Science Atlantic 2022
Biology, Aquaculture & Fisheries Conference

March
11th - 13th

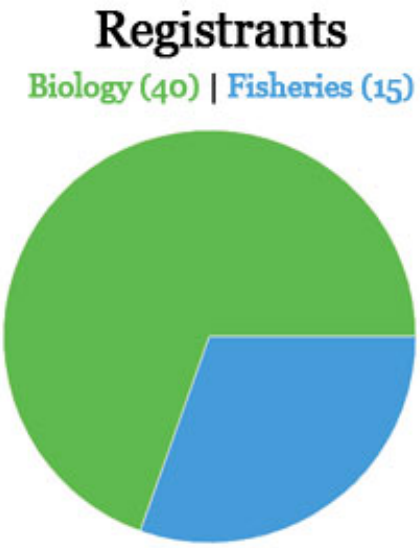
bit.ly/ScienceAtlantic2022

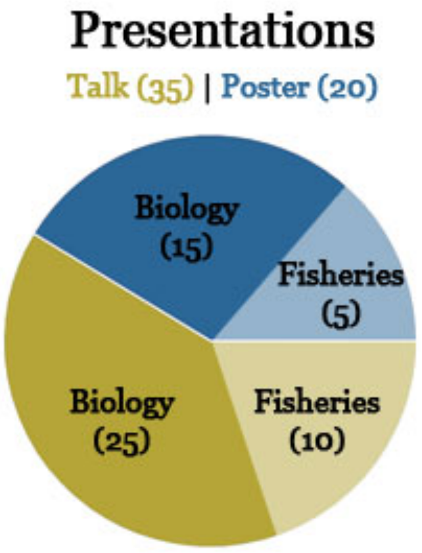
Science Atlantic 2022

Biology and Aquaculture & Fisheries Conference

March 11 to 13 2022

Hosted by Science Atlantic and UPEI Biology





Webpage

bit.ly/ScienceAtlantic2022

Join the Conference

bit.ly/ScienceAtlantic2022-Wonder

Conference Policies and Acknowledgements

Code of Conduct

scienceatlantic.ca/about-us/policies/conferencepolicies

Organizers of Science Atlantic-supported conferences are committed to providing a safe, inclusive, and productive meeting environment that fosters open dialogue and the exchange of scientific ideas, promotes equal opportunities and treatment for all participants, and is free of harassment and discrimination.

Territorial Acknowledgement (UPEI Faculty Association)

www.upeifa.ca/who-we-are/territorial-acknowledgement/

We begin by paying respect to the Mi'kmaq people of Abegweit in Mi'kma'ki. We acknowledge that Mi'kma'ki is the ancestral and unceded territory of the Mi'kmaq people, who, in 1725 first signed the Treaties of Peace and Friendship with the British Crown. Those treaties did not deal with the surrender of lands and resources, but instead recognized Mi'kmaq title and negotiated a path toward an ongoing relationship between nations. We acknowledge we carry out our daily work in Mi'kma'ki.

We convey our respect to all indigenous peoples living in this region, to the knowledge keepers, and to their brave and resilient leaders, past and present.

We acknowledge that any efforts we make as a collegial Association towards creating a fairer and more just workplace for more people, and the efforts we make to recognize and ameliorate the conditions that perpetuate injustices among us, must begin by also recognizing the injustice that lies at the base of the place we live and work. And then, together, we move towards a more just world for all of us.

Awards

Thank you to Science Atlantic (scienceatlantic.ca) and the Canadian Botanical Society (cba-abc.ca) for funding this year's student awards.

Organization

Thanks to Michelle McPherson from Science Atlantic. Trevor Avery and Russell Easy, chairs of the Science Atlantic Fisheries & Aquaculture and Biology committees. Larry Hale, Christian Lacroix, Kevin Teather, Nola Etkin, and the UPEI Biology Department. Special thanks to Kellie White from Cape Breton University (who organized this conference for the past two years!); who's help was invaluable. Thanks to the generous faculty who volunteered to evaluate talks and posters for awards.

Thank You!

Most importantly, thanks to all the student presenters for taking the time to share your research and interests. Your hard work makes this conference possible.

Schedule

	Friday	Saturday	Sunday
9:15		**Welcome – 9:15 AM**	
9:30		**Biology 1**	**Aquaculture 1**
9:45			
10:00			
10:15			
10:30			
10:45		**Break**	
11:00		**Biology 2**	**Aquaculture 2**
11:15			
11:30			
11:45			
12:00			
12:15			
12:30		**Biology 3**	**Posters**
12:45			
1:00			
1:15			
1:30			
1:45			
2:00		**Biology 4**	**Awards**
2:15			
2:30			
2:45			
3:00			
3:15			
3:30	**Technology: Test the Wonder Platform**	**Biology 5**	
3:45			
4:00			
4:15			
4:30			
4:45			
5:00		**Plenary – 5:00 PM**	
5:15			
5:30			
5:45			
6:00	**SA Meetings**		

Index – Name

Abel-Adegbite	Faith	*fabelade@unb.ca*	Poster	B01
Anand	Jaskaran	*jaskaran.singh.anand@smu.ca*	Poster	B02
Armstrong	Gabrielle	*GabiArmstrong@hotmail.ca*	Saturday	2:45
Ballard	Tanisha	*tanishalynn17@gmail.com*	Saturday	12:00
Barry	Kaelin	*x2018ygz@stfx.ca*	Sunday	10:30
Bath	Devon	*drbath@mun.ca*	Saturday	4:00
Best	Brianna	*brianna.best@smu.ca*	Poster	B03
Blackwood	Calum	*cl944944@dal.ca*	Sunday	9:45
Brown	McKenzie	*140899b@acadiau.ca*	Sunday	11:15
Cameron-Pack	Marybelle	*mcamero6@unb.ca*	Saturday	2:15
Campbell	Emma	*ecampbell2@upei.ca*	Saturday	11:00
Cao	Trung	*ttcao@mun.ca*	Poster	A01
Collet	Elise	*x2018xzx@stfx.ca*	Saturday	4:30
Conrad	Brian	*Brian.Conrad@smu.ca*	Poster	B04
Diesbourg	Emilie	*ediesbou@unb.ca*	Poster	B05
Doiron	Gabrielle	*egd4094@umoncton.ca*	Saturday	3:30
Fenech	Amanda	*afenech@unb.ca*	Poster	B06
Freeman	Emma-Jean	*147513f@acadiau.ca*	Saturday	12:30
Gaudet	Lauren	*lauren.g799@gmail.com*	Poster	B07
Gaudet	Seth	*sjgaudet@hotmail.ca*	Poster	B08
Ghasemieshkaftaki	Maryam	*mghasemieshk@mun.ca*	Poster	A02
Gravel	Cédric	*148112g@acadiau.ca*	Saturday	10:30
Grigg	Annie	*an304114@dal.ca*	Poster	A03
Hanrahan	Gracie	*cbu17fmb@cbu.ca*	Sunday	10:15
Hickey	Jill	*Jillian.Hickey@unb.ca*	Saturday	10:00
Issa	Jad	*147311i@acadiau.ca*	Saturday	1:00
Iyengar	Indhu	*ilyengar@unb.ca*	Poster	B09
Jones	Tahlia	*Tahlia.Jones2@msvu.ca*	Saturday	9:30
Khayol Muhammad	Sokhiba	*sohiba@dal.ca*	Saturday	11:15
Kromberg	Sarah	*sr972144@dal.ca*	Sunday	9:30
Kubelka	Jonathan	*Jonathan.Kubelka@unb.ca*	Poster	A04
Landry	Sophie	*sophie.landry@usainteanne.ca*	Saturday	3:45
Laver	Harriet	*hmlaver@upei.ca*	Saturday	1:15
Losier	Chloé	*ecl4682@umoncton.ca*	Poster	B10
MacIntyre	Leah	*lmacintyre2@upei.ca*	Saturday	1:30
Mader	Rebecca	*142554m@acadiau.ca*	Saturday	11:45
McIntyre	Trinity	*x2018zkh@stfx.ca*	Saturday	12:45
Noseworthy	Keshia	*keshian@mun.ca*	Poster	B11
Nunn	Sam	*samnunn@acadiau.ca*	Sunday	11:30
Onireti	Oluwatoyin	*obonireti@mun.ca*	Sunday	11:45
Randall-Scott	Caelin	*cl861623@dal.ca*	Poster	A05
Rowe	Kaileigh	*cbu17fmd@cbu.ca*	Sunday	10:00
Salt	Victoria	*cbu16dqf@cbu.ca*	Saturday	11:30
Samaraweera	Estelle	*es766984@dal.ca*	Saturday	9:45
Saulnier	Alexis	*alexis.saulnier@usainteanne.ca*	Saturday	3:00
Stacey	Erin	*erinstacey1999@gmail.com*	Poster	B12
Todoschuk	Jemma	*jmtodoschuk@upei.ca*	Poster	B13
Turner	Marco	*marco.turner@dal.ca*	Poster	B14
Vandeplas	Stormy	*st694494@dal.ca*	Sunday	12:00
Vasquez	Jose	*ivasquezsoli@mun.ca*	Sunday	11:00
Voitk	Triina	*tmvoitk@mun.ca*	Saturday	4:15
Wells	Molly	*m.wells@dal.ca*	Saturday	2:00
Weston	Liz	*Liz.Weston@dal.ca*	Poster	B15
Whittaker	Kira	*kwhittaker@mun.ca*	Saturday	2:30
Wood	Truman	*tfwood@mta.ca*	Saturday	10:15

Index – Biology Presentations

Jones	Tahlia	*Tahlia.Jones2@msvu.ca*	Saturday	9:30
Samaraweera	Estelle	*es766984@dal.ca*	Saturday	9:45
Hickey	Jill	*Jillian.Hickey@unb.ca*	Saturday	10:00
Wood	Truman	*tfwood@mta.ca*	Saturday	10:15
Gravel	Cédric	*148112g@acadiau.ca*	Saturday	10:30
Campbell	Emma	*ecampbell2@upei.ca*	Saturday	11:00
Khayol Muhammad	Sokhiba	*sohiba@dal.ca*	Saturday	11:15
Salt	Victoria	*cbu16dqf@cbu.ca*	Saturday	11:30
Mader	Rebecca	*142554m@acadiau.ca*	Saturday	11:45
Ballard	Tanisha	*tanishalynn17@gmail.com*	Saturday	12:00
Freeman	Emma-Jean	*147513f@acadiau.ca*	Saturday	12:30
McIntyre	Trinity	*x2018zkh@stfx.ca*	Saturday	12:45
Issa	Jad	*147311i@acadiau.ca*	Saturday	1:00
Laver	Harriet	*hmlaver@upei.ca*	Saturday	1:15
MacIntyre	Leah	*lmacintyre2@upei.ca*	Saturday	1:30
Wells	Molly	*m.wells@dal.ca*	Saturday	2:00
Cameron-Pack	Marybelle	*mcamero6@unb.ca*	Saturday	2:15
Whittaker	Kira	*kwhittaker@mun.ca*	Saturday	2:30
Armstrong	Gabrielle	*GabiArmstrong@hotmail.ca*	Saturday	2:45
Saulnier	Alexis	*alexis.saulnier@usainteanne.ca*	Saturday	3:00
Doiron	Gabrielle	*egd4094@umoncton.ca*	Saturday	3:30
Landry	Sophie	*sophie.landry@usainteanne.ca*	Saturday	3:45
Bath	Devon	*drbath@mun.ca*	Saturday	4:00
Voitk	Triina	*tmvoitk@mun.ca*	Saturday	4:15
Collet	Elise	*x2018xzx@stfx.ca*	Saturday	4:30

Index – Biology Posters

Abel-Adegbite	Faith	*fabelade@unb.ca*	Poster	B01
Anand	Jaskaran	*jaskaran.singh.anand@smu.ca*	Poster	B02
Best	Brianna	*brianna.best@smu.ca*	Poster	B03
Conrad	Brian	*Brian.Conrad@smu.ca*	Poster	B04
Diesbourg	Emilie	*ediesbou@unb.ca*	Poster	B05
Fenech	Amanda	*afenech@unb.ca*	Poster	B06
Gaudet	Lauren	*lauren.g799@gmail.com*	Poster	B07
Gaudet	Seth	*sjgaudet@hotmail.ca*	Poster	B08
Iyengar	Indhu	*ilyengar@unb.ca*	Poster	B09
Losier	Chloé	*ecl4682@umoncton.ca*	Poster	B10
Noseworthy	Keshia	*keshian@mun.ca*	Poster	B11
Stacey	Erin	*erinstacey1999@gmail.com*	Poster	B12
Todoschuk	Jemma	*jmtodoschuk@upei.ca*	Poster	B13
Turner	Marco	*marco.turner@dal.ca*	Poster	B14
Weston	Liz	*Liz.Weston@dal.ca*	Poster	B15

Index – Aquaculture & Fisheries Presentations

Kromberg	Sarah	*sr972144@dal.ca*	Sunday	9:30
Blackwood	Calum	*cl944944@dal.ca*	Sunday	9:45
Rowe	Kaileigh	*cbu17fmd@cbu.ca*	Sunday	10:00
Hanrahan	Gracie	*cbu17fmb@cbu.ca*	Sunday	10:15
Barry	Kaelin	*x2018ygz@stfx.ca*	Sunday	10:30
Vasquez	Jose	*ivasquezsoli@mun.ca*	Sunday	11:00
Brown	McKenzie	*140899b@acadiau.ca*	Sunday	11:15
Nunn	Sam	*samnunn@acadiau.ca*	Sunday	11:30
Onireti	Oluwatoyin	*obonireti@mun.ca*	Sunday	11:45
Vandeplas	Stormy	*st694494@dal.ca*	Sunday	12:00

Index – Aquaculture & Fisheries Posters

Cao	Trung	*ttcao@mun.ca*	Poster	A01
Ghasemieshkaftaki	Maryam	*mghasemieshk@mun.ca*	Poster	A02
Grigg	Annie	*an304114@dal.ca*	Poster	A03
Kubelka	Jonathan	*Jonathan.Kubelka@unb.ca*	Poster	A04
Randall-Scott	Caelin	*cl861623@dal.ca*	Poster	A05

Biology Talks – Saturday March 12

Session 1 (9:30 to 10:45)

9:30 Investigating the role of the cell cycle regulator CDK1 in the regulation of the spindle assembly factor Asp.

