Abstract Booklet

2026 Graduate Symposium

April 23-24

Contents

McNiven, Mackenzie

Degree Sought: MSc
Supervisor(s): Dr. Hans-Peter Loock, Dr. Jürgen Ehlting
Category: Forest Biology
Talk Type: 12 minute

Glowing AND Growing: Hyperspectral Fluorescence Imaging of Biological Samples

Fluorescence microscopy of complex heterogeneous systems provides a fascinating challenge and opportunity in developing optical instruments for the identification and quantification of chemical components. Here, we combine excitation-emission-matrix (EEM) spectroscopy with fluorescence microscopy to obtain a chemical classification for each pixel in an image.

Using an in-lab developed illumination technique, we explore chemical composition within biological contexts. Samples are excited according to Hadamard-Transform matrices, and emission is recorded with multi- and hyperspectral cameras. After inverse Hadamard transformation, we obtain an emission spectrum for each of the excitation wavelengths, providing near real-time data acquisition. By collecting an EEM for each pixel of an image, we can calculate the EEM signatures for each unique component of a heterogeneous sample. Components are further isolated both spectrally and spatially using optimized parallel factor analysis.

To explore the biological applicability of this technique we first consider both environmental contaminants and plant extracts in solution. For in vivo use of this technique, we next examine spatial and spectral isolation of green fluorescent protein variants in transgenic *Arabidopsis thaliana* plants expressing one to four fluorophores with known sub-cellular localization. Finally, to study fluorophores with broad excitation and emission ranges between the ultraviolet and visible spectrum, we examine cross sections of young woody plant tissues targeting autofluorescence from the phenolic biopolymer lignin while overcoming strong, overlapping fluorescence from chlorophyll, a strongly emitting and highly abundant fluorescent photosynthetic pigment. This project aims to develop a novel, rapid, high-throughput, quantitative imaging method, with economical and sustainable ecosystem health monitoring implications.

Houston, Sydney

Degree Sought: MSc
Supervisor(s): Dr. Peter Constabel
Category: Forest Biology
Talk Type: 12 minutes

A forest tale: Western redcedar and the rot within

This is a story about TREES. We love them, we need them, but what if I told you they had enemies… The protagonist of this story is **western redcedar**, an important conifer species native to our home, the Pacific Northwest. Its enemy? ***Coniferiporia weirii***, a plant pathogen known to cause butt rot in our beloved hero. You may be asking yourself, *who am I in this story?* Great question. You can call me somewhat of a forest detective, assigned by my PI to follow the clues of this case. Using molecular techniques including quantitative PCR, next-generation sequencing of the fungal ITS regions, and RNA-seq, I am able to detect the pathogen's movement through the host's roots and butt. By following *C. weirii* through the roots, I can uncover the wider fungal community, discovering fungal friends associated with redcedar roots or evil microbial foes that conspire with the enemy. I don't just investigate the enemy however; I also work with redcedar itself. Through gene expression and patterns of genetic diversity, I ask: how are you responding to this attack? Are some individuals stronger than others? Do you even need help or is resistance already written into your DNA? Altogether, by combining molecular insight with ecological understanding and a hint of whimsy, this work brings the secret life of western redcedar roots to light, revealing the complex microbial and host interactions that inform forest health and disease management.

Moran, James

Degree Sought: MSc.
Supervisor(s): Dr. Basudev Ghoshal, Dr. Jürgen Ehlting
Category: Forest Biology
Talk Type: 12 minute

Development of an Experimental Model for the Study of Blueberry Scorch Virus Infection

Widespread blueberry scorch virus (BlScV) symptoms throughout the major growing regions of BC threaten Canada's most valuable fruit export with an estimated export value of $382 million. Viral latency, co-infection with other viruses, and differing environmental conditions make the study of BlScV infection in the field difficult. Additionally, previous attempts at experimental study through graft inoculation can take up to 1-2 years to establish systemic infection, while attempts at experimental inoculation with aphids have had low success rates. Thus, there is a need to establish a faster and more reliable experimental model for the study of BlScV infection. To develop a model system, two different hosts (highbush blueberry cuttings and *Nicotiana occidentalis* '37B' plants), two temperature settings, and two inoculation methods were tested for BlScV accumulation and spread. Mechanically inoculated blueberry cuttings showed the spread of the virus to upper systemically infected leaves within 2-8 days post infection. *N. occidentalis* '37B' mechanically inoculated plants exhibited symptoms at both temperature settings between 2-4 weeks post infection. Although the outcome of the symptoms varied at the two temperature settings, BlScV accumulation and spread was confirmed by RtqPCR. These results indicate the high potential for the use of these experimental model systems in basic and fundamental research of BlScV.

Orr, Rachel

Degree Sought: MSc
Supervisor(s): Dr. Rana El-Sabaawi and Dr. Paul Weidman
Category: Ecology and Evolution
Talk Type: 12 minute

Stream Habitat Assessment Using Macroinvertebrates and Remote Sensing in the Xwulqw'selu Sta'lo'

Freshwater ecosystems are valuable yet increasingly threatened by human land use, making it essential to understand where and why stream conditions diverge from expectations. In this study, we used benthic macroinvertebrate community composition and remote sensing of land cover to assess habitat condition in the Xwulqw'selu Sta'lo' (Koksilah River) watershed. The objectives were to (1) classify the condition of Koksilah sites using the Canadian Aquatic Biomonitoring Network (CABIN) Reference Condition Approach (RCA), and (2) identify environmental variables associated with divergence of invertebrate communities from reference condition using instream habitat and water quality and forest and land cover metrics by remote sensing. Thirteen Koksilah test sites were compared to 66 reference sites from Vancouver Island with similar climate, geology, and channel characteristics. Invertebrate communities in Koksilah sites spanned the full range from reference to highly divergent conditions. Invertebrate community composition differed significantly between Koksilah and reference sites, with divergent sites showing greater dominance of disturbance-tolerant taxa and lower proportions of sensitive taxa. Redundancy analysis and generalized linear modeling showed that higher periphyton growth, greater canopy cover, and increased fine sediment were most consistently associated invertebrate community divergence from reference conditions. Remote sensing metrics identified spatial gradients in riparian condition, with divergent sites showing more non-forested land. Overall, the results suggest that cumulative effects of agricultural, urban, and forestry land use are contributing to degraded stream habitat condition in parts of the Koksilah watershed. These findings demonstrate the value of combining analysis of benthic bioindicators and remote sensing to better understand land use effects on stream ecosystems.

Robson, Bethany

Degree Sought: MSc
Supervisor(s): Dr. Barbara Hawkins
Category: Forest Biology
Talk Type: 12 minute

The tall and the small: mycorrhizal impact on drought response of Western redcedar and Bigleaf maple

Drought events in British Columbia are increasing in frequency and severity, and are now occurring in forest landscapes that are not resilient to water shortages. Plant roots and their mycorrhizal fungal symbionts exude low molecular weight organic compounds (LMWOCs) into the rhizosphere, including sugars, amino acids, and organic acids. These compounds aid in vital processes, including water and nutrient acquisition, and may contribute to drought tolerance. For native tree species *Thuja plicata* (Western redcedar) and *Acer macrophyllum* (Bigleaf maple), the production of LMWOCs under drought stress and their contribution to drought tolerance are unknown. Unlike many sympatric tree species, *T. plicata* and *A. macrophyllum* associate with arbuscular mycorrhizal fungi (AMF), which may further affect drought responses. Our objective was to test organic acid, sugar, and amino acid production by *T. plicata* and *A. macrophyllum* roots under well-watered and drought conditions, with and without AMF. This objective was tested using a novel approach where plants were grown with and without AMF in a soilless medium before being transplanted to aeroponic systems for the experimental period. Photosynthetic parameters were monitored and exudates were collected from the roots to determine drought responses and exudate composition of proline, sugars, and organic acids. We hypothesize that mycorrhizal association results in decreased production of LMWOCs in drought conditions compared to non-mycorrhizal seedlings, including drought-related LMWOCs, like proline and succinic acid. Results will help to elucidate the function of mycorrhizal association during drought stress and how root exudate composition is affected by the association in these species.

