interactions between metals and PAHs and their possible synergistic effects in contaminated environments.

Investigating the relationship between ionoregulatory mechanisms and salinity tolerance in early life stages of mummichog (Fundulus heteroclitus)

Evan Berthelot[1], Alex Zimmer[1]

[1]University of New Brunswick Saint John

In virtually all organisms, maintenance of ion homeostasis is critical for survival. In euryhaline fishes that inhabit both freshwater and saltwater environments, ionoregulatory mechanisms must be adjusted to respond to external salinity. Fish in freshwater environments actively absorb ions to compensate for the passive diffusion of ions, while seawater fish counteract the passive influx of ions through active ion excretion. In both freshwater and seawater, the active component of ionoregulation is coordinated by specialized cells known as ionocytes that are localized to the gill epithelium, and in some species the opercular membrane, of adult fishes. Though the ionoregulatory mechanisms of the adult stage of many fish species are well characterized, the mechanisms used by larval and embryonic stages are less studied, except for a few species. For instance, the euryhaline mummichog (*Fundulus heteroclitus*) is an invaluable model for studying ionoregulatory mechanisms, yet we lack an understanding of these mechanisms in early life stages of this species. Furthermore, larvae of this species have been shown to have a lower euryhaline capacity relative to adults, yet the physiological basis of this discrepancy has not been investigated. My thesis will investigate the mechanisms underlying early-life salinity tolerance in mummichog using a molecular approach to assess the expression of specific ionocyte subtypes and ion transporters in response to varying environmental salinity over early-life development. From this study, we hope to advance the current ionocyte model in mummichog and reveal mechanisms that underlie salinity tolerance across life history in this species.

The Effects of Chronic Hypoxia on the Lipid Metabolism of Brook Trout (Salvelinus fontinalis)

Hannah MacIntosh[1], Andrea Morash[1]

[1]Mount Allison University

Aquatic hypoxic events are becoming far more frequent, severe, and long lasting. To cope with periods of hypoxia, fish can decrease their oxygen requirements by reducing energetically costly activities such as locomotion, growth and feeding. During normal oxygen conditions fasting will typically upregulate fat metabolism, as fats can be stored in large quantities, and yield high levels of ATP per molecule. However, during periods of acute hypoxia, fat metabolism is typically downregulated as this process requires large amounts of oxygen and can produce harmful levels of reactive oxygen species. Instead, cells typically breakdown carbohydrates which use considerably less oxygen, but have limited stores. However, it is unclear how periods of chronic hypoxia may impact fat metabolism of fish when carbohydrate stores are exhausted. To determine the effects of chronic hypoxia and fasting we exposed brook trout (*Salvelinus fontinalis*) to 14 days of fasting and normoxia or fasting and hypoxia at 45% dissolved oxygen. We measured mitochondrial respiration using both a short-chain (sodium butyrate) and long-chain (palmitoyl-CoA) fatty acids, as well as the activity of various other enzymes important in lipid metabolism in cardiac muscle tissue. We found that fish exposed to chronic hypoxia had an increased capacity for long-chain fatty acid uptake and higher oxygen consumption in the heart than both fasted and control groups. This suggests that chronic hypoxia may induce fat oxidation to support cardiac function despite the potential negative side effects.

Taurine supports the cardiovascular response to hypoxia in marine fish

Radka Sevcik[1], Tyson MacCormack [1]

[1]Mount Allison University

Climate change is altering aquatic environments through processes like eutrophication. This is generating hypoxic conditions which may have adverse consequences for aquatic species. This may be exacerbated by taurine-deficiencies occurring due to a loss of taurine-rich prey. Taurine is a non-proteogenic β-amino acid that exhibits cardioprotective properties through osmoregulation and calcium homeostasis. Taurine is necessary for supporting cardiac function under hypoxic conditions. Taurine-deficient freshwater fish have an increased sensitivity to hypoxia but analogous studies in marine fish are lacking. The present study investigates this knowledge gap by determining the effect of taurine-deficiency on cardiac function in marine fish. Saltwater acclimated brook char (*Salvelinus fontinalis*) were used as a model marine fish to facilitate comparisons with existing data on freshwater brook char. Taurine deficiency was generated through a 5% β-alanine feed, which acts as a competitive inhibitor of tissue taurine transport. Heart rate (*fh*) was quantified using electrocardiograms (ECG) under normoxic or hypoxic conditions. Plasma osmolality and tissue taurine concentrations were determined to confirm taurine deficiency and understand the dynamics of taurine flux under hypoxic conditions. Results showed that control brook char exhibit a typical bradycardia in response to hypoxia with an average decrease in *fh* of 55%. Taurine deficient fish showed high interindividual variability and a blunted bradycardia. Additionally, control fish maintained plasma osmolality following hypoxia, while it increased by 57 mosmol/kg in taurine-deficient fish. Overall, taurine is important for the normal cardiac response to hypoxia through the maintenance of osmotic homeostasis in the heart.

Testing the tests: analysing and developing current methods of characterizing phenotypes of Saccharina latissima in Nova Scotia, Canada

Ainhoa Fournier[1]

[1]Undergraduate Researcher (Dalhousie University)

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

A Canadian marine pollutant review: The tracking methods and data analysis of reported lost, abandoned, and discarded fishing gear.

Ashley Lansley[1]

[1]Undergraduate student at St. Francis Xavier University

Marine pollution from abandoned, lost, or discarded fishing gear (ALDFG) poses a significant threat to marine ecosystems and the fishing industry. This presentation investigates the methods and trends for tracking ALDFG along the coastline and offshore waters of Atlantic Canada. Various techniques, including local knowledge, sonar scanning, ROVs and underwater cameras, diver surveys, and aerial or visual surveys, are used to track ALDFG. Coastal clean-up initiatives collect lost gear that washes ashore, contributing to data collection efforts. Through literature review and analysis of public datasets, this presentation examines the type, quantity, size, and distribution of retrieved fishing gear collected on beaches and in offshore waters. Gear type commonalities include lobster tags, buoys and floats, fishing lures and lines, plastic rope and small net pieces, and non-nylon rope and net pieces. Preliminary findings indicate that a significant portion (90%) of the retrieved gear found along Atlantic Canada falls under the category of plastic rope and small net pieces. Moreover, a dataset of retrieved lobster trap tags reveals valuable information such as the tag supplier, fishing season year, designated Lobster Fishing Area (LFA) or zone (located in the USA), and tag number. Data concluded tags found in Antigonish County and Guysborough County areas originated from the Atlantic coast of Nova Scotia, and as far as Maine, USA. Overall, the findings of this presentation show trends among retrieved ALDFG data that highlight the need for effective management strategies to mitigate the impact of ALDFG on marine ecosystems and communities along Atlantic Canada's coasts.

Towards a Baseline Behavioural Survey of Juvenile Lobsters (Homarus americanus) in the Southern Gulf of St. Lawrence Scallop Buffer Zone

Gavin Hiltz[1], Alexandra Reinhardt[1], Russell Wyeth[1]

[1]St. Francis Xavier University

Scallop Buffer Zones (SBZ) have been created in the southern Gulf of St. Lawrence by the Department of Fisheries and Oceans to protect juvenile lobster habitat by restricting scallop dragging. SBZ are new and therefore no data, to date, has been collected on their effectiveness. It is important to establish baseline behavioural data for juvenile lobsters in the SBZ for subsequent studies to build on. Over time, continued observations of juvenile behaviour and how it varies depending on different environmental factors can provide data to inform fisheries management decisions. In this project, we conducted an initial behavioural survey of juvenile lobsters at one site in the SBZ. We aimed to 1) collect baseline behavioural data of juvenile lobsters, and 2) describe patterns of juvenile lobster behaviour across environmental factors of food availability, depth, and substrate. We hypothesized that juvenile lobster behaviour will change across all three factors. We collected the data through continuous top-down underwater video from the shallow subtidal habitat of juveniles. For analysis, we determined abundances of lobsters in the videos and constructed a time budget for six broad behavioural categories. Quantitative analysis of this time budget revealed that some juvenile lobster behaviour changed across either food availability or depth and, similarly, that juvenile lobster behaviour can change across substrate types. Future studies will continue adding to this baseline data to help document changes in juvenile lobster populations through time