Tahlia Jones, BSc Student [1], Lori Borgal, PhD [1]
[1] Biology Department, Mount Saint Vincent University, Halifax, Nova Scotia B3M 2J6
Student Author Email: Tahlia.Jones2@msvu.ca

Mitotic spindle formation is required for cell proliferation, which is critical to propagation of all biological life. The spindle consists of microtubules and associated proteins that control chromosome segregation and pole focusing during mitosis. One of these proteins, called abnormal spindle (Asp), is the *Drosophilia* orthologue of the human Abnormal spindle microcephaly associated (ASPM) gene. In humans and flies, interrupted ASPM or Asp expression in the brain is linked with microcephaly, a neurodevelopmental disorder that causes reduced brain size. Despite these findings, the regulation of Asp/ASPM is not well understood. Sequence analysis has identified a phosphorylation motif within the Asp coding sequence for a major cell cycle regulator Cyclin-dependent kinase-1 (CDK1). Our lab has demonstrated that mutating this CDK1 phosphorylation motif resulted in sterile males defective in producing meiotic cells. To continue investigating how Asp and CDK1 phosphorylation contribute to meiotic precursor stem cell mitosis, current work aims to demonstrate that this motif is required for Asp-CDK1 protein interaction and CDK1-dependent Asp phosphorylation. To do this, we extracted *Drosophila* RNA to generate cDNA and amplified the CDK1 coding sequence which was then cloned into the pET28a vector. To optimize active kinase activity, two cloning strategies were attempted by using XhoI at the C-terminus and two different restriction enzymes at the N-terminus, SalI and NcoI. The resulting vectors will be used for protein expression in BL21 bacteria and downstream co-precipitation and phosphorylation experiments by expressing recombinant CDK1 with Asp truncations in vitro. Although transformation using NcoI was unsuccessful, additional attempts to troubleshoot this method are recommended as the additional amino acids present using the SalI cut site can interfere with kinase activity. If findings support that phosphorylation at this motif occurs, future projects can compare wildtype and mutant stem cell mitosis in the testis to further understand the role of Asp.

9:45 Investigation of the role of UFMylation in IAV infection

Estelle Samaraweera, BSc Student [1]
[1] Department of Microbiology and Immunology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: es766984@dal.ca

Ubiquitin-Fold Modifier-1 (UFM1) is a Ubiquitin-like (UbL) protein that can be covalently linked to lysine residues on target proteins. While relatively little is known about the consequences of protein UFMylation, the genes encoding the multicomponent UFMylation machinery are transactivated in response to endoplasmic reticulum (ER) stress, and the protein products operate on the cytosolic face of the ER, influencing protein homeostasis (or proteostasis). Enveloped viruses influence ER homeostasis in a variety of ways. For example, they require glycoproteins that traffic through the secretory pathway burdening the protein folding machinery, perturbing ER homeostasis, and giving rise to ER stress. Also, they can change the protein load via host shutoff, or steal ER membranes to build replication compartments. While there are few studies investigating the role of UFMylation in viral infections, the relationship between this cascade and Influenza A virus (IAV) infection has not been studied. In this study, I demonstrate how the UFMylation cascade regulates IAV infection. I used a CRISPR/Cas9 genome editing based approach to create human lung epithelial cell lines deficient in UFM1 or UFM1-specific cysteine protease 2 (UFSP2), which is required to deconjugate UFM1 from target proteins. I demonstrated successful deletion of UFM1 and UFSP2. These cell lines were infected with IAV to determine the effect of UFMylation on viral replication. I observed that UFSP2 deficiency had no effect on IAV replication and release of infectious progeny viruses. By contrast, UFM1 deficiency yielded variable results and requires further study.

10:00 Mechanical activation of the stretch-sensitive calcium channel Piezo1 regulates activation of matrix metalloproteinase-2 (Mmp2) in zebrafish

Jillian E. Hickey, BSc Student [1], Bryan D. Crawford, PhD [1]
[1] Biology Department, University of New Brunswick, Fredericton, New Brunswick, Canada E3B 5A3
Student Author Email: Jillian.Hickey@unb.ca

In order to grow and change shape during development, wound healing and regeneration, multicellular tissues must remodel their extracellular matrix (ECM). The matrix metalloproteinases (MMPs) are the primary effectors of ECM remodeling, making their proper regulation central to normal development, and their mis-regulation central to many diseases. All MMPs are synthesized as inactive pro-enzymes that must be post-translationally activated by the proteolytic removal of an auto-inhibitory N-terminal domain. Using a novel transgenic zebrafish, I can visualize the proteolytic activation of matrix metalloproteinase 2 (Mmp2) in embryos. Interestingly, Mmp2 is activated in a patchwork-like pattern in the epidermis of growing embryos, suggesting that the mechanical stretching of this tissue as the embryo grows may stimulate ECM remodeling. Piezo1 is a stretch-sensitive calcium channel expressed in the epidermis; I hypothesized that mechanical activation of the Piezo1 channel regulates activation of Mmp2, resulting in this patchwork pattern. To test this hypothesis, I used gadolinium to inhibit Piezo1, and Yoda-1 to activate it, and the epitope mediated Mmp2 activation (EMMA) assay to assess the effect on patterns of Mmp2 activation. Consistent with Piezo1 regulating Mmp2 activation, I see dramatic expansion of the patches of activated Mmp2 in the presence of Yoda-1, however the effect of gadolinium is less pronounced. I am using CRISPR/Cas9 to mutate Piezo1, which should clarify these results. These findings are the first to link mechanical stretching of epithelial tissues to the mechanisms of ECM remodeling in an intact tissue, and shed light on the feedback mechanisms regulating tissue morphogenesis in vertebrates.

10:15 The Effect of Cold Exposure on Glutamate Synaptic Transmission in the Dorsomedial Hypothalamus

Truman F. Wood, BSc Student [1], Karen M. Crosby, PhD [1]
[1] Biology Department, Mount Allison University, Sackville, NB, Canada, E4L 1E2
Student Author Email: tfwood@mta.ca

The dorsomedial hypothalamus (DMH) is a key brain region involved in thermoregulation, in part through activation of brown adipose tissue (BAT) (Labbé et al., 2015). The DMH functionally connects thermoreceptors in the skin to the sympathetic nervous system, which activates BAT and generates heat during cold exposure in mammals (Labbé et al., 2015) (Nedergaard et al., 2011). While it is known that the DMH is essential for BAT activation , how cold exposure affects neuronal communication in the DMH remains unknown. We hypothesized that cold exposure affects synaptic communication at glutamate synapses in the DMH by altering basal synaptic transmission and neuronal plasticity. To examine the potential effects of cold exposure on DMH synapses, we subjected young male Sprague Dawley rats to a 2-hour cold exposure (2 - 4°C). Patch clamp electrophysiology was then used to study glutamate signalling in the DMH of cold-exposed animals. Compared to naïve animals, we observed a decrease in basal glutamate transmission and a long-term decrease in the strength of glutamate synapses, suggesting decreased glutamate transmission in the DMH may be involved in the thermoregulatory response to cold. As the cold-exposure protocol entailed subjecting an animal to a loud cooling system and removing their bedding to ensure cold effects (Castillo-Campos et al., 2021), we performed control trials where the bedding was removed and similar noise levels were replicated for 2 hours in a room kept at 21°C . This allowed us to differentiate if our observed neuronal changes resulted from cold exposure or stress. We found that DMH neurons from control animals also exhibited a long-term decrease in synaptic strength but no decrease in basal transmission. This data suggests that cold exposure decreases basal glutamate transmission in the DMH, which could ultimately lead to BAT activation.

10:30 **The Vascular and Neuronal Effects of Astrocytic HmgB1**

Cédric Gravel, BSc Student [1, 2], Russell H. Easy, PhD [1], Baptiste Lacoste, PhD [2]
[1] Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6
[2] Department of Cellular and Molecular Medicine, University of Ottawa, Ottawa, Ontario, Canada K1H 8M5
Student Author Email: 148112g@acadiau.ca

Astrocytes surround brain capillaries using endfoot processes, which contribute to the regulation of the blood brain barrier (BBB). Astrocytes are involved in initiating synaptogenesis and regulating synapse formation. An astrocyte specific knockout (KO) of high mobility group box 1 (HmgB1) was performed using cre dependent gene KO in mouse models. After confirming successful genetic manipulation, brain sections were immunostained using NeuN and Tbr1 neuron markers. Distribution of neurons within the cerebral cortex was then assessed using ImageJ software and showed differences in cortical neuron distribution. To further evaluate this, immunostaining was performed using Ctip2 and Pou3F2 neuron markers. Neuronal cells were visible and counted using ImageJ and showed a significant difference in Pou3F2+ cells in the cortex ($n = 4$, $p= 0.0396$), relative to wild types ($n = 4$). This analysis will be repeated using Ctip2 to determine the effects on upper layer neurons. Claudin-5 immunostaining was performed and will be used to calculate percent coverage of claudin-5 on CD31. This will determine if astrocytic HmgB1 KO reduces tight junction expression between endothelial cells.

Session 2 (11:00 to 12:15)

11:00 **Reprogramming human skin fibroblasts to neurons using a single viral vector**

Emma J. Campbell, BSc Student [1], V. Shruthi Bandi, BSc [1], Shelby J. Squires, BSc Student [1], Brandon S. Smith, MSc [1], P. Joel Ross, PhD [1]
[1] Department of Biology, University of Prince Edward Island, Charlottetown, PE, Canada C1A 4P3
Student Author Email: ecampbell2@upei.ca

Human neurons are valuable model systems for studying neurodevelopmental disorders. However, they are difficult to obtain as they are post-mitotic and must be harvested through invasive procedures. Reprogramming the cell fate of human skin fibroblasts through forced expression of specific genes is a promising solution to obtaining human neurons. Most current approaches for fibroblast-to-neuron reprogramming use multiple viral vectors to deliver reprogramming genes. I aim to improve the conversion of fibroblasts to neurons using an inducible “all-in-one” reprogramming vector. We used molecular cloning approaches to engineer a single vector containing two neurogenic genes (Ngn2 and Ascl1), a selectable marker, and a gene required for doxycycline inducibility. Using this approach, the neurogenic genes will be turned on at specific time points by exploiting selectable gene expression through doxycycline stimulation. The identity of the vector was confirmed through a restriction enzyme digest. The vector was packaged as a lentivirus that we used to infect HEK-293T cells, BJ fibroblasts, and mouse embryonic fibroblasts. We confirmed the doxycycline inducibility and presence of neurogenic genes through immunocytochemistry assays in HEK-293T cells. In the coming weeks, I will converting the transduced BJ fibroblasts and mouse embryonic fibroblasts to neurons. qPCR gene expression studies will be conducted following stimulation of both human and

mouse neurons. The expression of specific genes linked to activity in the brain and neurodevelopmental disorders will compared between the human and mouse neurons. The results from this study will provide insight on the efficiency of the all-in-one reprogramming vector in obtaining human neurons. This model system will have widespread implications in studying the role of genetic factors in brain development and neurodevelopmental disorders.

11:15 **The Effect of Auxin (IAA) on Programmed Cell Death during Perforation Formation in Lace Plant Leaves (*Aponogeten Madagascariensis*)**

Sokhiba. Khayol Muhammad, BSc Student [1], Arunika.N. Gunawardena, PhD [1]
[1] Biology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: sohiba@dal.ca

Programmed cell death (PCD) is mechanism where cells death occurs in a controlled manner. The lace plant (*Aponogeten madagascariensis*) is an excellent model organism for studying developmentally regulated PCD, because it forms perforations via PCD throughout its leaf lamina in a highly predictable manner during leaf development. This process occurs in five distinct stages where PCD initiates in the center of areoles in early-stage leaves known as the "window" stage. Anthocyanin, a potent antioxidant, is abundant in window stage leaves and its loss from specific cells cues the beginning of cell death. Auxin, in its most common form, indole acetic acid (IAA), is a natural phytohormone important in plant growth and development. It is distributed in a polar manner where PIN1 efflux proteins direct its flow. The exact role and direction of flow of auxin in the lace plant remains unknown. This study aims to determine whether an increased amount of auxin hormone can alter perforation formation or affect key regulators of PCD by quantifying anthocyanin and determining the direction of auxin flow via immunolocalization of PIN1 proteins. Pharmacological experiments were conducted on lace plants with concentrations 0 (control),1,5,15,50 and 100 µM of IAA. Leaves were harvested, and data was collected on leaf length, number of perforations, microscopy analysis and anthocyanin extraction. Results indicated that plants treated with 5-100 µM IAA showed a slight decrease in perforation number per cm^2 and slight increase in leaf length in all treatments (1-100 µM). However, a significant difference was only observed in the 100 µM treatment in both parameters. All IAA treatments showed a significant decrease in anthocyanin concentration. This implicates the importance of auxin in perforation formation and suggests an optimal auxin concentration is crucial in the PCD mechanism. Immunolocalization of PIN1 proteins and ROS detection is still currently under investigation.

11:30 **Evaluating the efficacy of biopolymers as natural inhibitors of marine biofilms**

Salt, Victoria[1], Oakley, David[1], Roland, Joshua[1], Buffett, Jacob[1], Trask, Courtney[1], Ryan, Lenayah[1], Porro, Natalia[1], Jha, Kshitij[2], Carrier, Andrew[3], Mkandawire, Martin[3], Zhang, Xu[3], and Oakes, Ken[1]
[1]Biology Dept, Cape Breton University, Sydney, Nova Scotia, Canada B1P 6L2 [2] Kavacha, Canoe Cove, Prince Edward Island, Canada, C0A 1H7 [3] Chemistry Dept, Cape Breton University, Sydney, Nova Scotia, Canada B1P 6L2
Student Author Email: cbu16dqf@cbu.ca

Marine biofouling is a costly and time-consuming problem for marine aquaculture. Traditional tin and current copper-based antifouling coatings proved detrimental to marine ecosystems, demonstrating the need for effective and environmentally safe alternatives. A cost effective and non-harmful solution may lie in biopolymers which naturally exhibit anti-microbial properties. Using two naturally sourced waxes as a binding agent, the efficacy of antifouling coatings was determined over four months in 34 L aquaria. Coatings were applied to substrates commonly used in aquaculture including Aquamesh wire, vinyl siding, cedar, and pine substrates with controls (bare substrate), waxes alone, or waxes with added biopolymer and submersed at 18 or 32 ppt salinities using natural source waters (and hosted microbial communities). Eastern Oyster (*Crassostrea virginica*) were placed in half of the tanks. The balance was regularly augmented with water-soluble nutrients (24-8-16 NPK) and microbial growth was supported with full spectrum LED lights. Following a 4-month incubation, microbial fouling and coating effectiveness was determined by mass (wet and dry weight) accumulated and surface affinity/durability by methodically scrubbing of substrates with a soft-bristled brush. Additionally, a field experiment has been implemented in two marine locations to validate the laboratory findings. The results of both laboratory and field experiments will be discussed. Future implications of this research include the development of aquaculture coatings which are both economical and environmentally viable.