Wright-LaGreca, Marissa

Degree Sought: PhD
Supervisor(s): Dr. Amanda Bates and Dr. Timothy Green
Category: Marine Biology
Talk Type: 12 minutes

Microbial education: Exploring how early microbial exposures shape long-term microbiome composition and survival against disease in the Pacific oyster

Climate change events such as marine heatwaves (MHW) weaken marine organisms' defenses against disease, such as immune system and microbiome function. As marine diseases intensify with ocean warming, methods to improve survival against disease will be valuable for mitigation. Mass mortalities of up to 100% in the Pacific oyster (*Crassostrea gigas*) are linked to MHWs and infection by *Vibrio* bacteria. During early animal development, immune processes are activated and shaped by surrounding microbiota. Exposure to certain microbes early in life may alter immune development and host-microbe interactions, improving survival against disease, denoted *microbial education*. Here, I tested how different early microbial and environmental exposures impact Pacific oyster's microbiome formation and future survival against the wide-spread marine pathogen, *Vibrio aestuarianus*, during heat stress. These findings highlight that an organism's capacity to survive disease is shaped by microbes from both its past and present, and that microbial education processes can be used as a tool to combat marine diseases.

Capralov, Ilya

Degree Sought: PhD
Supervisor(s): Dr. Gautam Awatramani
Category: Neuroscience
Talk Type: 12 minute

Inhibition plays a major role in shaping orientation selectivity in mouse bifid wide-field amacrine cells

Orientation selectivity is the property of visual neurons to respond selectively to edges at specific orientations. It is a basic computation in vision, but the cellular and circuit mechanisms that generate it are still not fully understood. Bifid wide-field amacrine cells have unusually long, straight, unbranching dendrites. These dendrites receive excitatory input along much of their length, support active signal propagation, and are electrically isolated from one another, making them a plausible substrate for orientation selectivity. Consistent with this idea, bifid WAC dendrites showed orientation preferences that matched their morphological orientation. Surprisingly, however, weakening active propagation or reducing electrical isolation between dendrites did not measurably reduce orientation selectivity. By contrast, blocking inhibition significantly reduced orientation selectivity. Together, these results suggest that the geometry and active properties of bifid dendrites are not sufficient on their own to explain their orientation selectivity, which instead relies strongly on inhibitory circuit interactions.

Greentree, Wesley

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 12 minutes

Predator-prey size relationships of small pelagic fish

Small pelagic fish, such as herring and mackerel occupy a key position in marine food webs as abundant and nutritious prey for predatory fish, seabirds, and marine mammals. However, small pelagic fish also compete with and feed on the early life stages of their fish predators. Since the role of small pelagic fish as predators and competitors is likely size-dependent, we compiled available data from 29 small pelagic fish species to identify size-based ontogenetic changes in their feeding ecology. Predator-prey size relationships varied widely among species. Differences among closely related species suggested that prey community composition, not feeding morphology, determines the predator-prey size relationships of small pelagic fishes. Expanded data collection on predator-prey size relationships between small pelagic fish and their prey will be valuable to resolve the complex roles that small pelagic fish play as prey, competitors, and predators in marine ecosystems.

Kuperus, Akina

Degree Sought: PhD
Supervisor(s): Dr. Mark Lewis
Category: Ecology and Evolution
Talk Type: 12 minute

Should I stay or should I go? Modelling mother-calf movement in Svalbard reindeer

Why an animal moves, where it chooses to go, and how these decisions interplay with the external environment are driving questions in movement ecology. However, animals do not live in isolation; their movement both impacts and is impacted by the movement of others, necessitating methods to study inter-animal interactions. For Svalbard reindeer, the most significant inter-animal interaction is between mother and calf. Despite this, the changes in mother-calf interactions from attraction to avoidance and the timing of behavioural emancipation is unknown. In this talk I explore the movement dynamics of mother and calf Svalbard reindeer by introducing a coupled animal movement model. This framework uses movement data to obtain a quantitative description of interaction modes. Understanding these dynamics gives insight into parental investment and calf learning, both of which have consequences for fitness.

Bartlett, Mackenzie

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes
Category: Ecology and Evolution
Talk Type: 12 minute

Quantifying early marine survival and stressor impacts in threatened WCVI Chinook Salmon

West Coast Vancouver Island (WCVI) Chinook Salmon (*Oncorhynchus tshawytscha*) are threatened with local extinction, with multiple populations falling below Fisheries and Oceans Canada's limit reference point due to drastically reduced marine survival. Early marine mortality is widely recognized as a critical driver of population declines, yet mortality rates during this life stage remain unquantified for WCVI Chinook — a significant knowledge gap given their ecological importance, deep cultural significance to Indigenous communities, and historical support of commercial and recreational fisheries. My research aims to address this gap by characterizing stressors and their impacts on early marine survival through three integrated components: developing a modeling framework to generate survival estimates from PIT-tag detection data; analyzing temporal and spatial patterns in gene-expression derived stressor and pathogen exposure data to assess condition in the early marine phase; and examining survival outcomes in the context of individual stressor/pathogen profiles. Together, these components will help quantify estimates of early marine survival for WCVI Chinook, identifying key drivers of mortality to inform conservation and management of this threatened population.

Davies, Hailey

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes, Dr. Dana Haggarty
Category: Marine Biology
Talk Type: 5 minute

FishSounds Educate: Engaging the Public in Ocean Acoustics

Science literacy is essential to ensure public awareness of research findings and foster meaningful engagement with scientific endeavours. However, a disconnect persists between scientific research and public understanding, as outreach is frequently overlooked in favour of data collection, analysis, and publication. Our outreach initiative, *FishSounds Educate*, aims to increase the accessibility of ocean acoustics research, with a focus on fish sounds, noise pollution, and the broader effects of sounds on aquatic life. Bioacoustics provides an engaging entry point into topics such as fish and invertebrate biology, marine ecology, the physics of sound, and human impacts on aquatic environments. To cultivate public engagement, we developed interactive workshops, activity tables, seminars, and a colouring book, adaptable for all ages, from elementary to university-level students and lifelong learners. As of spring 2026, we have reached nearly 4,000 participants with more than 85 visits to schools, universities, aquariums, nature clubs, and public programs. Through FishSounds Educate, we have gained valuable insights into making bioacoustics research more accessible and have applied these lessons to other work, including adapting a recent meta-analysis for young readers. Our experiences highlight the benefits of integrating outreach into research from the outset.