Characterizing offshore lobster movement and distribution patterns within LFA 33 and 34 through a tagging program

Marco Turner[1], Alysa Czenze[1], Trevor Avery[1]

[1]Acadia University

The lobster fishery is Canada's most profitable fishery, with lobster exports valued at $3.26 billion in 2021. Profits are expected to continue increasing as lobster landings increase especially in the offshore, deep-sea fishery contingent. Lobster fishing areas (LFA) 33 and 34 are the largest and most profitable areas within Nova Scotia and include both inshore and offshore contingents. The primary goal is to characterize offshore lobster movements using a tag-recapture program. Lobsters were tagged using streamer tags and reported by fishermen after being caught during the fishing season. Data collected from 2021-2023 will be presented, with data collection being ongoing as the winter fishing season progresses for LFA 33&34. This project will also compare to a larger, existing dataset provided by Southwest Lobster Science Society. Understanding lobster movement and distribution patterns is crucial to informing and stewarding the lobster fishery for the future. The study also aims to relate temperature, depth, and bottom type to lobster movements, describe the contingents (Alysa Czenze's project focus), and describe by-catch (non-target fisheries effects). These relationships are described in other fishing areas that are generally inshore contingents. Circular analyses will characterize movement patterns based on directionality and relate them to physical and environmental conditions and lobster morphometric data. It is expected that temperature will be a major factor in characterizing movement patterns because previous studies indicate warming waters increase suitable habitat within the offshore contingent. Overall, improving the strength of offshore lobster research will inform conservation and management actions.

Section 1 – Biology

Posters

In the Belly of the Beast: Examining the Diet of a Domestic Invasive Amphibian to Gain Insight into its Impact and the Mechanisms that Promoted its Success

Maya Williams[1], James Baxter-Gilbert[1], Julia L. Riley[1]

[1]Mount Allison University

The island of Newfoundland, Canada, has no native amphibians or reptiles. Since colonization, however, six species have been introduced. The Eastern Red-backed Salamander (*Plethodon cinereus*) is the most recently described of these non-native herptiles with a self-sustaining population occurring in Conception Bay South. Little is known about their origins, invasion history, or invasive ecology. The introduction of species to environments outside of their native range can lead to detrimental changes, particularly for species that reach high biomass and drive energy flow within ecosystems - like *P. cinereus*. We posit that this salamander's successful establishment and proliferation may have been mediated by pre-existing invasive prey communities (i.e., the Invasional Meltdown hypothesis). To test this hypothesis, we examined the stomach contents of 133 *P. cinereus* from Newfoundland and identified their invertebrate prey. Stomach contents were obtained through dissection, with prey items identified to the lowest possible taxonomic level, using dichotomous keys, field guides, and crowd-sourced iNaturalist consultation. In total, we assessed 1073 individual prey items. We then compared the composition of the invasive diet to the native range, using data we generated from a systematic literature review, to examine any differences. As expected, 67% of the volume within the invasive salamanders diet was made up of invasive prey items. Our research provides foundational knowledge on what native prey are being consumed by this introduced predator, as well as some of the preexisting conditions (e.g., prior invertebrate invasions) that may have allowed the salamanders to colonise a previously salamander-free Newfoundland.

The Role of Supervillin in the Freeze-Tolerant Spring Field Cricket (Gryllus veletis)

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Gryllus veletis are freeze-tolerant crickets that can survive internal ice formation following acclimation to fall-like conditions for six weeks. Fall-like acclimation causes filamentous actin (F-actin) abundance to increase in fat body and Malpighian tubules (the main insect excretory organ) in *G. veletis*; These changes in F-actin suggest a potential role for the actin cytoskeleton in freeze tolerance. The peripheral membrane protein, Supervillin, tightly binds and reorganizes F-actin in mammalian cells and may therefore be involved in remodelling the cricket actin cytoskeleton during acclimation. Moreover, Supervillin mRNA expression increases following acclimation in *G. veletis* fat body, but this has not been confirmed at the protein level. I hypothesized that Supervillin would increase in abundance during fall-like acclimation in *G. veletis* fat body and Malpighian tubules, and that Supervillin would colocalize with F-actin and nuclei. I used immunocytochemistry to stain Supervillin and F-actin from fat body and Malpighian tubules in *G. veletis* acclimated for zero (control), three and six weeks to fall-like conditions. I imaged samples with confocal microscopy and used ImageJ software to quantify the mean fluorescence intensity of Supervillin staining. Supervillin protein abundance increased significantly following fall-like acclimation for three and six weeks in fat body. However, there was no significant increase in Supervillin abundance in Malpighian tubules. Furthermore, Supervillin colocalized with F-actin and nuclei in fat body, but only colocalized with nuclei, and not F-actin, in Malpighian tubules. These results suggest that Supervillin may be involved in tissue-specific remodelling of the actin cytoskeleton as a potential freeze tolerance mechanism.

Soil Microbiome Diversity of Coastal Heathlands and Marram Grasslands on Sable Island, Nova Scotia

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The soil microbiome is essential for environmental processes and influences both above and below-ground communities. Among many factors, feral horses are shown to have a negative effect on the soil microbiome by reducing microbial diversity and abundance. Sable Island (Nova Scotia, Canada) is a sand dune with a large feral horse population, but no literature on the soil microbes. Determining the microbial composition and the driving factors is crucial for effective ecosystem management. Our research goal was to determine differences in microbial diversity (α-diversity) and composition (β-diversity) across vegetation communities, along with soil pH, organic matter content, and phosphorous concentration. This study also serves as an overall taxonomic survey of bacteria and fungi. Using eDNA from soil samples, we identified bacteria with 16S and fungi with ITS2 DNA barcodes and performed soil analyses to get pH, organic matter content and phosphorous concentration across 16 sites on the island (five plots at each site, n=80). We identified a total of 812 bacterial taxa and 336 fungal taxa. Our results indicate bacterial sensitivity, as the vegetation community, soil pH, and organic matter content significantly affected the α-diversity ($p<0.05$), but phosphorous concentration did not ($p>0.05$). In contrast, fungi were robust to the environmental factors and α-diversity was not significantly affected by any variables ($p>0.05$). Both bacterial and fungal community composition did not vary significantly in the taxa present/absent across any variable ($p>0.05$). However, when accounting for abundance, the bacterial composition was significantly different across vegetation communities ($p<0.05$).

Effects of sweet fennel essential oil on the microsporidian pathogen of the two-spotted lady beetle, Adalia bipunctata L.

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The two-spotted lady beetle, *Adalia bipunctata* L., is commercially available for biological pest control in Europe and North America. It is susceptible to the microsporidium *Vairimorpha adaliae*, a spore-forming fungal pathogen which prolongs larval development. Sweet fennel essential oil, *Foeniculum vulgare* var. *dulce*, is known to have antifungal properties and has been used for the management of both the microsporidium *Nosema ceranae* in honeybees and the late blight pathogen, *Phytophthora infestans*, in tomato and potato plants. However, sweet fennel essential oil has not been investigated for the management of *V. adaliae* in *A. bipunctata*. In this study, the effects of sweet fennel essential oil on larval development time, larval mortality rate, adult sex ratio, and microsporidian infection (spore counts) in *V. adaliae*-infected *A. bipunctata* were examined. Development time, mortality rate, and sex ratio of larvae fed green peach aphids, *Myzus persicae*, and water did not differ significantly from larvae fed aphids and 10%, 20%, or 30% fennel, respectively. However, the 20% fennel had the highest mortality rate among all treatments. Although spore loads did not differ significantly, heavier infections were observed in increased fennel concentrations with an increase of 12.83%, 61.33%, and 58.24% in the 10%, 20%, and 30%, respectively. This study suggests that fennel essential oil is safe to use on *A. bipunctata* and may provide additional energy to the host beetle to withstand the effects of the microsporidian pathogen as larval development time was unaffected, despite heavier infections.