11:45 **Nature's pest control: antifungal activity of individual and combined thyme and cinnamon essential oils and their main components, cinnamaldehyde and thymol**

Rebecca Mader, BSc Honours Student [1], Nicoletta Faraone [2], Allison K. Walker PhD [1]
[1] Department of Biology, Acadia University, Wolfville, NS, Canada, B4P 2R6 [2] Department of Chemistry, Acadia University, Wolfville, NS, Canada, B4P 2R6
Student Author Email: 142554m@acadiau.ca

Essential oils (EOs) are concentrated, volatile plant extracts which have widespread pharmacological, agricultural, and cosmetic applications. Thyme EO (TEO) and cinnamon EO (CEO) contain antifungal natural products which may make them effective deterrents against plant pathogenic fungi, such as Botrytis cinerea, the causative agent of grey mold of many plants. To determine the effects of these extracts on B. cinerea growth, TEO, CEO, and their main components – thymol (TL) and cinnamaldehyde (CA), respectively – were tested for fungistatic and fungicidal activity using an agar dilution method. Cores of B. cinerea mycelium were grown on potato dextrose agar infused with different concentrations of treatments. After 7 days, growth area was measured. Combined treatments (CEO+TEO, CA+TL) were also tested in this way to identify interactive effects between EOs or their components. Additionally, combinations of CA/ TL and the commercial antifungal natamycin were tested for interactive antifungal activity using a broth dilution method, where treatments were mixed with potato dextrose broth and B. cinerea spore suspension in a 96-well microplate and visually assessed for turbidity after 7 days. All individual treatments produced fungistatic effects and completely inhibited B. cinerea growth at 500 µg/mL. Only cinnamon treatments (CEO, CA) were fungicidal, possibly due to the destruction of the fungal cell wall by CA. Components tended to produce similar results to whole EOs, indicating that the antifungal properties of CEO and TEO can be primarily attributed to their main components. Contrary to previous reports, no interactive antifungal effects were found in any treatment combinations in the agar and broth dilution trials. This may be explained by variations in the chemical composition of the EOs used. These findings supports previous documented antifungal activity in CEO, TEO, and their main components against B. cinerea, but does not confirm any antifungal interactions between these treatments or natamycin.

12:00 **The effects of Fictibacillus enclensis on collard greens and carrot plant growth**

Tanisha Ballard BSc Student [1], Clarissa Sit, PhD [1]
[1] Department of Biology, Saint Mary's University, Halifax, Nova Scotia, Canada B3H 3C3
Student Author Email: tanishalynn17@gmail.com

Food insecurity and food availability are emerging issues in the world as global populations are increasing and the yield and quality of crops are declining. Excessive use of agrochemicals to improve plant growth are very damaging to the environment, which warrants the need for sustainable alternatives. Exploitation of plant growth-promoting

bacteria is one alternative being considered due to the inherent relationship between plants and bacteria within the soil. Here we investigated the plant growth-promoting properties of *Fictibacillus enclensis* on collard greens and carrot plant growth by assessing the bacteria's impact on their vegetative growth. Carrots treated with *F. enclensis* exhibited little benefit in terms of carrot root weight and length, however collard greens treated with *F. enclensis* displayed improvements in leaf weight and average total leaf area. Collard greens treated with F. enclensis also exhibited a high leaf:shoot ratio. This high leaf:shoot ratio suggests that F. enclensis may be allocating resources towards the leaves rather than the shoots. These results reveal that the collard greens benefited from the application of *F. enclensis*, which provides evidence that *F. enclensis* has the potential to improve plant growth.

Session 3 (12:30 to 1:45)

12:30 **An Exploration of the Impacts of Temperature Stress on an Agricultural Insect Pest, the Oblique Banded Leafroller (*Choristoneura rosaceana*)**

Emma-Jean Freeman, BSc Student [1], Shelley Adamo, PhD [2], Suzanne Blatt, PhD [3], Russell H. Easy, PhD [1]
[1] Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6 [2] Department of Psychology and Neuroscience, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2 [3] Agriculture & Agri-Food Canada, Kentville Research and Development Centre, Kentville, Nova Scotia, Canada B4N 1J5
Student Author Email: 147513f@acadiau.ca

Management of insect pests is crucial to maintaining the sustainability and success of agriculture as it contributes to plant health, yield, and quality. As agricultural production is expected to double by 2050 to accommodate an ever-increasing human population, the success and stability of this sector are of particular importance. Further affecting agriculture is climate change. It is predicted that with a rise in global temperatures, the occurrence of heatwaves will increase and will have an impact on the overall efficiency of current pest control methods, e.g. chemical and microbial insecticides. This may be due to the differential expression of key genes involved in insect detoxification and immune pathways in response to temperature stress. Many gaps in knowledge exist concerning how insects, including agricultural pests, will be impacted by climate change and how pest management will need to adapt. To contribute to this area of interest, the response of a particular agricultural insect pest to a simulated heatwave was observed following treatment with a commonly used insecticide. The oblique banded leafroller (OBLR), a species of Tortricid moth that has a wide distribution in North America, was used as the model organism in this experiment as it is a common tree fruit pest in Nova Scotia. The overall goal of this project was to explore how this insect species reacts to heatwave exposure and to lay a foundation for further study on what changes may be occurring at the molecular level. Further research in this area will become increasingly important as our climate continues to change and as pest management strategies lose efficacy.

12:45 **Cold tolerance of the apple maggot fly and its endoparasitoid wasps**

Trinity A. McIntyre, BSc Student [1], Lalitya Andaloori, BSc [2], Glen R. Hood, PhD [3], Gregory J. Ragland, PhD [2], Jantina Toxopeus, PhD [1]
[1] Department of Biology, St. Francis Xavier University, Antigonish, NS, Canada B2G 2W5 [2] Department of Integrative Biology, University of Colorado, Denver, CO, USA 80204 [3] Department of Biological Sciences, Wayne State University, Detroit, MI, USA 48201
Student Author Email: x2018zkh@stfx.ca

Cold temperatures are known to challenge the fitness of many terrestrial organisms, and insects are no exception. The winter season can prove fatal for a number of species; therefore, several insect species have evolved strategies to survive the cold, known as their over-wintering physiology or cold tolerance. Three cold tolerance strategies have been identified: freeze-tolerant insects experience and

survive ice nucleation of their internal fluids, freeze-avoidant insects do not survive internal ice formation but survive chilling of their internal fluids, and chill-susceptible insects do not survive chilling or freezing of their internal fluids. While cold tolerance has been studied in individual species, very little investigation has been done with respect to competing species. The co-evoluntionary system of the apple maggot fly, *Rhagoletis pomonella*, and its endoparasitoid wasps (*Utetes canaliculatus*, *Diachasmimorpha mellea*, and *Diachasma alloeum*) are an excellent model system given the interspecific competition experienced by these wasps as they develop within the pupa case of the fly. The purpose of this study is to characterize and compare the cold tolerance of these three endoparasitoid species as it relates to interspecific competition by assessing their acute cold tolerance, chronic cold tolerance, and cold tolerance strategy. The apple maggot fly and its endoparasitoid wasps all survived chilling of their internal fluids, but did not survive freezing, therefore we classified them as freeze-avoidant. The species exhibited similar trends in acute cold tolerance and chronic cold tolerance as well. These results imply that cold tolerance likely does not affect interspecific competition of endoparasitoids.

1:00

Fungi on *Rana clamitans* (Green Frogs) Skin

Jad Issa, BSc Student [1] and Melanie R. Power Coombs, PhD [1,2].
[1] Department of Biology, Acadia University, Wolfville, NS, Canada, B4P 2R6 [2] Pathology Department, Dalhousie University, Halifax, NS, Canada, B3H 4H7
Student Author Email: 147311i@acadiau.ca

Although the bacterial microbiome of many Ranid frogs have been studied, there is limited data on their fungal microbiome. *Rana clamitans* are shoreline dependent species that are found widely in eastern Canada along with parts of Ontario. They present as mostly green and tend to breed in May, June, and early July. Given the changing climate, microbial interactions, and species-species interactions, investigating the fungal microbiome of Rana clamitans will provide a better understanding of beneficial and harmful factors affecting the species. For example, some fungi secrete antimicrobial peptides that protect these frogs from harmful pathogens and further studies into these fungi can potentially provide therapeutic uses that are not just exclusively applicable to frogs. During the months of June-July 2021, the frogs were collected from two different sites where cell scrapers were used to collect their skin secretions and stored at -80° C. The samples were sent to the Integrated Microbiome Resource Laboratory in Halifax, NS for ITS Amplicon DNA Sequencing. The results indicated that Basidiomycota overwhelmingly compromised the fungal sampled with over 90% abundance in all but one sample. Notable fungi are compromised from the families Russulales, Agaricales, and Malasseziales which was present in 9 out of 13 samples. Some of the fungi present in our samples have been shown to enhance or inhibit *Batrachochytrium dendrobatidis* (Bd), a fungal pathogen that is a threat to many frog species. Interactions between bacteria and fungi on amphibian skin can have dramatic effects on survival, colonization, and pathogenesis. They affect factors including antibiotics and antifungals, skin pH, and influencing gene expressions. By determining the fungal microbiota of Rana clamitans, further studies into various fungi-fungi, fungi-bacteria, and bacteria-bacteria interactions would be essential to the understanding of how the frog's microbiome affects the health of the frog.

1:15

Using Environmental DNA to Detect River Herring, *Alosa aestivalis* and *A. pseudoharengus* on Prince Edward Island

H.M. Laver, BSc Student [1], Kyle M. Knysh, PhD Candidate [1] Rosemary Curley, MSc [2], Simon C. Courtenay [3], M.R. van den Heuvel, PhD [1]
[1] Canadian Rivers Institute, Department of Biology, University of Prince Edward Island, 550 University Avenue, Charlottetown, PE, C1A 4P3, Canada [2] Nature PEI, P.O. Box 2346, Charlottetown, Prince Edward Island C1A 8C1 Canada [3] Canadian Rivers Institute, School of Environment, Resources and Sustainability, University of Waterloo, 200 University Avenue West, Waterloo, ON, N2L 3G1, Canada
Student Author Email: hmlaver@upei.ca

River herring (*Alosa pseudoharengus* (Alewife) and *A. aestivalis* (Blueback Herring)) spawn in eastern North American rivers late spring to early summer. The species are known to be in decline throughout their range. Both species are commercially fished in the Maritime region and hold

cultural importance to first nations. Ecologically, river herring are important nutrient sources to a variety of species and are glochidia hosts of the alewife floater mussel (*Utterbackiana implicata*). There is a lack of data regarding the spatial distribution of river herring spawning in Prince Edward Island rivers and little is known about their conservation status in the Maritime region. On PEI in particular, an abundance of dams has led to an obstruction of passage into upstream spawning grounds for river herring. We hypothesized that river herring DNA concentrations in river water would be more abundant when river herring were spawning and would decline as when juvenile river herring go to the ocean. Water samples from three systems, West, Hunter, and Winter Rivers, were taken biweekly from May until September 2021 and then monthly until October. These water samples were filtered to extract environmental DNA (eDNA). The extracted DNA was amplified using a river herring specific quantitative Polymerase Chain Reaction assay and comparing against known concentrations of DNA to quantify the amount of river herring DNA present in the water samples. River herring DNA was detected in all three rivers and the quantity of DNA decreased over time when the river herring were expected to leave the rivers. The results suggest that spawning increases eDNA abundance in rivers, and due to the relationship between eDNA abundance and behaviour, life history traits could be evaluated using eDNA. Furthermore, the results indicate that sampling eDNA between June and August will detect spawning populations in other river systems on PEI.

1:30 Comparing sample mediums for detecting invertebrates using eDNA on Prince Edward Island

Leah MacIntyre, Bsc Student [1], Mark Saunders, Msc Candidate [2], Kyle Knysh, PhD Candidate [1], Royce Steeves, PhD [3], Simon Courtenay, PhD [2], Michael Van Den Heuvel, PhD [1]
[1] Department of Biology. University of Prince Edward Island. Charlottetown. Prince Edward Island. Canada C1A 4P3 [2] School of Environment and Sustainability. University of Waterloo. Waterloo. Ontario. Canada N2L 3G1 [3] Aquatic Animal Health Section. Fisheries and Oceans Canada. Moncton. New Brunswick. Canada E1C 9B6
Student Author Email: lmacintyre2@upei.ca

Environmental DNA (eDNA) is a biodiversity monitoring strategy that can be faster and less costly than morphometric identification. Several shortcomings limit the use of eDNA for environmental monitoring, as eDNA surveys can suffer methodological difficulties because they rely on metabarcoding. PCR amplification bias may distort the taxonomic abundance in a sample, and gaps in the database may cause a survey to overlook particular species. This study uses novel 16S rRNA gene metabarcoding primers designed by Fisheries and Oceans Canada to survey estuarine arthropods on Prince Edward Island (PEI). In June and August of 2021, we collected water and sediment samples from estuaries on PEI and used next-generation sequencing to evaluate their eDNA content. We referenced the 16S sequences recovered from these samples to the NCBI database, and we compared sequence data to our results from crustacean traps set at the same time as sampling. This study found that eDNA could detect over 60 unique arthropods across both sample mediums, over double the taxa detected using invertebrate traps. However, 16S sequence databases are still missing entries for local species, and efforts to improve representation will increase reliability. Nevertheless, eDNA surveys are a promising supplement to existing biodiversity survey programs on PEI.