Weir, Ellie

Degree Sought: PhD
Supervisor(s): Dr. Amanda Bates
Category: Marine Biology
Talk Type: 5 minute

Constraint or choice? Beach morphology shapes nest placement in leatherback sea turtles

Climate change is accelerating coastal erosion and reshaping sandy beach habitats worldwide, with consequences for species that depend on these systems for reproduction. Leatherback sea turtles (*Dermochelys coriacea*) nest on high-energy beaches that are susceptible to rapid morphological change. Yet the extent to which local beach morphology constrains nest placement remains poorly quantified at the within-beach scale, with implications for nest vulnerability as shorelines change. Using nest position data from nightly surveys at Pacuare Nature Reserve (Caribbean Costa Rica, 2020-2023), I modelled nesting success across 57 100-m sectors spanning 5.7 km of beach and quantified cross-shore placement using a position ratio metric (0 = high water line, 1 = vegetation line). Beach width significantly predicted nesting success and accounted for observed interannual differences, indicating that variation among years is largely explained by spatial variation in beach morphology. Nest placement was also constrained by beach width, with turtles on narrower segments placing nests closer to the high water line. However, a shift in cross-shore placement in 2022-2023 was not explained by width alone, suggesting that additional morphological features, such as scarps or slope, may further constrain nest positioning. Together, these results indicate that nest placement at Pacuare is strongly shaped by physical constraints imposed by beach morphology, rather than deliberate site selection alone. Sectors that are consistently narrow or narrowing may warrant prioritization for nest relocation, particularly where morphological constraints concentrate nests closer to the tide line and increase exposure to inundation.

Sharpe, Deborah

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 5 minutes

Assessing ringed seal exposure to vessel noise in the Canadian Arctic using a novel perception-based approach

Ringed seals (*Pusa hispida*) are an ice-obligate species adapted to quiet underwater soundscapes. Although integral to both Arctic ecosystems and Indigenous communities, the extent to which they are impacted by increasing vessel noise is largely unstudied. A critical first step is to determine where and when seals encounter noise; however, standard methods for describing exposure often involve temporal or spatial averaging that may mask fine-scale patterns.

Here, we present the first estimates of ringed seal noise exposure and introduce a novel methodology for evaluating exposure at the level of individual seals and vessels. Predicated on biologging data, this workflow incorporates Automatic Identification System (AIS) vessel information, ringed seal hearing measurements, and oceanographic variables to model the range at which vessel noise is perceivable to seals at several frequencies (63, 200, 1000, 3200 Hz).

Results show that less than 5% of estimated seal locations were exposed to vessel noise at any frequency, with substantial individual variation in exposure rates. Vessel source level estimates had the strongest impact on detection ranges, which were often sizeable even in noisy ambient conditions. The greatest number of exposures occurred at 63 Hz, where seal critical ratios were lowest and vessel source levels were highest. No exposures occurred at 3200 Hz, despite vessel source levels often surpassing ambient levels.

This computationally efficient workflow assesses exposure within a meaningful spatial and temporal framework and can be easily applied to other datasets and species to enhance our understanding of noise exposure trends in the Arctic and beyond.

Timmer, Brian

Degree Sought: PhD
Supervisor(s): Dr. Julia Baum
Category: Ecology and Evolution
Talk Type: 5 minutes

Juvenile fishes temporally partition their use of kelp forests as nursery habitat

Kelp Forests are the foundation of coastal habitats, yet in many cases intra-annual biodiversity patterns in kelp forests are un-accounted for or poorly understood. Moreover, young-of-year fish species will often temporally partition their use of kelp forests for nursery habitat, making it important to understand how and when kelp forests are being used by fishes to properly conserve their ecosystem function. We used underwater timelapse cameras, ROV surveys, and SCUBA surveys to monitor fish biodiversity in a bull kelp (*Nereocystis luetkeana*) forest from May to August 2025. These surveys show the importance of early-season surveys for capturing nursery habitat function within kelp forests, and demonstrate the efficacy of underwater timelapse cameras as a tool for marine ecosystem monitoring.

Kolatkova, Viktorie

Degree Sought: PhD
Supervisor(s): Dr. Ryan Gawryluk
Category: Marine Biology
Talk Type: 5 minutes

The story of *Marinomyxa*, the doubted parasite

Marinomyxa (SAR: Rhizaria: Phytomyxea) is a genus of obligate intracellular parasitic protists infecting tropical seagrasses of the genus *Halophila*. Since its first description in 1913, the genus has followed a long and winding path, marked by scientific neglect, repeated renaming, and periods of being dismissed as a doubtful taxon. Even today, the galls it forms in *Halophila* petioles are still commonly mistaken for the plant's fruits! Recently, *Marinomyxa* has attracted renewed attention through its association with the seagrass *Halophila stipulacea*, a prominent invader in the Mediterranean and Caribbean Seas. It is now recognized that at least two parasite species exist, each associated with specific seagrass hosts: *Marinomyxa marina*, parasitizing *H. stipulacea*, and *Marinomyxa halophilae*, infecting shoots of *Halophila ovalis* and *Halophila major*. In our newest study, we expand the current knowledge by presenting new molecular and morphological data on *Marinomyxa* infections in two additional seagrass hosts from geographically distant locations. We show that the cosmopolitan *Halophila decipiens* from Puerto Rico serves as an additional host for *M. halophilae*, and that the vulnerable intertidal seagrass *Halophila beccarii* from Southeast Asia harbours a previously undescribed parasite, designated as *Marinomyxa denhartogi* sp. nov. We also provide evidence that *Marinomyxa* can be detected in environmental sequencing datasets from remote regions such as New Caledonia (South Pacific). Given these findings, it is time to give *Marinomyxa* the recognition it deserves: the status of a ubiquitous seagrass symbiont, one that has been co-evolving with its hosts for millions of years, and one that has outlived its skeptics.

Kecheliev, Vasil

Degree Sought: PhD
Supervisor(s): Dr. Kerry Delaney
Category: Neuroscience
Talk Type: 3 minutes

Mechanisms of activity-dependent cortical sensory adaptation in the rodent hindlimb somatosensory circuitry

Animals are continuously exposed to environmental stimuli to which sensory and central nervous systems have evolved to optimize their detection and processing. Cortical sensory adaptation (CSA) to repetitive stimulation (RS) is a hallmark feature of sensory systems. Despite this, the specific neural contributions and circuitry underpinning CSA are yet to be elucidated. Electrophysiological studies from our lab investigating cortical responses to hindlimb RS show short-term CSA (stCSA) characterized by a decrease in evoked cortical response over the course of a train of 7 tactile stimuli. Sustained RS applied for 30-45 minutes augments the amount of stCSA which persists for up to an hour after the cessation of RS. Our current studies investigate the neural substrate of stCSA and the basis for its persistence following sustained RS focusing on thalamocortical and intracortical circuitry using *in-vivo* two photon imaging of neuronal Ca2+ transients. Complex lateral and vertical interactions especially implicated in the cortex are mediated by both excitatory pyramidal cells and regulatory inhibitory interneurons including those expressing parvalbumin. Neural activity corresponding to Ca2+ reporter fluorescence was isolated to parvalbumin-expressing interneurons or pyramidal principal cells in cortical layers two to four of the primary hindlimb somatosensory cortex. The respective excitatory and inhibitory contributions to neural plasticity in the context of our stimulation paradigm yields insight into the possible mechanisms of neural adaptation in healthy adult mice.