Exploring the Space of Colour Changes in Jamaican Click Beetle Luciferase

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The natural glow of the Jamaican click beetle (*Pyrophorus plagiophthalamus*) is produced by a bioluminescent protein called luciferase. Four distinct colours of bioluminescence have been observed among beetles in their natural environment and the colour that a beetle glows depends on the amino acid sequence of its luciferase alleles (Stolz, 2003). There are two luciferase genes in click beetles, one expressed only in the dorsal light organ and another only in the ventral light organ. Field studies and phylogenetic inferences have shown that the ventral luciferase is evolving adaptively and that populations on the western islands of Jamaica are changing towards an orange glow (Stolz, 2003). Interestingly, there are only two amino acid changes between the yellow and orange alleles. This project aims to see if there is a mutational bias towards orange or if the changes in the frequency of orange individuals seen in natural populations could be due to selection on orange colour itself. We have created a saturation library, a collection of all possible mutations for every site in the colour-determining region of the luciferase protein. Starting with the two sites which differ between the yellow and orange allele I will be measuring the colour that each luciferase mutant glows. This empirical data will reveal how the availability of mutations guides natural evolution in this species of beetles.

Does the Symbiotic Sulfate Transporter (SST1) Actually Transport Sulfate?

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Many legumes form an endosymbiotic relationship with soil-bacteria called rhizobia, which fix atmospheric dinitrogen into accessible ammonium. The rhizobial nitrogenase enzyme requires a large amount of sulfur to function, and due to the endosymbiotic nature of the legume-rhizobia relationship, this sulfur must be provided by the plant. Krusell et al. (2005) previously reported that the *Symbiotic Sulfate Transporter* (*SST1*) was responsible for this sulfate transport; I sought to replicate their study. A yeast mutant in the BY4742 background deficient in all known sulfate transporters was developed to serve as a model system. *SST1* from two model legumes (*Lotus japonicus* and *Medicago truncatula*) was transformed into the mutant yeast, where it failed to rescue their growth on low or high concentrations of sulfate. When *SST1* was fused with Green Fluorescent Protein (GFP), epifluorescent microscopy revealed that it remained within the endoplasmic reticulum of the yeast and could not be found on the plasma membrane. Due to the localization of *SST1*, I could not determine its ability to transport sulfate. Further studies using a different strain of yeast or plasmid background for *SST1* transformation should be conducted.

Investigating the role of FOXA1 and DNA methylation in gene expression changes induced by ALDH1A3

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Aldehyde dehydrogenase 1A3 (ALDH1A3) enzyme is a cancer stem cell (CSC) marker whose expression in breast cancer is associated with triple negative breast cancer (TNBC) subtype and has been identified to promote tumour growth and metastasis. ALDH1A3 acts primarily by its conversion of retinal to retinoic acid (RA) which controls the transcription of thousands of genes. This study investigates an alternate mechanism by which ALDH1A3 alters gene transcription independent of RA. Microarray and 450K methylation data performed by the Marcato lab demonstrated that ALDH1A3 induced genome-wide methylation changes which were not observed when treated with exogenous RA, indicating another methylation mechanism of gene regulation independent of RA. One of the genes identified to be regulated by ALDH1A3 across TNBC cell lines was forkhead box A1 (FOXA1), a pioneer transcription factor with known effects on DNA methylation. We hypothesize that FOXA1 is responsible for the ALDH1A3-induced DNA methylation and gene expression changes. We have identified four genes, thrombospondin 1 (THBS1), keratin 4 (KRT4), and cysteine rich secretory protein 2 (CRISP2) in MDA-MB-468 cells and retinoic acid receptor beta (RARb) in MDA-MB-231 cells, with comparable expression in ALDH1A3 and FOXA1 knockdown cell lines. Furthermore, bisulphite sequencing of THSB1 in MDA-MB-468 cells revealed common methylation patterns in ALDH1A3 and FOXA1 knockdown cell lines. Bisulphite sequencing will be performed on KRT4, CRISP2, and RARb to validate the methylation mechanism. This data will provide new insights into the role of ALDH1A3 in TNBC and inform the development of future treatments for breast cancer.

The Effects of Cellular Cations on the Thermal Stability of the Human Proteome

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Proteins interact with a network of other molecules within cells. These interactions have significant implications for protein stability and thus cellular functioning as a whole; nonetheless, many of these protein interactors and interactions remain vastly understudied. While the protein-protein and protein-nucleic acid interactomes are largely understood, there exists a gap in our understanding of other protein interactions. This gap continues to decrease as more of these interactions are unveiled. Salts are one example of known protein interactors with the ability to stabilize or destabilize proteins, thus causing their respective “crashing out” via denaturation or “salting in” by solubilization. Such stability alterations may be revealed through variations in protein melting temperatures, which are thus indicative of protein-salt interactions. Dialysis against water or salt (K^+, Mg^{2+}, Na^+, Ca^{2+}) solutions was used to remove select salts from cell lysate solutions. This was followed by Thermal Proteome Profiling (TPP) to examine the resulting changes in protein stability across the proteome. These data revealed individual proteome thermal stability differences that were unique to each cation. The results indicate contributions to protein stability by intracellular cations. These interactions are of significance in human health and drug discovery.

Developing a Novel Thermal Proteome Profiling Method to Identify Phytochemical Target Engagement with the Human Proteome

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Phytochemicals are bioactive secondary plant metabolites known to affect mammalian cells, such as reducing oxidative stress and inducing apoptosis. Fruits such as blueberries contain an abundance of bioactive phytochemicals that bring about positive health effects. However, the molecular mechanisms underlying these phenotypic effects are not well understood. Thermal proteomic profiling (TPP) methods allow direct interactions between small molecules and proteins to be identified on a proteome-wide level, possibly serving as a method to define relevant phytochemical-protein interactions. Therefore, our goal was to develop a TPP-based method to identify phytochemical targets within the human proteome that may help the phytochemistry field improve understanding of phytochemical mechanisms of bioactivity. Previously established TPP methods were adapted to analyze fractions of phytochemicals derived from blueberries obtained from collaborators at Agriculture and Agri-Food Canada. Proteomic analysis revealed that eleven kinase proteins interacted with the control drug staurosporine, which is a known kinase interactor. Additionally, several novel proteins appeared to interact with blueberry anthocyanins, acylated anthocyanins, and flavanol glycosides. Western blotting also demonstrated clear interactions between methotrexate and its known protein interactor, DHFR, when subjected to this method. These data suggest that this TPP-based method may reveal several phytochemical interactions with the human proteome. Future experiments should validate these findings to determine the phenotypic effects of phytochemicals in mammalian cells so that they may be applied within the agriculture and natural product fields.

Neural Specific-Gene Expression in the Great Pond Snail, Lymnaea stagnalis

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Studies of gastropods have enhanced our understanding of how the nervous system controls animal behaviour. Immunohistochemical labelling has traditionally been the primary method used to investigate gastropod neuroanatomy, however, challenges persist regarding antibody availability and specificity. To address this, we explored a novel technique, *in situ* hybridization chain reaction (HCR), to label mRNA expression of neural-specific genes. This method offers higher versatility, as genetic sequence data allows for labelling a wider array of potential targets. Moreover, HCR inherently provides increased specificity by relying on genetic base-pairing, rather than the lock and key mechanism seen with antibodies. We conducted a comparative analysis of the techniques by parallel investigations of two enzymes associated with the synthesis of neurotransmitters in the nervous system of *Lymnaea stagnalis*. Tyrosine hydroxylase (involved in the production of catecholamines; e.g. dopamine) labelling with HCR was consistent with current and past immunohistochemical findings, albeit with lowered sensitivity. More substantial discrepancies emerged with Tyramine Beta Hydroxylase (involved in the production of octopamine) expression in the central nervous system. Furthermore, HCR failed to label neural fibres (axons and dendrites) with both enzymes, limiting anatomical detail compared to immunohistochemical labelling. Our results indicate complementary advantages of both techniques: while HCR offers stronger evidence and a greater target range, immunohistochemistry appears to provide superior visualization. Overall, the integration of both approaches could synergistically advance neuroanatomical exploration and facilitate future studies of neuron functions.