Session 4 (2:00 to 3:15)

2:00 Assessing the impact of visual media as an outreach tool for marine conservation: historical and present applications

Molly M.B. Wells, BSc Student [1]. Heike Lotze, PhD [1]. Jennifer Stamp, PhD. [2]
[1] Biology Department, Dalhousie University, Halifax, NS, Canada B3H 4R2. [2] Psychology & Neuroscience Department, Dalhousie University, Halifax, NS, Canada B3H 4R2.
Student Author Email: m.wells@dal.ca

There is often a disconnect between academic and public spheres in terms of knowledge and understanding of ocean issues, which limits conservation action. Throughout history, visuals have bridged this gap by facilitating ocean exploration by proxy. More recently, art-science collaborations have been promoted as a way to increase public engagement, emotional responses, and changes in behavior. Still, scientists hesitate to use art in outreach as it is considered unconventional and difficult to evaluate. The purpose of this study was to evaluate the usage of different types of visual media in marine science outreach over time, using historical and modern survey methods. First, a historical review investigated changes and trends in marine zoological illustration through time. European illustrations from 350 BC up to the 21st century were analyzed according to their purpose, execution, scientific and social impact. Trends were compared qualitatively between and within time periods. Overall, visuals were used to investigate, communicate, and popularize marine science. The coevolution of marine zoological illustration and public interest in marine life provides insight into the potential of contemporary marine art-science collaborations. Second, an online survey assessed the impact of different visual media types on university student responses to marine conservation topics. Participants read three articles and responded to 19 questions including Likert scales, multiple choice, and open answer formats. Attributes contributing to a person's likelihood to act on conservation issues were evaluated. Each article was accompanied by either an art piece, a scientific illustration, or a photograph. Responses were analyzed using Analysis of Variance and Chi-Square tests to measure effect of media type on responses. Results can inform marine science outreach strategies as to how visual presentation of topics may affect public opinion and action. Overall, this research can address concerns regarding art-science collaborations and encourage their use in marine conservation.

2:15 **Sensory Perception and the Social Brain: How ablation of the lateral line modulates expression of pth2, a social hormone in zebrafish.**

Marybelle Cameron-Pack, BSc Student [1], Alexandra Venuto, PhD [2], and Timothy Erickson, PhD [1]
[1] Biology Department, University of New Brunswick, Fredericton, New Brunswick, Canada E3B 5A3 [2] Department of Biology, East Carolina University, Greenville, North Carolina USA
Student Author Email: mcamero6@unb.ca

Our social interactions are an essential aspect of who we are and important to our well-being. Yet the influence of social interactions on the brain's chemistry and function is poorly understood. Parathyroid hormone 2 (Pth2) is a neuropeptide expressed in the thalamus that is involved in social behaviour in vertebrates. In zebrafish, pth2 expression is dynamically regulated by social context: socially-housed fish exhibit high pth2 expression while expression is lost in socially isolated fish. Fish assess their social context using sensory information from the mechanosensory lateral line, a sensory system in aquatic vertebrates that detects environmental water motion. Genetically inactivating or chemically ablating the lateral line results in decreased expression of pth2 in socially raised fish and prevents social-induced recovery of pth2 expression in previously isolated fish, respectively. However, it is unknown whether chemical ablation of the lateral line will affect pth2 expression in fish that have previously sensed the presence of conspecifics. My hypothesis is that repeated chemical ablations of the lateral line will result in similarly low pth2 expression levels as seen in socially isolated fish and lateral line mutants. I will be using neomycin to repeatedly ablate lateral line hair cells in socially-raised zebrafish larvae over a 36 hour period and perform mRNA in situ hybridization to detect pth2 expression. This work will help our understanding of the role of Pth2 in social behaviour by connecting the fish's ability to sense other fishes with pth2 production.

2:30 **Tracing camouflage: saliency effects on gaze patterns during visual search image formation**

Kira L. Whittaker BSc Student [1], Pierre-Paul Bitton, PhD [1]

[1] Department of Biology, Memorial University of Newfoundland and Labrador, St. John's, NL, Canada A1C 5S7 [2] Department of Psychology, Memorial University of Newfoundland and Labrador, St. John's, NL, Canada A1C 5S7
Student Author Email: kwhittaker@mun.ca

Search image formation is the process by which an organism, after repeated exposures to a type of camouflaged item, can optimize its search pattern to better detect the camouflaged target. While the concept of search image formation and the systems of visual information processing are well understood, little is known about how search image formation occurs, and if there are any particular visual patterns or approaches associated with the formation of search images. In my honours research, I investigated the visual processing methods used by participants searching for a camouflaged target as they undergo visual search image formation. This was done by assessing if participant attention was drawn to highly salient features in a landscape, and whether or not this changed over repeated exposures. Fixations made by participants were compared to areas identified to be of high saliency using a computer vision software, to determine if there was crossover between areas of focus of the participant and the areas indicated by the software. It was found that there was no indication that participants were fixating in more salient areas of the images, which indicates that computer-determined saliency is not a good model for human visual behaviours when searching for a target camouflages in a black and white landscape image. This investigation has, however, highlighted problems with this analysis which can be improved on and allow further investigation in the future by applying saliency in a novel way.

2:45

Nest material preferences among European Starlings (*Sturnus vulgaris*) with a focus on feathers and anthropogenic materials

Gabrielle C. Armstrong, BSc Student [1], Colleen. Barber, PhD [2]
[1] Department of Biology, Saint Mary's University, Halifax, Nova Scotia, Canada B3H 3C3 [2] Department of Biology, Saint Mary's University, Halifax, Nova Scotia, Canada B3H 3C3
Student Author Email: GabiArmstrong@hotmail.ca

Avian nests provide critical shelter for offspring and differ in structure according to the species. They typically consist of natural materials such as dried grass, feathers from other species, and anthropogenic materials woven into them. The European starling (*Sturnus vulgaris*) is an urban-thriving cavity-nesting species. Their nests consist of both natural and anthropogenic materials taken from the surrounding area. Anthropogenic materials have been shown to reduce fledging success in certain species. Passerine research has revealed birds prefer unpigmented over pigmented feathers to incorporate into their nest, although a mixture of both may be present. Studies have demonstrated that white feathers result in greater hatching success. Nests within nestboxes occupied by starlings in 2021 were examined after fledging to document the amount of anthropogenic materials and unpigmented vs. pigmented feathers. Of these, 17 nests were collected from early broods, and 21 from late broods. The amount of anthropogenic materials and feathers did not differ between early and late broods. Brood condition tended to be negatively correlated with the amount of anthropogenic materials and was significantly negatively correlated with total feather mass within a nest. However, I did not detect a relationship between hatching success and the amount of unpigmented feathers within a nest. Anthropogenic materials and feathers appeared to have adverse effects on nestling condition, so it is surprising that they are abundant in many of their nests.

3:00

Roseate Tern Diet and Foraging Specificity Amongst Nesting Terns on North Brother Island, Nova Scotia

Alexis V. Saulnier, BSc Student [1], Shawn R. Craik, PhD [1], Mark L. Mallory, PhD [2]
[1] Départment des sciences, Université Sainte-Anne, Pointe-de-l'Église, Nouvelle-Écosse, Canada, B0W 1M0 [2] Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada, B4P 2R6
Student Author Email: alexis.saulnier@usainteanne.ca

On the open ocean, seabirds can serve as important bio-indicators for assessing ecosystem health, as they form a dependency on fish prey. In southwest Nova Scotia, the monitoring of piscivorous terns has allowed for the study of diet composition of Common (*Sterna hirundo*) and Roseate Terns (*S. dougallii*). Elsewhere, it has been shown that Common Terns are more generalist predators than Roseate Terns. We tested the prediction that Roseate Terns specialize on a narrower range of fish prey species than Common Terns by undertaking a comparative analysis of the diet of two of the tern species on North Brother Island, home to Canada's largest Roseate Tern breeding colony. Data on the species of fish prey brought back to the island by adults to feed either mates or newly-hatched young were collected by assessing chick prey provisioning at individual nests and by photographing adults with food arriving to the colony. Consistent with expectations, we found that Roseate Terns limited the diversity of their fish prey species captured compared to Common Terns. We confirmed 12 prey species for Common Terns (n = 242 observations), whereas only five fish species were confirmed for the Roseate Tern (n = 78), the vast majority (82%) of which were either herring (Clupea spp.) or sandlance (Ammodytes spp.). The relatively narrow diet of the Roseate Tern may reflect a preference for specific foraging habitats. Thus, demonstrating the relevance of the essential breeding ground that is North Brother Island for the Canadian population of the Roseate Tern.

Session 5 (3:30 to 4:45)

3:30

Does size matter?: Prey selection by non-breeding Snowy Owls (*Bubo scandiacus*) in Igloolik, NU

Gabrielle Doiron. BSc Student [1], Cléa Frapin, MSc [1][2], Nicolas Lecomte, PhD [1]
[1] Département de Biologie, Université de Moncton, Moncton, New-Brunswick, Canada E1A 3E9 [2] Centre d'études nordiques, Kuujjuarapik, Quebec, Canada J0M 1G0
Student Author Email: egd4094@umoncton.ca

Due to the low productivity of the tundra, the Arctic food web counts amongst the simplest in the world. Most arctic predators, such as the snowy owl (*Bubo scandiacus*), feed primarily on lemmings (*Lemmus sp.* and *Dicrostonyx sp.*), whose prevalent cyclical population dynamics – during which populations can vary up to a hundredfold – largely impact the tundra's food web. With the advent of climate change, lemming population dynamics across the Arctic have demonstrated great losses in amplitude, if not collapsed in some cases. Such trophic shifts will impact the predators specialized on lemmings, such as the snowy owl. Here we aim to measure the impact of lemmings' fluctuations and low density on prey selection by the snowy owls. The study site was situated in Igloolik, a Canadian arctic island with a resident non-breeding population of snowy owls. The density and body mass of the lemmings available on site during each study year were determined using a capture-recapture design. We found low fluctuation of density between years, between 0.08 and 2.32 collared lemmings (*Dicrostonyx groenlandicus*) per hectare, demonstrating that Igloolik hosts much lower lemming densities relative to other study areas. The diet of the owls was studied from regurgitation pellets collected between 2015-2019. The body mass of the lemmings consumed, primarily collared lemming, was determined from a pre-established allometric relationship based on the size of the mandibles recovered from the pellets. No significant relationship was observed between lemming density and the size of the lemmings selected by the owls. However, it was determined that the size of the lemmings selected by the snowy owls was 20% lower than the size of lemmings available on site, likely due to the lower energy requirements of this non-breeding population.

3:45

Foraging Ecology of the Endangered Roseate Tern at Dennis Point, Nova Scotia

Sophie E. Landry, BSc Student [1], Shawn R. Craik , PhD [1]
[1] Département des science, Université Sainte-Anne, Church Point, Nova Scotia, Canada, B0W 1M0
Student Author Email: sophie.landry@usainteanne.ca

The Roseate Tern (S*terna dougallii*) is listed as endangered in both Canada and the United States, therefore understanding the species' ecology at key breeding and foraging sites will help guide recovery strategies. This research aims to understand the foraging ecology of Roseate Terns at Dennis Point, Nova Scotia, which has recently been found to be a key foraging site for terns breeding on nearby North Brother Island, the largest Roseate Tern colony in Canada. We observed tern foraging activity at Dennis Point in relation to breeding chronology, prey capture success rate, and the position of foraging tern flocks relative to tide and time of day. On North Brother Island, we collected data on tern nesting chronology and noted from a blind the direction in which terns returned to the colony with prey to feed either mates or newly-hatched young throughout the breeding period. Tern flock size and their feeding locations at Dennis Point were assessed during the breeding period. As many as 18 Roseate Terns were observed feeding at Dennis Point at once, which was equivalent to approximately 20% of all birds breeding on North Brother Island. Results indicated there was a relationship between Roseate Tern breeding chronology and use of Dennis Point as a foraging site; specifically, an increase in the proportion of tern returning to the colony with prey from the east (Dennis Point) was noted when most nests (>93%) had recently hatched, suggesting that Dennis Point is particularly important during the Roseate Tern chick rearing phase. Prey capture success rate averaged 50%, and we observed an average of 1.87 prey capture attempts per minute and 0.88 captures per minute. Preliminary data suggest that the distribution of foraging terns is influenced by the tide as terns foraged farther offshore at low tide, possibly due to shifts in availability of prey, notably juvenile herring, at the water's surface. In conclusion, this study highlights the importance of Dennis Point as a foraging site for this important breeding colony of Roseate Terns in Canada, particularly during the chick rearing period.

4:00

Warm predator rich waters produce few but large age-0 juvenile cod

Devon R. Bath, BSc Student [1], Robert Gregory, PhD [2], Paul Snelgrove, PhD [1]
[1] Ocean Sciences, Memorial University of Newfoundland, St. John's, NL, Canada A1C 5S7 [2] Ecological Sciences, Department of Fisheries and Oceans, St. John's, NL, Canada A1C 5X1
Student Author Email: drbath@mun.ca

Targeted seining of nearshore habitat refugia in conjunction with environmental data can offer insights into juvenile fish ecology and the factors that shape recruitment. Past studies propose predation and temperature as key influences on juvenile fish abundances. Predation evokes both direct and indirect effects through consumption of prey and spatially mediated avoidance behavior, respectively. Previous studies demonstrate the influence of temperature on spatial patterns and recruitment of fishes, with greater susceptibility of smaller fish to temperature stress than larger fish. Our study tests the hypothesis that higher temperature and greater predator abundance reduce juvenile abundance and truncates size distributions of age 0 Atlantic cod in nearshore habitat. We tested this hypothesis using eight years of historical data on nearshore fish abundance and benthic temperatures in Newman Sound, Newfoundland. We found significant effects of temperature on abundances of recently settled age 0 Atlantic cod, with lower temperature corresponding to higher abundance years and higher temperature to lower abundance years. We found no effect of temperature on predator abundance. The monthly mean length of age 0 Atlantic cod is found to be higher under high predator abundance. Years with high predator abundance and low prey abundance exhibited the highest mean length of age 0 Atlantic cod. Our study shows predators and temperature operate in tandem changing the abundance of age 0 Atlantic cod in nearshore refugia as well, the size-

frequency distribution. These results suggest that increased temperatures and predators have separate roles in determining age 0 Atlantic cod survival in coastal nursery habitats.

