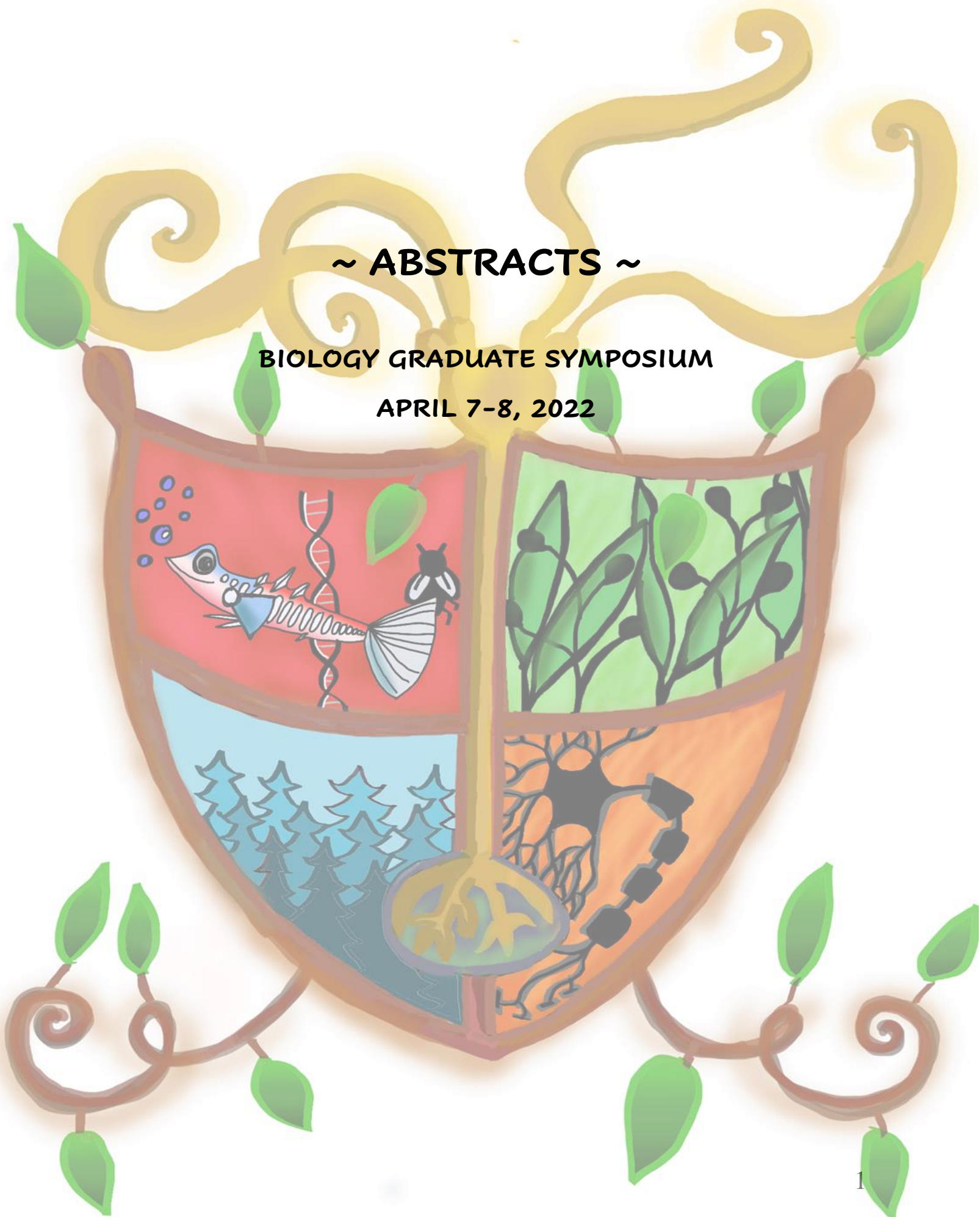


~ ABSTRACTS ~

BIOLOGY GRADUATE SYMPOSIUM

APRIL 7-8, 2022



INDEX

April 7, 2022

Session 1: Neuroscience, Cell, and Molecular Biology (9:00-9:50)

RUIZ DE CHAVEZ GINZO, Alberto	4
HANSON, Laura.....	5
YOUNG, Penelope	6
RAVI CHANDLER, Prathyusha.....	7

Session 2: Neuroscience, Cell, and Molecular Biology (10:45 – 11:50)

MOKARIASL, Niloufar	8
HIRABAYASHI, Kaede	9
DeROSENROLL, Geoffrey.....	10
BARNES, Hayley	11
ATHAR, Faria.....	12

Session 3: Forest Biology (1:05-2:10)

GORDON, Harley.....	13
NEHRING, Lise	14
LANE, Sarah	15
LIU, Yalin	16
PIIRTOLA, Eerik	17

Session 4: Ecology and Evolution (2:40-3:15)

MAY, Emily.....	18
LAWTON, Maggie.....	19
ELLIS, Sarah.....	20

April 8, 2022

Session 5: Marine Biology (9:00 – 9:50)

WYATT, Shea	21
KOLATKOVA, Viktorie	22
CRAWFORD, Rebecca	23
DAVIES, Hailey	24

Session 6: Marine Biology (10:45 – 11:50)

WRIGHT-LaFRECA, Marissa	25
BLACK, Morgan	26
CSORDAS, Matthew	27
REIDY, Rhonda	28

Session 7: Marine Biology (12:50 – 2:10)

BUZZONI, Daisy	29
LIVINGSTON, Michael	30
WOODS, Mackenzie	31
MURCHY, Kelsie	32
HEIMRICH, Annika	33

Session 8: Marine Biology (2:30 – 3:50)

INNES, Kathleen	34
CHALIFOUR, Lia	35
GAFFNEY, Leigh	36
QUALLEY, Jessica	37
QUINDAZZI, Micah	38

Acknowledgments	39
-----------------------	----

Author: Ruiz de Chavez Ginzo, Alberto

Degree Sought: MSc

Supervisor: Dr. Bob Chow

Category: Neuroscience, Cell and Molecular biology

The mechanisms underlying retinal bipolar cell subtype differentiation

Cell fate determination in the central nervous system is a highly regulated process in which dividing multipotent progenitor cells give rise to post-mitotic neurons. While much is known about how general neuronal classes are formed, little is known about the mechanism behind the differentiation of specific neuronal subtypes that comprise distinct neuronal classes. Bipolar cells are retinal interneurons that convey information from photoreceptors to retinal ganglion cells during visual processing. Fifteen bipolar cell subtypes have been identified but the mechanisms mediating their differentiation remain poorly understood. We hypothesize that bipolar cells are born as undifferentiated intermediate cells and that distinct subtypes require non-cell autonomous interactions in order to differentiate into distinct subtypes. To address this hypothesis and to gain mechanistic insight into how bipolar cell subtypes are generated, we have developed an in vitro retinal dissociation approach. This approach uses two transgenic mouse reporter alleles as well as immunolabeling that allow us to distinguish between the major subgroups of bipolar cells, such as rod versus cone and ON versus OFF. Our preliminary data demonstrates that this approach allows for robust survival of bipolar cell subtypes from postnatal mouse retinas during the time period in which they are generated in vivo. Using 5-ethynyl-2'-deoxyuridine (EdU) to metabolically label retinal progenitor cells, we are determining the role of cell autonomous and non-cell autonomous mechanisms underlying bipolar cell subtype development with the ultimate objective of identifying the molecular mechanism.