How repeatable is local adaptation? Re-use of standing genetic variation at three inversion loci during freshwater adaptation in Threespine stickleback (Gasterosteus aculeatus)

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Standing genetic variation can help to ‘jumpstart’ local adaptation, especially if past hybridization and gene flow has led to the presence of alleles beneficial in this new environment. Chromosomal inversions, which can group potentially beneficial loci, also appear to commonly underlie local adaptation. Indeed, in the Threespine Stickleback, standing genetic variation in three chromosomal inversions (Chromosome 1, 11, 21) is associated with repeated freshwater colonization in Pacific Stickleback and Eastern Atlantic populations. However, it is not clear if these loci are repeatedly used during freshwater colonization in other parts of the species’ range. As part of a global survey, we are testing if these inversions are associated with freshwater colonization in Atlantic Canadian populations. To this end, we genotyped fish from three marine and two freshwater populations in Nova Scotia. Since ‘freshwater’ and ‘marine’ alleles vary in size, we were able to genotype fish by separating amplified PCR products on an agarose gel. We found low frequencies of ‘freshwater’ alleles at all three loci. Indeed, one of our freshwater populations contained no freshwater alleles at any loci (n = 21 individuals). We are now analyzing the second Nova Scotian freshwater population (n = 7), and preliminary data absence of freshwater alleles for Chromosome 11 or 21, but that at least one individual does have a freshwater allele at Chromosome 1. Overall, these data suggest that standing genetic variation in these three inversions may be lower in Atlantic marine populations, but may still contribute to local adaptation, albeit less frequently.

Cracking the wall: immunolabelling of cell wall components in Ascophyllum nodosum

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The multicellular brown alga *Ascophyllum nodosum,* commonly known as rockweed, is a dominant plant found along the intertidal rocky shores of eastern Canada. A distinct phenomenon found in these plants is that they can shed the outer layer of their epidermal cell wall. We wanted to investigate the role of two major cell wall polysaccharides in this dynamic shedding process. We hypothesized that we could adapt methods previously developed for immunolabelling other species of multicellular brown algae and apply them to *Ascophyllum.* Hand sections of freshly fixed tissue or thick sections of plastic embedded tissue material were used. Various extraction and permeabilization methods reported by others were applied to improve antibody labelling. All sections were stained using monoclonal antibodies, some developed for brown algae cell walls, and others developed for flowering plant cell walls. To visualize immunolabelled cell walls of *Ascophyllum*, an epifluorescence microscope as well as a confocal laser scanning microscope was used. Combining a paraformaldehyde-based fixative with caffeine followed by extraction in a ClearSee solution gave the most reliable immunolabelling of hand sections. For thick sections of LR white-embedded tissue, heating at 60°C followed by hydrochloric acid treatment gave the most consistent staining. Immunolabelling revealed distinctive differences in cell wall polysaccharide staining in the epidermal and medullary cells of *Ascophyllum*.

Investigating Secondary Metabolites of the Lace Plant

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The lace plant, Aponogeton *madagascariensis*, is an ideal model for studying programmed cell death (PCD) because of the predictable perforations which form in its leaves. These perforations form during an early stage of leaf development (window stage) and are fully formed at the mature stage. Window-stage leaves show an accumulation of anthocyanins, a type of secondary metabolite (SM), which plays a vital role in PCD in the lace plant. The identities of the anthocyanins and other SMs involved in this PCD process are unknown. SMs are compounds produced by eukaryotic organisms that do not play a conserved role in their growth and reproduction. They fulfill roles in development and protect from environmental stressors through the plasticity of SM production and the diversity of chemical composition. This research project aims to profile the SMs produced in window and mature-stage leaves and to identify significant differences between the two leaf stages. Profiling was undertaken through untargeted and targeted, in progress, LC-MS-MS and analyzed through MS-DIAL - leaf stages were statistically compared using MetaboAnalyst. Untargeted LC-MSMS analysis found 22,367 features, unconfirmed compounds, produced by lace plant leaves, of which 6,967 are tentatively identified. Most features are shared between leaf stages, although significant differences exist in the abundance of approximately 5% of features between the window and mature stages, 753 and 418 features, respectively. The most abundant feature is a honokiol-like phenolic compound. Ongoing work seeks to quantify and confirm common SMs in lace plant leaves through targeted LC-MS-MS.

Phospho-regulation of ASPM throughout the cell cycle

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Pathologies such as cancer and microcephaly occur due to disrupted regulation of cell proliferation. *Assembly factor for spindle microtubules* (*ASPM*) gene codes for a protein required to organize the microtubules during cell proliferation. ASPM contributes to forming a mitotic spindle, which is required to accurately segregate genetic material into two daughter cells during animal cell division. The disrupted expression of ASPM is the leading cause of microcephaly (a brain 2 standard deviations smaller than average), and ASPM is overexpressed in various cancers. Cell proliferation is largely controlled via phospho-regulation by cyclin-dependent kinases (CDKs) and expression of cell-cycle phase specific CDK binding partners. This project studies ASPM overexpression in HEK293 cells with an *in-silico* analysis of ASPM regulation via CDK1. *ASPM* will be transfected into HEK293 cells to evaluate the number of mitotic (actively dividing cells) compared to the GFP treatment as a control. The cells will be fixed, stained with immunofluorescent dyes, including DAPI (a DNA stain) and tubulin, and imaged using confocal microscopy. We hypothesize ASPM overexpression in HEK293 cells will increase the mitotic index, and the analyzed spindle morphology will be abnormal. Researching the mechanisms underlying cell cycle regulation and spindle formation will improve understanding of how diseases like cancer and microcephaly occur.

Examining herring gull (Larus smithsonianus) diet through noninvasive bolus collection as an index of predation pressure on co-nesting allospecific seabirds

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In Nova Scotia, anthropogenic food sources support inflated numbers of American herring gulls (*Larus smithsonianus*), whose predation can detrimentally impact other local species. On Country Island in Nova Scotia, a predator management plan protected co-nesting seabird species-at-risk from significant predation by gulls and other predators from 1998-2019. During the current program cessation and subsequent return of gulls, we are reassessing the efficacy and necessity of predator management on the island. I evaluated the prevalence of at-risk seabirds in adult gull diet via noninvasive bolus collection, examining the frequency of occurrence of prey items in boluses, and how this varied with location (coastal, near gull nests, within the tern colony, etc.) and time (before or after gull chick hatch), using GLMMs with a binomial response for prey-type occurrence. Gulls primarily foraged on marine invertebrates (64.8% of samples), with at-risk seabird species occurring in their diet relatively infrequently (8.9% of samples). Prey types were more likely to occur near their respective source habitats, suggesting that gulls maximize time and energy budgets by resting near their preferred foraging sites. Gulls shift their diet during chick provisioning, consuming more marine invertebrate prey and likely providing more soft bodied prey such as birds and mammals to their chicks. Food items fed to chicks are not represented in adult boluses, implying that predation pressures on at-risk seabirds may be more severe than my findings suggest. This research will aid in the conservation of Country Island's at-risk seabird species and help inform future predator management strategies.

Liming as a Potential Restoration Method for Acid Rain-Affected Shrubs in Nova Scotia Forests

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Acid rain, characterized by sulphuric acid, poses threats to Nova Scotia's ecosystems, plants, and animals. Nova Scotia has a longstanding history of acid rain, influenced by both local sources from industry and air pollution, as well as atmospheric contributions from the northeastern United States. This situation is compounded by the natural acidity of the region's soils, primarily derived from the prevalence of granite bedrock. Lime, administered as calcium carbonate, offers restoration potential by neutralizing soil acidity. Despite successful applications in many Canadian forests, Nova Scotia's liming applications are limited. To address this, we applied sulphuric acid and lime to forest plots and monitored morphological and physiological responses of understory shrubs over a single growing season.

We found species-specific treatment effects, with an overall reduction in growth and function in the highest acid treatment. Lime positively influenced leaf physiology, evidenced by increased stomatal conductance and leaf calcium content, although its impact on leaf morphology and growth was minimal. A slight increase in leaf chlorophyll was observed in the highest acid treatment. Comparative analysis with plants from Sudbury, Ontario, subjected to long-term liming, showed more favorable growth outcomes in limed sites. This suggests the potential for positive lime effects on understory shrubs, possibly requiring extended periods for establishment. Future research should consider multi-year assessments for a comprehensive understanding of liming's impact on understory perennial shrubs. This study, though preliminary, provides valuable insights into using liming as a restoration strategy in regions impacted by acid rain in Nova Scotia.

