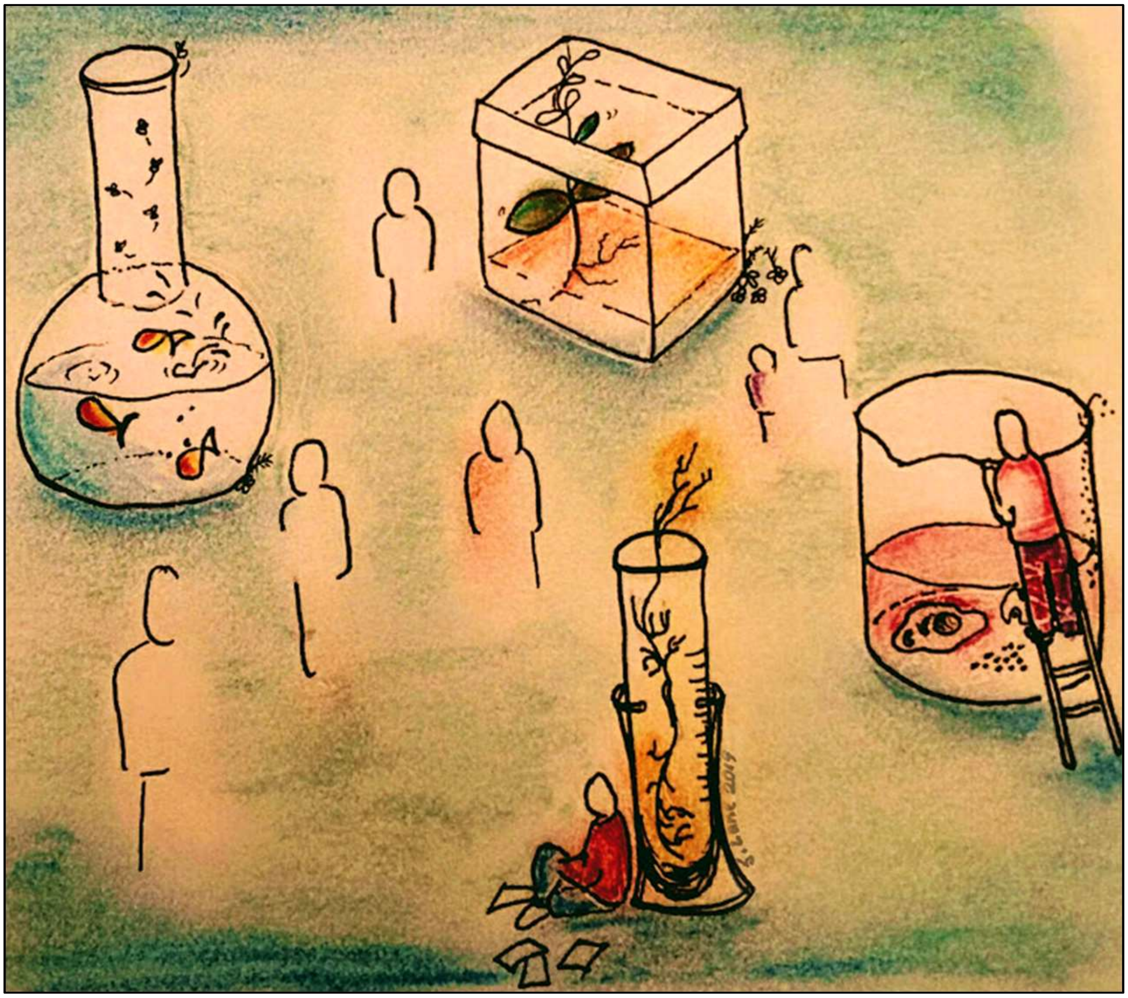
2019 UVic Biology Graduate Student Symposium



November 13 and 14
8:00 AM – 4:30 PM
Medical Science Building (MSB 160)

