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Abstract Booklet

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12 minute presentations (alphabetical order by last name)

Bolded Name (presenting author)

Investigating the resilience of kelp forests to harvest amid a rapidly changing ocean

Allchurch, A., Denley, D., Thompson, M., Peeler, M., Kowalchuk, K., Salomon, A.

While kelp-related activities have become a major component of the global blue economy, the resilience of kelp forests to forest-scale harvest remains understudied. To determine how kelp harvest affects ecological and biophysical characteristics of an entire kelp forest, we conducted a seascape-scale harvest experiment of giant kelp (*Macrocystis pyrifera*). In collaboration with Indigenous kelp harvesters, knowledge holders, and leaders from the Kwakiutl First Nation, in addition to government and university scientists, we established harvested and unharvested control sections in three large kelp forests which ranged from 6.91 to 25.62 hectares. Harvesters then decided which kelp forest to harvest based on a 20% harvest quota, sea condition, kelp condition, and travel time. While harvesters consistently removed an average of 7100 +/- 325 kg of kelp from the top 5.81 +/- 2.17m of the forest canopy per harvest event, overall removing <10% of surface canopy over the season, the occurrence, timing, and magnitude of kelp harvest varied across each experimental site. We found that kelp forests appear to be resilient to current kelp harvest levels and practices. The hand harvest of surface canopy fronds removing <10% of available canopy biomass had surprisingly small effects on kelp forest surface density, subsurface frond recovery, canopy kelp area, and potential reproductive output of kelp plants. Our results underscore the resilience, yet context-dependence, of kelp forests to harvest. More broadly, the co-design, co-production, and co-implementation of this experiment, conducted at ecologically and socially relevant scales, models an equitable way to inform a more resilient and just blue economy.

Does flow speed affect blade number in the bull kelp, *Nereocystis luetkeana*?

Breitkreutz, A., Martone, P.

The bull kelp *Nereocystis luetkeana* is a foundational species of temperate, nearshore environments. Its sporophytes, known for their large size and unique, multi-bladed morphology, begin life with a single blade. Additional blades are formed by dissecting existing ones lengthwise as the thallus grows. Blade morphology in this species is plastic and responsive to environmental flow speed. Mature thalli from more exposed sites tend to have more blades than those from protected sites, suggesting that blade number - not just blade morphology - may be plastic. The drag experienced by an intact bull kelp thallus is only a fraction of what its many blades experience in isolation, suggesting that splitting blades into increasingly subdivided parts has a hydrodynamic benefit. Thalli might respond to high flow by increasing their blade number, or blade number could be genetically determined, with site variations due to genetic drift or local adaptation. We investigated if blade number is plastic in response to flow by growing sporophytes from two different sites in four different flow treatments under otherwise identical culture conditions. Sporophytes developed significantly more blades in faster flow, suggesting that blade number may be a plastic trait in response to flow speed and that increasing blade number may be another drag-reducing strategy in the bull kelp.

Kelp culturing and thermal physiology research for collaborative industry restoration

Burns, R., Supratya, V., Martone, P.

Kelp forests are important marine ecosystems that are threatened by coastal development and climate change. In the Burrard Inlet, the canopy kelp species bull kelp (*Nereocystis luetkeana*) exists in small, fragmented populations along the heavily developed coast. A construction project at Neptune Terminals (Port of Vancouver) has led to a unique collaboration with the University of British Columbia to redesign a shipping berth with kelp in mind. The restoration goals are to establish a self-sustaining kelp population that retains the genetic diversity of the starting kelp bed while increasing resilience to heat stress. To achieve these goals, multiple initiatives are being undertaken in the lab that build off of recent and ongoing phycological research. Kelp germplasm from the terminal is being stored in a gametophyte library to be grown after construction. An ongoing strain selection experiment will determine the kelp individuals that are most resilient to heat stress, which will be outplanted in greater numbers. For outplanting, kelps are grown on tiles using recirculating flumes. Trial outplanting of these tiles in the terminal has produced sporophytes up to 40cm in length, and future outplanting efforts that match the window of natural bull kelp recruitment will determine whether this method can produce reproductive individuals. Kelp restoration in highly populated areas must be able to coexist with infrastructure, yet be resilient in the face of a changing climate. This project demonstrates how these at times conflicting values can work together to protect an ecosystem.

The Environmental Drivers of Isolumes and Impacts on Krill Vertical Migration

Chawarski, J.

Krill are an important component of coastal and continental shelf ecosystems. Through their diel vertical migration behavior, they mediate energy transfer throughout the water column, fueling the oceans biological pump. The timing and magnitude of their migrations varies seasonally, not only in response to changing photoperiod, but also due to variability in light penetration due to oceanographic conditions. Using a suite of environmental data from autonomous observatories, collected during productive summer conditions in Barkley Sound, I investigated the impact of bloom conditions on krill migration timing. I hypothesize that phytoplankton bloom strength, which can inhibit light penetration, is positively correlated with migration timing relative to photoperiod. This work contributes to an improved understanding of salmon prey and their impact on carbon cycling in coastal water.

The current relevance of creekwalking

Clavenger, I.

Escapement estimates of all five Pacific salmon species have relied on the persistent seasonal efforts of charter patrolmen or "creekwalkers" who count and keep track of salmon returning to their natal streams. Creekwalking has been the most widely adopted survey method for collecting spawning and habitat data on salmon in British Columbia since the mid 1900s. 40 years after its inception, budget cuts, changes in management objectives and government structure, have all led to the detriment of on the ground efforts coast wide. Currently, First Nations, NGOs and academic groups are working together to continue the long standing datasets and are taking matters into their own hands. Within this long standing methodology is an great opportunity to connect with our surroundings and ourselves. Salmon often exist in unison with weather, tides and other natural cycles. This forces those participating in creekwalking to abide by elements out of their control and witness one of natures most incredible migrations. This sense of connection to non-human cycles entices one to ponder on our purpose and place.

Cold region *Nereocystis Luetkeana* sporophytes outperform those from warm regions

Cross, S., Gray, A., Gregr, I., Parsons, A., Steell, C.

Rising ocean temperatures threaten marine ecosystems, impacting foundational species such as *Nereocystis luetkeana*. While warmer temperatures have been observed to cause declines in the macroscopic life stages of *N. luetkeana*, effects on the microscopic life stages are not well-documented. In this study we explored how warmer temperatures impact *N. luetkeana* gametophyte and sporophyte development from warm and cold source regions in the Salish Sea. We hypothesized resilience in gametophytes but changes in sporophyte development due to regional adaptation and plasticity. We cultivated Gametophytes from warm and cold regions and exposed them to temperatures of 10 and 14ºC. In 14ºC, gametophytes had significantly fewer reproductive structures and lower reproductive success than in 10ºC water, with the 10ºC treatment producing more sporophytes. Gametophytes from cold regions produced significantly more and larger sporophytes than those from warm regions. This suggests gametophytes exhibit plasticity by decreasing reproductive structures in warmer waters, leading to negative implications for *N. luetkeana* forests. Sporophytes from cold regions were less impacted by higher temperatures, possibly due to adaptation or number of parents and their fitness. Our research indicates that using cultures from cold regions, incubated in colder temperatures, enhances success in outplanting due to their adaptive and plastic qualities.

What happens to marine biota after we stop bottom trawling

De Capitani, J., Foster, S., Vincent, A.

Bottom trawling is a widespread fishing technique that has been associated with overfishing, high rates of bycatch and marine habitat destruction. My research investigates if marine spatial bans on bottom trawling are effective at mitigating impact and restoring biodiversity damaged by this fishing practice. I conducted a systematic mapping of studies (peer reviewed and grey literature) that have assessed the ecological outcomes of bottom trawling spatial exclusions. I also synthetized their findings using vote counting and correlated ecological outcomes to characteristics of the area and of the spatial planning, implementation, and management processes. Our preliminary results indicate that recovery after bottom trawling is possible and happens in a variety of contexts but can take a long time. Some 53% of the studies revealed improvement in the biological parameters assessed, while 40% showed mixed results or no statistically significant changes. Results will enhance the understanding of how ecological outcomes of bottom trawling spatial closures may vary depending on the ban history and on area characteristics. This knowledge can be used for guiding and improving conservation strategies and policies that aim at protecting and restoring biodiversity degraded by bottom trawling.

Life history tradeoffs in *Harmonia axyridis*

Desjardin, G., Williams, T.

Individual quality (variable and correlated with fitness) is determined by phenotypic (eg. Body size) or life-history traits (eg. fecundity). Although many studies have focused on phenology and fecundity, few studies have researched the causes and consequences of intraspecific variation of egg size. Fewer studies have considered the impact of warming temperatures due to climate change on ectotherms and their future fecundity. Climate predictions suggest insects are more sensitive to warming temperatures. Exploring individual quality in *Harmonia axyridis*, the Harlequin ladybird, a globally introduced predatory generalist, allows us to study a system without post-hatching care. We hypothesize that a) *H. axyridis* egg size will decrease under high temperatures as individual females will allocate more resources to larger clutch size and fewer resources to individual egg size (maximizing female fitness), but b) smaller egg size will not come at a cost in terms of offspring fitness because larvae from smaller eggs will have higher viability at higher temperatures. Our findings for individual egg size variability will provide base knowledge that can project population trends under warming temperatures. Further, it will contribute to a better understanding of the trade-offs and the mechanisms behind egg size variation within a species.

The Impact of Tire-Derived Toxicity

Garcia, J.

Storm water and urban roadways runoff contain a complex mixture of toxic pollutants originating from traffic-related emissions, including tire and road wear particles (TRWPs). These particles are generated by the friction between vehicle tires and road surfaces and contain rubber, metals, and other materials. Specifically, the chemical compound N-(1,3-dimethylbutyl)-N'-phenyl-p-phenylenediamine-quinone (6PPD-Q), a by-product of tire manufacturing, has been frequently detected in stormwater runoff and urban roadways. This substance has been shown to have adverse effects on aquatic organisms and is washed into waterways during stormwater runoff, posing a significant environmental threat. This research aims to examine how the chemical compound 6PPD-Q may impact the reproductive capabilities of *C. elegans*, a commonly used model organism. The study will consist of evaluating fifteen (n = 20) C. elegans per treatment using brood counting techniques across varying concentrations, including the control group dimethyl sulfoxide (DMSO) diluted with K buffer (potassium phosphate), a Nanaimo stormwater concentration of 6PPD-Q (3.5 µg/L), and the highest experimental concentration of 6PPD-Q in a scientific article by Hua et al., 2023 (10 µg/L). In this study, a t-test analysis will be conducted to assess the difference in reproductive capacity. Imaging analysis, including gonad development and DNA damage, will also be included for a comprehensive representation of how 6PPD-Q affects the reproductive health of these organisms.

Yesso scallop larval rearing: microbiome and husbandry practices

Gilchrist, K., Perlman, S., Leask, K., Loudon, A., Wiebe, A., Green, T.

Scallop farming provides job opportunities in remote coastal communities and is a sustainable avenue for improving food security. The Yesso scallop (*Mizuhopecten yessoensis*) is an economically important cultivated scallop species due to its fast growth rate, large size, and high market value. Access to seed (juvenile scallops) limits production due to frequent and unexplained mass larval mortality events linked to bacterial disease outbreaks. Suboptimal larval rearing conditions may cause unstable microbial communities in culture tanks and favor the proliferation of pathogenic bacteria. Many factors may contribute to mortality, as larval cultures are complex systems and scallops are highly sensitive to environmental fluctuations. This project aims to explore the effects of water change frequency, temperature, photoperiod, diet, and bacterial exposure on the growth and survival of scallop larvae, as well as on the microbial communities associating with larvae and tank water. Growth and survival will be measured throughout larval development from embryo to pediveliger in a hatchery setting. Microbiome will be characterized by 16S rRNA sequencing at several time points to access succession throughout development. Preliminary results demonstrate that reduction of water change frequency to half that of standard hatchery procedures does not affect growth and survival of larvae. This project aims to develop knowledge for successful production of scallop seed in aquaculture hatcheries by informing larval rearing methods that promote a microbiota that is natural and protective against bacterial pathogens.