4:15

The influence of microhabitats on life form composition within the arctic-alpine barrens of the Hawke Hills, Newfoundland and Labrador

Triina Voitk, BSc Student [1]
[1] Biology, Memorial University of Newfoundland and Labrador, St. John's, Newfoundland, Canada, A1C 5S7
Student Author Email: tmvoitk@mun.ca

Microhabitats influence the ability of plants, lichens, and mosses to colonize in a landscape. Microhabitats create small variations in microclimate within the mesohabitat, therefore, different life forms such as cryptogams and vascular plants must inhabit unique microhabitats when exposed to adverse conditions. I investigated the relationship between microhabitat and life form diversity in the Hawke Hills formation in eastern Newfoundland and Labrador: an arctic-alpine environment located below the latitudinal Arctic. I calculated the Shannon index as a proxy to determine the diversity of vascular plants, bryophytes, lichens, and exposed areas within 1 m x 1m quadrats and compared this to three different variables: microhabitat diversity, aspect, and relative location of the quadrat within the sample site. I predicted that quadrats with greater microhabitat diversity will have greater life form diversity than quadrats with lower microhabitat diversity, quadrats placed along north-facing aspects will have greater cryptogam diversity than quadrats placed on south-facing aspects, and quadrats placed along the edge of the sampling site (margin of the ecotone) will have greater life form diversity than quadrats placed near the middle of the sampling site. I tested these predictions at six different sites located in three regions. My results indicate that in my study, microhabitat diversity does not drive life form diversity (p-value= 0.739), aspect does not influence cryptogam diversity (t-value= -0.3378, p-value= 0.7399), and distance from ecotone does not influence life form diversity in the Hawke Hills (t-value= 1.4838, p-value= 0.1574). These results indicate that to better understand drivers of life-form diversity in the Hawke Hills, more sites should be sampled and other factors such as climate and elevation may be influencing the establishment of vegetation.

4:30

Light requirements and community structure of Black ash in Nova Scotia

Elise Collet, BSc Student [1], David Garbary, PhD [1], Nicholas Hill, PhD [2]
[1] Department of Biology, St. Francis Xavier University, Antigonish, NS, Canada B2G 2W5, [2] Fern Hill Institute of Plant Conservation, South Berwick, NS, Canada, B0P 1E0
Student Author Email: x2018xzx@stfx.ca

Black ash, Fraxinus nigra, is a native tree to central and eastern North America. In Nova Scotia, Black ash is rare compared to its abundant relative White ash, Fraxinus americana, that is also native to this area with the two species often present in the same habitats. We suspected that differences in abundance between Black ash and White ash were because of differences in their respective regeneration niches associated with light. On this basis we examined light intensity (using HOBO – light loggers) at both the seedling and adult life stages to evaluate microhabitat. Transects were conducted to identify seedlings of both species and describe the vegetation community associated with them. In a field experiment, seedlings of the two species were either left untouched or exposed to higher light by cutting away the herbaceous overstory. Growth and survival were measured for all seedlings over a 4-month period. We found that Black ash received more light than White ash trees at maturity, but not at the seedling stage and that increased light availability did not increase seedling growth. Therefore, light availability is likely not the limiting factor on Black ash seedling growth even though in paired experiments more mature trees occurred in a higher light environment.

Plenary Talk – Saturday March 12, 5:00 to 6:15

Adaptation and Diversification of Galapagos Island Land Snails

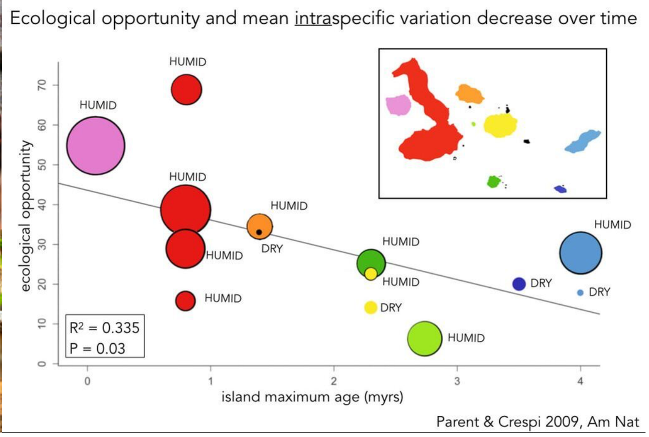
Christine E. Parent, University of Idaho

My students and I study how evolution to new environments shapes adaptation, diversification, and speciation. We approach these questions two ways:

1. We observe current patterns of biodiversity to infer past evolutionary processes.
2. We test those processes with manipulative experiments in laboratory populations.

Island systems (natural or experimental) are the focus of our research. We use many different approaches, new and old. Field observations, molecular phylogenetics and comparative analysis, and laboratory experiments. We bring these different approaches together with theoretical modeling.

My talk will introduce the work I've done over the past 20 years studying the adaptive radiation of 80 new land snail species on the Galapagos Islands. We will trace their history of movement within and between islands, and the ecological opportunities that drive their remarkable evolution.



Parent & Crespi 2009, Am Nat

[Parent Lab Website](#)

Aquaculture & Fisheries Talks – Sunday March 13

Session 1 (9:30 to 10:45)

9:30 **Analysis of Predatory Northern Sea Star Distribution and Abundance Suggests a Shift in the Benthic Community within the Bras d'Or Lake, Cape Breton Island**

Sarah T. Kromberg, BSc Student [1], Shannon Landovskis, Msc [1], Caelin Murray, Msc [1], Frederick Whoriskey, PhD [1,2]
[1] Biology Department, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
[2] The Ocean Tracking Network, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: sr972144@dal.ca

Sea stars (Asteroidea) and urchins (Echinoidea) are important but frequently neglected ecosystem components which can structure the communities in which they live either by exerting top-down pressures as predators or bottom-up controls as grazers (Schultz et al., 2016). Many sea stars are keystone species that control overall biodiversity within an ecosystem and can significantly disrupt the commercially valuable shellfish populations on which they prey (Bucci et al., 2017). The Northern Sea Star, Asterias vulgaris, is a primary subtidal predator within the western North Atlantic Ocean, however, there is currently little research on asteroids in subtidal regions (>15m depth) (Gaymer et al., 2001; Gale et al., 2015). My honours project aimed to categorize the epibenthic macrofaunal invertebrate community in the Bras d’Or Lake/Pitu’paq on Cape Breton Island/Unama'ki. Sea stars and green sea urchins dominate the benthic echinoderm fauna at the study site and are often associated and compete for space (Tremblay et al., 2005; Schultz et al., 2016). I examined the Northern Sea Star’s subtidal distribution, select behaviour patterns and co-occurrences with green sea urchins in the Bras d’Or Lake by analyzing ROV footage from 16 study transects (16-43m depth) within the East Bay region of the Bras d’Or Lake. The study tested for whether asteroids were equally likely to occur on all bottom substrate types encountered. I also examined aggregation behaviour by determining whether sea star aggregations were more often present on soft bottom substrate and, if aggregations were assembled according to size class. Finally, I compared present abundances of sea stars and urchins to historic reports of their abundances in order to estimate changes in ecosystem structure and function. I found no evidence of sea star habitat preferences, although low habitat diversity may account for this. There was evidence to suggest adult sea stars were capable of competing with green sea urchins while juvenile asteroids were not. Finally, urchin numbers were much reduced compared to historic values. The results suggest there has been a shift in benthic community structure and function in the Bras d’Or system. Changes to the benthic community structure can affect the health and resiliency of an ecosystem and sequentially, impact commercially valuable species.

9:45 **Comparing the physiology and morphology of geographically distinct sources of Blue Mussels (*Mytilus edulis*)**

Calum Blackwood, BSc Student [1], Laura Steeves, PhD Candidate [1], Ramon Filgueira, PhD [1]
[1] Biology Department, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
[2] Marine Affairs, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: cl944944@dal.ca

The Blue mussel (*Mytilus edulis*) is a widely distributed marine bivalve that is ecologically and commercially important. To predict mussel growth rates and optimize the production of mussels in spatially limited coastal regions, it is important to understand how physiological traits differ between geographically distinct sources of mussels. Mussel physiology is highly plastic, with feeding and respiration rates often changing significantly with respect to the local environment. This study was designed to compare the morphology and physiology of four groups of mussels initially collected as spat from different bays in Prince Edward Island, Canada and reared together in a common location. A common garden experimental design was used to account for plasticity, allowing for the observation of differences in physiology due to initial mussel settling location. Four mussels from each group were kept in individual flow through chambers. Key physiological traits including metabolism, pumping rate, and an indication of feeding were measured throughout the study using oximeters, particle counters and fluorometers. These physiological rates were compared between the 4 groups of mussels. The experiment was replicated 3 times, twice under laboratory conditions, and once using seawater taken directly from St. Peters Bay, PEI. This study will help determine if settling location has a lasting affect on mussel physiology and morphology. Further, quantifying differences in physiology and morphology between these groups will provide a deeper understanding of the limits of physiological plasticity, and may help to optimize mussel production.

10:00

Detection of *Haplosporidium nelsoni* in aquatic environments through passive DNA collection

Kaileigh N. Rowe, BSc Honours Student [1], Dr. Rod Beresford, PhD [2]
[1] Verschuren Centre for Sustainability, Sydney, NS, Canada B1M 1A2 [2] Biology Department, Cape Breton University, Sydney, NS, Canada B1P 6L2
Student Author Email: cbu17fmd@cbu.ca

For the past 65 years the causative agent of multinucleate sphere unknown disease (MSX), the protozoan parasite *Haplosporidium nelsoni*, has been causing mass mortalities in the eastern oyster (*Crassostrea virginica*) populations along the eastern seaboard. It was first detected in 2002 in the Bras d'Or Lake and it has been affecting the eastern oyster population in the Bras d'Or Lake since that time. Currently, the most common methods for detecting the parasite are histology and PCR through lethal sampling. This project focused on developing a non-lethal method for detecting the parasite in the environment. I attempted to passively collect *H. nelsoni* DNA by placing whiffle balls with cheese cloth inside at different depths and retrieving it for DNA extraction. Two different locations of known *H. nelsoni* activity were sampled, MacDonald's Pond and Nyanza Bay and two different extraction protocols were utilized. Samples from the whiffle balls and cheesecloth underwent DNA extraction, PCR for *H. nelsoni* detection, and were analyzed using agarose gel electrophoresis. These samples were also tested for the presence of oyster DNA to ensure the extraction protocols and PCR were uninhibited. I was unable to detect *H. nelsoni* in any of the samples; however, oyster DNA was detected in 64.6% of samples, thus this method does work for collecting DNA in this environmental setting. I will discuss the process and extraction protocols used for this project as well as recommendations that could result in the detection of Haplosporidium nelsoni in the water column.

10:15

Efficacy of *Haplosporidium nelsoni* testing protocols for the Eastern oyster (*Crassostrea virginica*)

Gracie Hanrahan, BSc Biology Honours Student [1], Rod Beresford, PhD [1]
[1] Biology, Cape Breton University, Sydney, NS, Canada, B1P 6L2
Student Author Email: cbu17fmb@cbu.ca

Haplosporidium nelsoni, more commonly known as MSX, is a protozoan parasite that has caused catastrophic oyster (*Crassostrea virginica*) losses along the mid-Atlantic coast of the United States since the 1950's. In 2002, an outbreak was first detected in Canada in the Bras d'Or Lake in Cape Breton, Nova Scotia where mortalities on oyster leases exceeded 90%. The oyster industry in the Bras d'Or Lake, Cape Breton, which previously accounted for approximately 80% of oyster production in Nova Scotia, still has yet to recover. Current detection protocols include testing gill sections for parasite presence using DNA analysis followed by confirmation of infection using histology. The presence of localized infections could be missed using standard detection protocols resulting in false negative results.

However, the testing of additional samples to detect localized infections would require more time, labour, and expenses, thus this approach would only be worth implementing if it proved more reliable (able to detect more infections) than the current protocol. This study involved using two different methods for analysis of tissues: (i) analysis of four additional samples from oysters previously tested using standard protocols, and (ii) analysis of samples from homogenized oysters. The results of this study suggest that the standard protocol does not detect all infections. A more thorough testing protocol may be a more reliable detection method for the presence of the parasite. For surveillance purposes where early detection is critical to assess and plan for disease presence and spread, analysis of additional samples may prove beneficial moving forward.

10:30 Oyster Cage Innovation: OysterGro versus BOBR Comparative Growth

Kaelin J. Barry, BSc Student [1], David Garbary, PhD [1]
[1] Aquatic Resources, St. Francis Xavier University, Antigonish, Nova Scotia, Canada B2G 2W5
Student Author Email: x2018ygz@stfx.ca

The comparison of the commonly implemented oyster cage technology to new cage models is important to the efficiency and progression of the oyster aquaculture industry. The newly developed BOBR (Benefit of Being Round) oyster cage has a dynamic shape that influences uniformity and therefore marketability of oysters. Oyster Grow is the commonly used cage technology for suspended oyster aquaculture. This study investigates the differences in volume, and morphology of oysters from each cage technology, grown over a period of four months. Qualitative analysis of biofouling on cages and respective oysters is considered in the overall comparison of technologies. Oysters from both technologies were photographed twice over the period of study. Oysters were measured using an open-source image processing package to determine growth and morphology. Continued research of these cage technologies would be beneficial in determining long-term effects of each cage on oyster morphology and biofouling.

Session 2 (11:00 to 12:15)

11:00 Transcriptome profile of Atlantic salmon (*Salmo salar*) primary macrophages response to Aeromonas salmonicida subsp. salmonicida infection.

Ignacio Vasquez, MSc Student [1], Manuel Soto-Davila, MSc [1,2], Hajarooba Gnanagobal PhD Student [1], Javier Santander, PhD [1]
[1] Marine Microbial Pathogenesis and Vaccinology Laboratory, Department of Ocean Sciences Memorial University of Newfoundland, NL, Canada, A1C 5S7 [2] Department of Biology, University of Waterloo, ON, Canada, N2L 3G1
Student Author Email: ivasquezsoli@mun.ca

A. salmonicida is one of the oldest known marine pathogens with a wide increasing host range from freshwater to marine fish species, mainly affecting salmonids, and currently emergent cultured fish species such as lumpfish, Atlantic cod, sablefish. *A. salmonicida* infection causes furunculosis, resulting in a systemic shock, organ failure and ultimately death. Understanding *A. salmonicida* infection development at early stages is critical for the disease output, including intracellular infection, immune response elusion, and propagation to lymphoid organs. Here, we performed a semi-dual RNA-seq based technology to identify relevant genes for *A. salmonicida* early infection in real-time in Atlantic salmon primary macrophages. RNA samples were taken after 1 h post-infection and 2 h post-infection, mimicking cellular attachment and intracellular infection. We identified a total of 871 differential expressed genes (DEGs) at 1 hpi and a total of 1,683 DEGs were identified at 2 hpi. Gene ontology (GO) of these DEGs during the attachment of *A. salmonicida* to the host cell showed a negative impact on the expression of genes related to cellular stimulus and biological processes, ion binding and

integral components of the membrane. In contrast, during an early infection process, expression of genes associated with cytoskeleton organization and actin polymerization, phospholipid binding, plasma membrane organization, cytokine activity, inflammatory response, wound healing, calcium transport and RNA polymerase II transcription factor activity are modulated. The enrichment of KEGG pathways showed that *A. salmonicida* hijacks pathways related to innate immune response, lipids synthesis, gene transcription, cellular transport, and apoptosis, mainly affecting cytokine-cytokine receptor interaction and protein processing endoplasmic reticulum, toll-like receptor signaling, RIG-1-like signaling, p53, and necroptosis pathways. These indicate that *A. salmonicida* induces and modulates phagocytosis and apoptosis to survive in an intracellular environment during the early stages of furunculosis.