Author: Hanson, Laura

Degree Sought: PhD

Supervisor: Dr. Gautam Awatramani

Category: Neuroscience

Orientation-selectivity in the direction-selective ganglion cells

Retinal ganglion cells split the visual information into many parallel channels, each conveying different features of the visual scene to higher order visual areas for further processing. Two prominent features detected in the retina are direction selectivity and orientation selectivity which are predominantly thought to be encoded by separate populations of ganglion cells, the direction-selective ganglion cells (DSGCs) and the orientation-selective ganglion cells (OSGCs), respectively. This contrasts with what has been observed in the visual cortex where all direction-selective cells are also orientation-selective. Using a combination of electrophysiology and 2-photon imaging we show that a population of ON-OFF direction-selective ganglion cells are also strongly orientation-selective, matching that seen in the visual cortex. We further show that this orientation selectivity arises from gap-junction mediated asymmetric spatial integration in the type 5a bipolar cells. These findings show that ON-OFF DSGCs utilize separate mechanisms to generate different feature selectivity, with starburst amacrine cells mediating DS and bipolar cells mediating OS and uncover a new role for electrical coupling in the retina.

Author: Young, Penelope

Degree Sought: MSc

Supervisor: Dr. Raad Nashmi

Category: Neuroscience

Investigating the role of the medial and lateral substantia nigra pars compacta in modulating voluntary movement

The substantia nigra pars compacta (SNc) is a population of dopaminergic (dopamine-producing) neurons (DANs) located in the midbrain that is a critical regulator of goal-mediated behaviour, learning, and voluntary locomotion. There is substantial evidence suggesting that the SNc is not a homogenous population of neurons, but in fact heterogenous along the medial-lateral axis with regards to projection targets, inputs, and firing properties. The aim of my research is to determine whether the optogenetic stimulation of DANs located in the medial versus lateral SNc has a differential effect on voluntary movement.

Author: Ravi Chander, Prathyusha

Degree Sought: MSc

Supervisor: Dr. Gautam Awatramani

Category: Neuroscience

Orientation selectivity in direction selective ganglion cells

The first step in the processing of visual information is performed by complex circuits in a light-sensitive layer of the eye called retina. In the retina, multiple overlapping microcircuits serve to extract distinct features of the visual world. A major challenge is to identify the cellular components of each circuit and understand their functional properties. To date, the direction-selective circuit is one of the best described circuits in the brain. Over the years, research devoted to deconstructing the circuitry underlying direction selectivity has led to the identification of several bipolar cells that serve as a major source of excitation to the direction-selective ganglion cells (DSGCs, amongst other cell types). Similarly, another such circuitry devoted to encoding orientation information from the visual scene has been taking stage in the last decade. However, the functional properties of direction selective ganglion cells in mediating orientation selectivity remains unclear.

By means of using electrophysiology and two-photon optogenetics, I intend to identify the circuit components which allow for extraction of directional and orientation information from the visual scene. Following this, I will describe the neural basis for two types of stimulus specificity – namely direction coding and orientation coding. Finally, I will introduce the complexities involved in differentiating stimulus types that enable the retina to encode directionally selective inputs from the visual field.

Author: Mokariasl, Niloufar

Degree Sought: PhD

Supervisor: Dr. John Taylor

Category: Neuroscience, Cell, and Molecular Biology

Characterizing the timing and location of melanopsin expression during development in the sablefish (*Anoplopoma fimbria*)

Sablefish live at depths of between 300m to 2000m in the eastern Pacific Ocean. Spawning occurs below 300m, and embryos and yolk sac larvae grow in the deep. By 40 days, the larvae move to the surface in search of plankton. At 2 years old, juveniles return to the depth. The Taylor lab has introduced the sablefish as a model for opsin research. Opsins mediate light-sensitivity. Zebrafish have 42 and many are expressed in the brain. What opsins are doing in the brain is the mystery. Zebrafish also express opsin as embryos and larvae. What their role is in development is not clear. Genome and transcriptome analyses have shown that sablefish has 36 opsins. The key difference between zebrafish and sablefish is exposure to light. If brain- and embryo-expressed opsins are light sensors, then we can formulate hypotheses about when and where they will be expressed in sablefish. I used qPCR and immunostaining to test these hypotheses. I have chosen to focus on the Opn4 family for investigation because it is well studied. Sablefish has five Opn4 opsins (*opn4m1*, *opn4m2*, *opn4m3*, *opn4x1*, and *opn4x2*) as non-visual opsins. I localized melanopsin in different tissues of the sablefish. *Opn4m3* has the highest expression in eye and *opn4m2* has the highest expression in hindbrain. I plan to characterize the location of this protein in sablefish embryos and larvae (1-42 days) to investigate the role of Opn4s family in teleost fish.

Author: Hirabayashi, Kaede

Degree Sought: MSc

Supervisor: Dr. Gregory Owens

Category: Neuroscience, Cell, and Molecular Biology

Science of DNA extraction – Why is DNA extraction from plants so hard?

Today, given the advanced tools readily available, extracting DNA from biological samples of interest in many molecular biology labs has become almost a monotonous task. For scientists who perform DNA extractions on countless number of samples a day, a DNA extraction protocol is like a daily routine to begin the main analyses of the day.

While it is straightforward to extract DNA from soft tissues like animal fluids or fish skins, it is not easy for plant cells because of their rigid cell walls and various metabolites that interfere with DNA during the extraction procedure. Additionally, long-read genome sequencing requires high-molecular-weight (HMW) DNA, meaning the DNA must be gently extracted and cannot be fragmented.

The goal of my thesis project is to sequence and assemble the whole genome of lingonberry, where the good quality of DNA is critical. To achieve this goal, my first objective is to optimize the method for HMW DNA extraction from lingonberry.

I tested several protocols that failed to produce any DNA from lingonberry. After a literature review, I decided on a two-step protocol: 1) isolate nuclei from plant tissue, then 2) extract and purify HMW DNA from the isolated nuclei. By testing multiple methods and species, I optimized an extraction protocol for lingonberry.

The species-specific challenges of DNA extraction in plants highlights their biochemical diversity. By comparing and testing multiple protocols, I learned the function of all reagents and steps, and have developed best practices.

Author: deRosenroll, Geoff

Degree Sought: PhD

Supervisor: Dr. Gautam Awatramani

Category: Neuroscience, Cell, and Molecular Biology

Investigating the relevance of sustained and transient bipolar cell input waveforms, and their distribution, to Direction Selectivity in Starburst Amacrine Cells

It has been shown previously with electron microscopy that different types of bipolar cells (BPs) (as determined by morphology and genetics) preferentially cover (surface area over dendritic arbour) starburst amacrine cells (SACs) at different somatic distances. They hypothesized that if these populations of BPs were representative of sustained (proximal to the soma) and transient (biased to be more distal), this could support centrifugal preference (soma outwards to tip) in SACs. More prolonged inputs close to the soma would be activated first while moving outwards, improving postsynaptic summation with the more transient inputs that follow along the remainder of the SAC dendrite. Centripetal movement (from the tips/outside the receptive field inward towards the soma), would lead to less optimal summation, as the more brief inputs would be activated first and run down, rather than ride on the wave of the sustained proximal inputs. This was modelled in the original paper (Kim *et al*, 2014) as well as others (Fransen and Borghuis, 2017), though with non-compartmental mathematical models, and without confirmation of what the inputs onto SACs actually look like. By directly imaging glutamate release from BPs onto SAC dendrites, we are now able to calculate release rate estimates for BPs proximal and distal to the SAC soma. Using these release rates, which we find to verify the hypothesis that proximal inputs are more sustained, we confirm that a proximal-distal arrangement of sustained and transient BPs along the SAC dendrite is sufficient to generate direction-selective signals at the dendritic terminals.