Evaluation of Endophytic bacterial strains for plant growth and development in Pine and Spruce

Goli, R.

Lodgepole Pine (*Pinus contorta*) and Hybrid White Spruce (*Picea engelmannii x Picea glauca*) are economically important trees in British Columbia that grow well in infertile, gravel soils. They are unique among conifer species in their ability to survive on nutrient-poor and fire-affected soils that are severely limited in nitrogen. Bacterial endophytes (the micro-organisms residing inside the plant tissues without causing symptoms of disease) have been found to fix atmospheric nitrogen in various plant parts through biological nitrogen fixation. Many studies have been done on individual and consortia of endophytic strains isolated from agricultural crops, however, little has been done with gymnosperms. This research evaluates individual and different combinations of endophytic strains to compare their performance in enhancing pine and spruce seedling growth. The selection of endophytic strains for the following experiments was based on previous studies demonstrating direct and indirect plant growth-promoting abilities by considering 12 potential plant growth-promoting mechanisms in lodgepole pine and hybrid white spruce (Puri, 2020). I have chosen 2 strains that performed best in pine and spruce when grown in an 18-month greenhouse trial. The strains to be examined for my research are LS-S2c isolated from low-nutrient stands of spruce at west Chilcotin and P2-b2r from internal tissues of pine. Both of these strains are capable of atmospheric nitrogen fixation, phosphate solubilization, phytate hydrolysis, production of plant growth-promoting substances, and siderophore production. My study will use a quantitative approach to determine the growth and development of pine and spruce seedlings in a 12-month greenhouse trial by measuring their shoot height, root length, and plant biomass at 6 and 12-month intervals after inoculation. The research objectives that I will address are: (i) To determine how inoculation with a combination of known endophytic PGPB strains affect pine and spruce seedling growth compared to individual strains in natural soil; (ii) To quantify the proportion of N-requirements of pine and spruce fulfilled by each combination of strains; and (iii) To evaluate endophytic and rhizospheric colonization by these bacterial strains in different tissues of pine.

Ticks utilize soil-dwelling fungi as indicators of suitable resting sites

Gooding, C., Gould, L., Gries, G.

Ticks are well known globally as blood-feeding parasites but despite this reputation, most ticks spend over 90% of their lifespans off-host. Off-host ticks are highly susceptible to desiccation and must efficiently locate high humidity, low sunlight resting sites in soil and leaf-litter to survive. How ticks choose these sites remains unknown. Microhabitats utilized as resting sites for ticks are also optimal environments for the growth of soil-dwelling fungi, which thrive in moist, low-light environments. *Beauveria bassiana* is one such fungus and is pathogenic to ticks. Working with six species of ixodid ticks in olfactometer bioassays, we tested the hypothesis that ticks avoid soil colonized by *B. bassiana* to mitigate the risk of infection. Contrary to our prediction, nearly all ticks sought, rather than avoided, *B. bassiana*-inoculated substrates. In further bioassays, we found that ticks oriented towards both pathogenic and harmless soil-dwelling fungi, implying that fungi – regardless of their pathogenicity – signal habitat suitability to ticks. Finally, we demonstrate ticks specifically detect metabolites associated with fungal cellulose decomposition to evaluate the long-term suitability of microhabitats.

Optimizing Seagrass Mapping with Drones and Machine Learning

Gwynifyre, T.

Seagrass meadows play a vital role in the protection of coastlines, support productive habitat for marine life, and act as significant carbon sinks. Experiencing a decline due to changing climate and human disturbances, accurate data on the spatial extent of seagrass meadows is integral to support coastal management decisions. However, field-based methods are expensive, time-intensive, and are difficult to replicate over extensive areas. In response to this need, collecting imagery using remotely piloted aircraft systems (RPAS) is increasingly popular. The flexibility and relatively low cost make RPAS an accessible tool, however, at present there is no established methodology for detecting and delineating seagrass meadows from this imagery. Coastal dynamics associated with seagrass habitat such as tidal conditions and growing season limits the extent to which seagrass can be accurately detected. In this study, I test a methodology for seagrass detection and evaluate how detection accuracy is impacted by tidal conditions, growing season, and the incorporation of multispectral sensors. Specifically, I compare classifications of two eelgrass (*Zostera marina*) sites in the Gulf Islands (Sidney and Moresby) in southwestern British Columbia. To do so, I tested the performance of popular classification algorithms (Random Forest, Support Vector Machine, Maximum Likelihood) in response to tidal heights and growing seasons. Further I compare the incorporation of near-infrared and red-edge spectra to traditional red-green-blue imagery to explore potential improvements in eelgrass detection. The results of this analysis will intend to support development of a provincial seagrass mapping methodology, supporting seagrass monitoring and conservation in British Columbia.

Ecotoxicological insights from the 2022-White Sturgeon (*Acipenser transmontanus*) mortalities in the Nechako River, British Columbia

Hassanaghaei, M., McAdam, S., Gantner, N., Keogh, K., Alava, J.J.

The Nechako White sturgeon is an endangered species under the Species at Risk Act (SARA), and the detection of 13 large dead fish in August /September of 2022 led to considerable conservation concern. Among those fish, 12 were male adults with unknown causes of dead and one was a juvenile that was by-catch mortality of a First Nations fishery. Muscle and liver samples were collected from dead fish for analysis of trace metals and micronutrients ([As], [Cd], [Cr], [Co], [Cu], Hg], [Zn]) polychlorinated dibenzo-p-dioxins (PCDDs) and polychlorinated dibenzofurans (PCDFs), and polychlorinated biphenyls (PCBs). After analyzing data for contamination levels, we observed that the Hg mean concentrations in muscle and liver were higher (muscle: 1.64,± 0.88 mg/kg wet weight (ww); liver: 2.96,± 1.84 mg/kg ww) in sturgeon from Nechako River compared to similar studies from lower Fraser and Columbia River fish. We estimated Selenium Health Benefit Value (HBVSe), which was negative ($-2.96 < \text{HBVSe} < -47.18$) for muscle and positive ($12.40 < \text{HBVSe} < 31.78$) for liver. For the juvenile fish, both tissues have positive HBVSe. While the majority of PCDD and PCDF concentrations were below the detection limit (2.00E-04 to 2.00E-03 mg/kg ww), the PCB mean concentration in muscle was 229 mg/kg lipid weight (lw). The PCB 153 + PCB 168 congeners presented the highest concentrations (23 mg/kg lw) in punch muscle tissue. While questions still remain on the toxic effects by metals and PCBs in this endangered fish species, our contaminant data contribute to ecotoxicological baseline information with implications for hazardous pollutant management and conservation of this species throughout its range.

Tenacibaculum maritimum susceptibility to Florfenicol at Atlantic salmon net-pen sites

Heese, B.

The Food and Agriculture Organization of the United Nations states that “antimicrobial resistance (AMR) is a One Health issue that affects food safety and the health of humans, animals, plants and the environment.” AMR monitoring programs are commonly implemented in terrestrial animal agriculture production. Resulting AMR data can then be utilized to better manage and monitor the emergence of resistant bacterial strains and subsequently help sustain healthy ecosystems. Florfenicol (FFC) is a broad-spectrum antimicrobial used only in veterinary medicine to treat disease in both terrestrial and aquatic animals. In Coho and Atlantic salmon production systems, FFC is used to treat bacterial diseases including tenacibaculosis caused by the Gram negative, ubiquitous marine bacteria Tenacibaculum maritimum (T.mar). Using microdilution minimum inhibitory concentration assays to evaluate antimicrobial susceptibility and resistance to FFC, we are collecting T.mar isolates from BC raised salmonids and studying potential FFC susceptibility and resistance trends over time. Results currently suggest minimal to no antimicrobial resistance identified or developed among the collected isolates. Results of this research will advance our understanding of Tenacibaculum spp. diversity, florfenicol susceptibility, and treatment efficacy in British Columbia. This work is important for monitoring and improving ecosystem health and critical for identifying novel ways to improve fish survival and welfare by reducing the occurrence and severity of T.mar – related disease outbreaks.

Spatial dynamics of animal-mediated nutrients in temperate waters

Lim, E., Attridge, C., Schuster, J., Cox, K., Kattler, K., Leedham, E., Maher, B., Bickell, A., Juanes, F., Côté, I.

Consumer-mediated nutrient dynamics (CND), through which animals metabolic waste products fertilize primary producers, is known to drive variability in nutrient availability and thus primary productivity and community functioning in tropical waters. Yet, examinations of CND as a driver of variation in nutrient availability in temperate systems are limited. Therefore, we aimed to quantify and explain spatial variation in CND by surveying fish and macroinvertebrates via Reef Life Survey methods and measuring their ammonium excretions at 27 rocky reefs (3 years) and 17 kelp forests of varying density (1 year) in Barkley Sound, British Columbia. Ammonium concentrations varied from 0.009 to 2.5 uM across rocky reefs, and the relationship between animal biomass and ammonium varied with tidal exchanges weakly positive at slack and ebb tides, but weakly negative at flood tide. Ammonium was significantly higher within than near kelp forests, a difference that increased with tide exchange, kelp and animal biomass. We found fine-scale ammonium variability and nutrient enrichment on a scale of meters was only possible under low flow conditions. Our results suggest CND-driven variability acts on scales ranging from a few meters to over 20 km, contributing to finer-scale variation in nutrient availability than allochthonous nutrient sources such as upwelling. Therefore, CND may play a previously unrecognized role in structuring temperate marine ecosystems from the bottom up.

Intertidal communities and stoichiometry on natural and artificial urban reefs

MacLennan, E., El-Sabaawi, R.

Cities, especially those near the sea, are expanding rapidly to accommodate a growing world population. As they do, more artificial structures are introduced into the coastal environment, often supported by pilings driven into the seafloor. These structures house communities of intertidal and subtidal organisms which likely differ from nearby communities on natural reefs, but the ways they vary and the impacts of those differences are still unclear. We are investigating whether and how community composition, biodiversity, and elemental composition of those organisms and communities differ, which may elucidate potential impacts on nutrient cycling and food webs. Pilings and natural rocky reefs were compared in Victoria, British Columbia, on the traditional and unceded territories of the Esquimalt and Songhees nations. We used quadrats to assess the percent cover of sessile species on both habitat types and sampled the dominant taxa for elemental and isotopic analysis. Sample processing is not yet complete, but it seems clear that communities on pilings do not represent communities on natural shores. Elemental composition data will contribute to the building of a stoichiometric database for these common intertidal organisms, and we will use it, along with the percent cover data, to estimate the community stoichiometry of each site. Marine structures will continue to be built as cities continue to grow. By understanding more precisely how communities are affected by urban development, we hope to inform meaningful management strategies and eco-engineering solutions.

Assessing Methods of Measuring Urbanization and Its Effects on Aquatic Ecosystems Across Vancouver Island

Mickens, A., Maucieri, D., El-Sabaawi, R.

Urbanization is increasingly altering the landscapes surrounding cities. Anthropogenic impacts associated with urbanization, such as increased nutrients, habitat degradation and loss, and the introduction of invasive species significantly alter the health and function of aquatic ecosystems. While many studies have looked at the relationship between increasing urbanization and water quality, fewer have looked at how urbanization alters traits (i.e., morphologic and phenotypic) and nutrient allocation of aquatic organisms. In this study, we examine the effect of urbanization on the morphology and elemental content of a common North American fish species, the Threespine Stickleback (*Gasterosteus aculeatus*). During summer 2022 and 2023, we surveyed 15 freshwater locations on Vancouver Island across a gradient of urbanization. This research increases our understanding of how urbanization influences the overall health of organisms in aquatic ecosystems by examining stickleback condition and nutrient allocation. We apply two methods of urbanization to our data and use a sensitivity analysis to support our results. Our work provides recommendations to urban planners and resource managers on where to focus conservation efforts and provides a framework for other researchers to carry out similar studies that can add to our understanding of the effects of urbanization on aquatic ecosystems.

Barnacle-infested Yesso scallops: Shell colour and microbiome as potential influences

Moody, D.