Kaban, Taylor

Degree Sought: MSc
Supervisor(s): Dr. Kerry Delaney and Dr. Craig Brown
Category: Neuroscience
Talk Type: 5 minutes

Brain-wide hemodynamic changes accompanying sensory adaptation and its impairment in a mouse model of Rett syndrome

Rett syndrome (RTT) is a neurodevelopmental disorder caused by *MECP2* mutation. As a transcription factor, MeCP2 plays a vital role in maintaining neural circuits and in activity-dependent plasticity processes. In RTT model mice our lab has shown dysfunction of cortical sensory adaptation (CSA), a form of activity-dependent plasticity. In the contralateral somatosensory cortex (ssCTX) and after an hour of repetitive hindlimb stimulation, neural activity to test pulses decreases by 40% compared to pre-adaptation levels in both control (WT) and RTT mice. After cessation of continuous stimulation, the cortical response to test pulses in WT mice remains persistently adapted, while RTT mice revert to pre-adaptation levels. It was unknown whether persistent CSA extends to distantly connected brain regions or if blood flow dynamics change with persistent CSA. Using intrinsic optical signal (IOS) imaging we show that the impaired persistence of CSA in WT mice extends to the ipsilateral ssCTX. Unexpectedly, we also find that persistent CSA in WT mice is accompanied by a large global stimulus-induced overshoot of the IOS signal which was absent during pre-adaptation measurements and is largest in the retrosplenial and frontal cortical brain regions. This IOS overshoot is consistent with a global increased stimulus-induced perfusion of tissue that develops in response to repetitive neural activity. In RTT mice, this global overshooting IOS response is not present after the cessation of repetitive stimulation, suggesting dysfunction in activity-dependent neuro-vascular coupling in RTT.

Kenny, Eve

Degree Sought: MSc
Supervisor(s): Dr. Jürgen Ehlting
Category: Forest Biology
Talk Type: 12 minutes

The foliar fungal endophyte community in Douglas fir and its role in Swiss Needle Cast mitigation

In the forest ecosystems of the Pacific Northwest, Douglas-fir (*Pseudotsuga menziesii*) supports diverse ecological communities. Despite extensive efforts to characterize these communities, comparatively little research has focused on one of its most inconspicuous components: microbial fungal endophytes. One notable exception, *Nothophaeocryptopus gaeumannii*, is an emerging fungal pathogen that causes the foliar disease Swiss Needle Cast (SNC). *N. gaeumannii* develops fruiting bodies which physically impede gas exchange, resulting in premature needle loss and reduced tree growth. Research from the last decade suggests that this system may emerge from a complex interaction between the host genome, environment, and co-occurring fungal communities. This project aims to (1) investigate the effect of environment and host genetics on foliar fungal endophyte communities and (2) determine whether differences in community structure reflect differences in disease severity at the needle and branch level. Together, these aims advance understanding of forest ecosystem function at the micro-scale while identifying candidate taxa and communities for further study in the context of foliar diseases. Samples were collected from 300 trees comprising 12 families across three sites on Vancouver Island. Culture-based and metabarcoding techniques were used in tandem to catalogue and assemble fungal taxa from within needles. Community structure will be assessed at the tree, family, and site scale, and compared to key disease metrics of needle loss and stomatal occlusion. Preliminary culture-based results indicate an overrepresentation of *N. gaeumannii* and several common benign endophytes across sites.

Tabert, Nathanael

Degree Sought: MSc
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 12 minutes

A Century of Salmon Diet Data

Forage fish play a critical role in marine food webs as energy dense prey for a variety of marine predators. Consequently, understanding shifts in forage fish communities that are likely to occur in response to climate change is essential for characterizing marine food webs. However, many forage fish are not exploited commercially, and fishery-independent surveys are resource intensive, meaning these populations are often not monitored. Predator diets provide an alternative method for sampling forage fish. In BC, Chinook salmon are a marine predator that feed primarily on forage fish; historical data on forage fish in Chinook salmon diets are available for the 1920's-60's. In 2017, the Adult Salmon Diet Program was created to address knowledge gaps in salmon diets and monitor forage fish populations; over 7000 Chinook salmon digestive tracts have been analyzed to date. We used Chinook salmon diets to characterize recent trends in the distribution and availability of forage fish in southern British Columbia. We compare our data to historical information, highlighting major trends over the past century. Herring have been an important prey for Chinook salmon across regions and years. Sand lance have been important across years in certain regions. Northern anchovy have become more common in diets in the Strait of Georgia in recent years. Sardine were important off west coat Vancouver Island prior to the 1950's but have been uncommon more recently. This research provides a novel understanding of shifting forage fish distributions and their availability to Chinook salmon in BC.

Qualley, Jess

Degree Sought: MSc
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 12-minute

Adult non-migratory herring in the Strait of Georgia

Migratory life histories of Pacific herring (*Clupea pallasii*) in the Strait of Georgia (SOG) are not well understood. Most adult herring (age-2+) migrate between spring spawning grounds in the SOG and summer foraging grounds off the west coast of Vancouver Island (WCVI); however, some adult herring remain in the SOG through summer, indicating an alternative non-migratory life history. Non-migratory herring are important prey for Chinook salmon and other predators, and mechanisms driving migratory decisions may influence long-term food web dynamics. This work highlights the ecological importance of non-migratory adult herring in the Strait of Georgia, a previously overlooked component of the ecosystem. Through the Adult Salmon Diet Program (Juanes Lab) and the Salmon–Herring Interactions Project (Pacific Salmon Foundation), we have documented the reappearance of this non-migratory life-history strategy and developed acoustic methods to track seasonal and interannual changes in herring abundance. Otolith stable isotope analysis reveals potential drivers of migration versus residency, differences in adult morphology, and links to increased spawning site diversity in the northern Strait of Georgia. These non-migratory herring provide critical prey for adult salmon, buffer predation on juvenile salmon, and support broader marine predators, while a substantial portion of roe fisheries overlap with these same herring, potentially affecting salmon growth and survival. By collaborating with First Nations, academics, government, and recreational fishers, this work **introduces new acoustic and otolith-based tools that were previously unavailable,** enabling us to monitor, understand, and manage herring populations in ways that support resilient salmon and sustainable fisheries.

Furlonger, David Douglas

Degree Sought: MSc
Supervisor(s): Dr. Steve Perlman, Dr. Katherine Bleiker
Category: Forest Biology
Talk Type: 12 minutes

A novel nematode on the Mountain Pine Beetle

The Mountain Pine Beetle (*Dendroctonus ponderosae*) harbours a diverse community of internal and external organisms, including mites, fungi, parasites, bacteria, and nematodes. Despite extensive research on this ecologically and economically significant forest pest, many of its organismal associates remain poorly characterised. Here, we describe a new species of nematode in the genus *Bursaphelenchus*. This nematode is an external, phoretic species that associates in a unique location beneath the beetle's hindwing in the jugal fold—a small membranous flap. Successful culturing of this nematode has been achieved on multiple different species of necrotrophic fungi and ground-phloem plates. Morphological identification was a collaborative effort and supports its classification as a new species. Phylogenetic analyses are based on multiple ribosomal genetic markers, small subunit SSU 18S and large subunit LSU 28S, helping place this new nematode amongst other described *Bursaphlenechus* groups. Future work will investigate nematode–beetle interactions, including vector switching between beetle hosts, and nematode-tree interactions to investigate whether the nematode is a pathogen to certain conifer tree species.