11:15 **Characterizing the effects of stress on CBD treatment**

McKenzie Brown, MSc Student [1], Russell Easy, PhD [1]
[1] Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6
Student Author Email: 140899b@acadiau.ca

Cannabidiol (CBD) has been used for treatment of nausea, pain and migraines in cancer patients, and has shown substantial therapeutic potential for the treatment of diverse ailments. CBD is the second-most abundant bioactive constituent of *Cannabis sativa*. Many valuable pharmacological activities of *Cannabis* have been documented, including anti-inflammatory, antibiotic, anticonvulsant, anti-spasticity, antioxidant, analgesic, antiemetic, anxiolytic, antipsychotic, and neuroprotective effects. While the therapeutic potential of CBD is well supported by scientific literature, scant empirical evidence exists to validate the effects of CBD treatment. There is a dearth of research on toxicological impacts and potential adverse effects of cannabis and cannabinoid treatments. Many factors such as drug potency, dosage, individual differences, and physiological state contribute to variable treatment effects. The relative influence and effects of these factors remains largely unknown and uncharacterized. This represents a risk to public health, as there are approximately 150 million *Cannabis* users globally ¾ an estimated 9% of which will suffer from dependency. The aim of this project is to identify and characterize possible differential effects of stress on CBD treatment. Protein profiles will be constructed from epidermal mucus samples of zebrafish subjected to differential stress and CBD treatments. Novel metabolites will be identified by comparing the protein profiles of control and experimental treatment conditions. We will then use RT-qPCR to explore differential expression of genes corresponding to target proteins. The objective of this research is to explore how stress affects the apparent benefits of CBD in a vertebrate model.

11:30 **Exploring differential gene expression in Striped Bass (*Morone saxatilis*) in response to mercury contamination**

Sam Nunn, MSc Student [1], Russell Easy, PhD [1]
[1] Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6
Student Author Email: samnunn@acadiau.ca

This project aims to explore how target genes in striped bass are differentially expressed as a result of mercury contamination. Mercury is one of the most widespread, toxic, nonessential environmental contaminants on the planet. Methylmercury bioaccumulates efficiently in aquatic environments due to retention in fat and inefficient excretion. Most organisms on the planet are chronically exposed to mercury, in humans often due to fish consumption. This has resulted in fish-consumption advisories in many countries to moderate human ingestion. Striped bass are a large, anadromous fish that are important to Aboriginal, recreational and commercial fishers including roles in cultural activities. Striped bass require high quality food sources and specific conditions for egg laying, and thus they can be used as indicators of ecosystem health. We will use RT-qPCR to explore changes in expression of target genes in Striped Bass following exposure to mercury. Genes of interest include elements of the Major Histocompatibility Complex (MHC) and sequences coding for Matrix Metalloproteinases (MMPs) Amino acids corresponding to novel peptides will be identified by Mass Spectrometry. We will use this data to identify biomarkers to be used in further assays exploring the effects of mercury in striped bass.

11:45 Evaluation of the protective efficacy of an autogenous vaccine in lumpfish (*Cyclopterus lumpus*) against V. anguillarum under controlled and field conditions

Oluwatoyin B. Onireti, MSc student [1], Trung Cao, PhD Student [1], Hajarooba Gnanagobal, PhD Student [1], Joy Chukwu-Osazuwa, PhD Student [1], Ignacio Vasquez, MSc Candidate [1], Ahmed Hossain, PhD Student [1], Vimbai I. Machimbirike, PhD [1], Jennifer Monk [1], Andre Khoury, [2], Nicole O´Brian [3], Andrew Swanson [4], Danny Boyce [1], Javier Santander, PhD [1].
[1] Department of Ocean Sciences. Memorial University of Newfoundland. St. John's. Newfoundland and Labrador. Canada. A1K 3E6 [2] Vacci-Vet. Saint-Hyacinthe. Quebec [3] Government of Newfoundland and Labrador. St. John's. Newfoundland and Labrador. Canada. A1B 4J6 [4] Cooke Aquaculture. New Brunswick. Canada.
Student Author Email: oboniretí@mun.ca

Lumpfish (*Cyclopterus lumpus*) has become the predominant cleaner fish species used in North American salmon aquaculture for sea lice (e.g., *Lepeophtheirus salmonis*) biocontrol. Lumpfish utilization has contributed significantly towards eliminating the utilization of chemotherapeutants by effectively controlling the abundance of this damaging pest of Atlantic salmon (*Salmo salar*) aquaculture. *Vibrio anguillarum* is a frequent pathogen of lumpfish in Atlantic Canada. Here, several vaccine trials against *V. anguillarum* were conducted. Fish health, including effective vaccine design, and vaccination programs have been identified as a high priority. In this study, the safety and efficacy of a *V. anguillarum* autogenous vaccine were evaluated. Five treatments with three replicates were used in this study. They were PBS (negative control), in-house vaccine (positive control), autogenous IP (intraperitoneally), autogenous deep and autogenous deep, and IP boost. Length and weight were taken, gross pathology was conducted. These treatments were bath challenged with *V. anguillarum* J360 (serotype O2) after 10 weeks post-vaccination, and the survival was bath re-challenged after 9 weeks of the first challenge with *V. anguillarum* J360 (serotype O2) and *V. anguillarum* J382 (serotype O1). Tissue samples were collected for tissue colonization count. No mortality after vaccination signified that the vaccine is safe. The gross pathology score indicated a normal immune response. The in-house IP, autogenous IP, and autogenous deep and IP boost had a relative percentage survival (RPS) of 76.12%, 72.12%, and 68.75% respectively in the first challenge. The vaccine only protects against *V. anguillarum* J360 (serotype O2) but does not confer protection against *V. anguillarum* J382 (serotype O1).

12:00 Effects of an Aquaculture Fish Farm to the Sediment Geochemistry of a Naturally Anoxic Basin.

Stormy Vandeplas, MSc Student [1], Christopher, Algar, PhD [1]
[1] Oceanography, Dalhousie University, Halifax, NS, Canada
Student Author Email: st694494@dal.ca

Whycocomagh Basin is a deep, naturally anoxic basin located in the Bras d'Or Lakes, Nova Scotia.Presently a Steelhead Trout (*Oncorhynchus mykiss*) aquaculture farm leased by the Waycobah First Nation operates as an economic resource. However, hazards associated with free sulfide accumulation following anaerobic processes pose challenges to sustainable management practices for the fish farm pens. Accumulation of total dissolved free sulfide (S2-= H2S + HS- + S2-) concentrations can reach toxic levels in the bottom water and sediment, and it could impact fish in floating pens at the surface and the surrounding biogeochemical environment. Porewater chemistry, microsensor profiling, and CHN analysis of the sediment-water interface, both below and away from fish pens, were collected to assess the fish farm impacts on the sediment geochemistry and to understand the influence of the farm on the natural biogeochemical cycles.

Poster Session – Sunday March 13, 12:30 to 1:45

Biology (B01 to B15, Alphabetical)

B01 Assessing the effects of Barley, Plantago, and Red Clover photometer plants on the functioning of soil biological communities that affect plant growth.

Faith. Abel-Adegbite, BSc Student [1], Cameron. Wagg, PhD [1], Amy Parachnowitsch, PhD [1]
[1] Agriculture and Agri-food Canada and University of New Brunswick
Student Author Email: fabelade@unb.ca

This experiment used Barley (*Hordeum vulgare*), Narrow-leaf plantain (*Plantago lanceolata*) and red clover legume (*Trifolium pratense*), a grass, forb, and legume, respectively, as phytomer plants to assess the effects of the soil biotic feedback effects of the two years of the previous rotation crops. It can be challenging to identify all the soil organisms that inhibit or promote plant growth. One method is the use photometer plants; plants grown in a controlled environmental condition are used to determine the cause and effect between plants and their habitat. It has been observed that the use of photometers plants to access and influence the functioning of soil biological communities can support plant growth under different cover crop histories. The result in this study will be the first step in determining if the photometer plant under a healthy productive cover crop soils would cause an increase in successive plant growth. Additionally, if it enhance the performance of the soil by reducing crop-specific pests and promoting beneficial soil organisms.

B02 Wearable electrochemical surface enhanced Raman spectroscopy (EC-SERS) sensor used to detect biomarkers for early diagnosis of PTSD

Jaskaran Anand, BSc Student [1], Christa Brosseau, PhD [2]
[1] Department of Biology,Saint Mary's University, Halifax, Nova Scotia, Canada, B3H 3C3
[2] Department of Chemistry, Saint Mary's University, Halifax, Nova Scotia, Canada, B3H 3C3
Student Author Email: jaskaran.singh.anand@smu.ca

Early diagnosis of Post-Traumatic Stress Disorder (PTSD) is challenging. The prevalence rate of PTSD in Canada is 9.2%. cortisol is a glucocorticoid stress hormone. Experiencing stress for a longer period can lead to prolonging the release of cortisol that causes negative feedback which leads to a decrease in cortisol levels in PTSD patients. Electrochemical Surface Enhanced Raman Spectroscopy (EC-SERS) utilizes chemical enhancement of metal nanoparticles with the analyte under application of voltage which enhances the signal. EC-SERS is advantageous for detecting biological samples. Here we report developing a functional fabric sensor and using EC-SERS to detect cortisol for early diagnosis of PTSD. A blend fabric (37% silk, 35% hemp, 28% org. cotton) was used to synthesize a functional fabric sensor. the fabric sensor is made of the counter electrode, reference electrode, and working electrode. The counter electrode and working electrode are imprinted on fabric with carbon ink and the reference electrode is imprinted on fabric with silver conductive ink. The silver nanoparticle is deposited on the working electrode area. For proof-of-concept studies, a 1 mg mL-1 analytical standard of cortisol in methanol was used for these investigations. To start, 50 µL of this 1 mg mL-1 cortisol standard was deposited onto the surface of the fabric sensor and EC-SERS measurements in 0.1 M supporting electrolyte were conducted. The spectra were acquired at 785 nm excitation for 30 seconds at a laser power of 42.6 mW. Cortisol peaks were reported in 1600 to 800 cm-1 of the EC-SERS plot. Cortisol signal increased with an increase in the application of negative voltage. Quantitative analysis of signals intensity with cortisol concentration was also detected. To determine the relationship between peak intensity and analyte concentration, replicative EC-SERS studies were conducted with 50 µL, 65 µL, 75 µL, and 100 µL of 1 mg mL-1 cortisol.

B03 Conservation Genetics of the St. Lawrence Beluga Whale (*Delphinapterus leucas*)

Brianna Best, BSc Student [1], Dr. Timothy Frasier, PhD [1]
[1] Department of Biology, Frasier Lab, Saint Mary's University, Halifax, Nova Scotia, Canada, B3H 3C3

Student Author Email: brianna.best@smu.ca

Beluga whales (*Delphinapterus leucas*) first inhabited the St. Lawrence River after the ice age had ended, and when the climate warmed, the Atlantic rose. With time, the land re-emerged and the basin dried, causing a population of belugas to become stuck; unable to migrate to arctic regions. Decades after a ban on the hunting of the beluga whale, the lack of recovery noticed in the St. Lawrence Estuary (SLE) population has puzzled researchers in the field of population and conservation genetics. The St. Lawrence River has been known for its industrialization, as well as its large amounts of vessel traffic, contributing to entanglements, as well as pollution to the river and its inhabitants. The current population of belugas inhabiting the SLE are ~1000 or less, and declining, which is concerning because the species as a whole are endangered. This research project focuses on the threat of inbreeding and low genetic diversity on the small, isolated population of the SLE beluga. In order to estimate the degree of inbreeding, as well as the loss of genetic diversity within the SLE beluga population, Arctic samples from Nunavik were genotyped using multiplex PCR and capillary electrophoresis for the creation of microsatellite profiles for each individual to be scored with GeneMarker v.2.7.4. The microsatellite profiles of the Nunavik individuals will then be compared with the SLE beluga data that have already been genotyped in order to gain insight into the genetic constraints of the SLE beluga population. The effective population size (Ne) will also be estimated for each population using the COLONY program in order to determine how many individuals are truly contributing their alleles to further generations.

B04 Sex differences in oxygen consumption in Japanese medaka (*Oryzias latipes*)

Brian R. Conrad, BSc Student [1], Laura K. Weir, PhD [1]
[1] Department of Biology, Saint Mary's University, Halifax, Nova Scotia, Canada B3H 3C3
Student Author Email: Brian.Conrad@smu.ca

A defining characteristic in sexual dimorphism is that there are morphological differences between the sexes in an animal species. Sexual dimorphism usually acts on the males of a species in order for them to stand out as good mates for females. In Japanese medaka (*Oryzias latipes*), sexual dimorphism can be observed in the larger size of male anal fins, which aids in reproduction, and larger body size in females which results in increased fecundity. Larger body size in males is attributed to greater mating success compared to smaller body size males. I examined the rates of oxygen consumption between the sexes in order to determine whether increased body size or anal fin size contributed to differing oxygen consumption. Each trial included a single medaka placed into a container with water, and the percent oxygen saturation of the container in mg O_2/L was measured for 30 minutes. Increasing weight had a weak positive correlation to increasing oxygen consumption, and males had a higher average weight than females (0.168g vs. 0.159g). Females tended to consume more oxygen than males during the trials, suggesting that physiological differences are responsible for the difference in oxygen consumption between the sexes.