Barnacles are a group of marine invertebrates common to the Pacific Northwest of British Columbia. These animals colonize submerged surfaces, often en masse. This poses a significant problem in shellfish aquaculture where they settle on crops and compete for available resources, such as food and oxygen. This competition can result in reduced growth rates, increased stress, and even mortality among the cultured species. One aquaculture species at risk of such occurrences is the Yesso scallop (*Mizuhopecten yessoensis*). However, certain scallops seem to be more at risk than others. Yesso scallops farmed at the Deep Bay Marine Field Station in Bowser, BC exhibit highly variable degrees of colonization. In this study, we assessed two physical parameters to look for differences between scallops that became heavily colonized by barnacles, and those that did not, after one year in the same environmental conditions. First, we analyzed the shell colour of 122 scallops. Second, we characterized the bacterial microbiome sampled from the shell surface of 28 scallops. Comparing these physical traits between the two groups may provide insight into the factors contributing to the variable levels of colonization noted between individuals; information that may prove useful to BC's shellfish aquaculture industry to enhance the production, revenue, and sustainability of scallop farming.

Measuring Genetic Diversity Across Populations

Niloufar A., Colijn, C., Mooers, A., Tupper, P.

At the sharp end of biodiversity loss, it is estimated that millions of genetically distinct local populations are lost annually. While various strategies for measuring among-species diversity have emerged (e.g. Phylogenetic Diversity (PD), Split System Diversity (SSD) and entropy-based methods), extensions to populations are rare. An understudied problem is how to assess the diversity of a collection of populations where each has its own internal diversity. Relying solely on measures that treat each population as a monomorphic lineage (like a species) can be misleading. To address this problem, we present four population-level diversity assessment approaches: Pooling, Averaging, Pairwise Differencing, and Fixing. We extend these approaches, which can be applied to any diversity measure that is primarily defined for a group of individuals, to collections of populations. We then apply the approaches to two conservation metrics -- Heterozygosity (Het) and Split System Diversity (SSD) €“ across a dataset comprising 50 Atlantic salmon populations. We investigate convergence and divergence of the approaches and also identify alternative optimal sets of salmon populations for conservation. The study extends beyond salmon SNP data, raising questions about the generalizability of observed correlations and optimal preservation subsets across different scenarios. The findings emphasize the need for clearly defining what aspects of biodiversity we aim to both measure and optimize to ensure meaningful and effective conservation decisions.

Measures of Smoltification in Aquaculture Chinook Salmon

Nowlan, J., Britney, S., Heese, B., Canon, B., Leme, R., Griffiths, P., Milligan, B., Russell, S.

Smoltification and designations of smolt-status is a crucial transition and practice in salmon aquaculture respectively. However, most information on these topics is based on Atlantic salmon (*Salmo salar* L.) and rainbow trout (*Oncorhynchus mykiss* W.), while less information is available for Pacific salmon. With Chinook salmon (*Oncorhynchus tshawytscha* W.) being a valuable aquaculture species in British Columbia (Canada), developing novel techniques such as reverse-transcriptase qPCR (RT-qPCR) assays may assist designations of smolt-status in aquaculture and conservation fish. Novel techniques to clarify Chinook salmon smolt status could improve survival and growth when transferred to marine waters. Two production groups (spring and fall) of Chinook salmon were collected monthly from freshwater to saltwater entry. Fish were evaluated using classical techniques (i.e., condition factor, ATPase activity, parr marks, silvering, and black fin margins) and three developed RT-qPCR assays (NKA Î±1a, NKA Î±1b, and NKCC). The inclusion of RT-qPCR assays along with other techniques explained significant variation between collections in freshwater and saltwater for both production groups. The application of RT-qPCR also led to the interpretation of desmoltification within the fall production group based on the reduced expression of target genes prior to saltwater transfer and increased mortality post saltwater transfer. A decrease in ATPase activity for both production groups contradicts what is classically seen as salmon enter saltwater, indicating that genetic applications may also help alleviate anomalous enzymatic results. In conjunction with previous techniques, developed assays may further clarify smolt-status and improve fish welfare.

Substrate complexity reduces prey consumption in functional response experiments: implications for extrapolating to the wild

Oishi, E., Kattler, K., Watkins, H., Howard, B., Côté, I.

Understanding the density-dependent impacts of an invasive predator is integral for predicting potential consequences for prey populations. Functional response experiments are used to assess the rate of prey consumption and a predator's ability to search for and consume prey at different resource densities. However, results can be highly context-dependent, limiting their extrapolation to natural ecosystems. We examined how simulated habitat complexity affects the functional response of invasive European green crabs foraging on two different bivalve species. Green crabs feeding on varnish clams shifted from a Type II hyperbolic functional response in the absence of substrate to density-independent consumption when prey could bury. Green crabs ate so few Japanese littleneck clams under all densities, such that no functional response curve of any type could be produced and their total consumption was always density independent. However, the probability of at least one Japanese littleneck clam being consumed increased significantly with initial clam density and crab claw size across all treatments. The proportion of varnish clams consumed increased with crab claw size and was higher across both substrate conditions than the proportion of Japanese littlenecks consumed; however, the proportion of Japanese littleneck clams consumed increased faster with claw size than that of varnish clams. Our results suggest that including environmental features and variation in prey species can influence the density-dependent foraging described by functional response experiments. Incorporating replicable features of the natural environment into functional response experiments is imperative to make more accurate predictions about the impact on prey populations by invasive predators.

The enigmatic life of LEX01, a strain of *Lotharella globossa*

Perovich, R., Livingston, S., Keeling, P.

Rhizria is a clade full of interesting taxa, with none as enigmatic as the Chlorarachniophytes. They live as single-celled marine algal mixotrophs, thanks to a secondary endosymbiosis event between their Cerozoan ancestors and a green alga closely related to Bryopsidales. This was discovered via sequencing the highly reduced vestigial nucleus of the ancestral green algal, known as the nucleomorph. Recent sequencing of the nucleomorph of what was thought to be a new species showed a 100% ITS match with the holotype of *Lotharella globossa*. This new variant, named LEX01, is morphologically distinct as it forms 3 life stages - coccoid, flagellate, and amoeboid, the latter of which is never observed in the holotype. There is limited documentation of life stage transformation, differences in form and function of life stages, or population demographics over time, and no scanning electron microscopy (SEM) work has been conducted to characterize morphological features of LEX01. To bridge this research gap, we used a combination of SEM and correlative LM time-course assays to detail all three life stages within LEX01. We found that coccoids dominated low and high-density cultures, with amoeboids and flagellates appearing after ~48hrs and peaking ~96hrs. Various life-stage transformations were also observed for the first time including instantaneous flagellate to amoeboid. Cell boundaries and connectivity between cells via reticulopodial networks were characterized for each life stage. We conclude that the amoeboid life stage is the defining character of LEX01, which has been maintained due to recent differing selective pressures on the holotype and LEX01.

Seasonal patterns of macronutrient collection and proximate mechanisms of foraging ants

Renyard, A., Gooding, C., Gries, G.

Adequate nutrition is vital for ant colony growth. Ant foragers upregulate recruitment behaviour, resulting in both colony-level selection of profitable food sources and optimal colony fitness. Few studies have investigated the relative contribution of specific nutrients to momentary and season-long foraging responses by ants and whether or not colony-level responses are driven by increased recruitment of ants or larger amounts of food taken per ant. Using western carpenter ants, *Camponotus modoc*, and European fire ants, *Myrmica rubra*, as model species, we: (1) tested preferential consumption of various macro- and micro-nutrients; (2) compared consumption of preferred macro-nutrients; (3) investigated seasonal shifts in nutrient preferences; and (4) tested whether colony level nutrient consumption is driven by higher recruitment and/or larger amounts of food taken per ant. In laboratory and field experiments, we measured nutrient consumption by weighing tubes containing aqueous nutrient solutions before and after feeding by ants. Laboratory colonies of *C. modoc* favored nitrogenous urea and essential amino acids (EAAs), whereas *M. rubra* colonies favored sucrose. Field colonies of *C. modoc* and *M. rubra* preferentially consumed EAAs and sucrose, respectively, with no sustained shift in preferred macro-nutrient over the course of the foraging season. Recruitment counts and volumetric measurements of individual feeding bouts in *C. modoc* ants indicate that colony level feeding responses are likely driven both by increased recruitment and amount of food taken by ants. Foraging responses in ants are likely driven intrinsically by colony demographics and extrinsically by resource availability in the ants' habitat.

Effects of *Rhizobium* and *Caballeronia sordidicola* Inoculation on Growth and Nitrogen Fixation of Intercropped Field Pea and Poplar

Sandhyarani S.

The research aim is to determine N fixation by inoculating field peas with rhizobia and non-rhizobia strains (LS-S2r) alone and in combination when intercropped with poplar. The research objectives are to evaluate the amount of N fixed in poplar when intercropped with field peas inoculated with LS-S2r, enhance the plant growth of poplar with both rhizobial and non-rhizobial strains, and examine whetherLS-S2r fixes nitrogen in poplar. Methodology: The experiment carries greenhouse trials and involves nine treatments as follows: Poplar + Field pea (with rhizobia), Poplar+ field pea(with LS-S2r), Poplar+ Field pea (with rhizobia+LS-S2r), Poplar (with rhizobia), Poplar (with LS-S2r), Poplar (with rhizobia+LS-S2r), Field pea (with rhizobia), Field pea (with Ls-S2r), Field pea (with rhizobia+ LS-S2r). LS-S2r will be cultured in the lab by growing them on culture plates and CCM Broth, while field pea seeds will be surface-sterilized. Rhizobial strains will be obtained from previous fieldwork. The treatments will be grown in greenhouse pots. Findings from this research will allow agroforestry and tree plantation practitioners to make land management decisions on soil health and tree nutrition by utilizing fewer fertilizers.

Biodiversity in British Columbia

Schafers, E., Janes, J.

A decrease in biodiversity is cause for rising concern worldwide. In Canada, biodiversity metrics and monitoring has several gaps, including in British Columbia. Lack of biodiversity research has implications that can lead to poor management practices and conservation. In this paper we focused on biodiversity in Stone Mountain and Mt. Robson provincial park. Stone Mountain is particularly understudied, compared to Mt. Robson, where several conservation projects are already being managed. We evaluated species biodiversity using a Jaccard dissimilarity test, alpha, beta, gamma tests, and principal component analysis. Analysis of these sites yielded surprising results, with higher layer gamma values being 211and 168 for Stone Mountain and Mt. Robson respectively, indicating that even with conservation practice in place for Mt. Robson, the diversity is lower than that of Stone Mountain. Stone Mountain has no other biodiversity metrics reported, and such we cannot make any conclusive statements on whether this is a rich or poor site. Results from this study can direct future management, and provide as a baseline for any future research.

Exploring Novel Applications and Advancements of Passive Integrated Transponders (PIT) in Fisheries.

Scurfield, D.

Passive Integrated Transponders or PIT tags are small tags that require no internal battery, applied across ecological studies. PIT technology is a form of low-cost telemetry that is a great tool that can be used to determine growth rates, survivorship, food webs and movement patterns via “hands-off” mark-recapture. We highlight the importance of our various PIT study designs in systems across British Columbia. Exploring the unique challenges each system and study species brings, and improved data collection through advancements in the technology through antenna design and deployment strategies. Touching on results from Keogh River steelhead (*Oncorhychus mykiss*), Portage creek Chinook salmon (*Oncorhynchus tshawytscha*), Peace River bull trout (*Salvelinus confluentus*), and Pitt Lake white sturgeon (*Acipenser transmontanus*).

Long-read sequencing reveals complete plasmids in three *Tenacibaculum* species

Sies, A., Nowlan, J., Lumsden, J., Russell, S., Cameron, A.