Penkova, Latina

Degree Sought: MSc
Supervisor(s): Dr. Barbara Hawkins & Dr. Marty Kranabetter
Category: Forest Biology
Talk Type: 12 minute

Linking Ectomycorrhizal Fungal Species, Peroxidase Genes, and Activity in Coastal BC Forests

Forest ecosystems are critical carbon sinks, with soil organic matter representing one of the largest terrestrial carbon reservoirs. Fungal communities regulate how carbon and nutrients move through these systems, yet the role of ectomycorrhizal (ECM) fungi in decomposition remains poorly understood. Traditionally, decomposition of complex plant material such as lignin was attributed to saprotrophic fungi, but emerging evidence suggests ECM fungi may also contribute through oxidative enzymes. This contribution is mediated by class II peroxidases, including manganese peroxidase (MnP), which enable the breakdown of recalcitrant organic matter. Despite this growing recognition, the extent to which ECM fungi actively participate in decomposition, and under what environmental conditions, remains unclear.
This study aimed to quantify and compare ECM MnP activity across nutrient-rich and nutrient-poor soils, identify fungal species associated with high MnP and generalist peroxidase activity, and characterize MnP gene sequences to link genetic capacity with observed enzymatic function. Root samples were collected from Douglas-fir (*Pseudotsuga menziesii*) forests across sites with varying fertility on southern Vancouver Island. Individual root tips were analyzed using colorimetric enzymatic assays to measure MnP and broad-spectrum peroxidase activity. DNA was subsequently extracted from these root tips and used for sequencing to identify fungal species and characterize decomposition-related genes.
Preliminary findings reveal distinct taxonomic patterns in enzymatic activity and gene presence, including unexpectedly high activity and gene abundance in groups not typically associated with peroxidase production. Together, these results suggest that peroxidase gene presence is more broadly distributed across ECM taxa than previously recognized.

Liu, Martin

Degree Sought: MSc
Supervisor(s): Dr. Gregory Owens
Category: Ecology and Evolution
Talk Type: 12 minute

A population genetics approach to resolving the disjunct populations of wild, White-whorled Lupine (*Lupinus microcarpus*).

One of BC's most critically endangered plants is *Lupinus microcarpus*, found only in three locations in Victoria. Although it is also found in the San Juan Islands, the next closest populations are found in California, over 700 km away. Two main hypotheses explain the disjunct population distribution. One hypothesis is that *L. microcarpus* had a continuous ancestral range along the Pacific Coast, but glaciers largely extirpated northern populations. In this idea, the BC populations represent a relict population that survived in a glacial refugia. In the second hypothesis, California is the native range, and European Colonizers or First Nations activity introduced *L. microcarpus* to BC. Currently, these hypotheses have not been tested. I will use population genomics and morphological characteristics to explain the disjunct nature of the populations. Seeds from across the range of California and BC have been collected and will be genotyped using Restriction-site Associated DNA sequencing. Genetic Demographic Modelling using the sequenced markers will identify how long ago the BC and California populations separated. A divergence of over 20,000 years would indicate a glacial relict, while a divergence of less than 10,000 years would indicate human-assisted migration with a specific date differentiating between European or First Nations activity. The results could help inform conservation efforts for the endangered *L. microcarpus* in Canada. A recent divergence suggests that assisted migration from California could restore BC populations. However, an older divergence suggests that the BC population is unique, and supplementation from California would not be beneficial.

Lancaster, Darienne

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes, Dr. Dana Haggarty
Category: Marine Biology
Talk Type: 45 minute exit seminar

Hydrophones, sonars, and fish grunts, oh my! Investigating non-destructive acoustic methods for monitoring vulnerable rocky reef fish

There are 41 rockfish species in British Columbia (BC) and many are important to local fisheries, but multiple species are listed as threatened. Increased monitoring of rockfish populations has been recommended by the Department of Fisheries and Oceans. However, common survey methods require the use of lethal hook and line sampling or visual surveys. These methods can be destructive to fishes or are time consuming and expensive. Active and passive acoustic monitoring techniques are non-invasive and growing in popularity for fisheries research. However, there is a lack of information on how to use these methods to monitor rockfish. To address this lack of quantitative tools, this research project develops new acoustic methods for monitoring rockfish. We use a passive acoustic localization array to identify wild, species-specific fish sounds. We identify calls for eight soniferous fish species, five of which have never been documented or described. We then use random forest models to test the feasibility of differentiating species-specific fish calls. This project also explores the complexities of fish vocalizations including behaviour specific sounds like chasing and feeding, the influence of fish size on sound characteristics, and species-specific calling patterns. We also explore diel patterns in fish calling and compare acoustic and video abundance estimates. Finally, using active acoustics, we develop a novel method for detecting rockfish hotspots in Mowachaht/Muchalaht territory using paired echosounder and ROV surveys. This project lays the groundwork for developing quantitative, acoustic methods for monitoring rockfish using species-specific fish sounds and rapid echosounder surveys.

Csordas, Matt

Degree Sought: PhD
Supervisor: Dr. Julia Baum
Category: Marine Biology
Talk Type: 12-minute

Using multiple ocean models to evaluate the distributional drivers and future of BC kelp forests.

Recently, climate change driven kelp forest declines have inspired a global focus on kelp forest conservation and restoration. However, prioritizing actions that will likely be successful long-term requires understanding where suitable kelp forest habitat is currently and how this may change. Species distribution models (SDMs) have been used for decades to assess conservation priorities in changing environments, however, projecting SDMs to future scenarios can emphasize issues with niche truncation in regional models or poor data resolution at larger spatial domains. In British Columbia bull kelp and giant kelp form complex kelp forests, have experienced climate change related losses, and are conservation and restoration priorities. We fit SDMs for these species using three different predictor datasets (two regionally parameterized ocean models and one global dataset) across two different spatial domains (BC-wide and coastwide (California to BC)) to explore how these factors influence model predictions, projections, and occurrence/predictor relationships. Our results showed considerable agreement between models when predicting present-day distributions but massive differences in future projections. SDMs fit to regional ocean models predicted large losses of suitable habitat while SDMs fit to the global dataset predicted stability regardless of spatial domain. This was driven by differences in the importance of and response to predictor variables between models and highlighted the global dataset's inadequacy in BC's complex nearshore. Our study emphasizes the importance of considering predictor dataset limitations when using SDMs in planning future ecosystem stewardship and underscores the need for datasets representing future ocean conditions at fine scales over large spatial domains.

Black, Morgan

Degree Sought: PhD
Supervisor(s): Dr. Sarah Dudas, Dr. Francis Juanes
Category: Marine Biology
Talk Type: 12 minute

Clam gardens foster diverse, productive nearshore communities.

Clam gardens, ancient intertidal rock-walled terraces built and maintained by Indigenous peoples of the Pacific Northwest Coast, support distinct, diverse, and more productive nearshore marine communities than unmodified reference beaches. We surveyed fish and mobile invertebrate communities across 46 surveys at 18 sites on Calvert and Quadra Islands, in the spring and summer of 2016 and 2017. Clam gardens supported a significantly different community composition. They were home to 44 of the 47 taxa recorded, including 11 taxa exclusive to walled beaches—among them juvenile pink salmon (*O. gorbuscha*), steelhead trout (*O. clarkii*), and California spot prawn (*P. platyceros*)—while reference sites yielded only 3 unique taxa from 36 total. Mean abundance was approximately double, and biomass was one and a half times greater on clam gardens. Invertebrate abundance was significantly higher on clam gardens, and the interaction between beach type and season was a significant predictor of fish abundance, with clam gardens exhibiting a stronger summer increase in abundance. Across all sites, distance to a structural refuge was a significant predictor of fish abundance and invertebrate biomass, pointing to a potential mechanism driving faunal productivity. Clam gardens increase biodiversity and productivity in nearshore ecosystems, which is a testament to the enduring ecological effectiveness of Indigenous mariculture and its potential relevance to contemporary coastal conservation.