Differential Impacts of pH and Acid Type on Brassicaceae Seed Germination and Seedling Growth: Implications for Acid-impacted Environments

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Elevated acidity can be a considerable stressor for plants. Acids can arise from anthropogenic sources such **as acid rain, characterized by inorganic acids like sulphuric acid.** Beyond anthropogenic influences, various habitats exhibit inherent acidity due to bedrock properties, such as granite's limited buffering capacity or peatlands with low pH resulting from biological activity, featuring an abundance of weak organic acids. While low pH (<4) is generally considered stressful for plants, differential impacts of distinct acid types—organic versus inorganic, strong versus weak—on plant growth and function remain unclear. To address this knowledge gap, we conducted a controlled experiment to determine whether acid responses are solely pH-dependent or if acid type specificity plays a role in plant functional responses. We grew two Brassicaceae species under factorial combinations of four pH levels (pH 1-5.5) and three acids (hydrochloric, sulfuric, and acetic) with water as control, and measured seed germination, seedling growth, leaf size, shoot and root length. Seed germination, growth, and morphology increased with increasing pH across all acids. However, acid type influenced plant responses. Hydrochloric acid promoted higher seed germination but hindered seedling growth, while acetic and sulphuric acids had the opposite effects. These results highlight the influence of acid types on plant functions, specifically affecting distinct developmental stages. Our study has implications for restoration efforts in acid-impacted environments, challenging the assumption that pH alone dictates plant stress responses. Understanding the differential effects of acid types on various growth parameters provides insight into acid stress and potential tolerance mechanisms.

Foraging ecology of Roseate Terns breeding on North Brother Island

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The Roseate Tern (*Sterna dougallii*) is a piscivorous seabird listed as Endangered in Canada. Nearly 75% of the entire Canadian breeding population currently breeds on North Brother Island, Nova Scotia, yet very little is known of the foraging ecology of these birds. I examined the diets and foraging routes of adult and newly hatched Roseate Terns on North Brother Island 2022 and 2023. Using two data collection techniques (high-resolution photography and GoPro video footage), I identified prey species foraged by Roseate Terns and determined the prey recipient (partner/self or chick) and size of prey. The direction from which terns returned to the colony with prey was observed from a blind, and which provided information on key foraging routes used by terns. For both 2022 and 2023, the most common prey observed were juvenile herring (*Clupea* sp.) and sand lance (*Ammodytes* sp.). Data obtained from photography and GoPro footage showed similar tern diet composition. Diets varied by age class as adults' diet was comprised mostly of sand lance, whereas chick diets consisted of more juvenile herring. Furthermore, sand lance that were fed to chicks were generally longer than those consumed by adults. Terns returning to the colony with sand lance were almost always observed coming from a southerly direction whereas juvenile herring were foraged from more easterly directions. Together, my results help support the premise that Roseate Terns are dietary specialist (i.e., limited prey diversity). Differences in diet observed between adults and chicks may reflect dietary needs of growing offspring.

Developing and testing a lab protocol to study the feeding ecology of American lobster (Homarus americanus) larvae

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There is very little known about the feeding ecology of American lobster larvae and how this impacts their survival and development. Through a lab experiment that used different size fractions of natural zooplankton as a food source, this study aims to develop a lab protocol to raise lobster larvae on a natural zooplankton diet, which will be able to be used to test feeding ecology questions. This protocol was successful in raising lobster larvae from stage I to stage IV. It also shows promise to be able to be used to address feeding ecology questions since there were differences in survival rate and inter-moult period depending on the size fraction of zooplankton they were given. With improvements, this protocol shows promise to be used to raise lobster larvae and test feeding ecology questions.

Drivers of Functional Diversity Across Ericaceae in Nova Scotia

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Plant species are diverse in many ways, from physical appearance to the way they function. Plants can be diverse in function due to abiotic factors such as light availability or due to evolutionary history such as a common ancestor. This study investigates why functional traits of closely related plant species may differ across habitats and between species. Twenty-four Ericaceae species across three habitat types (Barren, Bog, and Forest) in Nova Scotia were collected to provide extensive variation in environmental factors and evolutionary history. Morphological traits such as specific leaf area (SLA), leaf dry matter content (LDMC), leaf thickness (Lth), and leaf size (LS), chemical traits such as leaf pH, and categorical traits such as leaf lifespan (evergreen or deciduous), leaf arrangement (opposite or alternate), and flowering strategy (precocious or serotinous) were used to test functional diversity between species and between habitats. Analysis of variance and phylogenetic signal were used to test what influenced functional diversity of Ericaceae species across habitats. This study found that most traits were influenced solely by environmental factors such as SLA, Lth, LDMC, and flowering strategy, and some traits were influenced by both evolutionary history and environmental factors such as leaf arrangement, leaf lifespan, and leaf pH. This study shows that Ericaceae species are highly adaptable to their environment and are heavily influenced by environmental factors, especially light, and evolutionary history plays a partial role in shaping some traits.

From Field to Lab: Developing qPCR Primers and Probes for Monitoring Novel 3ANX Producers in North America

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Fusarium head blight (FHB) is an economically important disease of cereal crops globally. FHB is caused by numerous fungal pathogens in the genus *Fusarium*, but the greatest concern is *Fusarium graminearum (F. graminearum)* within the filamentous fungi genus *Fusarium*, for it's contamination of grain with mycotoxins such as DON and the emerging toxin 3-alpha-acetoxy, 7-alpha,15-dihydroxy-12,13-epoxytrichothec-9-ene (3ANX). Unlike traditional *F. graminearum* chemotypes, a novel chemotype lacking the C-8 keto group in the *Tri1* gene, but structurally similar to Type B toxins, has been identified as a unique variant of the trichothecene Type A toxin class. The absence of the C-8 keto group allows 3ANX to evade detection using conventional high-performance liquid chromatography with ultraviolet (UV) signal. It is important for agricultural practices to have rapid monitoring detections for biovigilance of pathogens such as that of 3ANX producers. In this study, I developed cost-efficient and rapid quantitative polymerase chain reaction (qPCR) assays for detecting 3ANX. Through consensus alignment of a collection of *Tri1* gene sequences of 3ANX isolates, I identified 3ANX-specific single nucleotide polymorphisms (SNPs) used to design probe (Pr_J) and primer assays (FA and FB) for *in vitro* testing for functionality with DNA extracted from 3ANX, 3ADON, 15ADON and 12 other *Fusarium spp*. Assays with specific amplification were tested *in vivo* with wheat heads, seeds, and soil. The developed assays offer a new tool for rapid and early detection of 3ANX-producing isolates in plant tissue and soil, advancing research on the epidemiology and geographic distribution of this novel chemotype.

Development of a sugar kelp biobank in Atlantic Canada

Eliza MacDonald[1, 2], Stephen O'Leary[1], Flora Salvo[2]

[1]NRC, [2]Merinov

Seaweeds are used globally in industries such as food, medicines, and cosmetics, while also serving as an important marine ecosystem engineer. Kelp species, including sugar kelp (*Saccharina latissima),* have a bi-phasic life cycle; they spend a portion of their lives as macroscopic blades, the sporophyte phase, and another portion as microscopic, sexually reproductive gametophytes. Historically in Nova Scotia, the sporophytes reproduce in late summer as the ocean cools - but with climate change, this is occurring later, and reproductive success is decreasing. However, sporophytes can be artificially matured in the lab allowing for spore collection independent of changing environmental conditions. Each spore produces a gametophyte, and an abundance of spores released by mature sporophytes may be collected for germination. Resulting gametophytes are stored under cultivation conditions that keep them growing vegetatively while remaining sexually immature. Growing kelp germplasm in a lab environment supports the propagation of kelp without overexploiting wild populations. The goal of this project is to develop a Nova Scotian sugar kelp gametophyte bank for use in research, environmental restoration, and aquaculture while protecting natural resources. Female and male *Saccharina latissima* gametophytes are easily distinguishable and can be isolated and stored separately for selective crossing. A germplasm bank created from gametophytes exists to help preserve genetic diversity in vulnerable species. Research into the population genetics of Nova Scotia's sugar kelp, as well as phenotypic data for cataloging is required for effective use of the bank. Establishing protocols for gametophyte banks is a first step towards improving seaweed aquaculture.