Tenacibaculum is a genus of Gram-negative, filamentous, marine bacteria. Several species can induce a disease, called 'tenacibaculosis', in marine aquaculture fish populations. While *Tenacibaculum* mechanisms of infection remain cryptic, techniques to research the pathogen are improving. We recently sequenced ten *Tenacibaculum* isolates collected in British Columbia with Oxford Nanopore long-read technology. In addition to assembling complete or nearly complete chromosomes for 9 of 10 isolates, we assembled complete putative plasmids in five isolates, representing three distinct species. Plasmids are extrachromosomal DNA structures which are most often circular, and encode 'accessory' genes which are not necessarily essential to the survival and replication of the microbe. Nonetheless, plasmids impact bacterial physiology and evolution in several ways. For instance, many well-studied plasmids in enteric and soil bacteria provide their host with functions and phenotypes that are beneficial in specific environments, such as antibiotic resistance. Some plasmids have an ability to transmit themselves 'horizontally' between bacterial cells, meaning that plasmidic genes and their associated functions can reach many cells in a bacterial community in a short amount of time. No plasmids have been identified in previous whole genome sequencing efforts of *Tenacibaculum* isolates, to our knowledge. Here, we describe the contents of the first complete putative plasmids in *Tenacibaculum*, then test experimental approaches other than long-read sequencing for plasmid identification in the marine microbial genus. Finally, we compare the complete putative plasmids to contigs in existing *Tenacibaculum* assemblies, identifying probable plasmid fragments in several other isolates.

Moonlight influence on the vocal activity of Western Screech-Owls

Williams, N., Kennedy, J., Demers, E.

Populations of the coastal Western Screech-owl (*Megascops kennicottii kennicottii*) on Vancouver Island, BC, are declining. Passive acoustic monitoring through autonomous recording units (ARUs) depends on call detection to monitor owl populations. Therefore, it is crucial to account for exogenous factors such as moonlight that may impact owl vocal activity when passively monitoring. Previous studies have shown that moon illumination levels positively impact owl vocal activity. This project aims to determine if moon illumination levels throughout a lunar cycle, and within individual nights as moonlight fluctuates between a nightly minimum and maximum, can impact the number and frequency of vocalizations detected from the coastal Western Screech-owl through passive acoustic monitoring. ARUs were deployed on 5 transects within the Sitika Valley and Carmanah Valley in Vancouver Island, between March-April 2022 by the

Pacific Megascops Research Alliance (PMRA). Vocalization data was processed as a 15-minute cycle, with the ARU recording for 3 minutes and off for 12 minutes from one hour before sunset to one hour after sunrise for 5-9 nights throughout the deployment period from each ARU station. Moonlight illumination values were calculated using the R package moonlit, a package that uses location, elevation, date, and time to calculate relevant moonlight values. Using linear modeling, the lunar illumination values were compared to coastal Western Screech-owl vocalizations. Understanding how moonlight impacts coastal Western Screech-owl vocalizations may allow for an understanding of when maximum vocal activity occurs, to improve the probability of detecting this species when monitoring.

Mechanisms impacting the short-term survival of released Chinook salmon in Barkley Sound

Zinn, K., Johnston, S.., Bass, A., Hinch, S.

Although Chinook salmon (*Oncorhynchus tshawytscha*) are the least abundant species of Pacific salmon, they are the most sought-after in the marine recreational fishery. As a result, catch-and-release fisheries will play an increasingly important role in fishery management and public fishery opportunities in the future to protect stocks of concern. In partnership with the Sport Fishing Institute of British Columbia, we undertook a holding study in 2022 and 2023 to better understand some of the intrinsic and extrinsic mechanisms that may affect the physiological state and survival of Chinook salmon following catch-and-release. While some earlier studies have investigated the impacts of recreational angling on Pacific salmon in freshwater, research on the effects of marine recreational catch-and-release angling, specifically on Chinook salmon have not been conducted at appropriate time scales and are technologically outdated (20+ years ago). 492 adult and subadult Chinook were captured using typical marine recreational angling practices and held for up to 14 days in tanks following capture. Hook type (single vs. treble), gear type (bait vs. artificial), in-line flasher, and gaff release treatments were tested over seven 2-week holding studies. Physiological status, health and injury were closely monitored, as a means of assessing the latent impacts of specific fishing and release practices on physiology and survival. Scale loss, fin damage, sex, and fork length (cm) were the largest determinants of survival. For smaller bodied fish, treble hooks resulted in lower survival. By lessening physiological impacts through improved fish handling and release practices, it may be possible to improve the fitness of released fish and enhance the sustainability of the British Columbia public recreational fishery.

3 minute presentations (alphabetical order by last name)

Egg Size Variation and Lifetime Reproductive Success in European Starlings

Barbera, R.

Across a wide range of taxa, the distribution of lifetime reproductive success (LRS) is highly skewed – most breeding individuals fail to produce any recruiting offspring, while only a small proportion of the breeding population successfully contribute to future generations. The reasoning of why so few individuals succeed has remained a key question in biology; however, it has largely been attributed to heterogeneity in individual "quality". Individual quality has historically been estimated with a suite of phenotypic traits positively correlated with fitness. Among birds, laying dates and clutch size have most often been used as measures of individual quality. In contrast, other life history traits (egg size, parental care) have rarely been considered as factors influencing individual quality and LRS. These traits vary widely within a population; in our study of European starlings (*Sturnus vulgaris*), the largest mean egg size was 47% larger than that of the smallest. Here we assessed how these traits, as well as laying date and clutch size, contribute to LRS (total number of chicks fledged) among nest box-breeding starlings over a 20-year period at our study site in Langley, BC. Preliminary analysis shows a slightly positive relationship between egg size and LRS, although most of the variation was unexplained. Our next step is to perform model selection to understand the relative contribution of all four life history traits to variation in LRS.

Understanding the Role of Attributes and Patterns in the Segmentation and Development of Global Shark Ecotourism

Basok, L. D., Cisneros-Montemayor, A.

Due to the growing popularity of non-consumptive utilization of natural resources, such as ecotourism, shark watching has gained increasing attention both on a global and local scale. This interest is fueled by the potential conservation benefits it offers in the face of declining shark populations worldwide. Making development decisions for shark ecotourism calls for information on the suitability of potential sites such as ecological, spatial, and socio-economical features. Literature sources and web pages were reviewed to determine the currently active global shark ecotourism sites and shark ecotourism attributes. Then, a principal component analysis (PCA) approach was used to identify the common grounds and diversity of the sites that the PCA suggests. Selective biological, physical, and managerial variables were used to understand the potentially important combinations of variables that define shark ecotourism. According to the results, this study aims to examine how hypothetical new operations or the growing industry can be conducted with sustainable and equitable management between stakeholders, government, and non-governmental organizations.

Arctic Lake Methane Cycling: Whos Who?

Burns, L., Goordial, J., Fowler, J., Lesack, L.

The production and consumption of methane is a key biogeochemical process in the global carbon cycle, comprising the final step in the reduction of carbon from the decomposition of biomass in anaerobic environments. While the production of methane is a natural biological and climatic process, methane is also a powerful greenhouse gas with a warming potential 84 times greater than carbon dioxide over a 20-year period. The Arctic is experiencing climate change at a rate faster than the rest of the world but the impacts on methane dynamics, emissions, and ecosystem processes within Arctic lakes are poorly understood. My research aims to identify species of methanogens and methanotrophs present in Mackenzie River Delta lakes from peak methane concentrations before spring ice melt through the summer open water season along gradients of select environmental variables, including river-to-lake connectivity and macrophyte cover, using 16S rRNA amplicon sequencing and qPCR. This will clarify the methane cycling component of microbial carbon processing, which, in future work, could support the development of more appropriate modelling for lakes in river floodplains and improve understanding of how Mackenzie delta lakes, and other large lake-rich deltas in the Arctic, may respond to the complex multiple forcings of global climate change.

Ocean acidification influences gene expression in ‘resilient’ and ‘susceptible’ lineages of late life-history stage Pacific oysters (*Crassostrea gigas*)

Chapman, B., Wright-LaGreca, M., Mackenzie, C., Green, T.

The Pacific oyster (*Crassostrea gigas*) is a cultivated bivalve species of substantial economic and ecological value that is adversely affected when exposed to ocean acidification (OA) conditions. This is particularly evident during early life stages when developmental delays, shell deformities, reduced shell growth and decreased survivorship are most noticeable. However, deleterious effects may be observed across life stages. Oyster lineages displaying resiliency to OA have arisen from selective pressures associated with OA. Research investigating these adaptation mechanisms has primarily focused on early-life stages and has yet to determine if resiliency persists across life history. Pacific oysters exhibit dramatic shifts in gene expression across developmental stages, indicating that resiliency may have life stage dependence.

Previously, the expression of 23 shell matrix and pH regulatory genes were analyzed under experimental OA conditions in larvae of Pacific oyster lineages bred to be OA ‘resilient’ or ‘susceptible.’ Herein, I aim to expand on previous work by analyzing the expression of the same 23 genes under experimental OA conditions at later life-history stages of three ‘resilient’ and three ‘susceptible’ larval Pacific oyster lineages. Oysters were distributed among four experimental OA seawater treatments (control: pH 8.0, 16°C, experimental: pH 8.0, 20°C; pH 7.6, 16°C; pH 7.6, 20°C). Sampling occurred after 12 weeks of exposure and target genes were analysed using RT-qPCR. We observed the resilient lineages grew faster in OA conditions (ANOVA, $p < 0.05$), and select shell matrix genes were differentially expressed between ‘resilient’ and ‘susceptible’ lineages.

Disparity between acclimation rates in climate change experiments and predicted rates of ocean warming

Côté, I., Kattler, K., Oishi, E., Konrad, C.

With global ocean surface temperatures continually rising, it is imperative to understand how temperature stress impacts marine organisms. Many experiments are conducted to predict responses to long-term warming, but often do not include ecologically or environmentally relevant rates of temperature change before measuring organism responses. These experimental constraints may be inaccurately predicting, or even exaggerating the conclusions drawn from ocean warming studies. To understand these potential limitations, we conducted a meta-analysis to examine the disparity between the rate of ocean warming and the acclimation rates used in climate change experiments. Our searches yielded 51 studies which met our inclusion criteria. Twenty-seven percent of these studies did not incrementally acclimate their organisms to higher temperatures before recording their responses. Furthermore, we aim to explore the trends of acclimation rates used in published experiments between organism taxa, lifestage, and experimental duration. We will also examine how responses of marine organisms varied between individuals that were exposed to raised temperatures and those that were held at control temperatures, when considering the acclimation rates used. The results from these analyses will aim to persuade future research to include ecologically relevant acclimation rates, as well as how results from past studies may be more accurately predicted when accounting for acclimation rate. Studies exploring the impacts of ocean warming on marine organisms have high importance, which underscores the necessity to make reliable predictions regarding their responses as the ocean continually warms.

Investigating the Impacts Early Microbiota Disruption have on Pacific oyster, *Crassotrea gigas*, Survivorship against Bacterial Inoculation of *Vibrio* spp

Dennis-Orr, J., Loudon, A., Green, T.

Microbes can have a tremendous impact on the health and development of animals. Pacific oysters (*Crassostrea gigas*) are a widely cultured species in BC; however, they are increasingly susceptible to summer mortality events related to climate change-associated heatwaves. While Pacific Oyster microbiomes have been studied under various developmental stages and rearing conditions, little is known about early-life microbial exposures impact on host fitness. In this experiment the effects of early-life microbial dysbiosis were tested on Pacific oysters through administration of antibiotics (AB) and high temperature (HT) during larval development for just the first 24 hours of life. Changes in microbiome were followed throughout development and oyster survivorship was tested at the three-month-old spat phase through inoculation with known pathogen Vibrio spp. Early larval rearing followed a factorial design including treatments: 1) a Control (20 °C no AB), 2) Disturbed or dysbiosis microbiome (20 °C and AB - penicillin streptomycin), 3) Heatwaves (high Temperature 27 °C no AB), and 4) disturbed and high temperature (27 °C and AB). Following the development, each treatment underwent Vibrio spp. challenges at the juvenile stage (3-month-old spat); survivorship challenge revealed that all forms of early microbial dysbiosis conferred increased susceptibility to Vibrio pathogenesis, with the high-temperature disturbance being most influential with a 7.3x lower survival rate than the control. These results indicate that just 24 hours of early-life microbial disturbance profoundly affect life-long organismal susceptibility to disease. Microbial communities were be further evaluated using 16S ribosomal rRNA sequencing, where samples were taken every other day for 15 days.