Author: Barnes, Hayley

Degree Sought: MSc

Supervisor: Dr. John Taylor

Category: Neuroscience, Cell, and Molecular Biology

Light sensitive brains? Melanopsin expression and localization in the deep-sea sablefish (*Anoplopoma fimbria*).

Light regulates many biological processes through light-sensitive proteins called opsins. Opsins are involved in vision, but they are also expressed in extra-retinal tissue, where their roles are far less clear. Fish have large opsin repertoires, derived from a long history of gene duplication and divergence. I introduce sablefish (*Anoplopoma fimbria*) as a model for opsin research. Like zebrafish, we have access to large numbers of individuals at all developmental stages. Unlike zebrafish, this is a deep-sea species. My survey of the genome showed that they have 36 distinct opsin genes even though they spend most of their lives in the dark. To test the hypothesis that opsin expression is higher during the comparatively brief period of time when this species is exposed to light (the free-swimming larval stage through to reproductive maturity), I quantified the expression of five paralogous genes from a well-studied non-visual opsin family (OPN4's) in the brain across life stages. Data show stable expression of some paralogs across life stages, while others are roughly associated with age and light environment. I localized proteins encoded by the most highly expressed class of OPN4 genes in the brain, the *Opn4m* genes, to the surface of the optic tectum just below a cranial 'window'. Thus, expression appears to be correlated with light exposure not only temporally, but also spatially.

Author: Athar, Faria

Degree Sought: PhD

Supervisor: Dr. Nicole Templeman

Category: Cell and Molecular Biology

Deciphering the nutritional control of reproductive aging.

One of the strongest modulators of reproductive function is nutrition and environmental cues such as food availability. Severe undernutrition restricts reproduction, while overconsumption, as seen in conditions like obesity, causes reproductive dysfunction. As food consumption patterns shift towards high-fat, high-sugar processed foods, the rates of obesity, diabetes and their associated reproductive disorders are rising putting the vulnerable, especially the elderly, at further risk.

Insulin/IGF-1 signaling (IIS) is a highly conserved nutrient-sensing pathway that is activated due to elevated levels of nutrients such as glucose, leading to a suite of cellular and gene expression changes that mediate physiological responses to nutrients. It is well established that dysregulated insulin signaling, as seen in disorders like obesity, is associated with poor reproductive health, but the mechanistic role of insulin in reproductive aging is unknown. This project aims to delineate this puzzle by investigating how insulin signaling modulates ovarian aging, fertility, and reproductive function. Using two animal systems to model a moderate reduction in IIS, the reproductive repercussions of high-fat, high-glucose diets will be studied in detail. High-fat, high-glucose diets are typical of modern society and understanding the crosstalk between food intake, nutrition and reproductive health has potential in extending reproductive longevity for women, decreasing age-associated disorders, and promoting healthy living.

Author: Gordon, Harley

Degree Sought: PhD

Supervisor: Dr. Peter Constabel

Category: Forest Biology

Rescuing phenotypes: Using degenerate nucleotides to avoid CRISPR/Cas9 cleavage

Poplar trees are widely distributed across the northern hemisphere and are an ecological keystone species. Widespread and prolific growth of poplars can be attributed, in part, to a robust defense to herbivory. Poplars produce high concentrations of constitutively present specialized metabolites known as salicinoids which function to prevent insect herbivory. Salicinoids are glycosylated phenolic compounds, and it has been shown that CRISPR/Cas9 knockout of the salicinoid biosynthetic gene UGT71L1 in poplar has widespread and unexpected impacts on tree growth, development, and sprouting efficiency. Salicinoid deficient plants lacking functional UGT71L1 are smaller, with different leaf morphology and branching patterns when compared to wildtype plants. Due to the widespread and dramatic phenotype presented by salicinoid deficient plants, our work aimed to restore and rescue the phenotype of salicinoid deficient plants by introducing a synthetic CRISPR/Cas9 resistant UGT71L1 gene and demonstrate that interruption of a single salicinoid biosynthetic gene, UGT71L1, is responsible for the observed growth patterns. Interrupting salicinoid biosynthesis results in metabolic overflow diverting into the plant hormone salicylic acid. Reintroduction of a modified CRISPR/Cas9 resistant salicinoid biosynthetic gene prevents salicylic acid over-accumulation and restores nominal growth and development in poplar. Furthermore, salicinoid concentrations are restored to wildtype levels, despite promoter differences between native UGT71L1 and the introduced transgene.

Author: Nehring, Lise

Degree Sought: MSc

Supervisors: Dr. Barbara Hawkins & Dr. Marty Kranabetter (FLNRO)

Category: Forest Biology

Assessing the contribution of *Alnus rubra* to *Pseudotsuga menziesii* stand nitrogen budgets using tree ring $\delta^{15}\text{N}$

Alnus rubra (Red Alder) is the most abundant native coastal hardwood in British Columbia and has evolved a symbiotic relationship with the nitrogen-fixing actinobacteria *Frankia*. While nitrogen is the most abundant gas in the atmosphere, it cannot be directly absorbed, making it one of the most common limiting nutrients. Only nitrogen-fixing bacteria and archaea can convert nitrogen gas into plant-accessible compounds (NO_3 ; NH_4 with H_2O).

The question “what does nitrogen do under and around alder?” has been thoroughly researched over the past 50 years, yet a knowledge gap exists within the wood. This research uses $\delta^{15}\text{N}$ signatures to assess the contribution of *A. rubra* to neighbouring *Pseudotsuga menziesii* (Douglas-fir) nitrogen budgets. I propose increased *A. rubra* will increase the percent nitrogen and $\delta^{15}\text{N}$ signature within *P. menziesii*. The sites in this study are part of the Ministry of Forests’ long-term Experimental Project 1121.01 examining the interactions between conifers and *A. rubra*. Planted in 1994, the Holt Creek site contains stands of *P. menziesii* and *A. rubra* in five proportions (*A. rubra*: *P. menziesii* proportions: 1.0:0, 0.5:0.5, 0.25:0.75, 0.11:0.89, 0:1.0). Increment cores from 5 trees per species per plot were taken along with soil and foliar samples.

Statistical analyses confirm that *P. menziesii* grown in 50% alder plots have increased N% ($p=0.010$) and $\delta^{15}\text{N}$ ($p=0.0001$) compared to pure *P. menziesii* plots. Knowledge of how *P. menziesii* responds to *A. rubra* in mixed stands can help improve the success rates and biodiversity of tree planting after logging.