Nov. 13, 2019

Time	Chair	Name	Supervisor	Title
9:00-9:15 - Coffee				
9:15	**Dr. Jürgen Ehlting**	**Nicholas Planidin**	**Introductory Remarks**	
9:30		Kathryn Erceg	Dr. B. Koop & Dr. J. Taylor	Eco-evolutionary impact of chromosomal inversions in rainbow trout populations
9:45		Ainsley Fraser	Dr. R. El-Sabaawi	Characterizing phenotypic diversity in marine populations of the threespine stickleback
10:00		Hollie Johnson	Dr. B. Koop & Dr. John Taylor	Northern pike of North America: population genomics and sex determination
10:15		Emily May	Dr. R. El-Sabaawi	Experimentally evaluating phosphorus release in fish excreta and egesta
10:30-10:50 - Coffee				
10:50	**Ainsley Fraser**	Anna Curtin	Dr. H. Buckley	Mitigating biofouling on reverse osmosis membranes: applying greener preservatives to biofilm treatment
11:05		Audrey McPherson	Dr. S. Perlman & Dr. P.l Abram	Genomics and microbial symbionts of spotted wing *Drosophila*
11:20		Nicholas Planidin	Dr. T. Reimchen	Spatial, sexual and rapid temporal differentiation in neuromast expression in Haida Gwaii stickleback.
11:35		Candice Powell	Dr. S. Perlman	Characterization of a selfish genetic element in *Drosophila testacea*
11:50 - 12:50 - Lunch				
12:50	**Carmen Lea**	Chloe Christensen	Dr. F. Choy	Investigating therapeutic applications for lysosomal disease
1:05		Geoffrey deRosenroll	Dr. G. Awatramani	Applying machine learning techniques to decode retinal ganglion cell activity to see what they saw.
1:20		Farnoosh Farhoomand	Dr. K. Delaney	Sensory-evoked activity in somatosensory cortex as a model to probe cortical plasticity in a mouse model of Rett syndrome
1:35		Laura Hanson	Dr. G. Awatramani	“Silent” synapses in the mature mouse retina and their response to graded signaling
1:50		Keyrian Le Gratiet	Dr. R. Nashmi	Spatial profiling of co-transmitted acetylcholine and GABA inputs onto substantia nigra dopaminergic neurons
2:05-2:25 - Coffee				
2:25	**Shea Wyatt**	Marie Vance	Dr. P. von Aderkas	Population genomics of a high-elevation conifer, subalpine larch (*Larix lyallii*)
2:40		Yuriko Carrington	Dr. J. Ehlting	The functions of QDH genes in plants
2:55		Gerry Gourlay	Dr. C.P. Constabel & Dr. B. Hawkins	High condensed tannin levels protect poplar against oxidative damage generated by UV-B exposure or drought stress
3:10		Sarah Lane	Dr. J. Ehlting & Dr. P. Walter	The potential of plant root compounds as iron chelators for human medicinal use
3:25		Carmen Lea	Dr. C. P. Constabel	Purification and biological activity of a diarylheptanoid compound found in the leaves and bark of red alder
3:40		Dawei Ma	Dr. C. P. Constabel	MYB transcription factor, MYB117 induces anthocyanin production and increases hydroxylation of flavonoids in poplar

Nov. 14, 2019

Time	Chair	Name	Supervisor	Title
9:00-9:15 - Coffee				
9:15	**Dr. Barbara Hawkins**	Will Duguid	Dr. F. Juanes	Regional and seasonal variation in adult Chinook Salmon diets in British Columbia
9:30		Morgan Black	Dr. F. Juanes & Dr. S. Dudas (DFO)	Marine macrofaunal communities of First Nations' clam gardens
9:45		Malcolm Cowan	Dr. P. von Aderkas	Influence of *Vibrio* spp., temperature, reproductive development, and stocking density on Pacific oyster summer mortality in Baynes Sound, BC.
10:00		Kieran Cox	Dr. F. Juanes & Dr. S. Dudas	Shellfish subsidies along the Pacific coast of North America
10:15		Sean Dimoff	Dr. J. Baum	Kiritimati's coral reef soundscapes: Can listening to the reef inform us about its health?
10:30		Michael Livingston	Dr. D. Varela	The role of transparent exopolymer particles in the biological carbon pump in the North East Pacific Ocean
10:45-11:05 - Coffee				
11:05	**Morgan Black**	Kelsie Murchy	Dr. F. Juanes	Behaviour of Chinook Salmon (*Oncorhynchus tshawytscha*) after acoustic tagging in Cowichan Bay, BC
11:20		Geoffrey Osgood	Dr. J. Baum	Chondrichthyans as an umbrella species complex for conserving South African biodiversity
11:35		Rhonda Reidy	Dr. F. Juanes & Dr. L. Cowen	Echo sounding humpback whale prey
11:50		Kristina Teitjen	Dr. J. Baum	Coral recruitment on an isolated atoll following mass coral mortality
12:05		Shea Wyatt	Dr. D. Varela	Ocean acidification effects on the growth physiology of subarctic and subtropical siliceous phytoplankton
12:20		**Dr. Jürgen Ehlting**	**Closing Remarks**	

November 13, 2019

Session One

ERCEG	Kathryn	pg. 1
FRASER	Ainsley	pg. 1
JOHNSON	Hollie	pg. 2
MAY	Emily	pg. 2

Session Two

CURTIN	Anna	pg. 3
McPHERSON	Audrey	pg. 3
PLANIDIN	Nicholas	pg. 4
POWELL	Candice	pg. 4