Microbiome Enrichment, Host Genetics, and Long-Term Resilience of Pacific Oysters

Detillieux, S., Wright-LaGreca, M., Loudon, A., Green, T., Janes, J.

Pathogenic diseases such as Pacific oyster mortality syndrome (POMS), which is linked to Vibrio infection (Vibriosis), pose a significant threat to oyster aquaculture efforts. Vibrio is a bacterial pathogen of particular concern not only because it causes high mortality in oysters but also because it is a causative agent of human foodborne illness. Recent evidence suggests a healthy microbiome significantly contributes to the disease resilience of oysters. However, hatchery-raised larvae are often reared in heavily sterilized conditions and are therefore not exposed to the microbes needed to develop a healthy microbiome. While experimental evidence has pointed to microbiome enrichment as an effective potential technique to raise more resilient animals, it is not well understood which specific microbial species are responsible for this increase in resilience; nor is it known whether it is even attributable to any specific species present or simply due to the presence of any external microfauna during the crucial stages of larval development. To address these limitations in our knowledge, we employ a factorial experiment wherein larvae from two distinct families of oysters, differing in their field-tested resilience to external stressors, are administered two distinct microbiome enrichment treatments using these oyster families The questions we hope to answer are twofold: (1) Will microbiome composition of the larvae differ between treatment groups, and if so, (2) will the oysters display different levels of resilience to Vibrio infection later in life based on their microbiome enrichment treatment as larvae?

Fit the bill: Rapid adaptation in a changing community

Duchesne, M., Arcese, P.

Climate and land use change facilitate rapid range shifts and novel competitive interactions among species, but case studies of the eco-evolutionary responses of native and colonist species remain rare. Grant & Grant (2006) reported rapid evolution in bill size in response to competition between native and colonist finches on Isle Daphne (Galapagos) with similar preferences and abilities to exploit seeds, demonstrating rapid divergence in morphology via natural selection. I am developing a parallel analysis of temporal change in traits affecting competitive ability in Song Sparrows (*Melospiza melodia*) resident on XOX DEL, BC, using 49 years of morphology and fitness data for ~3,500 birds subject to increasing competition for seeds following colonization by Fox Sparrows (*Passerella illiaca*). I predict that competition and temporal variation in seed abundance and diversity have caused rapid evolution in Song Sparrow bill size with two possible outcomes. 1) if seed diversity is limited, I expect bill dimensions to converge on those of Fox Sparrows, a socially dominant competitor, but nevertheless drive declines in Song Sparrow abundance (Abrams 1986). Alternatively, 2) given sufficiently diverse resources, natural selection may instead promote divergent evolution and facilitate the coexistence of both species on this small island (Grant & Grant 2006). My results will offer a novel test of theory (cf Abrams 1986) and advance our understanding regarding the role of rapid evolution in the coexistence of competing native and colonist species in a system wherein trait heritability and selection strength were extensively demonstrated when very few Fox Sparrows were present.

Landscape connectivity influence on genetic structure of coastal wolves

Hoang, M., Maraj, R., Roffler, G., Marshall, S., Boyce, M.

Functional connectivity provides insight into population structuring and gene flow within and among populations of organisms. Wolves that inhabit coastal British Columbia and Southeast Alaska are considered genetically, morphologically, and ecologically distinct from their mainland conspecifics. The current literature and available data on genetic population structuring for coastal wolves in BC is limited and there is a gap in our knowledge regarding the genetic variation and gene flow among populations, particularly across the international border. This projects main objectives are to: 1) characterize the genetic diversity and population structuring of coastal wolves in northern BC; 2) examine landscape connectivity between subpopulations; and 3) identify how geographical features impact gene flow. To accomplish these goals, I have collected over 500 genetic samples, consisting of hair and scat, which will be used for DNA extraction and genotyping by Wildlife Genetics International. I will use the program STRUCTURE to identify subpopulation differentiation. Then, using the software package Omniscape, I will use habitat attribute layers such as land cover, digital elevation models, hydrology layers, and prevailing ocean currents to model the terrestrial landscape connectivity and connectivity between islands and the mainland. Identifying corridors that are valuable for gene flow will provide a planning tool for recreation and urban planning, forestry, and other industrial activities.

Bird-window collisions: a window of opportunity to implement effective solutions

Hum, V., Green, David. Gow, Elizabeth.

Window collisions in Canada cause 16 – 42 million bird deaths annually, a significant contributor to anthropogenic bird population decline. Simon Fraser University's Burnaby campus, situated in a high elevation forested area along the Pacific flyway, offers valuable insights into seasonal collision patterns. My study assesses seasonal collision variations, species susceptibility, and building features contributing to mortality, aiming to evaluate bird window deterrent effectiveness. Year-round collision surveys were conducted across buildings of varying sizes and surrounding vegetation over five seasons. Scavenging and detection trials were also performed to quantify biases such as scavenging rates and detection efficiency. Preliminary findings reveal peak collision frequencies in spring and lowest in winter. This research illuminates the impact of collisions on declining avian populations in western North America. Identified high-risk facade features can inform mitigation strategies, including policy development and bird-friendly films, with potential applications beyond the study site. Ultimately, this work provides a foundation for implementing effective solutions to mitigate bird-window collisions and protect avian biodiversity.

Potential drivers of catch and release mortality of recreationally captured coho salmon

Johnston, Q.

Pacific salmon (*Oncorhynchus* spp.) play a vital role economically, culturally, and ecologically across their entire range. In an effort to slow the widespread declines of

Pacific salmon, many regulations have been implemented across all fisheries. In recreational fisheries, these regulations often result in an increase in catch-and-release (C/R) as a method to protect specific species, size classes, and populations. Coho salmon (*Oncorhynchus kisutch*) are one of the primary target species in British Columbia's marine recreational fisheries and, in southern waters, are subject to mark-selective fisheries, which require all wild coho salmon to be released. Coho salmon escapement estimates include models that incorporate post-release mortality (PRM) estimates based on short-term holding studies. Recent tagging and tracking studies have suggested that PRM rates may be higher than those currently used by fisheries managers. Our study aims to further investigate the mechanisms of mortality, the physiological response, and the relationship of infectious agents on the PRM rate of recreationally caught and release Coho salmon. Further, we aim to hold these fish for a minimum of 10-days to observe any latent mortality effects that may occur as a result of the fishery interaction. This study will advance our knowledge regarding the relative impact of different fishing techniques on *O. kisutch*, which will inform regulations implemented in the recreational fishery and the use of C/R as a conservation tool.

Understanding Trophic Dynamics in a Canadian Freshwater Jellyfish *Craspedacusta sowerbii* Population Through Zooplankton Analysis

Lambert, B., Halay, D., Pakhomov, E.

The Peach blossom jellyfish (*Craspedacusta sowerbii*) is one of the world's few freshwater cnidarians, and the only species to have a documented presence in North America. A non-native species that is believed to have originated in the Yangtze River basin of China, *C. sowerbii* has now been observed globally (excluding Antarctica), with future predictions expecting a species range expansion in high-latitude regions. Zooplankton communities in high latitude freshwater bodies are suspected to suffer from *C. sowerbii* expansion, with both life phases (benthic polyp and planktonic medusae) feeding on such communities. This research aims to investigate trophic dynamics of the often-overlooked invasive species *C. sowerbii* within the freshwater ecosystem of Hotel Lake (49°38 N, 124°02 W) on the Sunshine Coast of British Columbia. During the analysis we expect to observe differences in size and species composition of zooplankton between two sampling years, accounting for both high and low abundances of *C. sowerbii*. Increased abundance of *C. sowerbii* is expected to impact Hotel Lake trophic dynamics, leading to elevated predation pressure on the crustaceous zooplankton community. Zooplankton samples in a time-series taken from Hotel lake will be analysed using both modern and traditional methods to determine the predation impact of *C. sowerbii* on the lakes zooplankton population. This study addresses the urgent issue of invasive species, specifically examining the widespread but understudied *C. sowerbii*. Research proposed here will be the first of its kind in

North America, as there is currently no research examining the impacts of *C. sowerbii* blooms on zooplankton through lake sampling.

Robbing behaviour of bald eagles

Linton, A.

Kleptoparasitism, a foraging strategy characterized by the theft of food items from other animals, is a fascinating aspect of avian behaviour. This foraging tactic is common in various taxa, particularly among species that are predators or opportunists. Often referred to as “piracy” or “robbing,” kleptoparasitism is particularly notable in ecological conditions in which the animals are feeding on large, visible food items, and crucially, periods of food scarcity. Previous research identifies kleptoparasitism as a sub-optimal strategy and has predominantly focused on overwintering birds, observing an increase in kleptoparasitic behaviour in times of limited food. The scarcity of resources often leads to more instances of competition and fighting over these limited resources. However, few studies have described kleptoparasitism in systems in which food is relatively abundant. Here, we describe a system in which bald eagles often kleptoparasitize live prey, the plainfin midshipman (*Poricthys notatus*) at Crescent Beach, British Columbia, during the breeding season when resources are abundant. Using a mathematical model combined with observational data, we show that the rate of return for bald eagles self-feeding is low, indicating kleptoparasitism is a highly profitable strategy for these bald eagles.

Employing Environmental DNA to Resolve Spatial Differences in Marine Biodiversity

Melchers, G.

Environmental DNA is an emerging methodology in the field of marine ecology and conservation that holds immense potential for conducting non-invasive, non-expert, and rapid species detection across different ecosystems. Where standard dive and ROV surveys require laborious training, specialized identification skills, and safety concerns, eDNA can provide an alternative method for surveying underwater biodiversity, especially cryptic species that divers and cameras might miss. This study, in collaboration with members of The Marine Ecology Lab and The Juanes Lab, collected eDNA samples at the surface and bottom of three *Macrocystis pyrifera* kelp forests and non-kelp adjacent areas in the Deer Group Islands of Barkley Sound, the traditional territory of several Nuu-chah-nulth First Nations, in June 2023. The collected DNA was then processed using metabarcoding with 12S primers that can discern certain fish species. The aim of this study was to compare fish biodiversity from eDNA samples within and outside of *Macrocystis pyrifera* kelp beds, and also to compare results for fish biodiversity that members of The Marine Ecology Lab and The Juanes Lab obtained during their dive surveys, conducted within weeks of the eDNA collection date. These results will help to inform us of whether eDNA can detect potential cryptic fish species that dive surveys did not, the approximate accuracy of our eDNA results, and whether there are differences in fish communities between kelp and non-kelp forested areas at a very fine spatial resolution.

COVID-19 variant wave dynamics

Molan, S., Smith, N., Gandhi, V., Li, M., Murall, C. L., Stockdale, J., Colijn, C.

Our study aims to predict the amplitude of forthcoming COVID-19 variant waves using statistical modelling and a unique global dataset from throughout the pandemic. Utilizing publicly available datasets, we compiled relevant features such as demographics, geographic distribution, mobility patterns, epidemiological data, immunity levels, and viral genomic characteristics, which influence the spread and severity of COVID-19 waves. To train our model, we used the amplitude of consecutive COVID-19 waves, specifically Delta, BA.1, and BA.2 waves. For feature selection, we employed elastic net regression, given the model's effectiveness in handling diverse and multi-scale data types, with an emphasis on predictive accuracy. We implemented a leave-one-out cross-validation strategy that respects the time series nature of the data from each country. We then applied a random forest model using the same cross-validation strategy. Our preliminary findings indicate an underestimation of subsequent peaks in countries with a larger BA.1 compared to Delta and a larger BA.2 compared to BA.1. Addressing this underestimation is our current focal point, as it could potentially diminish the predictive utility of our model in critical situations. These observations guide ongoing refinements to our approach as we continue to investigate the complex dynamics involved in predicting COVID-19 variant waves.

Investigating Terrestrial Predation in the Intertidal Zone

Penno, Z.