Effects of mechanostimulation on adult bone homeostasis in Zebrafish

Florence Joseph[1], Juan David Carvajal-Agudelo[2], Tamara Franz-Odendaal[3]

[1]Student, [2]Supervisor , [3]Research instructor

Effect of mechanostimulation on adult bone homeostasis in zebrafish (*Danio rerio*)

Authors: Florence Joseph, Juan David Carvajal-Agudelo, Tamara Franz-Odendaal

Mechanical influence has been observed to affect adult bonetissue. Adult zebrafish (*Danio rerio*) scales were exposed to vibration or simulated microgravity for 6 hours or for 18 hours in order to compare the effects across instruments and exposure durations. These machines were placed in a 28 ◦C incubator during the experiments. Scales were pulled from the lateral body and then cultured in either petri dishes or small tubes for the vibration or SMG treatment respectively. After the incubation was complete, the fish scales were removed from the cultural media and placed into tubes containing RNAlater. Gene expression analyses on bone-related genes, such as *runx2a* and *osx* (for osteoblasts) and *rankl* and *opg* (for osteoclasts) will be examined. We hypothesize more negative effects on the bone after the longer duration exposure compared to the shorter duration. Furthermore, we hypothesize that both larval and adult tissue will be affected and that both types of mechanical stimulation (vibration vs. microgravity) will negatively affectbone homeostasis, however it is unclear which will have the stronger effect or which bone cell type will respond first. This study will improve our knowledge of how different types of mechanical inducers affect adult bone and development.

Toward Healing Waters: Inflammation in the Brain and Gut and The Role of INSL5 in Recovery from Traumatic Brain Injury in Zebrafish

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The role of insulin-like peptide 5 (INSL5) in inflammation and fibrosis has not been studied despite the known anti-inflammatory and anti-fibrotic properties of other relaxin family peptides. Inflammation following traumatic brain injuries (TBI) is a global cause of concern due to the puzzling crossover between gastrointestinal and neurological disorders via the gut-brain axis. With high expression in the brain and gut, we hypothesized INSL5 would affect inflammation in these areas following TBI. A zebrafish (*Danio rerio*) TBI model was used to study the effect of INSL5 treatment on inflammation in the brain and gut following brain damage. Anesthetized zebrafish received a puncture wound in the left telencephalic hemisphere with the undamaged hemisphere serving as a control. They were placed in ambient water containing 10-9M INSL5 or vehicle as a control for 60 min. Two days post-injury, the fish were euthanized. Brains were processed for immunohistochemical detection of L-Plastin and PCNA, while gut protein isolates were analyzed using Western blotting for pro-inflammatory cytokines IL-1β and TNF-α. There was a significant decrease in L-Plastin immunoreactivity in the telencephalon of fish treated with INSL5, but no significant effect on PCNA immunoreactivity. In the gut, there was a significant increase in both pro-inflammatory markers in brain-damaged fish, but no significant effect of INSL5 treatment. These data suggest that gut inflammation increases in brain-damaged fish. In addition, INSL5 treatment might reduce inflammation in the brain following injury permitting neurogenesis to occur.

Gene expression changes in larval zebrafish (Danio rerio) after microgravity and vibration exposure

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As the era of long-duration space missions is fast approaching, it is now more important than ever that we broaden our understanding of how bone cells react to the microgravity environment of space. Using a random positioning machine to simulate microgravity and a vibration machine, we subjected anesthetized larval zebrafish at 3.5 dpf to microgravity or vibration to examine the effects on bone tissue. Previous studies showed that an exposure of 24 hours resulted in a decrease in ossification, an increase of expression in osteoclast genes such as RANKL and a decrease in Runx2a-positive (osteoblast) cells. Here, we exposed the larval zebrafish for 18 or 6 hours in order to more precisely identify the point at which the effects on bone tissue can be observed. We hypothesize that similar results will be observed in the 18-hour experiment when compared to previous 24-hour experiments, but that the effect will be reduced after only 6 hours of exposure. This research provides valuable insight into how SMG and vibration can significantly impact bone tissue and holds important implications for future studies investigating the effects of microgravity on human bone cells, the challenges posed by long-term space travel, and the advancement of regenerative medicine.

The effects of conspecific brood parasitism (CBP) on hatching success and embryonic development in Red-breasted Mergansers (Mergus serrator).

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Conspecific brood parasitism (CBP) is an alternative reproductive tactic in which a female lays at least some of her eggs in the nest of another individual of the same species. In waterfowl, nests that are heavily parasitized can suffer from reduced hatching success, presumably because of inefficient incubation. However, embryonic development in unhatched eggs has not been assessed in most populations that exhibit CBP, so the extent in which CBP is linked to disruption in embryonic development is not known. Our project aimed to determine whether there was a correlation between the hatching success of nests and their maximum clutch size, as well as the impact of bigger clutch sizes on embryonic development, in Red-breasted Mergansers (*Mergus serrator,* a species of sea duck). We hypothesized that (1) larger clutch sizes would have a lower hatching success and (2) embryonic development in unhatched eggs would decrease in large clutch sizes. Unhatched eggs were collected from 52 nests in Kouchibouguac National Park, New Brunswick in 2022 and 2023 after monitoring clutch size and hatching success. Those with identifiable embryos were classified based on their embryonic development. Overall, the results of these analyses were not significant. However, there were tendencies in the data which suggested that as clutch size gets bigger, both hatching success and embryonic development of unhatched eggs decreases. These results suggest that as clutch size is enlarged through CBP, incubation of some eggs may be inefficient.

Mercury concentrations in migrating Semipalmated Sandpipers (Calidris pusilla) and Semipalmated Plovers (Charadrius semipalmatus) at an autumn stopover site in the Western Atlantic Flyway

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Migratory shorebirds have been experiencing significant population declines and face an array of threats throughout their range. Mercury is a toxic trace element of primary concern, as it is non-essential and widespread throughout the environment. Elevated concentrations of mercury can have adverse impacts on bird health, including reproductive, neurological, and behavioural effects. Shorebirds have the potential to be exposed to mercury throughout their extended range, from breeding grounds in the Arctic to stopover sites in Atlantic Canada. Yet the extent to which shorebirds in the western Atlantic flyway pick up mercury from these areas is relatively unknown. Semipalmated Sandpipers (*Calidris pusilla*) and Semipalmated Plovers (*Charadrius semipalmated*) are two species of arctic breeding migratory shorebirds that utilize Atlantic Canada as a critical stopover site on their southbound migration. These two species of shorebirds were caught at Petit Cap, NB, and their blood was collected for mercury analysis. Concentrations in the blood reflect recent dietary exposure or mobilization from storage tissues. Blood mercury concentrations, standardized based on the mean relative fuel load for each species, were not significantly different between the two species. Both Semipalmated Sandpipers and Semipalmated Plovers had mean blood mercury concentrations below known thresholds for adverse effects, but a few Semipalmated Sandpipers were at levels of concern.