Author: Lane, Sarah

Degree Sought: PhD

Supervisors: Dr. Jürgen Ehling & Dr. Patrick Walter

Category: Forest Biology

Poplar root extracts as novel iron chelators in treatment of iron-overload related disease

Iron is an essential mineral required for life. However, it is highly reactive and under tight homeostatic control in living systems. When this is disrupted, iron can accumulate to uncontrollable levels, with devastating consequences. In humans, this iron overload is increasingly recognized as a contributor to the pathology of diseases including cancer, diabetes, and Parkinson's Disease. Treatment with iron chelators (iron-binding compounds, ICh) is a promising therapy, but few ICh are approved for clinical use, and those can have severe adverse effects with prolonged use. Some ICh also have reduced mobility in the body, limiting utility as a treatment. In the search for new chelators that address these challenges, plants are a good source of novel ICh. They produce a variety of iron-chelating secondary metabolites, including phenolic acids in the roots as a response to low bioavailable iron in soil. These plant-based ICh could have similar activity in humans. To begin looking for plant-based ICh, I grew poplar plants in a reduced iron environment to stimulate production of iron-chelating secondary metabolites. The roots were harvested and extracted to isolate ICh for further characterization. Untargeted metabolomic analysis revealed a subset of metabolites that are more abundant in iron-reduced poplar than in iron-normal controls. I then applied plant-based ICh or chlorogenic acid (a phenolic compound prevalent in poplar used as a model) to human THP-1 monocytic cells cultured in iron-overload conditions. 100 μ M chlorogenic acid and some plant-based ICh reduced iron comparably to desferroxamine, a clinical iron chelator.

Author: Liu, Yalin

Degree Sought: MSc

Supervisor: Dr. Peter Constabel

Category: Forest Biology

The regulation and function of Proanthocyanidins (PAs) in poplar roots

Secondary metabolites play important roles in tree defense. Proanthocyanidins (PAs), one of the most common secondary metabolites, are widely distributed in trees and woody plants, and are abundant in poplar. In my research, molecular biology and biochemistry techniques are used to investigate the function of two important transcription factors, MYB115 and MYB134, in regulating the PA pathway in hybrid poplars. The importance of these transcription factors in regulating PA synthesis in leaves has recently emerged, but their roles in roots are unknown. MYB134- and MYB115-overexpressing transgenic poplars showed a strong high-PA phenotype in leaves, but how these two regulators interact *in vivo* is still a mystery. This research aims to test the function of both MYBs in the regulation of PAs in poplar roots, and to explore the antimicrobial functions of root PAs. Both alleles of the MYB genes were sequenced in wild type poplars to design gRNAs for creating transgenic poplars with knocked-out (KO) MYB115 and MYB134, using CRISPR Cas9 system. Chemical and genetic phenotype characterization of both single- and double-KOs showed reduced PA content and down-regulated flavonoid genes in leaves. In poplar roots, only double-KOs showed significant change in PA and salicinoid metabolism. These results indicate that the regulatory pathways of PA biosynthesis may differ in poplar leaves and roots. Additionally, the antimicrobial function of PAs was tested by disc inhibition assay *in vitro* and mycorrhizal co-culture sandwich assay *in vivo*. Pure PAs showed no inhibition towards pathogen fungus, *Armillaria*, but displayed slight inhibition to mycorrhiza, *Laccaria bicolor*.

Author: Piirtola, Eerik

Degree Sought: PhD

Supervisor: Dr. Peter Constabel

Category: Forest Biology

Chemistry and biochemistry of methylated flavonoids in *Populus* leaf bud resin

Poplar trees, such as black cottonwood (*P. trichocarpa*) and balsam poplar (*P. balsamifera*), are known to secrete resinous exudate from their leaf buds. Leaf bud resins contain diverse phenolic secondary metabolites, especially hydrophobic flavonoids, which are shown to be biologically active. Due to the rich flavonoid composition, bud resins from poplars have been widely used in traditional medicine for their antimicrobial properties. Leaf bud resins have also been found to be particularly important for honeybees, which utilize them as a building material and antibiotic protection for their hives.

The objective of this research is to characterize the biosynthesis of secreted flavonoids in bud resin of different poplar species using a combination of analytical chemistry and molecular biology. The chemical composition of poplar bud resins will be analyzed utilizing liquid chromatography and mass spectrometry to identify and quantify flavonoids. In parallel with the chemical analysis, transcriptomics will be used to identify novel *O*-methyltransferases that are associated with the production of bioactive methylated flavonoids in bud resin. The identified candidate *O*-methyltransferases will be tested as recombinant proteins to characterize and verify their function.

Based on phylogenetic analysis, I have identified flavonoid-specific *O*-methyltransferases expressed in both *P. trichocarpa* and *P. balsamifera*. Characterization of resin-specific *O*-methyltransferases will lay the foundation for studying the gene expression and biological functions of enzymes involved in leaf bud resin production. Studying the gene expression of resin-specific genes will allow me to identify the most active time period for the accumulation of leaf bud resin in *Populus*.

Author: May, Emily

Degree Sought: PhD

Supervisor: Dr. Rana El-Sabaawi

Category: Ecology and Evolution

Elemental content of non-fish vertebrates: Causes and consequences

In ecological stoichiometry, researchers use mass-balance to predict how an organism's elemental content may affect nutrient cycles. Since bone is high in phosphorus, vertebrates store uniquely high quantities of phosphorus in their bodies. This, along with their relatively long lives and high mobility, makes them impact nutrient cycles differently than other animals. However, despite their unique characteristics, vertebrate elemental composition is poorly characterized in ecological stoichiometry. Furthermore, studies that evaluate vertebrate elemental composition primarily occur in aquatic ecosystems, leading to an overrepresentation of fishes in the current literature.

My goal was to identify factors affecting elemental content in diverse vertebrates and to identify gaps in the literature. I performed a meta-analysis and compiled 179 measurements of whole-body percent phosphorus (%P), percent nitrogen (%N), and N to P ratio (N:P) in non-fish vertebrates; then, I analyzed these data with weighted general linear models. I found that variation stemmed mainly from taxonomy (class and order) and from life stage (larvae/neonate, juvenile, adult/paedomorph), with habitat and diet having small and inconsistent effects. Reptiles (especially turtles) drove taxonomic relationships in %P and N:P, as they had high %P compared to other vertebrates. Passerine birds and bats drove taxonomic relationships in %N, as they had low and high %N respectively. %P increased with age in vertebrates, causing a simultaneous decrease in N:P, but %N was essentially constant across life stages. Overall, most taxa and life stages were poorly represented, showing that further research is needed.

Author: Lawton, Maggie

Degree Sought: MSc

Supervisor: Dr. Ryan Gawryluk

Category: Ecology and Evolution

Characterizing protist diversity in oxygen minimum zones using molecular sequencing techniques

Oxygen minimum zones (OMZs) are oceanic regions with low levels of dissolved oxygen. Despite being inhospitable to aerobic organisms like animals, they contain diverse microbial communities that mediate gas and nutrient cycling, and thus are key components of oceanic ecosystems and biogeochemical cycles. Anthropogenic activity has led to the expansion of these regions, altering the function and composition of their communities. While the prokaryotic component of these environments has been extensively studied, the eukaryotic component has not. A common model system used for studying OMZs is the Saanich Inlet, a seasonally anoxic fjord in Vancouver Island, British Columbia. This project will investigate the eukaryotic diversity within the Saanich Inlet over both seasonal and temporal variations in oxygen levels, with a particular focus on identifying novel species, metabolisms, and symbioses. To achieve this, a combination of molecular methods will be developed, tested, and used for the best accuracy and resolution, including metabarcoding, metagenomics, single-cell genome sequencing and single-cell transcriptome sequencing. It is expected that more taxa of known anaerobic protists will be found in the anoxic layer, as well as possible previously unidentified species. In addition, novel adaptations for surviving in anaerobic conditions will likely be identified, including metabolic strategies and symbioses. This investigation will improve our overall understanding of protists, anoxic metabolism, and OMZs, as well as the effects of climate change.

Author: Ellis, Sarah

Degree Sought: MSc

Supervisor: Dr. Rana El-Sabaawi

Category: Ecology and Evolution

Does preservation alter bone phosphorous concentrations?