The importance of energy pathways between aquatic and terrestrial ecosystems is increasingly recognized with advances in technologies that detect animals and their behaviours in remote habitats. Fragmented evidence points to the transportation of marine nutrients to terrestrial environments. A classic example is the role of Pacific salmon (*Oncorhynchus*), a crucial resource for black bears (*Ursus americanus*) and gray wolves (*Canis lupus)* on Vancouver Island, British Columbia (BC) during their migration from the oceans to rivers to spawn. There are likely additional roles played by terrestrial mammals that transfer marine nutrients to land. Indeed, less studied are foraging behaviour by terrestrial species which take advantage of the rich food subsidies available during low tide such as the non-native European green crab (*Carcinus maenas*; EGC). Intertidal shellfish may thus subsidize nutrients on land influencing coastal soil chemistry as well as plant ecosystem diversity and productivity. Yet patterns of exploitation of intertidal habitats by terrestrial mammals and factors which moderate their behaviours and foraging intensity has been inconsistently addressed in scientific literature. My MSc will collect empirical evidence quantifying marine-terrestrial trophic linkages in a region where large mammalian predators are abundant (Barkley Sound, Vancouver Island, BC) using camera traps in the intertidal zone.

Microbial Source Tracking In Baynes Sound Using Pacific Oysters

Pettit, I., Green, T.

Food production practices can become polluted due to contamination relating to the water source. A major source of water contamination in coastline areas stems from human fecal waste. Fecal waste is known to carry many different microorganisms, many of which are pathogenic to humans and ecosystem health. Fecal presence in water is commonly detected using a Fecal Indicator Bacteria (FIB). Previously, *Escherichia coli* (*E. coli*) has commonly been used as a FIB, as it can be found in many different gut biotas in both humans and other animals, as well as having a higher tolerance to salinity than other microorganisms. Different strains of *Bacteroides* offer themselves as a more species-specific FIB than *E. coli*. Humans, dogs, seagulls, and sealions all act as potential sources of contamination in the Baynes Sound region, with many species-specific bacteria. Pacific oysters are a common product in the shellfish farming industry, which filter-feed for nutrition. Shellfish are unable to differentiate between fecal contaminants, other pollutants, and food, allowing them to be suitable sample subjects in contamination tracking. By utilizing quantitative PCR and geospatial programs, it is possible to identify trends and sources of contamination to better inform agricultural practices and health authorities. Due to the high volume of contamination sea lions can produce and lack of identified sea lion specific bacteria, we aim to identify a FIB marker that allows for the identification of sea lion sourced contamination.

Is colour a good metric of stress in coralline algae?

Porcher, E., Martone, P.

Coralline algae are important foundational members of rocky shore communities, but are increasingly under threat from environmental change. When exposed to stressors such as high light, increased temperatures, or desiccation, corallines may “bleach”, a process where pigments are lost, causing them to visibly lighten in colour. Bleaching is often considered synonymous with tissue death and has frequently been used as a metric of mortality. However, recent evidence suggests that some bleached corallines may still be photosynthetically active, which calls into question whether colour alone is a valid measure of health in corallines. We investigated the relationship between colour and health in *Chamberlainium tumidum*, a common intertidal coralline crust by quantifying both colour and stress in freshly collected crusts from across a shore height gradient, as well as in crusts subjected to a desiccation stress. Stress was quantified as maximum quantum yield (Fv/Fm, using Pulse-Amplitude Modulated (PAM) fluorometry), while colour was quantified using a colour-card system that incorporated both lightness and tone. We found no relationship between Fv/Fm and colour in freshly collected *C. tumidum*, indicating that colour is a poor indicator of health in situ for this species. However, colour shifts occurring after the application of a desiccation stress were correlated with changes in Fv/Fm, suggesting that tracking colour changes may be useful under specific, controlled circumstances. Future researchers should proceed with caution when using colour as a metric of health in corallines, especially in the field.

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Unraveling seasonal growth and fatty acid changes in estuarian biofilm

Racz, A.

Despite their seemingly barren appearance, mudflats harbor a diverse ecosystem of invertebrate and meiofaunal communities. Comprised of fine sediments, these intertidal mudflat assemblages are founded upon complex communities of microscopic algae and bacteria, playing a pivotal role in primary production. These microbial communities, often referred to as biofilm, serves as the cornerstones of numerous intertidal food webs globally. However, detailed insights into their ecology remain elusive. One of the primary uncertainties concerns the growth and nutrient composition dynamics of biofilms over time. Prevailing theories suggest that biofilm populations undergo significant booms during specific periods of the year, likely influenced by key environmental factors such as fluctuations in temperature and salinity. To further examine this hypothesis, we collected physical samples of biofilm throughout the spring growing season (February to May) at Roberts Bank estuary. This period is marked by elevated biofilm levels, crucial as a food source for migrating shorebirds, specifically Western Sandpipers (*Calidris mauri*). Through chemical analysis of biofilm samples, we examined fluctuations in biofilm levels on the Roberts Bank mudflat in relation to this critical migratory period. Our findings confirm a steady increase in biofilm levels throughout the spring season, closely correlated with the extension of the photosynthetic period. However, notable spikes in chlorophyll and fatty acid content were observed near the spring equinox. This insight enhances our comprehension of the fluctuating dynamics of biofilms during the spring season and offers valuable information for informing conservation efforts concerning Western Sandpipers.

Investigating urchin distributions and control methods to inform restoration of threatened kelp forest ecosystems

Rehill, T.

As one of the most abundant coastal ecosystems in the North Pacific, kelp forests provide critical habitat to a diversity of ecologically, economically, and culturally important species. However, kelp forests in many areas, including British Columbia (BC), are now threatened by climate change-driven marine heatwaves and sea urchin expansion, prompting greater interest in potential restoration strategies, such as urchin removal. Yet, the potential viability of such measures is still unclear given our limiting understanding of the intensity and spatial variability of urchin grazing, particularly in BC where canopy forming kelps (giant and bull kelps) have historically been understudied relative to other systems. To address these challenges and upscale kelp restoration, we seek to comprehensively map urchin distributions and assess the effectiveness of various urchin mitigation strategies across varying density gradients. I will first build species distribution models (SDMs) for three urchin species across the BC coastline using density data collected via Remote Operated Vehicle (ROV) and dive surveys and integrating environmental factors as predictors. I will then conduct in situ urchin culling and exclosure experiments at different urchin densities in Barkley Sound (Bamfield Marine Science Center), in partnership with the Kelp Rescue Initiative. These experiments will allow us to assess the effectiveness of different urchin mitigation strategies across densities. This integrated approach, merging predictive mapping with real-world implementation, strives to drive targeted, effective, and sustainable kelp restoration efforts in British Columbia, ultimately aiding the conservation of these invaluable coastal ecosystems.

Ecology of two *Haematoloechus* spp. in Invasive Bullfrogs on Vancouver Island

Reumkens, C.

The invasive American bullfrog (*Lithobates catesbeianus*) has introduced the non-native digenean trematode, *Haematoloechus longiplexus*, to Vancouver Island. Recently, a morph distinct from *H. longiplexus* has been observed. This study aimed to 1. Identify the morph species through morphological analysis; 2. quantify both flukes' prevalence, abundance, and degree of aggregation; and 3. correlate host biology with infection data at two sites in Nanaimo, British Columbia, Canada. Seventy-one bullfrogs from Diver Lake and Green Lake were examined, yielding 901 parasite samples. All morph specimens were compared against morphological descriptions and identified to be most similar to *H. parviplexus*. At Diver Lake (n = 36), *H. longiplexus* showed 86.1% prevalence, a mean abundance of 16.25 ± 27, and *H. parviplexus* had 19.4% prevalence, a mean abundance of 0.78 ± 2.3, with an aggregated frequency distribution (VMR = 6.4). At Green Lake (n = 35), *H. longiplexus* exhibited 80.0% prevalence, a mean abundance of 6.09 ± 7.4, and *H. parviplexus* had 11.4% prevalence, a mean abundance of 0.23 ± 0.69, with an aggregated frequency distribution (VMR = 2.0). H. longiplexus had a notably high non-site specific frequency distribution (VMR = 34.1). At Green Lake, *H. parviplexus* abundance moderately correlated with bullfrog snout-vent length and slightly with weight (Pearson’s r = -0.45, p = 0.0069; r = 0.32, P = 0.065). Genetic barcoding is recommended for accurate morph identification, and further research is vital to determine the morph's range, prevalence, abundance, and aggregation at other Vancouver Island sites.

On a collision course: reconciling wind and wildlife futures

Rolfe, K., Popescu, V., Palen, W.

In response to growing climate change concerns, many jurisdictions are accelerating renewable energy development globally. Plans to rapidly decarbonize and electrify British Columbia (BC) are providing opportunities for smaller, distributed renewable energies such as biomass, geothermal, and especially wind. Over half of the potential development projects included in BC Hydros 2021 integrated resource plan are onshore wind facilities, many of which are planned for the Peace River region in northeastern BC. A primary conservation concern of this rapid wind energy development is bird fatalities due to collisions with turbines. Turbine collisions account for hundreds of thousands of bird fatalities annually in Canada and the United States, and with some subset of 73 potential wind facilities coming into operation in BC over the 20 years, the province is uniquely situated right now to proactively assess the potential environmental risks of different wind resource options. Using metrics such as conservation status, trait-based factors (e.g., body size, flight behaviour, nesting behaviour, etc.), and migratory patterns, I propose calculating a wind farm vulnerability score for each bird species in BC. With a focus on the Peace River region, I will use spatial conservation planning software to determine the potential environmental risk of each planned wind project based on the extent of project overlap with bird distributions and weighted by species vulnerability. This will allow for the intelligent prioritization of wind farm sites based on actualized risk to different bird species, thereby using actionable science to balance the interests of conservation and energy development.

The effects of climate change on food security in Tla'amin

Saleh, M.

Traditional foods are at the core of Indigenous values. However, over the last 60 years, diet has changed significantly due to climate change, altering the availability of marine species for Coastal First Nations (CFNs), constraining access to traditional seafood and elevating the risk of food insecurity. Unreliable access to sufficient, affordable, nutritious food is experienced disproportionately among CFN households, 41%, compared to 8.8% in the rest of BC households. I will focus on the Tla'amin Nation, where my research question will be "How do nature and biocultural climate risk-reduction solutions using a socioecological trait-based approach help support food security and biodiversity conservation in Tla'amin Nation under climate change?". I hypothesize that socioecological traits can help support community adaptations, climate mitigation measures, and food security status in Tla'amin. The project will consist of (1) Systematic review: I will identify traits in three dimensions related to traditional marine species in Tla'amin, and the three dimensions I will focus on are a) sensitivity, b) bridging human and natural systems and c) decision support. (2) Trait analysis: I will collaborate with the Nation's resource managers to assess the significance of the identified traits and nature-based solutions regarding their contributions to climate risk reduction, biodiversity conservation, and food sovereignty. (3) Trait-model integration: I will combine the trait data with existing simulation model projections to depict changes in local marine species under various climate change scenarios and adaptation options. These steps will empower the Nation to achieve their desired future in the face of climate change.

Juvenile salmon response to jetty breaching in the Fraser River estuary, BC.

Scott, D.

Estuaries provide critical nursery habitats for juvenile Pacific salmon, but many are highly fragmented by anthropogenic structures. The Fraser River is the largest producer of Pacific salmon in Canada with millions of juveniles out-migrating each spring, however many populations are of significant conservation concern. Migration pathways through the Fraser estuary have been altered by numerous jetties and causeways totaling greater than 26 km in barriers. In 2019, we began a restoration initiative that constructed three 50-meter linear breaches in the Steveston North Jetty, an 8km long barrier, and in 2022, one 30-meter-wide breach was created in the North Arm Jetty, a 5km long barrier. We directly monitored juvenile salmon (*Oncorhynchus* spp.) movement through the breaches using beach seines and fyke nets for four years from 2019 to 2023. We found that juvenile salmon immediately began using the breaches as new migratory corridors during peak outmigration periods, with all five species captured at breach locations. Juvenile chum showed the highest passage rates, along with large bursts of juvenile pink salmon, and consistent captures of juvenile Chinook salmon. Genetic analysis demonstrated that juvenile Chinook salmon captured were primarily subyearling migrants from the Lower Fraser River however individuals from the full suite of Fraser Chinook populations including yearling migrants and hatchery produced individuals were captured at breach locations. Overall, our results demonstrate that restoring estuary connectivity is a potentially effective restoration technique particularly in large river systems where a diversity of populations and species can benefit from a single project.