Investigating the Biological Activity of Organic Compounds Containing a Novel Michael Acceptor Functional Group

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Discovering new drugs is a constant challenge in the pharmaceutical industry. Recently drugs containing a Michael Acceptor functional group (MAF) have become attractive drug candidates. They can be highly selective for enzyme active site nucleophiles such as thiols and amines. This makes them powerful covalent inhibitors of enzymes as seen in the ground-breaking drug Ibrutinib, for chronic lymphocytic leukemia. New MAFs open an avenue for combatting resistance to current drugs. To investigate the biological activity of a novel MAF developed in the Grant lab at Mount Allison, we measured the cytotoxicity of three compounds containing this functional group. These were examined alongside two compounds with a known MAF and two control drugs, Cisplatin (non-Michael Acceptor based) and Ibrutinib. We used the MTT assay to quantitively measure colon cancer cell (HCT116) viability after exposure to the treatments. Brightfield imaging allowed us to assess whole cell morphology, and fluorescent images of Hoechst-stained nuclei allowed us to assess nuclear morphology. Within the range of concentrations tested, one of the compounds with the novel MAF had comparable cytotoxicity to the control drugs while the other compounds produced varying levels of cytotoxicity. The images captured qualitatively visualize the reduction in viable cells induced by each treatment in comparison to untreated cells and suggests that the treatments are leading to apoptosis. This research highlights the bioactivity of this novel Michael Acceptor on human cells and provides motivation for further investigation into its mechanism-of-action and its effect on other biological systems.

Effects of temperature and water on canola during critical stages of plant growth

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Plants are continually subjected to more frequent and extreme changes in climate, such as increased temperatures and soil water deficit. Although plants may tolerate some of these changes via acclimation, climate change brings forth increased risk to important crops worldwide, thus threatening food security. Many studies have shown the individual effects of these factors on plants, but their combined effects during both vegetative and reproductive growth received little attention. We used canola (*Brassica napus*) as a model plant species and grew them through their entire life cycle under two temperature regimes (20/10°C and 24/14°C, 16 h light/8 h dark) in controlled-environment growth chambers. Half of the plants were watered to field capacity (well-watered) and the other half at wilting point (water-stressed). Growth (e.g., stem height and diameter, leaf area and mass) and physiological traits (e.g., chlorophyll fluorescence, photosynthetic pigments, and nitrogen balance index) were measured during vegetative and reproductive stages. Floral morphology and silique and seed traits were also measured. Higher temperature decreased chlorophyll fluorescence and leaf flavonoids during vegetative growth, delay flowering, silique appearance, and petal width, but increased nitrogen balance index, leaf area, photosynthetic pigments (chlorophyll *a*, chlorophyll *b*, carotenoids, and total chlorophyll), and nectar amount per flower. Water deficit decreased stem height, sepal width, nectar production and delayed budding, silique appearance and maturation, but increased chlorophyll *a:b* ratio and nectar sugar concentration. In conclusion, higher temperatures and water stress had a more pronounced effect during plant reproductive stage than during vegetative stage.

Investigating the effects of pathogen infection on EHMT2 expression in ticks and humans

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Restoring homeostasis is a crucial component of organismal stress responses. If an immune reaction is not terminated, excessive activation of the immune system risks damaging the body. Increasingly the epigenetic regulator *euchromatic histone lysine methyltransferase-2* (*EHMT2*) is recognized as resolving the stress response. Pathogens stress the immune system, and ticks are a prime vector for transmission of many pathogens, such as *Borrelia burgdorferi*, the cause of Lyme disease. There is limited research into the role of *EHMT2* in modulating pathogen infections in vectors or hosts. The present study aimed to investigate the effects of pathogen infection on *EHMT2* expression in a vector-host duo: ticks and humans. Ticks were screened for pathogens. RNA was extracted from infected and uninfected specimens, cDNA was synthesized, and qPCR was performed to measure *EHMT2* expression. Human sera from patients with post infectious syndromes, and healthy controls, was monitored for *EHMT2* expression via an ELISA. Results show that uninfected ticks express *EHMT2* over 200X higher than infected ticks. Similarly, humans with fibromyalgia, chronic fatigue syndrome, and long covid all had significantly lower levels of *EHMT2* than healthy controls. *EHMT2* expression in individuals with Lyme disease was not significantly different from healthy controls, but this may be related to treatment. This study is among the first to identify a gene that may contribute to epigenetic differences in ticks depending on infection status. This study also implies epigenetic changes in individuals with post infectious syndromes, shedding light on chronic diseases that have thus far been poorly understood.

Section 2 – Applied Aquatic Science

Posters

Predicting habitat suitability for the basking shark (Cetorhinus Maximus) in the Northwest Atlantic

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The basking shark (*Cetorhinus maximus*) is a globally endangered filter-feeding elasmobranch, observed seasonally throughout the Atlantic continental shelf in Canada. The Atlantic population is currently considered of “Special Concern” by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), however recent trends in this species’ abundance and distribution remain poorly understood as the last assessment was performed over 16 years ago. Gaps in data, seasonal changes and interannual variability in the regional distribution of basking sharks further complicate effective management and conservation efforts. Here, I present an analysis of over 9,000 opportunistic basking shark sightings in Atlantic Canada, these data informed an ensemble species distribution model that included suspected environmental drivers of basking shark distribution and predict past to present-day, near-future, and mid-future habitat suitability under a business-as-usual climate scenario (doubling of pre-industrial CO_2). Results suggest that areas of high current and future habitat suitability are strongly driven by sea surface salinity, temperature, and net primary productivity and that areas of high habitat suitability will be primarily restricted to the Gulf of Maine, Georges Bank, and the Lower Bay of Fundy and less towards the poleward range of the Northwest Atlantic in the future. This research improves our ability to forecast changes in habitat quality and provides an opportunity to design dynamic spatial protections that reduce overlap with known threats such as vessel collisions and bycatch.

Effect of Vibrio anguillarum infection on lumpfish (Cyclopterus lumpus) gut microbiome using full-length 16S rRNA amplicon sequencing

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The gut microbiome is a vital component in all organisms including fish. The microbiotaexists in symbiosis with the host providing several beneficial functions, such as nutrientmetabolism and mucosal immune regulation. Anti-inflammatory and pro-inflammatorybacterial species maintain a healthy mucosal immune balance. How this balance couldbe affected by pathogens in marine teleost is unexplored. V. anguillarum is a significantpathogen in aquaculture, affecting various economically important fish species,including lumpfish, which are used for the biocontrol of sea lice in salmon farms. Thisresearch aims to understand how V.anguillarum infection alters the lumpfish gutmicrobiota, a key organ of the innate immune system. I hypothesize that V. anguillaruminfection will lead to compositional changes in the gut microbiome of lumpfish, with anincrease in pathogenic microbes and a decrease in beneficial bacteria. Here, I aminvestigating the impact of V. anguillarum on the gut microbiome of lumpfish(Cyclopterus lumpus) at the early stages of the infection. The gut microbiome oflumpfish will be studied in samples from previously conducted infection trials by full-length 16S rRNA amplicon sequencing (Nanopore-Minion). DNA from hindguts of bothinfected and non-infected lumpfish at 6, 24, and 48 h were collected. Extracted DNA isevaluated for integrity and purity followed by library preparation and nanoporesequencing. Preliminary results are expected to reveal significant shifts in the gutmicrobial community in response to V. anguillarum infection, providing insights into thepathogen-host interaction and potential strategies for improving fish health and survivalin aquaculture settings.

The impacts of sampling scale on kelp abundance estimates

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In recent years, the focus on kelp beds as a potential source of blue carbon has increased due to emerging evidence suggesting long-term storage through sequestration. To better understand their potential role in carbon sequestration and manage their conservation, the distribution of kelp species must be well quantified. However, because of their expansive suitable habitat, large-scale studies (100s km) are often favoured over small-scale assessments (100s m - 10s km). This bias towards large-scale sampling could overlook important patterns in species distribution and abundance patterns that occur at smaller scales. My research aims to address the contribution of site-specific (100s m) variability in kelp abundance and its relation to larger scale patterns in kelp distribution. To do so, I am investigating how the addition of site-specific data affects the explanation of kelp abundance variability. For this study, kelp abundance data consisted of density, percent cover, and biomass sampling at 6 and 9 m depth from 3 islands on the Eastern Shore of Nova Scotia. To compare the contribution of site-specific and island-wide scales in explaining the variance in kelp abundance, PERMANOVA tests were run for each kelp abundance proxy (density, percent cover and biomass) per kelp species. Preliminary results from the density model outputs have shown notable differences between site and island scale factors in explaining kelp abundance variability. Ongoing analysis is underway to further elucidate the differences in variability able to be explained by site and island factors and to determine the benefits of conducting small-scale kelp abundance assessments.