There is increasing interest in using organism nutrient composition to understand nutrient flow through ecosystems. Aquatic organisms are often phosphorous-limited, and a major source of available phosphorous can be through nutrient recycling of metabolic wastes and carcass decomposition. Threespine stickleback (*Gasterosteus aculeatus*) have phosphorous-rich bony armor that can evolve quickly, perhaps altering their contributions to phosphorous recycling. Skeletal phosphorous content, or bone mineral density, varies over time; yet current nutrient recycling models do not include flexible phosphorous content, and little is known about marine stickleback bone density. Additionally, while many studies preserve stickleback in ethanol or by freezing, it is unclear whether preservation significantly alters their nutrient composition.

This study explores interannual variation in bone phosphorous of marine stickleback collected from several Vancouver Island populations. It also tests the effect of preservation method and duration on recovered bone phosphorous by using fish preserved over a variety of time spans—from fresh fish dissected a few hours after collection to fish that were frozen or soaking in ethanol for more than 16 months. Preliminary results currently indicate that bone phosphorous may not vary significantly between ethanol and freezing treatments. Understanding the interaction between preservation and nutrient recovery is key to unlocking a rich archive of historical fish specimens, allowing broader comparisons across studies and timeframes, and enabling a deeper understanding of nutrient recycling in aquatic ecosystems.

Author: Wyatt, Shea

Degree Sought: PhD

Supervisor: Dr. Diana Varela

Category: Marine Biology

Feeling the heat: is diatom productivity in the Pacific Arctic responding to long-term warming?

Primary producers mediate the transfer of nutrients through the food web and link biogeochemical cycles of Si, C, and N in the ocean. Here we present summer trends in phytoplankton and nutrient dynamics in the Northern Bering and Chukchi Seas from 2006 to 2021. We will discuss variations in upper ocean rates and stoichiometric ratios of carbon and nitrate uptake, and diatom-specific productivity (silicic acid uptake) across different regions that have experienced significant increases in ocean temperature. Biomass and ratios of particulate carbon, nitrogen, biogenic silica, chlorophyll-a and ambient dissolved macronutrients will also be discussed relative to the respective uptake rates under both nutrient-replete and nutrient-limiting conditions. Sampling was conducted along oceanographic transects crossing areas of high productivity and biodiversity that have been exposed to dramatic climatic changes in sea ice coverage, seawater temperatures, and biological communities. By studying the dynamics of Si relative to other nutrients and primary productivity over time in a broad Arctic region, this work will provide critical insight towards understanding both present-day and future ecological and biogeochemical shifts in the Pacific Arctic Region.

Author: Kolatkova, Viktorie

Degree Sought: PhD

Supervisor: Dr. Ryan Gawryluk

Category: Marine Biology

Under every stone? Phytomyxid parasites in seagrass meadows

Seagrasses are an ecological, polyphyletic group of flowering plants which recolonized marine environments independently on multiple occasions approximately 70–100 million years ago. They are important primary producers and keystone species of many temperate and tropical coastal habitats, where they provide complex ecosystem services, serving as seafloor stabilizers, and food, shelter and spawning grounds for countless marine organisms. Unfortunately, seagrasses are experiencing a continuous and rapid decline in both their abundance and distribution worldwide. Although the disappearance is predominantly caused by human-related activities in coastal areas and global climate change, natural pathogens and parasites are also believed to have played a role in weakening seagrass meadows. Phytomyxids, gall-forming obligate intracellular biotrophic protists, represent one of three microbial groups recognized as parasites of seagrasses. However, unlike other parasites, phytomyxids are typically found incidentally, and have long been considered rare in marine environments. To challenge this perception, I report here that when systematic screening and modern molecular approaches are applied, marine phytomyxids are proved to be ubiquitous and highly diverse inhabitants of seagrass beds. In the Salish Sea (British Columbia, Canada), phytomyxid parasites were found in >99% of *Zostera marina* and *Zostera japonica* specimens investigated. Phylogenetic analyses of the 18S rRNA barcoding gene moreover indicate that seagrass-associated phytomyxids are genetically variable and highly host-specific microorganisms, and were co-introduced to new regions with invasive hosts on several occasions. As the effect of phytomyxids on seagrass health remains poorly understood, experimental studies are required to further clarify their pathogenic potential in these ecosystems.

Author: Crawford, Rebecca

Degree Sought: MSc

Supervisors: Dr. Diana Varela & Dr. Ryan Gawryluk

Category: Marine Biology

Distribution of phytoplankton and parasitic fungi within Arctic and Subarctic Oceans

In recent years, shifts in environmental conditions in Arctic and Subarctic oceans have brought increased attention to the biodiversity of these regions. The Arctic is warming twice as fast as the rest of the world, which has serious implications for biological productivity. Environmental changes in the Bering and Chukchi seas are especially concerning, as they are among the most productive regions in the world's oceans, and their fisheries are crucial to supporting people on a local and global scale. Better predictions about how these oceanic regions may respond to climate change require that we fully understand the biodiversity and community structure of eukaryotic phytoplankton, given that they are the major primary producers in marine environments. To this end, we have sequenced the V4 hypervariable region of the 18S rRNA gene from water samples collected from the Chukchi and Bering Seas in order to assess phytoplankton community composition. In addition, this work also investigates the impact that chytrids, a notable group of parasitic zoosporic fungi, are likely to play in phytoplankton community dynamics. Chytrids are known to parasitize phytoplankton in freshwater and marine environments and have more recently been found to be ubiquitous across Arctic oceans. Here, a combination of metabarcoding and microscopy is being used to assess the diversity and geographic distribution of chytrids, along with their host range and specificity. This study intends to add to the growing body of knowledge on phytoplankton biodiversity in the Arctic and Subarctic, and the role that parasitism plays in shaping it.

Author: Davies, Hailey

Degree Sought: MSc

Supervisors: Dr. Francis Juanes & Dr. Dana Haggarty

Category: Marine Biology

Barotrauma injuries in Pacific rockfish species around Entrance Island, British Columbia

Rockfishes (*Sebastes* spp.) are a highly diverse group, with at least 41 species found off the British Columbia (BC) coast. These fish have a physoclistous swim bladder (no connection to the esophagus) which limits them to gradual adjustments in buoyancy. Consequently, rockfishes often suffer from barotrauma injuries when forced to the surface during capture due to expansion of gas in the swim bladder. Inshore rockfishes are targeted by many groups and industrial fishing has led to devastating declines in most populations. Despite conservation measures in BC, there has been little evidence of population recovery. We collected field data to quantify species differences in barotrauma symptoms using hook-and-line methods to capture rockfishes (9 species, n = 353) on a reef surrounding Entrance Island, BC in 2020 and 2021. Each rockfish was assessed for six external barotrauma symptoms: esophageal eversion, pop eye, tight abdomen, bulging membrane, membrane emphysema, and ocular emphysema. We found that there were differences in the type and severity of barotrauma between species. Yelloweye (*Sebastes ruberrimus*) and Canary (*Sebastes pinniger*) rockfishes experienced the most severe symptoms including esophageal eversion more frequently than other species, while Quillback (*Sebastes maliger*) experienced less severe injuries, and Yellowtail (*Sebastes flavidus*) only suffered mild barotrauma. Drivers of these differences could include physiological, life history, or behavioural characteristics (e.g., benthic versus pelagic schooling behaviours). These results add to the existing literature on rockfish barotrauma symptoms, including data deficient species in BC.