Session Three

CHRISTENSEN	Chloe	pg. 5
deROSENROLL	Geoffrey	pg. 5
FARHOOMAND	Farnoosh	pg. 6
HANSON	Laura	pg. 6
LE GRATIET	Keyrian	pg. 7

Session Four

VANCE	Marie	pg. 7
CARRINGTON	Yuriko	pg. 8
GOURLAY	Gerry	pg. 8
LANE	Sarah	pg. 9
LEA	Carmen	pg. 9
MA	Dawei	pg. 10

November 14, 2019

Session Five

DUGUID	Will	pg. 11
BLACK	Morgan	pg. 11
COWAN	Malcolm	pg. 12
COX	Kieran	pg. 12
DIMOFF	Sean	pg. 13
LIVINGSTON	Michael	pg. 13

Session Six

MURCHY	Kelsie	pg. 14
OSGOOD	Geoffrey	pg. 14
REIDY	Rhonda	pg. 15
TIETJEN	Kristina	pg. 15
WYATT	Shea	pg. 16

Author: **Erceg, Kathryn**
Degree Sought: MSc
Supervisors: Dr. Ben Koop and Dr. John Taylor
Category: Ecology and Evolution

Eco-evolutionary impact of chromosomal inversions in rainbow trout (*Oncorhynchus mykiss*) populations

Almost a century after their discovery in 1921, chromosomal inversions are still being identified in new populations and continue to contribute to the understanding of evolutionary processes. Occurring when a section of a chromosome is broken off and rejoined with the rest of the chromosome in its reverse orientation, inversions can suppress recombination and affect phenotypes related to eco-evolutionary processes. Two large inversions have been identified in the fifth (Omy05) and twentieth (Omy20) chromosomes of rainbow trout (*Oncorhynchus mykiss*). Using PCR and Sanger sequencing, these inversions were identified in individuals from populations across western North America as well as offspring from mate pairings of inverted and non-inverted parents. These inversions were found to be common in populations in northwestern North America for the Omy05 inversion and southwestern North America for the Omy20 inversion except for one hatchery population in Fraser Valley in which both inversions commonly occur. Though inversions can supress recombination, it was inconclusive whether recombination suppression occurred for the offspring families. For example, one mate pair's offspring resulted in significantly fewer heterozygotes than those with the inversion, suggesting recombination suppression and underdominance of heterozygotes. Contrarily, a different mate pair's offspring in which the parents had the same inversion status as the aforementioned parents were found to be in Hardy-Weinberg equilibrium. In addition to the offspring analysis, phylogenetic analysis of re-sequenced individuals will be used to study the evolutionary relationships of these inversions.

Author: **Fraser, Ainsley**
Degree Sought: MSc
Supervisor: Dr. Rana El-Sabaawi
Category: Ecology and Evolution

Characterizing phenotypic diversity in marine populations of the threespine stickleback

The threespine stickleback (*Gasterosteus aculeatus*) is an important model for studying evolution. Sticklebacks are widely distributed in the northern hemisphere and inhabit freshwater, brackish, and marine waters. Anadromous populations (hereafter marine) are assumed to be homogenous in space and invariant in time in their phenotypic characteristics, despite marine environments varying on regional and local scales. Recent studies suggest there is in fact genetic and phenotypic structure in marine sticklebacks, yet the ecological causes of these differences remain unclear. My goal is to asses trait variation in marine stickleback populations around Southern BC, and whether oceanographic and habitat characteristics explain this variation. Between May-July 2019, I sampled ~600 sticklebacks from 20 sites in Southern BC. This semester in the lab I will characterize trait variation using geometric morphometric analysis comparing individuals between these sites, as well as male and females of each site because sticklebacks are sexually dimorphic. My study will be the most comprehensive characterization of the phenotypic heterogeneity of marine sticklebacks to date. Research on traits that determine stickleback success in these environments will provide valuable insight into the viability of other marine populations. Researchers have shown that sticklebacks can be an indicator species to assess effects from pollutant exposure. Marine sticklebacks are known to overlap diets with complex pelagic fish and share nursery grounds with salmonids, perch, and pike. My project will allow us to refine our assumptions about using marine sticklebacks as the contemporary ancestors in studies of morphological evolution, thereby significantly advancing the field of study.

Author: **Johnson, Hollie**
Degree Sought: MSc
Supervisors: Dr. Ben Koop and Dr. John Taylor
Category: Ecology and Evolution

Northern pike of North America: population genomics and sex determination

Genetic variation is considered pivotal in a species' ability to adapt to new habitats and environments. Based on microsatellite and mitochondrial data, the economically and ecologically valuable Northern Pike (*Esox lucius*) has been reported to have low levels of genetic variation. Yet they have a circumpolar distribution and a great capacity to colonize and adapt to new environments. Here, high-resolution resequencing data from 47 Northern Pike from across North America was used for SNP discovery and population analysis. Results illustrate a genome-wide lack of polymorphism and suggest that two distinct groups of Northern Pike exist in North America, separated by the North American Continental Divide. Northern Pike west of the Continental Divide have an average of one heterozygous SNP every 6,250 bases. Their eastern counterparts possess just one heterozygous SNP every 16,500 bases. For comparison, an average of one heterozygous SNP per 309 bases has been reported in herring, one per 750 bases in Coho and chinook salmon, and one per 1000 bases in humans.