Identifying Markers Related to Bacterial and Viral Resistance in Pacific Oysters

Surry, L., Green, T., Sutherland, B., Loudon, A.

In the face of persistent pathogenic challenges, enhancing disease resistance within oyster populations emerges as a critical imperative in securing the sustainability of global oyster aquaculture. Since 2008, there has been an increase in mass oyster mortalities globally, decreasing Pacific oyster aquaculture worldwide. These mortalities are caused by viral and bacterial components: Ostreid herpesvirus 1 (OsHV-1) and Vibrio. There has been extensive focus on selectively breeding oysters with increased resistance to OsHV-1; however, it is currently unknown how Vibrio affects these OsHV-1-resistant oysters. We aim to assess how Pacific oysters with the presence of an OsHV-1 resistance genetic marker differ in susceptibility to Vibrio infection using a Genome-Wide Association Study (GWAS) and a PCR-based genotyping assay. Additionally, we aim to identify any additional genetic components related to bacterial susceptibility. We propose performing a disease challenge by exposing families of OsHV-1-resistant Pacific oysters to *Vibrio aestuarianus*, a known pathogen causing mortality. Oysters will be categorized based on being resistant or susceptible to Vibrio, and DNA will be extracted for genotyping. We hypothesize that homozygous recessive Pacific oysters will have a higher mortality rate due to the absence of critical genetic factors, making them more susceptible to Vibrio infections. The study aims to raise awareness about the importance of genomics in safeguarding oyster populations and global aquaculture.

Identification of the loci involved in ocean acidification resistance in Pacific oysters (*Crassostrea gigas*)

Wiebe, A., Green, T., Sutherland, B., Loudon, A.

Ocean acidification (OA) is a major consequence of climate change, which negatively impacts many marine organisms, such as Pacific oysters (*Crassostrea gigas*). OA inhibits early shell formation in Pacific oysters, resulting in arrested development, decreased size, shell deformities, disease susceptibility, and mortality. Some oysters have an innate resistance to OA, resulting in higher survival, but the loci associated with OA resistance have yet to be identified. We used a genetic-selection programs for C. gigas to create 137 genetically unique families. The larvae from each family were incubated with ambient and aragonite-undersaturated water for 24 hours to evaluate their resistance to OA. The parental genotypes were sequenced by whole-genome resequencing, and the offspring's genotypes were inferred. A genome-wide association study (GWAS) was conducted to identify the loci associated with OA resistance. This provides the genomic resources required to implement selective breeding in hatcheries, increasing the prevalence of OA resistance in the cultured population.

Vessel noise effects on anti-predator behaviour in Pacific sand lance

White, M., Carlson, N., Juanes, F.

The oceans acoustic environment has drastically changed due to the steep rise in human-generated or anthropogenic noise. This noise can elicit negative behavioural and physiological effects on numerous marine animals, such as fishes. With commercial shipping and recreational boating representing the main sources of anthropogenic noise in coastal areas, there is a growing concern for coastal marine organisms, many of which rely on sound for navigation, communication, and environmental perception. Compared to marine mammals, fewer studies have investigated how vessel noise influences fish behaviour, especially anti-predator behaviour. In a laboratory setting, I investigated how vessel noise impacts the anti-predator behaviour in Pacific sand lance (Ammodytes personatus), a coastal forage fish that is a major prey item for numerous seabirds, fish, and marine mammals. For ten days, schools of A. personatus were held in two different tanks, in one of which I played pre-recorded vessel noise, and in the other played computer-generated silence. Using underwater cameras, I recorded and analyzed fish anti-predator behaviour (e.g., startling and burrowing). I predicted that exposure to vessel noise would 1) initially increase startling and burrowing behaviour, and 2) elicit a long-term response of increased startle and burrowing behaviour. This study will be the first to investigate how vessel noise affects Pacific sand lance anti-predator behaviour, which can contribute to our understanding of how their individual fitness will be impacted by noise, and how their marine predators will be indirectly impacted through trophic linkages.

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Estimating Bryozoan Coverage on Kelp Surfaces Using UAVs

Wright, A.

This project will propose and test a methodology for monitoring Kelp-Encrusting Bryozoans (KEB) using Un-crewed Aerial Vehicles (UAV). Previous work in the remote sensing of Macrocystis pyrifera and Nereocystis leutkeana at regional scales has established robust methods of estimating kelp bed biomass using UAV-derived imagery. Here, I plan to (1) characterize the reflectance spectra of bryozoan-encrusted kelp at hyperspectral and multispectral resolutions, and (2) define a methodological framework to quantify percent coverage of bryozoans on floating kelp blades from high spatial-resolution UAV-derived multispectral images. This research will be performed at seven latitudinally distributed sites along the BC coast as part of the larger KEB monitoring project initiated by the SPECTRAL lab at UVic. To address objective (1), in-situ hyperspectral measurements of KEB and other end-members will be collected by boat. This spectral library can later be used to match end-members of UAV imagery to targets using spectral angle mapping (SAM). To address objective (2), a transect of very low altitude UAV images with high overlap and side-lap will be collected across the center and edges of a floating kelp bed. Orthomosaics of UAV transects will be constructed using Agisoft Metashape. Sunglint as well as overall kelp extent will be masked using the Hakai Institute Kelp-O-Matic and Glint Mask Generator software. Cover-type classifications will be performed using Convolutional Neural Networks (CNN) trained with images classified using supervised minimum-distance algorithms. With accurately masked KEB features and overall kelp bed surface area, an estimate of bryozoan coverage will be calculated using GIS software.

Posters (alphabetical order by last name)

Managing a tuc̓up Garden

Burtlake, C., Smith, S., Zayonc, D.

Food sovereignty, community engagement, and climate change guide Huu-ay-aht First Nations' marine monitoring program. The guiding topics are exemplified in four primary projects which include European Green Crab trapping and population management, the assessment of Dungeness Crab toxicology, the management of kelp extent and health, and monitoring our oceanographic conditions. An ongoing project, managing a tuc̓up garden, highlights the interconnectedness of our program. To manage a tuc̓up (Sea Urchin) garden, the HFN Lands and Natural Resources team, West Coast Kelp (WCK), and several youths in the Nuuchahnulth Warriors program harvested tuc̓up from a traditional harvest site at huʔii. 307 tuc̓up were harvested and distributed to Huu-ay-aht Citizens and Elders by Warriors. This work supports kelp growth as we re-establish the balance HFN managed in the ḥahuułi.

Assessing effects of acclimation temperature on thermal tolerance of stream-type juvenile Chinook salmon (*Oncorhynchus tshawytscha*) under ecologically relevant temperatures

Butler, N., Eliason, E., Lotto, A., Hinch, S.

We evaluated thermal tolerance in Chinook fry and parr using three approaches. Fish were acclimated for two weeks at temperatures spanning present and expected future summer levels (15°C, 18°C, 20°C, 24°C). Using fish from each acclimation temperature, we measured: 1) endurance swimming (E swim), where swimming fish were exposed to increasing speeds at each temperature, 2) critical thermal maxima (stationary) (CT max stat) where water was heated (0.3°C/min) in a stationary tank, and 3) critical thermal maxima (swimming) (CT max swim) where water was heated (1°C/30min) while fish swimming at a fixed speed. Fish acclimated to higher temperatures generally exhibited higher thermal tolerance, based on CT max stat and CT max swim trials, though fry exhibited a greater sensitivity to increased temperatures. However, swim performance impairment was greater at the 24°C acclimation treatment for both CT max swim and E swim trials in parr and fry, indicating an upper thermal limit with differing responses between life stages.

Female Meiotic Drive and its Effect on Nondisjunction

Clark, M., Perlman, S.

Meiotic drivers are selfish genetic elements that hijack meiosis to ensure their overrepresentation in the next generation. While meiotic drivers are widespread and diverse, we still know little about the mechanisms by which they operate. We recently discovered a selfish X chromosome in the fruit fly species Drosophila testacea that causes meiotic drive in females, resulting in it being passed on significantly more often than a wildtype X chromosome. In this study, we examined whether this selfish X chromosome increases the rate of nondisjunction, resulting in individuals with either too many or too few chromosomes. To test this, we crossed female flies with either two, one, or no selfish X chromosomes with males with a non-selfish X chromosome that carries a recessive bright orange eye color mutation. With this cross, any individual that did not inherit any X chromosomes from their mother (i.e. nondisjunction) would be clearly identified as a male with bright orange eyes, with XO genotype. We found that female flies with two selfish X chromosomes produced significantly more XO sons than females with only 1 or no selfish X chromosome, demonstrating a clear connection between female meiotic drive and nondisjunction, and highlighting some of the potential negative fitness consequences of meiotic drivers.

Evolution of the transitional retina in the young sablefish

Dove, G.

Vision within the vertebrate eye begins with light entering the eye and being absorbed by the photoreceptors within the retina. The retina has photoreceptors with distinct modus operandi; rods operate in dim environments whereas cones operate in bright environments. This study examines the arrangement of cone photoreceptors within the retina, the uniquely lattice-like formation of cones in teleosts. The pattern occurs regularly across the retina and is called a cone mosaic. In indirectly developing teleosts (fish that experience substantial phenotypical changes between larval and adult stages) the cone mosaic transitions between patterns. These larval teleosts have single cone-dominated retinas, each cone is surrounded by six neighbouring single cones. The adult retina is composed of single and double cones (two single cones juxtaposed), the double cones form a square around a single central cone. The retina of the indirectly developing Atlantic halibut, *Hippoglossus hippoglossus*, expresses these two distinct patterns during development. Moreover, the mosaic transition of the halibut is accompanied by a habitat change from shallow water to deep water, and an extreme metamorphosis in which the eyes migrate to one side of the head. The sablefish, *Anoplopoma fimbria*, shares an indirect life history and migration pattern with the flatfish but does not undergo the same degree of metamorphosis. A comparison of retinal structures between these two teleosts infers the role of metamorphosis and life history on the evolution of the transitional retina.

Mesozooplankton in the Lazarev Sea: Community structure and spatiotemporal dynamics

Gordon, H., Pakhomov, E.

In the Southern Ocean, zooplankton are the dominant component of pelagic biomass and play a significant role in carbon and nutrient cycling, structuring food webs, and sustaining commercial fisheries. Despite their ecological importance, zooplankton communities in many areas of the Southern Ocean remain poorly characterized. In this study, zooplankton community composition in a marginal sea of the Southern Ocean during early austral summer 1994-1995 was described across a latitudinal gradient and distinct zooplankton assemblages, along with their associated water masses, were identified. The results highlight the utility of zooplankton communities as indicators of boundaries between hydrologically distinct water masses. They also demonstrate how water mass modifications, due to sea ice melt and intrusion, restructure the pelagic community. Greater understanding of how lower trophic level communities are impacted by physical processes can help us to make better predictions about how ecosystems may be impacted by a changing climate. Additionally, historical zooplankton community data can provide indication of shifts in community structure, species distributional ranges, and phenology, all of which can have profound implications for higher trophic levels and overall ecosystem functioning.

Understanding Trophic Dynamics in a Canadian Freshwater Jellyfish *Craspedacusta sowerbii* Population Through Zooplankton Analysis

Halay, D., Lambert, B., Pakhomov, E.