Author: Wright-LaGreca, Marissa

Degree Sought: MSc

Supervisors: Dr. Amanda Bates & Dr. Timothy Green

Category: Marine Biology

Investigating the potential of probiotics to improve survival of the Pacific oyster (*Crassostrea gigas*) against bacterial infection

Mass die-offs of shellfish are occurring due to disease outbreaks that are growing in frequency and intensity, causing significant ecological and socioeconomic impacts.

Increasingly, the microbiome is being recognized as having a primary role in resisting the harmful effects of disease agents. Here, I focus on host-pathogen interactions in Pacific oyster (*Crassostrea gigas*) larvae and spat (early-adult). I will test if infection by *Vibrio* bacteria may be reduced by the presence of competing bacteria within the oyster, which constitute a portion of the oyster's microbiome, using bacterial fluorescent *in situ* hybridization (FISH) probes and bacterial inhibition assays. The bacterial genus, *Roseobacter*, is suspected to compete with *Vibrio spp.* in crustaceans but this is not yet proven in molluscs.

I will use FISH method to probe for *Roseobacter spp.* and *Vibrio aestuarianus* in whole oyster larvae and spat tissue to describe their distribution. If co-localization within the oysters occurs, this further supports a competitive relationship between the bacteria species. I will further conduct bacterial inhibition assays to investigate if *Roseobacter spp.* release antimicrobial peptides that inhibit *Vibrio aestuarianus* growth.

My results will be used as a stepping-stone towards the efficacy of probiotics to promote resiliency to bacterial infection. For instance, if *Roseobacter spp.* prevents *Vibrio* infection, it could be supplemented into seawater as a probiotic to encourage the formation of a favourable microbiome. This work has potential to reduce mass die-offs linked to *Vibrio aestuarianus*, and thus support the sustainability of the shellfish industry with implications for shellfish conservation.

Author: Black, Morgan

Degree Sought: PhD

Supervisors: Dr. Francis Juanes & Dr. Sarah Dudas

Category: Marine Biology

How ancient indigenous clam gardens alter marine community structure

Biodiversity monitoring is a relatively modern concept, with impact assessments focusing on post-industrial activities. Here we examine how Indigenous resource management practices, specifically clam gardens constructed and managed over thousands of years, shape biotic communities today. We compared fish and mobile invertebrates on walled (clam garden) and non-walled beaches (reference). Quantifying the differences in community assemblages between these beach types, we found that habitat modifications and the influence of structural complexity drive near-shore marine biodiversity patterns in this temperate system.

Author: Csordas, Matthew

Degree Sought: MSc

Supervisor: Dr. Julia Baum

Category: Marine Biology

Quantifying changes in *Postelsia palmaeformis* distribution and abundance along the south-western coast of Vancouver Island

Climate change is driving species redistributions, losses, and ecosystem transformations globally through gradual warming and acute marine heatwave events. Throughout the Pacific Northwest intertidal temperatures are poorly predicted by latitude and are instead mediated by local factors such as wave exposure and tidal patterns leading to the patchy loss of species throughout their ranges. *Postelsia palmaeformis* is a canopy forming kelp found high in the wave exposed intertidal on coastlines from mid-California to Hope Island, BC. Due to reports of decreased abundance near its southern range edge, patterns of intertidal kelp diversity and abundance loss associated with the 2013-2016 marine heatwave, and *Postelsia*'s inability to reliably disperse over long distances, there is concern that climate driven temperature increase may be causing *Postelsia* to decline across its range. Here we use historical (2007) and current (2021) coastal imagery to assess how the abundance and distribution of *Postelsia* has changed on the south-western coast of Vancouver Island. Both sets of data were obtained using a low flying helicopter and provide complete coverage of the coast from Sombrio Beach to Cape Beale. Using these images, we created and compared a georeferenced distribution and abundance dataset for *Postelsia* at each time point. We are currently overlaying this data with environmental data layers to build an understanding of what environmental changes may be associated with *Postelsia* presence or absence. This study assesses the current condition of *Postelsia* in BC and develops a framework which could be applied to other conspicuous intertidal taxa.

Author: Reidy, Rhonda

Degree Sought: PhD

Supervisors: Dr. Francis Juane & Dr. Laura Cowen

Category: Ecology and Evolution

Humpback whale subsurface feeding in Juan de Fuca Strait

Data on humpback whale foraging in the Salish Sea are biased toward prey types conducive to surface feeding, with no information on the whales' feeding behaviour at depth on alternative prey sources. Here, we present evidence that a solitary humpback whale in Juan de Fuca Strait was feeding on fish at 100 m depth. We combined data from a multisensor animal-borne tag with a vessel-mounted Acoustic Zooplankton and Fish Profiler to describe the foraging effort of the whale relative to its prey. Acoustically detected prey layers were consistent with dense schools of walleye pollock (*Gadus chalcogrammus*) distributed above diffuse aggregations of pollock. Analysis of a fecal sample from the tagged whale also revealed pollock. Integrating the whale dive profile with the prey data revealed that feeding lunges were initiated under the densest prey schools. A higher feeding rate occurred at higher prey densities but declined to zero at lower prey densities, suggesting dive-by-dive foraging decisions that minimized foraging costs.

Author: Buzzoni, Daisy

Degree Sought: PhD

Supervisor: Dr. Julia Baum

Category: Marine Biology

Metabarcoding reveals a variety of partner specificity responses between reef-building corals and their algal symbionts under an onslaught of local and global disturbance.

Climate change-amplified marine heatwaves are causing more frequent and severe mass coral bleaching events and now pose the greatest global threat to the future of coral reefs. Simultaneously, most coral reefs are exposed to some degree of local human disturbance, such as poor water quality. The Pacific Island of Kiritimati (Kiribati) was the epicentre for the 2015-2016 global coral bleaching event (experiencing a 10-month heatwave), and it also harbours reefs exposed to very high levels of local human disturbance. As such, Kiritimati is a microcosm representative of the global coral reef crisis. Bleaching represents the breakdown of the relationship between corals and their algal symbionts (family *Symbiodiniaceae*), so the symbiont communities hosted can have dramatic consequences for coral thermotolerance and heatwave survival. Whilst differing degrees of coral and symbiont partner specificity have been reported previously, this has not yet been explored across a major stress event, such as a heatwave. The use of ITS2 metabarcoding (a DNA sequencing technique) in this study has allowed fine-scale identification of putative symbiont taxa in samples from tagged corals of a long-term dataset from Kiritimati. Here we report analyses from over 2,500 samples taken from 7 different species of coral across different families and life-history strategies, at sites exposed to varying levels of human disturbance, spanning the heatwave. This study explores changes in both coral and algal partner-specificity in relation to local disturbance and the 2015-16 heatwave, with clear implications for coral resilience in an increasingly disturbed ocean.

Author: Livingston, Michael

Degree Sought: PhD

Supervisor: Dr. Diana Varela

Category: Marine Biology

Estimating spatiotemporal trends in surface ocean exopolymers using a modelling approach

Transparent exopolymer particles (TEP) form a gelatinous matrix within the upper surface of the world's ocean and are important for the efficiency of the biological carbon pump. While TEP can facilitate organic matter aggregation, the TEP matrix is also less dense than seawater, and can accumulate near the surface ocean. Owing to their low density, high TEP concentrations, relative to those of other types of organic matter, can reduce the sinking potential of organic aggregates and can even induce upward flux. Due to the characteristics of TEP and their ubiquity in the global ocean, it is critical to understand how changes in ocean conditions, such as warming and a shoaling of the mixed layer, influence TEP concentrations. Here we show that TEP concentrations can be estimated using multivariate regression models from predictor variables such as chlorophyll, particulate organic carbon, temperature, and time of year in Northeastern Pacific region. These regressions satisfy all model assumptions and are accurate in estimating TEP concentrations when tested on validation data sets. The models were applied to satellite derived data sets to provide large scale approximations of surface TEP concentrations. The results from these models provide a deeper understanding of surface distribution and changes in TEP concentrations in the Northeast Pacific.