Herrington, Cara

Degree Sought: PhD
Supervisor(s): Dr. Amanda Bates
Category: Ecology and Evolution
Talk Type: 12 minutes

A century of expansion in a generalist scavenger demonstrates distinct range shift stages

Range shifts are some of the most well documented responses to environmental change, yet few studies trace how migratory species shift across both breeding and winter seasonal ranges simultaneously at a poleward range edge. The Turkey Vulture (*Cathartes aura*) offers a data-rich system for examining this process, with over 130 years of records in British Columbia (BC) across museum specimens, historical archives, and contemporary public datasets. Using these sources, we document the species' northward expansion through three distinct, cumulative phases: (1) initial colonization and establishment at the range edge, (2) population increase and spatial range filling, and (3) emerging winter occupancy as individuals begin persisting year-round at locations typically considered part of the species' breeding range. We show that species-specific traits that facilitate breeding-season expansion such as obligate thermal soaring and olfactory carrion detection, simultaneously impose biophysical constraints on winter persistence at high latitudes. The progressive relaxation of these constraints through climatic warming and anthropogenic resource subsidies, as well as the presence of geographic barriers such as the Juan de Fuca Strait appear to be driving a transition from obligate seasonal migration toward year-round occupancy in parts of the province. Breeding-range expansion and winter-range expansion do not advance at equal rates, as latitudinal extent of winter occupancy lags behind breeding presence. By examining expansion as a sequential, multi-phase process in a migratory species expanding across both seasonal realms, this synthesis provides a structured framework for interpreting migration-to-residency transitions in other partial migrants experiencing poleward range shifts under ongoing environmental change.

Lawton, Maggie

Degree Sought: PhD
Supervisor(s): Dr. Ryan Gawryluk
Category: Neuroscience, Cell, and Molecular Biology
Talk Type: 12 minute

A seriously squishy flagellate: Phylogeny and anaerobic metabolism of an undescribed Rhizarian

In most eukaryotic organisms, mitochondrial ATP production relies on oxygen. However, there are groups scattered across the tree of eukaryotes that are capable of living in environments that lack oxygen. These organisms often have modified mitochondria known as mitochondria related organelles (MROs) with alternate metabolic pathways that allow for continued ATP production in anoxic environments. Several such anaerobic taxa are found within supergroup Rhizaria, including the currently undescribed 'seriously squishy flagellate' (SSF). SSF is a sediment-dwelling anaerobic eukaryovore found in a poorly classified lineage of Rhizaria. This study used single-cell sequencing techniques to obtain the transcriptome of SSF for phylogenomic and metabolic analyses. The transcriptome was used to identify MRO-targeted genes and map their ATP-generating metabolic pathways. SSF was identified as having a hydrogenosome-like MRO, which possesses an alternate hydrogen-producing version of substrate-level phosphorylation. In addition, SSF appears to contain a mostly complete tricarboxylic acid (TCA) cycle, but only complexes I and II of the electron transport chain. The missing enzymes suggest that the TCA cycle of SSF may act in reverse to utilize ATP-generating steps earlier in the cycle, a strategy commonly seen in anaerobic eukaryotes. This degree of reduction in mitochondrial proteins is unique within known Rhizarians, but similar features are found in distantly related anaerobes. Further study of these anaerobic metabolic strategies and their taxonomic links will help us understand how these organisms can survive in anoxic environments, as well as provide hints towards their origins.

Rastello, Kevan

Degree Sought: PhD
Supervisor(s): Dr. Mark Lewis
Category: Ecology and Evolution
Talk Type: 12 minutes

Beetle the cold: does winter temperature affect post-emergence fecundity?

Insects are ectotherms that rely on external temperatures to regulate their metabolic rate and energy use. Historically in temperate ecosystems, cold winters have kept insect pest populations in check by causing increased mortality rates. However, accelerating climate change is warming winters faster than summers, increasing overwinter survival of pest species. Climate warming has significantly contributed to the spread of the Mountain Pine Beetle (MPB) (*Dendroctonus ponderosae*), a bark beetle pest from Western North America. Warmer temperatures have facilitated MPB expansion eastwards into the boreal forest and across Canada. Recent outbreaks in the 2000s have killed approximately 54% of the merchantable pine in British Columbia. The freeze-avoidant MPB successfully overwinters by accumulating cryoprotectants, such as glycerol, which lower its freezing point as temperature decreases in winter. Synthesizing these compounds has long been recognised as energetically costly, yet how this investment affects post-winter fecundity across varying winter thermal conditions remains unquantified. As winters warm and cold-induced mortality decreases, we hypothesise that reduced cryoprotection demands free energy that is reallocated to growth with impacts in other fluxes such as reproduction. To test this hypothesis, we present the first Dynamic Energy Budget (DEB) model to explicitly incorporate energy allocation to cryoprotection as an additional energetic cost within somatic maintenance. This work has implications for understanding the magnitude of future MPB outbreaks, and more broadly for pest populations whose dynamics are shaped by cold-hardiness mechanisms under climate change.

Nikoo, Mitra

Degree Sought: PhD
Supervisor(s): Dr. Amanda Bates
Category: Marine Biology
Talk Type: 12 minute

Liberté, égalité, égoutté: Synergies between sanitation, tourism, and the UN Sustainable Development Goals

Coastlines with coral reefs offer attractive vacation destinations and many locations are actively growing their tourism economy; however, it can lead to environmental problems. Excess nitrogen pollution from sewage can harm coral biodiversity, increasing risk of bleaching and disease. We estimated dietary coastal resident nitrogen (CRN) and coastal visitor nitrogen (CVN) for 20 hotspots from the Caribbean, Red Sea, and Indo-Pacific. We then examined whether the global tourism collapse due to the covid-19 pandemic persisted, if a pandemic signal could be detected in the chlorophyll response to nitrogen, and the overall relationship between nitrogen from both residents and inbound visitors and chlorophyll.
We found a persistent tourism decline lasting from 2020-2022, but this disruption did not cause a detectable pandemic signal in the response of chlorophyll to nitrogen. The overall relationship between CRN, CVN, and chlorophyll was nonlinear: as CRN increases, the rate at which chlorophyll increases dampens; and an increase in CVN is associated with a decrease in chlorophyll with a stronger effect in an improved sanitation scenario. Our results highlight the importance of sanitation infrastructure in controlling how nitrogen from residents and visitors enters coastal waters and suggests that tourism-related pollution may decrease where tourism revenue supports improved infrastructure and governance. Considering the relationships between tourism, sanitation, inequality, and governance, rather than a purely ecological discourse to explain a pollution response, can inform policies for achieving the UN Sustainable Development Goals.

Bohlender, Nick

Degree Sought: MSc
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 12 minute

Evaluating Survival of Wild Coho Salmon Using PIT and Coded Wire Tagging Methods

While Coho Salmon (*Oncorhynchus kisutch*) are of significant ecological, cultural, and economic importance, many populations have declined due to environmental change and increasing anthropogenic pressures. Effective monitoring of these populations relies on accurate estimates of marine survival, which have traditionally been derived using coded wire tags (CWTs). CWTs have been widely used in hatchery programs to estimate survival and stock composition. However, their application in wild populations is limited, as estimates rely on extensive sampling in fisheries and spawning areas and do not provide individual level data needed to determine fine-scale drivers of survival. Passive Integrated Transponder (PIT) tags provide an alternative approach, enabling continuous, non-lethal detection of individuals and the collection of detailed biological data. Long term monitoring programs on Vancouver Island have generated multi-year datasets for wild Coho Salmon that include both PIT and CWT tagging. However, it remains unclear whether PIT tags provide survival estimates comparable to, or more accurate than, those derived from CWTs, and to what extent differences between methods reflect methodological bias. The purpose of this study is to (1) compare marine survival estimates derived from PIT and CWT tagging methods, and (2) evaluate using PIT tags how smolt size, migration timing, and freshwater environmental conditions influence survival across four Vancouver Island rivers. Together, these findings demonstrate how methodological differences influence survival estimates and highlight the value of individual-based tagging for understanding survival dynamics of Coho Salmon.