B05 Genetic and phenotypic variation of Atlantic salmon young-of-the-year (*Salmo salar*) in the Upper Salmon River, NB, Canada

Emilie Diesbourg, BSc Student [1], Kurt, Samways, PhD [2], Cassidy D'Aloia, PhD [3]
[1] Department of Biological Sciences, University of New Brunswick, Saint John, NB, Canada, E2L 4L5 [2] Department of Biological Sciences and the Canadian Rivers Institute, University of New Brunswick, Saint John, NB, Canada, E2L 4L5 [3] Department of Biology, University of Toronto Mississauga, ON, Canada, L5L 1C6
Student Author Email: ediesbou@unb.ca

Determining the spatial scale at which genetic structuring occurs is one of the main goals of conservation genetics because such data can help identify management units. This study assessed the hierarchical genetic structure of Atlantic salmon young-of-the-year in the Upper Salmon River, NB at a fine spatial scale (~12km). Using seven microsatellite loci, genetic clustering analyses and FST estimates were computed to determine the strength of genetic structure within the river. Observed patterns of genetic structure were then tested to see whether they aligned with previously identified morphological groupings, from the same salmon individuals. Subtle genetic differentiation and a weak isolation by distance pattern was found to exist within this 12km stretch of river (r2=0.044, $P < 0.01$). Additionally, not all genetic groupings corresponded to the morphological groupings. This study highlights the importance of considering within-river genetic structure across small spatial scales for more informed conservation design.

B06 Concentration of potential microplastics in soft-shell clams (*Mya arenaria*) is size dependent

Amanda R. Fenech, BSc Student [1], Krista Beardy, MSc Candidate [1], Heather Hunt, PhD [1]
[1] Department of Biological Sciences, University of New Brunswick, Saint John, New Brunswick, Canada, E2K 5E2
Student Author Email: afenech@unb.ca

Microplastics (MP) are a widespread pollutant in the marine environment. These contaminants are found in benthic organisms, including the soft-shelled clam (*Mya arenaria*), an ecologically and economically important filter-feeding bivalve. This study aimed to quantify the relationship between concentration of potential MP and clam size (mm and mean tissue weight). Since filtration rates are thought to effect MP ingestion in bivalves, it is hypothesized that smaller individuals will possess a higher concentration of MP per gram of soft tissue due to their greater filtration rate. We also examined whether MP type was independent of juvenile size. Juvenile and adult M. arenaria were collected from Kouchibouguac, NB and digested in KOH to extract potential MP, which were identified under a dissecting microscope. Potential MP concentration had a significant non-linear relationship to M. arenaria size, with the highest concentrations (per g of soft tissue) in small juveniles. Potential MP type was independent of juvenile size. 90% of potential MPs identified in this study were fibers and their concentration shared the same non-linear relationship to size (mm) as total potential MPs. Our results suggest that juvenile *M. arenaria* may be more vulnerable to any negative effects of MP ingestion than larger individuals.

B07 Bioaccumulation of contaminants in amphibians in historical gold mining areas of Nova Scotia.

Lauren Gaudet, BSc Student [1], Catlin J. Bradbury BSc [2], Donald F. McAlpine, PhD [3], Dr. Linda M. Campbell, PhD [2]
[1] Department of Biology, and [2] Department of Environmental Science, Saint Mary's University, Halifax, Nova Scotia, Canada, B3H 3C3. [3] New Brunswick Museum of Natural History, Saint John, Canada, NB E2K 1E5
Student Author Email: lauren.g799@gmail.com

Nova Scotia has a long history of gold mining that dates back to the mid-1800's. Early mining techniques that used liquid mercury, along with little or no environmental regulations at the time, resulted in over 3 000 000 tonnes of mine waste (tailings) being released into the environment. These tailings can contain high concentrations of the toxic chemicals mercury (Hg) and arsenic (As). These chemicals have negative effects on the environment, as well as on the animals living in the area. Frogs are often used as indicators of environmental conditions as they have thin, permeable skin and live a semi-aquatic lifestyle. These factors can contribute to the bioaccumulation of toxins in frog tissues. This study looks at bioaccumulation in frogs collected in 6 historical gold mining wetland sites in Nova Scotia and compares these to frogs collected at one reference site. Dried, ground, frog leg tissues were analyzed for mercury content using a Milestone DMA 80 machine. The hypothesis that the concentration of Hg found in the frog leg tissues will reflect the level of contaminants seen in their original environment is tested. This project, as part of the legacy gold mine contaminants research lead by the Dynamic Environment and Ecosystems Health Research (DEEHR) team at St. Mary's University, will enhance our understanding of the impact of historical human activity on aquatic ecosystems.

B08 Effect of hematophagous parasites on nestling condition in European starlings (*Sturnus vulgaris*)

Seth Gaudet, BSc Student [1], Colleen Barber, PhD [1]
[1] Department of Biology, Saint Mary's University, Halifax, Nova Scotia, Canada B3H C3C
Student Author Email: sjgaudet@hotmail.ca

Nest-dwelling ectoparasites are commonplace among cavity nesting birds such as the European starling (*Sturnus vulgaris*), and have been shown to be a detriment to the health of nestlings. To determine if this was the case for *Sturnus vulgaris* as well, parasite load and signs of parasites such as blood spots found on eggs of multiple nests were compared to the average nestling condition of each nest. Nests were divided by early and later broods to determine if time of breeding played a role in parasite load. There was significantly more parasites found in the later broods than in early broods, possibly from the colder climate at the start of the summer. Egg spots were found to be positively correlated with parasite load. The effect of parasite load on nestling condition was found to not be significant.

B09 The effect of deuterium-depleted water and glucose deprivation on the fitness of circulating tumour cell clusters

Indhu Iyengar, BSc Student [1], Aurora M. Nedelcu, PhD [1]
[1] Biology Department, University of New Brunswick, Fredericton, NB, Canada, E3B 5A3
Student Author Email: ilyengar@unb.ca

Cancer is the second cause of death around the world. Most cancer deaths are due to the ability of tumours cells to enter the circulatory system and disseminate throughout the body – a process known as metastasis. The main players in this process are the so-called circulating tumours cells (CTCs) that can exist as either single cells or cell clusters, with the latter being responsible for the majority of secondary tumours. Nevertheless, despite the fact that CTCs generally have an increased resistance to chemotherapies relative to tumours cells, there are no therapies that specifically focus on decreasing their fitness. In addition, most frequently used chemotherapy drugs (such as cisplatin) have severe negative side effects that limit their potential success. Recently, less toxic strategies such as glucose deprivation and the consumption of deuterium-depleted water (DDW) have been shown to reduce tumour growth, but their effects on CTC clusters have not been addressed. In this project, I used a lung cancer cell line that grows as clusters in suspension – as an in vitro model-system for CTC clusters, and investigated the effectiveness of deuterium depletion alone and in combination with glucose deprivation and chemotherapy on both cell proliferation and cell viability. I found that at physiological glucose levels, a combination of DDW and cisplatin decreased cell proliferation at concentrations that neither of them individually had an effect. Furthermore, glucose deprivation increased the effect of both DDW and cisplatin alone as well as in combination. My data also showed that DDW and glucose deprivation could be as effective as cisplatin at decreasing the fitness of CTC clusters. Overall, this study argues that alternative therapies – either alone or in combination with chemotherapy, could improve the outcome of current treatments and reduce the negative impact on patients.

B10 Colder temperatures alter decomposition patterns and insect succession on animal carcasses

Chloé Losier, BSc Student [1], Denis R. Boudreau, MSc Student [1], Kathleen LeBlanc, BSc, Jean-Philippe Michaud, PhD, Gaétan Moreau PhD [1]
[1] Département de Biologie, Université de Moncton, Moncton, Nouveau-Brunswick, Canada E1A 3E9
Student Author Email: ecl4682@umoncton.ca

The decomposition of large vertebrate carcasses is the result of a series of complex processes that are considerably influenced by ambient temperature. Thus, cold temperatures can slow and even stop decomposition by limiting tissue autolysis, bacterial decomposition, and insect activity contributing to necromass removal. In this study, we tested the hypothesis that the constraints imposed by cold temperatures on insect colonization will alter interspecific interactions among insects of forensic interest, thereby disrupting their ecological succession on carcasses as well as their functions. To test this hypothesis, a comparative analysis of insect activity on domestic pig carcasses in summer and fall was conducted. The results showed that at our latitudes, carcass decomposition is significantly slower in the fall than in the summer during the most advanced stages of decomposition and can sometimes be incomplete. In addition, the arrival, presence, and departure from carcasses of insects of forensic interest differed between summer and fall. While some insects were seldom documented on carcasses in the fall (e.g., beetles of the family Histeridae and Oiceoptoma noveboracense of the family Silphidae), others increased in abundance during the same season (e.g., Diptera of the genus *Calliphora* and the beetle *Necrodes surinamensis*). All of this supported our hypothesis and indicated that in cold weather conditions such as those found in New Brunswick, the ecological succession patterns of insects developed in summer studies have little forensic utility for cadavers found in the fall.

B11 Inferring the level of mixotrophy and endosymbiotic success through radular wear in a hydrothermal vent snail

Keshia Noseworthy, BSc student [1], Nova Hanson, PhD student [1, 2], Amanda Bates, PhD [2, 3], Suzanne Dufour, PhD [1]
[1] Department of Biology, Memorial University of Newfoundland, St. John's, NL, Canada A1C5S7 [2] Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL, Canada A1C5S7 [3] Department of Biology, University of Victoria, Victoria, BC, Canada V8P5C2
Student Author Email: keshian@mun.ca

Hydrothermal vent ecosystems are some of the harshest environments on Earth. Regardless, they tend to exhibit a high biomass, supporting vast invertebrate communities. Hydrothermal fluid consists of dissolved metals and minerals that provide ample opportunity for chemoautotrophic bacteria to produce energy, forming the base of these productive ecosystems. Many species form endosymbiotic relationships to support life in these environments. *Alviniconcha* snails host chemoautotrophic bacteria in their gills, forming a complex symbiotic relationship. These gastropods are present in multiple hydrothermal vent locations, including the Mariana Back-Arc Basin. Within this basin, there is an environmental gradient with differences in fluid chemistries such as pH, temperature, and hydrogen sulfide concentrations, which decrease in intensity from North to South. Little is known about how reliant *Alviniconcha* snails are on their endosymbionts, considering they retain the ancestral feeding structure of gastropods, an extendable ribbon of teeth called the radula. Here, I examine the radular wear of *A. hessleri* from four different hydrothermal vent sites in the Mariana Back-Arc Basin to determine the level of mixotrophy this species shows and how this might change with fluid chemistry, and thus the success of the symbiosis. Radulae from four sites were dissected out and tissue was removed by digestion using proteinase K. The tissue-free ribbons were then air dried, sputter coated with gold and visualized with an SEM. The percent wear of teeth in each specimen was measured by tracing the area of worn and unworn teeth with ImageJ and calculating the difference in area. Preliminary results suggest that *A. hessleri* exhibits mixotrophy, indicated by obvious wear on the radular teeth of all specimens examined. The degree of wear varied across sites, and between individuals, with those collected at a vent between the Northernmost and Southernmost sites exhibiting significantly more wear than all other sites ($P<0.0001$). This result may indicate that feeding relies less on symbioses, and thus fluid chemistries, than originally thought. Further, this suggests that site-specific differences may be due to competition, local food availability, or the biotic composition of the community.

B12 Assessing the Effects of Whaling on the Genetic diversity of North Atlantic Blue Whales (*Balaenoptera musculus*)

Erin Stacey, BSc Student [1], Dr. Timothy Frasier, PhD [1]
[1] Department of Biology, Frasier Lab, Saint Mary's University, Halifax, Nova Scotia, Canada, B3H 3C3

Student Author Email: erinstacey1999@gmail.com

Industrial whaling in the early to mid 20th century severely depleted the population of blue whales in the North Atlantic. Due to this reduction in population it is likely that the current population of blue whales in the North Atlantic have low genetic diversity. Low genetic diversity limits the ability of a species to withstand threats such as disease. Blue whales are an essential part of the oceans ecosystem and are currently considered endangered. Our research looks to assess the levels of genetic diversity amongst the contemporary North Atlantic blue whale population compared with the ancient pre-whaling population. The ancient samples were collected by archaeologists from ancient viking sites found in Iceland. The contemporary samples were collected from various blue whale carcasses that had washed ashore. The mitochondrial DNA of the samples were extracted using phenol: chloroform DNA extraction method and will undergo amplification and sequencing PCR. The ancient samples have already had the DNA extracted, amplified and sequenced and are undergoing analysis. From our preliminary results we expect that the contemporary samples will have lower values of genetic diversity compared to the ancient samples.

B13 Why Plants Lie: Modelling Pollinator Deception

Jemma M. Todoschuk, BSc Student [1], Stevan A. Springer, PhD [1]
[1] Department of Biology. University of Prince Edward Island. Charlottetown. Prince Edward Island. Canada C1A 4P3
Student Author Email: jmtodoschuk@upei.ca

When you can't move, sex can be a challenge. Sexual plants depend on pollinators to move pollen between flowers for them. To encourage pollinators to visit similar flowers, plants provide rewards (such as nectar or pollen). These incentives benefit the pollinator and cost the plant. Some plants have evolved deceptive rewards that increase pollinator preference but are not costly to the plant and not valuable to the pollinator. We simulated plant-pollinator interactions to model how pollinators respond when plants provide deceptive rewards. Our model follows a population of plants and their pollinators. Pollinators visit plants and receive nectar based on compatibility. When plant and pollinator match, plants give a large nectar donation and vice versa. Large nectar donations increase the chance that a pollinator will visit a similar plant in the future. Pollinators have more offspring when they receive more nectar. Plants have more offspring when their pollinators visit similar plants. We modelled a deceptive trait that allows plants to manipulate pollinator behaviour, increasing visitation without rewarding the pollinator. The dynamics of this model suggest that there are four extremes of plant-pollinator interaction across two trait dimensions: plant honesty and plant-pollinator match. 1) Pollinators evolve to match honest plants. 2) Honest plants respond by becoming deceptive. 3) Pollinators evolve to avoid deceptive plants. 4) Plants re-evolve honest rewards. If plant influence depends on the size of the reward, then the model can cycle between these four states. Plants also often maintain polymorphism in the deceptive trait, and natural surveys also show that deceptive plants are more phenotypically variable than honest ones. Our model helps us move toward a full-circle understanding of how honesty and dishonesty shape plant-pollinator interactions.