Author: Woods, Mackenzie

Degree Sought: MSc

Supervisors: Dr. Francis Juanes & Dr. Sigal Balshine (McMaster University)

Category: Marine Biology

Context-dependent effects of anthropogenic noise on nest defence in a singing toadfish

Anthropogenic noise has drastically changed natural soundscapes, affecting both terrestrial and aquatic ecosystems and their inhabitants. Noise pollution leads to a myriad of behavioural and physiological consequences for marine life, including fishes. Most studies have focused on the effects of noise on fish in controlled laboratory settings; however, these experimental conditions sometimes lack ecological validity, and it is largely unknown whether the effects observed in aquaria are representative of real-world responses for animals experiencing noise in the wild. In this study, we used a combination of laboratory and field playback experiments to assess the effects of noise on nest defence and parental behaviour in an intertidal-breeding toadfish, the plainfin midshipman (*Porichthys notatus*), which relies on acoustic communication for mate attraction and defence. Nest guarding males (without eggs) in aquaria exhibited a nearly fourfold increase in defensive behaviours during boat noise playbacks compared to ambient conditions. However, in the field, we observed no clear changes in the defensive or parental behaviours exhibited by guarding males (with eggs) during exposure to noise. Our study demonstrates that anthropogenic noise can alter nest defence behaviour in plainfin midshipman fish, but also that its impact depends on contextual cues, such as testing environment, presence of eggs, and type of noise stimulus used. Our results highlight the importance of considering testing environment when designing experiments and interpreting results, and the need for more field studies and lab-field integrative studies to quantify and mitigate the harm noise pollution causes to marine animals and populations in coastal environments.

Author: Murchy, Kelsie

Degree Sought: PhD

Supervisor: Dr. Francis Juanes

Category: Marine Biology

Underwater noise produced by anthropogenic activities on Vancouver Island, British Columbia

In recent decades, shipping traffic has been increasing, leading to elevated ambient underwater noise. Extensive research has been conducted on the changes to ambient noise levels of moving ships, but little is known about ships at anchor. Vancouver Island, British Columbia (BC) has many anchorage locations where freighters stop prior to entering the Port of Vancouver. Additionally, Vancouver Island has logging activities that occur in estuaries and surrounding waters. These human activities raise concerns about what impacts they might be having on the soundscape and marine organisms that inhabit these key locations. Cowichan Bay, BC is an industrialized bay and a key migration corridor for Pacific Salmon (*Oncorhynchus* spp.). To understand changes to the ambient noise levels in Cowichan Bay, with different anthropogenic activities, seven stationary hydrophones were deployed during Fall 2019 and 2020. Results show substantial changes in the soundscape with both anchored freighters and logging activities for the duration of their presence in the bay, with elevated sound pressure levels (SPL) detected throughout the bay for anchored freighters. Our results demonstrate the impact anchored freighters and logging activities have on underwater soundscapes and are the first step in understanding the impact these activities have on marine organisms and important ecosystems.

Author: Heimrich, Annika

Degree Sought: PhD

Supervisors: Dr. Francis Juanes & Dr. William Halliday

Category: Marine Biology

Temporal distribution of marine mammals and fish near Cambridge Bay, Nunavut in 2017-2019

The Arctic Ocean is an ecologically important ecosystem, offering either a temporary or long-term habitat for numerous migrating and resident marine mammal and fish species every year. Characterized by the annual cycle of sea ice, the Arctic Ocean has less noise disturbance from anthropogenic activities than other marine areas. However, as climate change causes longer ice-free periods during summer, and ship traffic continues increasing, underwater noise in the Arctic may increase in the future. Given that the underwater soundscape is a crucial habitat feature, it is important to monitor this environment.

This study will present the first year-round soundscape analysis based on passive acoustic data collected in the Kitikmeot Region of Nunavut, Canada, using data recorded between August 2017 and March 2019. > 500 hours of acoustic data were analyzed for vocalizations by marine mammals and fish, as well as for the presence of ship noise. Ringed seal (*Pusa hispida*) and Arctic cod (*Boreogadus saida*) vocalizations were present in nearly every month of the year, whereas bearded seal (*Erignathus barbatus*) vocalizations were present between October and August, but peaked during the breeding season. Beluga whale (*Delphinapterus leucas*) vocalizations were only detected on a single day in October 2017. Underwater sound levels were strongly driven by wind, sea ice concentration, and ship noise; however, ship noise only occurred between August and September.

This study presents the first long-term passive acoustic measurements in the Kitikmeot Region, and can be used as a baseline for future studies on underwater noise within this region.

Author: Innes, Kathleen

Degree Sought: MSc

Supervisor: Dr. Francis Juanes

Category: Marine Biology

The composition and quality of juvenile Chinook Salmon winter diets in the Strait of Georgia

Declines in Chinook Salmon abundance in recent decades are generally attributed to reduced survival during marine residence. A large portion of Chinook Salmon mortality is believed to occur in the first winter following ocean entry. High mortality rates may be caused by limited feeding in the preceding summer which prevent juvenile Chinook Salmon from building up enough energy reserves to last them throughout the winter months, a period of supposed starvation. However, despite the hypothesized importance of winter in regulating survival, little is known about juvenile Chinook Salmon ecology during this time, including a lack of information on winter diets throughout the Strait of Georgia. We sample juvenile Chinook Salmon by microtrawling (non-lethal hook and line capture) on an on-call basis from October to March in the Strait of Georgia; samples include fish length and weight, scales for genetic stock identification, and stomach contents by gastric lavage. A subset of intact prey from the diets are retained for energy density (ED) determination by the ash-free dry weight to wet weight ratio, a reliable predictor of ED. The overall diets and ED of juvenile Chinook Salmon prey throughout winter are assessed by stock, site, and date, and these values will later be used in bioenergetic models. These results will fill critical knowledge gaps and contribute to testing the hypothesis that nutritional stress in winter is linked to elevated mortality of juvenile Chinook Salmon in the Strait of Georgia.

Author: Chalifour, Lia

Degree Sought: PhD

Supervisors: Dr. Julia K. Baum & Dr. Tara G. Martin (UBC)

Category: Marine Biology

Identifying a pathway toward recovery for depleted wild Pacific salmon populations in a large watershed under multiple stressors.

Pacific salmon (*Oncorhynchus spp.*) support coastal and freshwater ecosystems, economies, and cultures, but many populations have declined. I used Priority Threat Management (PTM), a decision-support framework for prioritizing conservation investments, to assess management strategies to support thriving populations of wild salmon over 25 years. I evaluated the potential benefits of 14 strategies spanning fisheries, habitat, pollution, pathogens, hatcheries, and predation management dimensions to 19 conservation units (CUs) - genetically and ecologically distinct populations - of Pacific salmon in the lower Fraser River, British Columbia, Canada.