Lucyrio, Daniel

Degree Sought: MSc
Supervisor(s): Dr. Diana Varela
Category: Marine Biology
Talk Type: 12 minute

Beyond Diatoms: Silicon Uptake Along the Pacific Northeast

For decades, marine biogeochemistry has treated silicon cycling as a "diatom story." Because diatoms require silicic acid to build their frustules and often dominate export-driven blooms, silicic acid uptake has commonly been used as a proxy for diatom activity and, by extension, for larger phytoplankton that drive carbon export. While useful, this framework assumes that small phytoplankton contribute minimally to silicon uptake, an assumption that remains poorly tested. This study challenges that view by quantifying size-fractionated silicic acid uptake across Line P, the world's longest-running oceanographic time series, during April and September 2025. Shipboard incubations were conducted alongside measurements of chlorophyll *a*, biogenic silica, carbon and nitrogen uptake, taxonomy, and hydrography to evaluate how size structure regulates silicon assimilation. Preliminary results reveal a clear seasonal shift in phytoplankton size structure. In April, silicon uptake was primarily driven by larger (>20 µm) cells, despite substantial contributions of smaller cells to biomass offshore. By September, larger cells continued to dominate both uptake and biomass, indicating a shift toward a less classical size structure. However, for the first time, picophytoplankton (<2 µm) silicon uptake were measured and consistently exhibited measurable silicic acid uptake and biogenic silica stocks in both seasons, challenging the assumption that they are functionally negligible. These findings indicate a decoupling between biomass and biogeochemical function and suggest that silicon demand may persist even when large diatoms are not dominant. This has important implications for future ocean scenarios, where shifts toward smaller phytoplankton are expected under climate change predictions.

Rozanski, Sarah

Degree Sought: MSc
Supervisor: Dr. Rana El-Sabaawi
Category: Ecology and Evolution
Talk Type: 12 minutes

How the River Shapes the Fish: Characterizing Morphological Diversification along River Gradients Using the Threespine Stickleback.

Such wonder lies in the diversity of life—countless iterations of form and function shaped by natural selection and chance. How does such diversity arise? The threespine stickleback (*Gasterosteus aculeatus*) provides a powerful model for studying early stages of adaptive divergence. Following glacial retreat approximately 12,000 years ago, marine populations repeatedly colonized freshwater environments across North America. These environmental transitions have led to parallel evolution, with marine and freshwater populations evolving distinct morphological traits—for example, heavily armoured marine fish and lightly armoured freshwater forms with different feeding strategies. In this study, I investigate patterns of phenotypic and genomic divergence across three river gradients on southern Vancouver Island (Sooke, San Juan, and Koksilah), where marine and freshwater forms come into secondary contact. Using geometric morphometrics, environmental data, and chromosomal inversions as genetic markers, I test whether adaptive divergence is repeatable across rivers, whether it varies among functional trait groups, and whether different chromosomal inversion regions contribute unequally to divergence. I find that divergence is structured along environmental gradients but is not fully parallel across rivers and that different trait groups and genomic regions contribute unevenly to divergence. These results suggest that while environmental gradients promote adaptive divergence in sticklebacks, the outcomes are contingent on river-specific conditions and genomic architecture. Overall, this work provides insight into how adaptive divergence can proceed in the presence of gene flow. It also demonstrates limits to the predictability of parallel evolution, with implications for the conditions under which divergence may ultimately lead to speciation.

Angeley, Maxine

Degree Sought: MSc
Supervisor(s): Dr. Steve Perlman
Category: Forest Biology
Talk Type: 12 minute

Characterizing a novel fly-nematode-bacteria system

Intracellular bacteria often heavily influence parasite fitness, yet bacterial symbionts of insect-parasitic nematodes remain almost entirely unexplored. My research focuses on a fascinating and unusual system: sphaerocerid ("lesser dung") flies parasitized by an undescribed *Howardula* nematode that harbors a highly reduced *Wolbachia* symbiont. This association is especially intriguing because no other insect-parasitic nematode is known to host *Wolbachia*. The symbiont's extremely reduced genome and ubiquitous presence in the nematode suggests a long-standing obligate relationship, but its functional role remains unresolved. My aims are to describe the nematode's morphology and life cycle, quantify the effects of infection on host fitness, and test whether *Wolbachia* is required for nematode survival or reproduction. To address these questions, I combine field collection, laboratory culture, controlled infections, 18S/COI barcoding, 16S microbiome profiling, DIC microscopy, FISH localization, and antibiotic-curing experiments. A major recent advance has been successfully maintaining the nematode in laboratory fly culture, which now makes experimental manipulation possible. Together, this work introduces a promising new model for understanding how intracellular bacteria emerge, persist, and influence the evolution of intimate symbioses.

Jiaxin, Zhang

Degree Sought: MSc
Supervisor(s): Dr.Constabel Peter
Category: Molecular Biology
Talk Type: 12 minutes

Overexpression of SARD1 Reveals Its Role in Salicylic Acid Biosynthesis in Diploid Potato MSEE737-05

Salicylic acid (SA) is a plant hormone and plays an important role in inducing host defense responses upon pathogen infection. Although its function in plant defense is well studied, its biosynthesis in plants is not completely understood. It has been demonstrated that there are two pathways to synthesize SA: isochorismate synthase (ICS) and phenylalanine ammonia-lyase (PAL) pathway. The ICS pathway has been fully elucidated in *Arabidopsis thaliana*. Systemic acquired resistance deficient 1 (SARD1) was found to be a key transcription factor that positively regulates SA accumulation in the ICS pathway in *Arabidopsis thaliana*. Potato is a relatively easy plant to transform, which has played a significant role in the recent application of biotechnology. In this study, SARD1 overexpression transgenic potato (*Solanum tuberosum*) lines were generated in diploid potato MSEE737-05 to investigate its regulatory role in SA biosynthesis. The transgenic lines were evaluated for changes in SA contents and the expression levels of SA biosynthesis-related genes. Overall, this study aims to elucidate the function of SARD1 in regulating SA biosynthesis in diploid potato.

Centeno Duque, Manuel

Degree Sought: MSc
Supervisor(s): Dr. Nicole Templeman
Category: Neuroscience, Cell, and Molecular Biology
Talk Type: 5 minute

Effect of reversal of hyperinsulinemia on female reproductive function

Obesity, a widespread health concern, is often tied to poor reproductive health in women (e.g. irregular menstrual cycles, infertility, gestational diabetes). Obesity is correlated with increased levels of circulating insulin, hyperinsulinemia, often resulting from a poor diet and lack of exercise. Insulin, a hormone crucial for regulating blood sugar, has been demonstrated to accelerate the decline in fertility with age, reproductive aging. While lifelong prevention of hyperinsulinemia has shown increased fertility in female mice, it remains unclear if reversing hyperinsulinemia in adulthood can slow reproductive decline. This study aims to explain the effects of reducing insulin gene dosage in adult females to slow the decline of reproductive function. Using an adeno-associated virus, mice will have a partial reduction in insulin production during adulthood. All mice will be divided into two groups based on diet: one fed a standard diet and the other a high-fat, high-sugar diet to induce obesity. To assess mice's metabolic health, body weight and glucose and insulin levels will be measured. To assess reproductive health, hormone levels, reproductive cycles, fertility, and pregnancy outcomes will be monitored. The effects of lowering insulin levels in adulthood will shed light on how combatting hyperinsulinemia may improve fertility and reduce pregnancy complications, even after lifelong exposure to an obesity-inducing diet. As the age at childbirth continues to arise in Canada, this proposed work will elucidate the impacts of a reduction of hyperinsulinemia on female reproductive aging.