The Peach blossom jellyfish (*Craspedacusta sowerbii*) is one of the world’s few freshwater cnidarians, and the only species to have a documented presence in North America. A non-native species that is believed to have originated in the Yangtze River basin of China, *C. sowerbii* has now been observed globally (excluding Antarctica), with future predictions expecting a species range expansion in high-latitude regions. Zooplankton communities in high latitude freshwater bodies are suspected to suffer from *C. sowerbii* expansion, with both life phases (benthic polyp and planktonic medusae) feeding on such communities. This research aims to investigate trophic dynamics of the often-overlooked invasive species *C. sowerbii* within the freshwater ecosystem of Hotel Lake (49°38 N, 124°02 W) on the Sunshine Coast of British

Columbia. During the analysis we expect to observe differences in size and species composition of zooplankton between two sampling years, accounting for both high and low abundances of *C. sowerbii*. Increased abundance of *C. sowerbii* is expected to impact Hotel Lake trophic dynamics, leading to elevated predation pressure on the crustaceous zooplankton community. Zooplankton samples in a time-series taken from Hotel Lake will be analysed using both modern and traditional methods to determine the predation impact of *C. sowerbii* on the lakes zooplankton population. This study addresses the urgent issue of invasive species, specifically examining the widespread but understudied *C. sowerbii*. Research proposed here will be the first of its kind in North America, as there is currently no research examining the impacts of *C. sowerbii* blooms on zooplankton through lake sampling.

Hypoxia and heat stress on heart characteristics of *Corella* tunicates

Krohman, R., Ogushi, R., Fox, J., Ivy, C.

Marine habitats are experiencing changes in temperature and dissolved oxygen due to climate change, but how these changes are influencing the physiology of subtidal sessile invertebrates has not been well studied. Tunicates are a common subtidal invertebrate with a unique heart, in that their heartbeat can reverse directions. Tunicate heartbeats can be influenced by environmental stressors, but how low oxygen (hypoxia) and heat combined affect heart rate and heartbeat reversal is unknown. *Corella* spp. were collected and acclimated to lab conditions for 16-24 hours (~13°C, ~92% O2), then exposed to warm (~18°C), hypoxic (~31% O2), or warm and hypoxic (~17°C and ~31% O2) conditions for six hours. Heart rate and time between heartbeat reversals were measured after collection, acclimation to lab conditions, exposure to a stressor, and recovery from the stressor. There was a positive correlation between time between heartbeat reversals and heart rate when tunicates were measured immediately after collection, but not after lab acclimation. Heart rate increased with exposure to heat, hypoxia, and heat and hypoxia, with the greatest increase after exposure to both stressors. Time between heartbeat reversals increased with exposure to heat, but not hypoxia or heat and hypoxia. Our findings show that temperature and oxygen availability influence *Corella* heart rate and time between heartbeat reversals differently, suggesting that tunicates may be able to optimize oxygen and nutrient movement when exposed to abiotic stressors. As marine environments continue to change, studies such as these could provide insight into predicting how tunicates will respond to changing conditions.

Female-female socialization and cohabitation in intertidal jumping spiders (*Terralonus californicus*)

Mali, P., Punzalan, D.

Sociality and cooperation in jumping spiders are rarely observed. Female-female conflicts and aggression often arise from competition over resources or defensive nesting behaviour. We investigated the effects of residency status and egg-laying on the social repulsion and attraction between female intertidal jumping spiders (Terralonus californicus). Simulated 'intruders' were introduced to the nests of residents with or without egg clutches. Both female spiders generally displayed low rates of aggression and repulsion regardless of the presence or absence of the residents eggs. After some time, intruder and resident females were shown to nest and lay eggs together. Furthermore, we found that egg sacs were more frequently laid in the trials where residents' eggs were already present. We propose that female intertidal jumping spiders may receive benefits from cohabiting and cooperative egg-laying, though identifying what those might be is still a mystery and the subject of ongoing work.

You are what you eat: Humpback whale diet composition in the Strait of Georgia

Melica, V., Hunt, B., Thornton, S., Christensen, V.

Humpback whale (*Megaptera novaeangliae*) populations in the North Pacific are recovering rapidly after being severely depleted by commercial whaling. As large predators, their recovery is likely to have implications for food web dynamics; thus, diet studies are necessary to assess the ecological role of humpback whales. The goal of this project is to determine diet composition of humpback whales foraging in the Strait of Georgia, British Columbia, Canada. For this study, humpback whale skin (n = 63), juvenile herring (n = 181), adult herring (n = 23), euphausiids (n = 46), and amphipods (n = 5) were collected in the summer months of 2022 and analysed for carbon (δ^13 C) and nitrogen (δ^15 N) stable isotopes. These isotope data were then applied in a Bayesian mixing model to estimate the proportional contribution of each prey item to the humpback whale diet. Preliminary results indicate that humpback whales forage predominantly on euphausiids (80.9%) and juvenile herring (11.7%), with adult herring and amphipod representing a small portion of their diet. These findings align with stomach content analysis performed on captured humpback whales in the North Pacific during the whaling period. This local study provides insight into diet composition of humpback whales in the Strait of Georgia which may be used in model development to help inform conservation policies of both predator and preys. Additional diet analysis from other foraging areas in Pacific Canadian waters can further help understand regional dietary differences and overall food web effects of humpback whale recovery.

Investigating Behavioural Patterns in Ringed Seal Calls Through Acoustic Analysis

Nicholls, C.

This study addresses climate change and its impact on the Arctic ecosystem, with a specific focus on ringed seals, a vulnerable pinniped species. The research explores the dual threats of diminishing sea ice cover and increased shipping density, and their potential effects on the behavioural patterns of ringed seals. The study employs acoustic and photo analyses at sea ice cracks, where ringed seals gather during spring haul-outs. The first hypothesis proposes a diel pattern in calling behaviour, anticipating variations in vocalizations throughout the day. It predicts a decrease in calls during midday, coinciding with the presumed primary haul-out time, and an increase in vocalizations during morning and evening periods. The second hypothesis focuses on identifying distinct vocalizations associated with specific haul-out behaviours exhibited by ringed seals. This includes an analysis of acoustic call patterns concerning haul-out events, seeking to determine if unique vocalizations correspond to specific behaviours during these crucial moments. To investigate these hypotheses, a hydrophone was deployed near Ulukhaktok, Northwest Territories. Raven software is utilized for acoustic analysis to categorize calls. Trail cameras capture images to conduct a photo analysis of seal behaviours during the same period. The study aims to contribute valuable insights into the vocal repertoire and behaviours of ringed seals, offering a baseline for future research to monitor changes in patterns as environmental conditions evolve. The methodologies employed in this study, combining acoustic and photo analyses, provide a comprehensive approach to understanding the impacts of climate change and noise pollution on Arctic marine ecosystems.

Reconnecting salmonid habitats at watershed scales using spatial conservation tools

Persram, M., Palen, W., Popescu, V.

Freshwater ecosystems are highly connected and play important ecological, biological and cultural roles. However, barriers, such as road culverts, dams, and dykes, have fragmented river ecosystems creating a myriad of watershed-scale issues, posing problems for mobile freshwater species as fragmented connectivity leads to habitat loss. One challenge of restoration is that the number of potential sites exceeds current resource capacities, leading to restoration that is done opportunistically, tackling issues at local sites or aimed at specific species. To confront the challenges of watershed-scale restoration, I propose combining spatial datasets and conservation prioritization software to streamline decision-making when choosing potential restoration sites. Conservation prioritization software is frequently used for planning protected areas and generates spatial priorities for conservation or environmental planning, aimed at informing decision-making. The project goal is to develop a prioritization framework that can guide the implementation of freshwater restoration by identifying the cumulative benefits provided to multiple species and ecosystem processes. I will combine spatial datasets (salmonid habitats, barrier removal potential and cost) using conservation planning software to identify sets of potential freshwater restoration sites. This combines information across scales to provide guidance on the sets of sites that return the biggest restoration benefit based on costs, accessibility, stability, and number of species. This framework would demonstrate how a watershed-scale perspective of restoration could lead to sustained biodiversity and ecosystem function. By making connectivity the focus of restoration there is the opportunity for habitat improvement not only in local areas but also at the watershed scale.

Understanding controls on nutrient cycling in aquatic ecosystems

Rozanski, S.

Animals play an important role in nutrient cycles by uptaking dietary nutrients and storing them, but also by recycling a subset of these nutrients as waste. In freshwater ecosystems, fish can affect the standing stock and turnover rates of biologically important elements like carbon, nitrogen, and phosphorus. Fish waste shows considerable variation in the concentrations and proportions of elements, and the goal of my thesis is to understand this variation. To accomplish this goal, I used ecological stoichiometry (ES), which expresses biological entities as elemental ratios and uses mass-balance to predict elemental proportions of animal waste based on the elemental content of their bodies (their “organismal stoichiometry”, OS) and their diets. Current research in ES focuses either on invertebrates, or on interspecific variation in vertebrates. I use ES to predict how intraspecific variation in OS of vertebrates affects elemental proportions in excreted and egested wastes. I hypothesise that variation in OS will be high, and, in accordance with ES predictions, the elemental content of waste will be negatively related to OS. To test this hypothesis, I used the threespine stickleback, a fish with well-documented variation in OS stemming from its variation in bony armour. I collected stickleback from five sites along the Sooke River and measured their excretion rates in the field. I quantified the carbon, nitrogen and phosphorus content of their bodies, gut contents (proxy for egestion), and excreted wastes. As expected, variation in OS is high, but the relationship between OS and waste must be further analysed.

Self-Grooming in *Aedes aegypti* exposed to formulated *Metarhizium humberi* Conidia

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Mosquitoes play a crucial role in vector-borne disease transmission, and a better understanding of their interactions with entomopathogens is vital to improve control

strategies. This study investigated a possible intended removal of Metarhizium humberi conidia adhering to the cuticle of Aedes aegypti, a key vector of dengue, Zika and chikungunya fevers in the tropics. Adults were exposed to conidia (C), micronized carnauba wax (MCW) as an additive, a combination of both (C+MCW), or to no treatment (control), and then locomotion and friction behavior, and the number of conidia on adults up to 24 h post-treatment assessed. All treatments (C, MCW and C+MCW) significantly increased friction behavior ($p \leq 0.0013$) compared to the untreated control, while locomotion remained unaffected ($p \geq 0.087$). Increasing post-treatment period significantly reduced conidia numbers on mobile adults treated with C (5.1x10^5 conidia/adult after 0 h down to 9.2x10^4 conidia/adults after 24 h) and C+MCW (5.3x10^5 conidia/adult after 0 h down to 8.1x10^4 conidia/adult after 24 h; $p < 0.0001$). On immobilized adults the loss of conidia (C or C+MCW) on the cuticle was less distinct during the same period. The decline of conidial numbers on the cuticle found here suggests a potential self-grooming behavior of A. aegypti adults treated with this fungus that is highly infective to this vector. Findings emphasize the importance to consider post-treatment self-defense behavior in this important mosquito vector for the development of a mycoinsecticide as the final number of conidia that invade the insect determine further fungal infection and host death.

Exploring sea spider (Pycnogonida) species diversity in British Columbia

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The Pycnogonida, known as sea spiders, is a clade of marine arthropods generally accepted as the sister group to all other Chelicerata, including arthropods like arachnids and horseshoe crabs. Sea spiders have a cosmopolitan distribution and can be found intertidally to a depth of 7000 meters. Due to their generally small size and cryptic coloration, pycnogonids go largely unnoticed, and many questions remain surrounding their species diversity, phylogeny, and ecology. I hypothesize there are several undescribed species of littoral pycnogonids in British Columbia which have been overlooked due to their small size and crypticity. Here, I explore the littoral species diversity of pycnogonida in BC using SCUBA diving for specimen collection and a combination of imaging techniques to describe their morphology and ultrastructure including light microscopy (LM), scanning electron microscopy (SEM), and confocal laser scanning microscopy (CLSM). Additionally, by genetically barcoding the species collected for CO1 and 18S genes, I identify and place these sea spiders in their respective phylogenies. This project will fill gaps in our understanding of the diversity and distribution of an entire class of marine arthropods, pycnogonids, which are still poorly understood. In light of a rapidly changing climate, documenting marine biodiversity is more important than ever as species extinctions continue, and range shifts redesign our planet's ecosystems. The future of ecology and conservation

depends on reliable records of species and their distributions, and overlooked species such as sea spiders need to be described for us to recognize their role in marine ecosystems.