B14 A Comparative Analysis Of Striated Muscles In Non-Bilaterian And Bilaterian Animals

Marco B. Turner. BSc Student [1], Nicanor Gonzalez-Morales, PhD [1], Roger P. Croll, PhD [2]
[1] Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4J1. [2] Department of Physiology. Dalhousie University, Halifax, Nova Scotia, Canada B3H 4H7.
Student Author Email: marco.turner@dal.ca

Evidence of striated muscles has been documented in both bilaterian and non-bilaterian animals. Striated muscles have been documented within both ctenophores and cnidarians, which are the two phyla of non-bilaterian animals with defined muscle systems. Prior work has found that ctenophores and cnidarians lack relevant orthologs for some of the key proteins that make up striated muscles. Considering that these proteins are conserved throughout the rest of the animal kingdom, this observed phenomenon brings forth the potential for striated muscles to have evolved separately, once in Bilateria and once in ctenophores and cnidarians. The broader goal of this study is to support this theory and contribute to the ongoing discussion pertaining to the evolution of striated muscles. To achieve this, there are two major methodologies that were employed. The first is to perform dissections and document the presence of striated muscles within ctenophores available off the coast of Nova Scotia (*Pleurobrachia pileus*). This was done by staining the samples with phalloidin, which binds to actin and allows for a clear view of the striations under fluorescence microscopy. The second methodology is to repeat the bioinformatics work surrounding the relevant orthologs across more species of ctenophores, as the preliminary work was only done for a single species of ctenophore. This was done using the available genomic data across 29 species of ctenophores, along with several bilaterian and cnidarian controls. The preliminary results of this work indicated that *P. pileus* does not have striated muscles, although the work has provided a foundational understanding of the muscle systems within the animal. It has also been determined that ctenophores and cnidarians are missing several orthologs related to Z-disc proteins, some of which are documented to be crucial to muscle structure and function within Bilateria. Future work for this project involves sampling other species of ctenophores or cnidarians and following similar dissection and staining techniques, with the goal of identifying striated muscles within other species. Overall, the results of this study were unable to definitively support the prior theory of convergent evolution, however, this work adds to the ongoing discussion.

B15 Characterization and phylogenetic placement of a novel groove-bearing flagellate

Liz J. Weston, BSc Student [1], Alastair G. B. Simpson, PhD [1]
[1] Biology Department, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4R2
Student Author Email: Liz.Weston@dal.ca

The majority of described eukaryotes are macroscopic organisms from the kingdoms Plantae, Animalia, and Fungi; however, single-celled protists represent the bulk of eukaryotic diversity. To improve the resolution and utility of the Eukaryotic Tree of Life, more cell morphological and molecular data for undescribed, deep-branching protists are needed. Soap-colp (SC) is an undescribed flagellate with a conspicuous ventral groove, a trait observed in distantly related lineages across the breadth of eukaryote diversity. Preliminary 18S rDNA phylogenies weakly suggest that SC may be a deep branching stramenopile. Together, this implies that SC may be of outsize importance for understanding aspects of early eukaryotic evolution, including the cellular characteristics of the Last Eukaryotic Common Ancestor (LECA). In this study, a dieukaryotic culture containing SC and the haptophyte alga Isochrysis galbana was established using single-cell isolation. The prey range of SC was explored using 8 other species of marine algae in triplicate cultures with SC abundance measured at 10-day intervals. SC growth plateaued at low abundance after 20 days in 6 out of 8 prey trials. By contrast, after 30 days, SC that fed on the diatom Phaeodactylum tricornutum grew to an abundance (2.0 x104 cells/mL) similar to controls fed with I. galbana (2.8 x104 cells/mL), while SC that fed on the cryptophyte Guillardia theta grew to a much greater abundance (1.2 x105 cells/mL). Preliminary electron microscopy indicates that SC possesses tubular mitochondrial cristae and flagellar hairs on one flagellum, consistent with stramenopile phylogenetic affinities. Additional 18S rDNA analyses will be reported that focus on improved taxon sampling and limiting potential long branch attraction. Nuclear genome sequence data are available for G. theta and P. tricornutum, thus, cultivation of SC on either of these prey species will facilitate future transcriptome or genome sequencing to better infer the placement of SC using multigene phylogenetics.

Aquaculture and Fisheries (A01 – A05, Alphabetical)

A01 Isolation and characterization of outer membrane vesicles from Moritella viscosa and protection induced in lumpfish (*Cyclopterus lumpus*).

Trung Cao, PhD Student [1], Ignacio Vasquez MSc Student [1], Hajarooba Gnanagobal PhD Student [1], My Dang MSc Student [1], Setu Chakraborty PhD Student [1], Ahmed Hossain PhD Student [1], Danny Boyce [2], Javier Santander, PhD [1]
[1] Marine Microbial Pathogenesis and Vaccinology Laboratory, Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL, Canada; [2] The Dr. Joe Brown Aquatic Research Building (JBARB). Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, NL, Canada A1K 3E6; Email: ttcao@mun.ca; jsantander@mun.ca.
Student Author Email: ttcao@mun.ca

Outer membrane vesicles (OMVs) are nano-sized proteoliposomes shed from the cell envelope of all Gram-negative species. OMVs are now recognized as a generalized secretion pathway that provides a means to transfer cargo to other bacterial cells and eukaryotic cells. OMVs play an important role in pathogenesis, delivering virulence factors to the host cells, including toxins, adhesins, and immunomodulatory molecules. *Moritella viscosa* is a Gram-negative pathogen and the causative agent of winter ulcer disease in several marine fish species. *M. viscosa* OMVs have not been characterized and their role in the infection process and utilization as potenitial vaccine is unknown. Here, we develop a *M. viscosa* infection model in lumpfish, characterized the *M. viscosa* OMVs, and evalaue its toxicity and immunogenicity in vivo lumpfish model. We determined that lethal dose (LD50) of *M. viscosa* in lumpfish was 8.1 x107 CFUfish-1. Lumpfish intraperitoneally (i.p.) injected with 3.1 x 107 colony-forming units (CFU) fish-1 showed a rapid mortality and typical clinical signs of winter ulcer disease after 5 days post-infection. Iron is an essential nutrient for microbes that influence pathogenesis. To characterize *M. viscosa* OMVs the bacteria strains was cultivated under iron-rich and iron-limited conditions. *M. viscosa* purified OMVs were characterized by transmission electron microscopy and protein analysis. *M. viscosa* OMVs in both growing conditions showed spheres of 39.8–370 nm diameter that contains RNA and DNA. The most abundant proteins in *M. viscosa* OMVs have a molecular size of 45, 30 and 20 kDa. OMVs isolated from iron-limited condition harbor an additional protein of approximately 60 kDa which is absent in OMVs isolate from bacteria grown under iron-rich conditions. Protein identification analyses of the 60 kDa protein band indicated the presence of enzyme of Metal-dependent carboxypeptidase, Glucose-6-phosphate isomerase, Glucose-6-phosphate isomerase, and transport systems including the peptide ABC transporter, extracellular solute-binding protein, and oligopeptide transport system, and permease protein B. The results provide strongly that *M. viscosa* could induce the ulcer disease in lumpfish. *M. viscosa* OMVs contain various bacterial components, including proteins, DNA/RNA, and did not show toxicity in lumpfish. These OMVs products may partially explain the play an important roles in the pathogenesis of *M. viscosa*.

A02 Comparative Genomics Analysis of a Novel Strain Isolated from Winter Ulcer Disease in Atlantic Salmon

Maryam Ghasemieshkaftaki, MSc Student [1], Ignacio. Vasquez, MSc Student [1], Trung. Cao, PhD Student [1], Ahmed. Hossain, PhD Student [1], Vimbai I. Machimbirike, PhD [1], Anthony K. Gamperl, PhD [1], Javier. Santander, PhD [1]
[1] Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, Newfoundland and Labrador, Canada A1C 5S7
Student Author Email: mghasemieshk@mun.ca

Winter ulcer disease (WUD) is a recalcitrant issue in the salmon farming industry, usually caused by *Moritella viscosa*. Although different types of polyvalent vaccines are used against this pathogen, WUD outbreaks are continuously reported in Atlantic Canada. Currently, it is unknown whether undescribed bacterial pathogens are also causing WUD in vaccinated farmed Atlantic salmon (*Salmo salar*), or the effectiveness of current vaccines is not sufficient. In this study, we described the phenotype and genomic characteristics of *Vibrio* sp J383 strain isolated from internal organs of Atlantic salmon displaying clinical signs of WUD. Infection assays conducted in vaccinated Atlantic salmon revealed that Vibrio sp J383 can cause low mortalities when is intraperitoneally administered in high concentration (107 - 108 CFU/dose). *Vibrio* sp J383 persisted in the blood of infected fish at 10 and 12°C, clinical signs increased at 12°C, and no mortality and bacteremia were observed at 16°C. *Vibrio* sp J383 genome is composed of two chromosomes with a total genome size of ~5.9 Mb with ~3.6 Mb and ~2.0 Mb in chromosomes one and two, respectively. Phylogenetic and comparative analyses indicated that *Vibrio* sp J383 is closely related to *Vibrio splendidus*, with 93% identity. However, phenotypic studies showed significant differences between them. For instance, the optimal growing temperature for most of the *Vibrio* species is 28°C. In contrast, *Vibrio* sp J383 does not grow well at 28°C and displays an optimal growth between 15-18°C and substantial growth at 4°C. Also, Vibrio sp J383 displays hemolytic activity and siderophore synthesis at 15°C. Our finding suggests that *Vibrio* sp J383 could be a pathogen associated with WUD-like events in Atlantic Canada that may be adapted to cold temperatures and its distinctive characteristics compared to other *Vibrio* species suggest a novel species. Keywords: Winter ulcer disease, *Moritella viscosa*, *Vibrio* sp J383, genomic.

A03 Plastic Effects of Thermal Variability on Body Shape in Zebrafish (*Danio rerio*)

Annie Grigg BSc Student [1], Melanie Massey PhD Student [1], Talia Lowi-Merri PhD Student [1], Jeffrey Hutchings PhD [1], Paul Bentzen, PhD [1]
[1] Biology Department, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: an304114@dal.ca

Changing climatic conditions have profound impacts on ectothermic organisms. In particular, human-driven climate change is predicted to increase the amplitude of thermal variation over the coming decades which could vastly alter the thermal landscape for many species. Despite this knowledge, little research has been performed to examine the responses fish may have to thermal variability. In the present study, using zebrafish (*Danio rerio*) as a model organism, we applied morphometric analyses to examine how diel thermal fluctuations impact adult body shape and condition. To explore plastic morphological changes, we exposed zebrafish to diel thermal fluctuations during early ontogeny (days 0-30), late ontogeny (days 31-210), or a combination of both. Thermal fluctuations spanned the species' viable developmental range (22 - 32 °C). We found that body shape, size, and condition were affected, especially by the late ontogenetic fluctuating treatment. Specifically, fish that experienced wider thermal fluctuations in late ontogeny presented shorter body lengths and poorer body condition . Our data suggest that there are non-trivial energetic costs associated with the necessary internal regulation of bodily functions as a result of variable temperatures.

The present study provides insight into the environmentally-driven processes that create morphological consequences in zebrafish. Our findings may be generally illustrative of morphological changes in wild populations of freshwater fish in the coming years.

In-situ validation of lobster embryo hatch time based on presence and abundance of stage I larvae

A04

Jonathan A. Kubelka, BSc Student [1], Lydia White, MSc [1], Rémy Rochette, PhD [1]
[1] Department of Biological Sciences, University of New Brunswick Saint John, Saint John, NB, Canada, E2L 4L5
Student Author Email: Jonathan.Kubelka@unb.ca

Hatch time of American lobster is important to the dispersal and settlement success of lobster larvae, as it impacts the prey, temperature, and current conditions they encounter. In Canada, hatch mostly occurs during summer months, when fishing is closed, preventing its monitoring with the fishery. Two functions have been developed in the lab to model the relationship between water temperature and embryo development and hatch, a linear and a power function. However, little has been done to validate these functions in nature. In this study, the hatch of 2000 lobster embryos sampled in southwestern Bay of Fundy in June 2021 was predicted using both of these functions, and different assumptions concerning the movement of ovigerous lobsters and associated small differences in the temperature their embryos experienced. These predictions were compared to the hatch period observed in situ based on the presence and abundance of stage I lobster larvae in plankton tows. Hatch predictions generally aligned well with the observed hatch period, particularly those made using the power function of embryo development. This function predicted up to 87.50% of the 64-day hatch period and had up to 99.45% of its hatch predictions fall in this observed hatch period, compared to 87.50% and 71.80% for the linear function, respectively. Furthermore, inter-sample variation in hatch numbers predicted by the power functions was significantly related to the observed variation in abundance of stage I larvae in plankton tows, which was not true of the linear function. The results of this study support the use of models constructed using the power function in conjunction with lobster embryo sampling within the fishing season to predict hatch of lobster embryos in southwest Bay of Fundy. Additional validation efforts should be performed to assess the efficacy of these functions at predicting lobster hatch in different years.

A05 Human impacts on coral and macroalgal benthic cover among sites in the Mesoamerican reef, Northwestern Caribbean Sea

Caelin Randall-Scott, BSc Student [1], Heike Lotze, PhD [1]
[1] Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2
Student Author Email: cl861623@dal.ca

Coral reefs are diverse ecosystems that provide a multitude of social and economic benefits to human societies. A healthy reef ecosystem can be measured by the ratio of coral:macroalgal cover, with greater coral cover indicating a healthier reef. Human activities have been a major factor in the loss of over 50% of the world's reefs since 1980. The Bay Islands National Marine Park (BINMP) of Honduras in the Caribbean is experiencing intense human pressures, specifically from tourism. My research aimed to (i) determine the coral:macroalgae ratio and species composition among 23 study sites in the BINMP, (ii) quantify the level of human impacts at each site, and (iii) link coral:macroalgae ratio and species composition to the level of human impacts among study sites. Underwater photographs taken by SCUBA diving along six 30-meter transects at each study site in Roatan (n=21) and Cayos Cochinos (n=2) were used to estimate the % cover of coral and macroalgae in each photograph and determine the coral:macroalgae ratio for each site. Nested analysis of variance was performed to test whether coral cover or coral:macroalgae ratio differed across study sites within 5 regions (North, South, East, West, Offshore). A cumulative impacts model was created to quantify the level of human impacts related to tourism at each site. Regression analyses were used to determine the relationship between cumulative and individual human impacts, respectively, and each of the coral:macroalgae ratio, coral cover, species richness, diversity, and evenness, across study sites. Preliminary results suggest that human impacts are indicative of reef health, with lower reef health (i.e., less coral cover, more macroalgae) at sites with greater levels of impact. Further analyses will reveal which impacts (individual or cumulative) have the most influence on the coral:macroalgae trade-off and species composition in the studied area, which can inform management and conservation.