Maher, Bridget

Degree Sought: MSc
Supervisor(s): Dr. Francis Juanes
Category: Marine Biology
Talk Type: 5 minute

Prostrate “canopy” kelps on the coast of Vancouver Island

Canopy-forming kelps are foundation species in temperate ecosystems. Abiotic and biotic conditions can alter the physical structure of these kelps, which then influences the habitat they provide for biological communities. Prostrate forms of Macrocystis in Barkley Sound, British Columbia, are a notable example of this process. Yet, limited data exists on these unique ecosystems’ physical attributes and the biological communities they support. Here, we examine kelp forest metrics (e.g. density, biomass, length and environmental conditions at sites with prostrate and standing Macrocystis morphologies. We found that depth, temperature, substrate ratio and relative wave exposure mediated the presence of prostrate Macrocystis forms to varying degrees. The composition of biological communities varied across site types, with a reduction in herbivorous grazers at prostrate sites likely due to the high proportion of soft substrate. Uniquely, these prostrate kelps have persisted in areas where standing kelp forests have been extirpated during recent marine heat waves. Integrating the presence of these sites and the conditions that allow them to occur into current remote sensing methods and species distribution models will benefit efforts to monitor Macrocystis populations within changing coastal ecosystems.

Donaldson, Braeden

Degree Sought: PhD
Supervisor(s): Dr. Francis Juanes
Category: Ecology and Evolution
Talk Type: 5 minute

Enhancing Predator Avoidance, Neuroplasticity, and Survival in Hatchery-Reared Coho Salmon (*Oncorhynchus kisutch*)

Hatchery supplementation of Coho salmon aims to restore recent population declines. Captive-reared fish, however, often lack survival skills such as predator detection and avoidance needed to survive after release. This study applies an iterative approach to improve antipredator behaviour and post-release survival in juvenile Coho salmon using high-risk conditioning. High-risk environments can be simulated in hatcheries using damage-released alarm cues. Alarm cues are passively released from damaged epidermal tissue, such as during an attack by a predator, and elicit predator avoidance responses in nearby conspecifics. Alarm cues can be isolated by macerating the dermal tissue of donor fish. The method of donor fish euthanasia, however, may influence alarm cue integrity. Standard euthanasia protocols use blunt force trauma (BFT), as chemical euthanasia using tricaine methanesulfonate (TMS) is thought to interfere with cue effectiveness. Here, we tested behavioural responses of hatchery-reared Coho parr to alarm cues derived from donors euthanized using BFT versus TMS. Both types reduced movement compared to controls. Cues derived using BFT produced an immediate reduction in movement. TMS-derived cues also reduced movement, but the response was smaller in magnitude. These results show that hatchery-reared Coho respond to alarm cues and that donor euthanasia method may affect the magnitude of behavioural response. Alarm cues derived using TMS elicit antipredator behaviour, but detection of this response may require larger sample sizes. This insight provides a foundation for future work to use alarm cues to prepare hatchery Coho for high-risk conditions and improve survival after release.

Jewett, Emily

Degree Sought: MSc
Supervisor(s): Dr. Nicole Templeman
Category: Molecular Biology
Talk Type: 5 minute

Metabolic and Reproductive Effects of Insulin Levels on a Mouse Model of Polycystic Ovary Syndrome

Polycystic ovary syndrome (PCOS) is estimated to impact 6-13% of reproductive-aged females globally, making it the most common endocrine condition experienced in this age range. Hormonal dysregulation in PCOS patients negatively impacts their reproductive system, often leading to infertility and additional complications such as heightened risk of gestational diabetes and miscarriage. However, PCOS affects more than just the reproductive system, it is also associated with impacts to metabolic health, such as the development of insulin resistance and/or increased circulating insulin levels, hyperinsulinemia, seen in 50-70% of patients. Increased circulating insulin has previously been seen to contribute to PCOS pathogenesis in a variety of ways, yet it remains unknown if PCOS symptoms can be improved by reducing hyperinsulinemia in patients. To further explore the possible benefits of reducing insulin levels in PCOS patients this study uses a previously established prenatal androgenized PCOS mouse model in mice with genetically modulated endogenous insulin levels. This model will allow for the observation of how reduced endogenous insulin levels may impact the onset and progression of metabolic and reproductive dysfunction in PCOS-like mice, expanding current knowledge of insulin's role in the development of symptoms in this prenatal androgenized PCOS mouse model.

Clark, Lindsay

Degree Sought: PhD
Supervisor(s): Dr. Amanda Bates & Dr. Cherisse Du Preez
Category: Marine Biology
Talk Type: 5-minute

Incorporating biological interactions in climate change vulnerability frameworks for the deep Northeast Pacific

Climate change vulnerability frameworks are essential conservation tools for the management and monitoring of ecosystems undergoing rapid environmental change. By estimating the exposure, sensitivity, and capacity to adapt to changing conditions using species-specific traits, these frameworks attempt to identify species with increased vulnerability and therefore increased need for conservation intervention. However, interactions between species, an inherent feature of ecosystems effecting overall biodiversity, functioning, and stability, are often neglected in traditional frameworks, potentially reducing accuracy of vulnerability assessments. Here, using a trait database developed for the Offshore Pacific Bioregion of the Northeast Pacific, we examine the effects of including biological interactions within traditional climate change vulnerability frameworks, focusing on species with a dependence on biotic substrate occurring below 200 m depth. We find that biological interactions can have varying impacts on the overall vulnerability of dependent species, with the potential to ameliorate exposure, reduce sensitivity, and increase adaptive capacity. However, the beneficial impacts of biological interactions are heavily dependent on the vulnerability and quantity of the associated species involved, with fewer or more vulnerable associated species increasing the vulnerability of dependent species. These findings suggest that including biological interactions within climate change vulnerability frameworks can improve assessments essential for conservation efforts and highlights the importance of additional research on biological interactions, particularly in remote habitats such as the deep-sea.

Many Thanks To:

2026 Graduate Symposium Organizing Committee

Co-Chairs:

Bethany Robson and Mika de Breuyn

Finance Committee:

Martin Liu, Bridget Maher, Roderick Y, Hailey Davies, Milos Ristovic

Abstract Committee:

Kinga Kotulska, Alec Jones, Sarah Ronzanski, James Moran, Liam Hoogewerf

Tech Committee:

Jake Dingwall, Brian Timmer, Madeleine Abbott, Nick Benson, Vasil Kecheliev

Media Committee:

Ethel Wai, Sydney Houston, Colby Sandberg, Bryce O'Brien, Nadja Burkart

Social Committee:

Nathanael Tabert, Maddy Thomson, Sema Abu Shamleh, Emily Jewett, Manuel Centeno Duque

Coffee Committee:

Maxine Angeley, Mackenzie McNiven, David Furlonger, Maggie Lawton, Latina Penkova, Mackenzie McNiven, Joel Bourgeois

Financial Contributors

Department of Biology
Graduate Student Society
UVic Bookstore
Fernwood Coffee Company

Session Chairs

Eve Kenny
Muskan Karmani
Rachel Orr
Deborah Sharpe
Vasil Kecheliev

We would also like to thank the following individuals for their contributions:

Doug Briant
Steve Perlman
Michelle Shen
Jenica Enquist
Mitra Nikoo
Judges

Sponsors


UVIC
UNIVERSITY OF VICTORIA


FERNWOOD
COFFEE COMPANY
VICTORIA, BC, CANADA