Under 'business as usual', zero CUs were predicted to have >50% chance of thriving in 25 years. Implementation of all management strategies at an annual investment between 45-110 million CAD was, however, predicted to achieve >50% chance of thriving for 16 of 19 CUs, with seven above 60% chance, indicating there is a pathway toward recovery for most populations if we invest now. In fact, substantial gains could be made by investing in five combined habitat strategies, costing 20M CAD annually. These habitat strategies were estimated to bring 14 of 19 salmon CUs above this 50% threshold. Indigenous-led co-governance to manage salmon populations and harvest, and improved CU-level monitoring emerged from expert elicitation as critical 'enabling' strategies, underpinning the successful management of wild salmon in this region.

This research demonstrates the successful application of PTM to prioritize conservation investments for migratory species subject to multiple stressors and complex management structures. Our results emphasize the ability of holistic management approaches to support resilient wild salmon populations.

Author: Gaffney, Leigh

Degree Sought: PhD

Supervisor: Dr. Francis Juanes

Category: Marine Biology

Abnormal otoliths: Causes and consequences of vateritic otoliths in hatchery-reared Coho Salmon

Although Coho Salmon are of particular cultural, ecological, and economic importance throughout their range, anthropogenic activities have led to widespread declines in natural populations. To mitigate such declines, federal, provincial, and private organizations have undertaken large-scale hatchery-rearing of juvenile Coho Salmon. Unfortunately, once released into the wild, hatchery-reared Coho Salmon juveniles survive at generally low rates compared to wild-origin juveniles, such that hatcheries have proven much less effective than initially hoped.

Recently, differences have been observed between the sagittal otoliths of hatchery-reared and wild-origin Coho Salmon. Sagittal otoliths are essential sensory structures that enable fish to hear and maintain balance. Sagittal otoliths are normally composed of aragonite, a polymorph of calcium carbonate, but otoliths with inclusions of vaterite, an abnormal polymorph, also occur. Although vateritic otoliths have been shown to occur in less than 10% of wild-origin Coho Salmon, they are extremely common in hatchery facilities, affecting 60-80% of hatchery-reared Coho Salmon. Vaterite deposition reduces otolith function and causes hearing impairment in salmon; potentially leading to compromised marine survival rates and restoration efficiencies. Despite long-standing evidence of the occurrence of vateritic otoliths, the causes and consequences of vaterite formation is largely unknown.

This study aims to investigate which hatchery-rearing conditions and practices cause vateritic otoliths to form in Coho Salmon juveniles and whether vateritic otoliths influence the marine survival rates of hatchery-reared Coho Salmon. This research has the potential to increase the generally poor success rates of Coho Salmon restoration efforts and improve the welfare of hatchery-reared salmon worldwide.

Author: Qualley, Jessica

Degree Sought: MSc

Supervisor: Dr. Francis Juanes

Category: Marine Biology

Otolith microchemistry-based identification of migration life history variation in Pacific Herring (*Clupea pallasii*) in the Salish Sea

Most adult (age-2+) Pacific Herring (*Clupea pallasii*) in the Strait of Georgia (SoG) spawn in early spring before migrating to the west coast of Vancouver Island to summer foraging grounds. Herring begin returning to the Salish Sea in late fall (Nov–Dec) prior to spawning (Hay, 1985). Some adult herring are also observed in the SoG year-round, suggesting an alternative resident life history. However, the relative abundance of residents and the degree of variation in migratory behaviour are unknown. While resident herring likely constitute a small component of the aggregate stock, they may be disproportionately important to the SoG ecosystem. My research focusses on the development of an otolith elemental tag to differentiate resident and migratory individuals. As otoliths grow, elements derived from the surrounding aquatic environment are laid down as an elemental fingerprint and a snapshot of the ambient seawater chemistry in which the fish grew. Element composition in specific otolith regions can be quantified with mass spectrometry techniques to reconstruct movements of individuals that migrate between different environments. The application of a useful otolith elemental tag for migration life history types will allow us to test hypotheses about factors that influence divergent migration strategies and resident herring dynamics in the Strait of Georgia population. Adult herring dominate adult Chinook Salmon diets in the Salish Sea in summer (UVic Adult Salmon Diet Program) (Quindazzi *et al.*, 2020) and, therefore, resident herring distribution may have consequences for growth and survival of Chinook Salmon.

Author: Quindazzi, Micah

Degree Sought: PhD

Supervisor: Dr. Francis Juanes

Category: Marine Biology

Comparative microchemical techniques to infer marine residency history of Chinook and Coho Salmon

During their marine life stage, Chinook and Coho Salmon from watersheds connected to the Salish Sea either remain resident within the Salish Sea or migrate outside of the Salish Sea. The population of Chinook/Coho that remain resident within the Salish Sea has collapsed in the past three decades, and current conservation strategies have been inadequate in protecting them. Our knowledge of their marine migrations is limited to the tagged fish caught by anglers, and short research surveys. Furthermore, it is unclear what causes some Chinook and Coho to remain within the Salish Sea and others to migrate offshore. This study aims to provide a microchemical stock identification technique that can be used on Chinook and Coho returning to their watersheds (escapements) to determine which marine migration they undertook. Microchemical profiles from the otoliths of known offshore and known Salish Sea resident Coho differ in terms of trace elements, with offshore coho having significantly more barium in their second summer growth ring ($p < 0.001$). The study will also investigate the endogenous effects that influence the marine migration strategies of Chinook and Coho. The ultimate goal of this research is to provide the means to differentiate marine migration life history phenotypes of Chinook and Coho, as well as determine the relative endogenous effects influencing these phenotypes.

Acknowledgements

We thank the following:

Financial Contributors

Biology Department
Centre for Biomedical Research
Dean of Science
Faculty of Graduate Studies
Centre for Forest Biology

Island Medical Program
Department of Vice President
Research
Ocean Networks Canada
Thermo Fisher Scientific

Symposium Organizing Committee

Co-Chairs: Sarah Lane and Shea Wyatt

Tech Committee: Viktorie Kolatkova, Rebecca Crawford, Maggie Lawton, Lise Nehring, Nicholas Ens

Finance Committee: Jessica Qualley, Leigh Gaffney, Kathleen Innes, Hailey Davies, Darienne Lancaster

Media Committee: Katie Wiese, Penelope Young, Lia Chalifour, Laura Hanson, Michael Livingston

Abstract Committee: Olivia Melville, Sierra Gray, Camille Giuliano, Emily May, Sarah Ellis

Social Committee: Kelsie Murchy, Mackenzie Woods, Matthew Csordas, Dominique Maucieri, Megan Davies

Food Committee: Hayley Barnes, Faria Athar, Niloufar Mokariasl, Clair McPolin, Alberto Ruiz De Chavez Ginzo

Session Chairs

Morgan Black
Prathyusha Ravi Chander

Ashley Mickens
Julianne Radford

We would also like to thank these individuals for their contributions

Michelle Shen
Janice Gough
Dr. Rana El-Sabaawi

Dr. Peter Constabel
Laura Alcaraz-Sehn
Judges

Thanks to all our contributors and donors!



CENTRE FOR
BIOMEDICAL
RESEARCH
UNIVERSITY OF VICTORIA



University
of Victoria

Biology



University
of Victoria

Research



OCEAN
NETWORKS
CANADA



University
of Victoria

Island Medical Program



CENTRE for
FOREST BIOLOGY
University of Victoria



SCIENCE



THE UNIVERSITY OF BRITISH COLUMBIA
Faculty of Medicine



University
of Victoria



University
of Victoria

Graduate Studies



VWR™

part of avantor



fisher scientific

part of Thermo Fisher Scientific