Exploring the Phylogenetic Classification of Freshwater Mussel Nephronaias tempisquensis in Costa Rica

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Freshwater mussels (Family: Unionidae) are integral invertebrates in freshwater ecosystems and play crucial roles in nutrient cycling and water quality. However, this lineage of bivalves is among the most vulnerable groups of animals due to climate change and anthropogenic factors. Therefore, monitoring of bivalve population numbers and distribution is imperative as their environments continue to change. However, research on the phylogeny and distribution of freshwater mussels is described as geographically biased as monitoring activities in some parts of the world, including Mesoamerica, has been limited. A lack of available molecular sequence data for many Mesoamerican species of freshwater bivalves has also limited evolutionary analyses in this group. Three morphologically distinct collections of freshwater mussels collected in 2019 in Guanacaste, Costa Rica were subsequently identified as *Nephronaias tempisquensis, Anodontites trigona,* and the invasive species *Sinanodonta woodiana*. These specimens were further examined for doubly uniparental inheritance, an uncommon form of mitochondrial DNA inheritance only observed in some bivalve species. Phylogenetic analyses of *N. tempisquensis* revealed a close association with a recently recognized tribe of Mesoamerican freshwater mussels the Popenaiadini. The project presented here not only expands our knowledge of aquatic diversity in Costa Rica but also aims to provide crucial molecular sequence data currently lacking for Mesoamerican bivalves. This information can be used in future identification efforts and analyses of the molecular evolution of Mesoamerican bivalves. Ultimately, these efforts will become increasingly significant as monitoring strategies are developed (e.g., eDNA surveys) to assist in maintaining the health and diversity of freshwater ecosystems.

Increasing Metabolic Analytic Accessibility: Cryogenic Preservation of Tissue

Julia Smyth[1], Andrea Morash[1]

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Mitochondria produce the majority of cellular energy, which is used to power vital processes. Mitochondrial activity is studied via respiration analysis, an indispensable tool used by physiologists across many domains of research. Currently, mitochondrial respiration analysis must be performed on fresh tissue samples as traditional freezing methods damage mitochondrial membranes. This becomes challenging if researchers do not have access to the required equipment or when tissue samples are collected in field environments. A possible solution is cryopreservation, which allows tissue samples to be frozen, stored, and later thawed, while maintaining similar structure and function to fresh tissue. The current study focuses on developing a field-accessible cryogenic tissue storage technique so that respiration analyses may be performed on freeze-thawed tissue samples. Using a within-subjects study design, we collected ventricle tissue samples from brook trout. We measured the fresh tissue's respiration, and the remaining tissue was stored in cryopreservation solution (1M trehalose solution rich with antioxidants including catalase, histidine, vitamin E, glutathione, etc.) and frozen using either a -80°C freezer or in dry ice at a rate of ~ -1°C /min. The samples were later thawed, and their respiration analyzed again to compare to the fresh counterparts. Preliminary data analysis suggests that OXPHOS II and CCO are similar between fresh and frozen samples, although frozen samples displayed a higher level of membrane damage, Leak respiration, and lower OXPHOS I respiration. In conclusion, the proposed cryopreservation method is a promising alternative for fresh tissue respiration analysis and could increase accessibility to mitochondrial analyses.

Consistency in a Newfoundland Coastal Fish Community in Response to Warming

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Juvenile fishes utilize many nearshore marine habitats, particularly during their highly vulnerable first years of life. Such habitats provide food and protection from predators. Eelgrass beds in Newman Sound, Terra Nova National Park, for example, provide nursery habitat for economically important species, such as Atlantic cod (*Gadus morhua*). As global sea surface temperatures continue to increase, such species may encounter environmental changes to which they cannot adapt, leading to modified distributions. From 2007 onwards, annual Atlantic cod recruitment within Newman Sound increased noticeably. To determine whether this shift was species-specific, I analyzed the relationship between water temperature and local fish communities for the years immediately before (2000-2006) and after (2007-2013) the temperature shift. I hypothesize that changing water temperatures within Newman Sound contributed to increases in Atlantic cod abundances, and that other species experienced similar relative increases resulting in increased species diversity. To test my hypothesis, I analyzed fourteen years of catch and mean water temperature data from September using generalized linear mixed models. Preliminary analyses suggest significant differences in mean water temperature between the two year groupings, with cooler mean water temperatures post-2007. Temperature had no effect on species abundance between the two 7-year groupings; however, species richness increased with temperature for the post-2007 group.

Success of Conserving Genetic Diversity among Atlantic Salmon (Salmo salar)

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Atlantic salmon (*Salmo salar*) populations from the inner Bay of Fundy (iBoF) have been in rapid decline since the 1970's. Various management actions have been undertaken to conserve genetic diversity and restore populations, but genetic diversity remains low. In Fundy National Park and Fort Folly, supportive breeding programs are still ongoing to increase abundances and maintain genetic diversity within the rivers. In this study, we will use a panel of 60 microsatellites to assess genetic diversity levels and conduct parentage analysis in four rivers undergoing supportive breeding: Point Wolfe River, Upper Salmon River, Pollett River, and Little River. Genotyping will be performed on juvenile salmon obtained from each river in July 2024. Genetic diversity will be assessed by calculating allelic richness, observed heterozygosity, inbreeding coefficient (F_{IS}), and effective population size (N_e) for each river. Based on the level of genetic diversity and successful spawning seen in each river, supportive breeding programs can be continued, expanded, or adjusted to better support salmon populations within the iBoF.

Photosynthetic Adaptations of Polar Phytoplankton to Extreme Light Limitation

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Polar phytoplankton are vital for global aquatic ecosystems, driving primary production, biogeochemical cycling, carbon sequestration, biodiversity, and climate regulation. The slow but significant productivity of polar phytoplankton at exceptionally low light suggests possible adaptations for low-light photosynthesis. We hypothesized that maintaining photosynthesis under extremely low light involves suppressing energetically wasteful charge recombinations in Photosystem II. These recombinations desynchronize the four-step cycle of Photosystem II oxygen evolution. Therefore, we used single turnover variable chlorophyll fluorescence to detect changes in recombination in polar diatoms and green algae in response to temperature and photon delivery frequency. Prolonged synchronous cycling indicates fewer wasteful recombination reactions and, thus, more efficient photosynthetic energy conversion under low light. Within taxa, we observed that higher photon delivery rates and colder temperatures result in less recombination. Further, polar taxa synchronized cycles for longer durations than temperate taxa under comparable conditions. Our findings support our hypothesis that diverse polar phytoplankton have evolved capacities to sustain photosynthesis under extreme low light. This research challenges the conventional understanding of the limits on photosynthesis under light limitation, helping unravel polar ecosystem dynamics and predict ecosystem responses to climate change.

Conserving Marine Biodiversity Through Climate Change: Challenges and Prospects of Adaptive Management

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Canada's international commitment to protect 30% of biodiversity by 2030 necessitates a rapid doubling of the current protected area within a decade. The Eastern Scotian Shelf and Bay of Fundy region currently hosts three Marine Protected Areas (MPAs) conserving valuable marine ecosystem networks with unique habitats and rich biodiversity. However, the escalating severity of climate change impacts has prompted questions about the future effectiveness of static MPA's when species of interest can no longer endure the conditions in their protected habitats. Scientists and experts on marine conservation have developed forward-thinking actions in marine spatial planning and are calling on MPA managers to revise current conservation tools and implement a framework to address dynamic climate change. To comprehensively build a climate-focused adaptive management policy, experts propose a network based-ecosystem approach that incorporates purposeful monitoring and establishes long-term conservation objectives to inform climate-smart management decisions. Despite an abundance of evidence supporting these recommendations, the integration of a climate-resilient focus into Canadian marine conservation policy has faced challenges. These challenges include stakeholder priorities, complex regulatory processes, and conflicting political interests. Here, using global examples of adaptive management in practice and conceptual forward-looking research, this study investigates climate-focused management approaches for the Scotian Shelf and Bay of Fundy Region. Based on literature reviews, I identify the barriers in place that prevent the implementation of a climate-adaptive management framework and the systematic changes that are required to overcome these barriers.