We observed a recently described master sex-determining gene, *amhby*, in three western North American populations but not in populations east of the Continental Divide. We could not resolve any signals indicating a genetic sex determination system was present in populations from southern Manitoba or the St. Lawrence River. This may indicate that environmental sex determination is at play in these populations. We found evidence of a possible female-heterozygous, male homozygous ZW-ZZ genetic sex-determination system in Northern Pike from New Jersey.

Author: **May, Emily**
Degree Sought: MSc
Supervisor: Dr. Rana El-Sabaawi
Category: Ecology and Evolution

Experimentally evaluating phosphorus release in fish excreta and egesta

In many freshwater ecosystems, internal phosphorus (P) recycling is as important as external P input. In these ecosystems, P release in fish wastes can sustain primary production during periods of low external P input. Previous research in this field primarily focuses on liquid waste production (excretion), as excreta contains soluble inorganic phosphate that can be immediately used by primary producers. However, researchers often ignore solid waste production (egestion) because egesta must be processed before the nutrients can being taken up by primary producers and because egestion is logistically difficult to measure in the field and laboratory. Our research aimed to (1) develop methods for quantifying egestion and (2) collect preliminary data on how much P is released in egesta *versus* excreta. To accomplish this, we performed laboratory experiments with field-caught threespine stickleback (*Gasterosteus aculeatus*).

We allowed stickleback to fast for 24 hours, fed them to satiation with chironomid larvae, and incubated them individually in 3L chambers for 24 hours. Then, we collected water and fecal samples to quantify excretion and egestion respectively. Stickleback consumed a mean of 157.273 ug of P (sd: 61.205) and released 27.5% of this P as waste. Stickleback egested a mean of 7.256 ug of P (sd: 7.044 ug) and excreted a mean of 35.939 ug of P (sd: 26.147 ug). The mean ratio of excreted to egested P was 16.629 (sd: 23.244), implying that egested nutrients contribute less to nutrient recycling in this system.

Author: **Curtin, Anna**
Degree Sought: MSc
Supervisor: Dr. Heather Buckley
Category: Marine Biology

Mitigating biofouling on reverse osmosis membranes: applying greener preservatives to biofilm treatment

Water scarcity is characterized by a lack of access to clean and affordable drinking water, as well as water for hygienic and economic needs. The amount of people effected by water scarcity is expected to increase in the coming. In response, scientists are pursuing cost effective drinking water treatment methods. Desalination of brackish water via reverse osmosis (RO) is one promising alternative method. RO, however, is limited significantly by biofouling of the filtration membrane. Biofouling is the buildup of microorganisms in a biofilm at the water-membrane interface. It clogs the membrane, decreasing the efficiency of filtration, consequently increasing operational and maintenance costs. Although effective, existing biofouling treatment methods can damage the membrane, decreasing the lifespan of the membrane; create antibiotic resistance; and cause harm to humans and the environment if the chemicals pass through the membrane. The current project focuses on applying safer preservatives used in home and personal care products to RO membranes to investigate the biofouling treatment efficacy. Many of these safer preservatives have only been tested on cells in planktonic phase in suspension cultures, not on cells in biofilms. The results of suspension culture tests are not applicable to biofouling scenarios because organisms in suspension cultures exhibit different characteristics than those in a biofilm. In this study, biofilms will be grown on 96-well-plates and minimum inhibitory concentrations (MIC50 and MIC90) and log-reductions will be calculated for various safer preservatives. Results from these tests will be used to guide doses for tests of safer preservatives in a bench-scale RO system.

Author: **McPherson, Audrey**
Degree Sought: MSc
Supervisors: Dr. Steve Perlman and Dr. Paul Abram
Category: Ecology and Evolution

Genomics and microbial symbionts of spotted wing *Drosophila*

Insects introduced from other parts of the world can cause major crop yield losses, and keeping them at non-damaging levels often requires the application of costly and non-specific chemical pesticides. Spotted wing Drosophila (SWD), which arrived in British Columbia in 2009 from Asia, are unique because females have a serrated ovipositor allowing them to lay their eggs in small fruits (blueberries, raspberries, blackberries, cherries, strawberries), causing them to rot and become unmarketable. There are currently no effective, environmentally friendly tools available to reliably manage this pest. Biopesticides, which are highly specific pesticides that infect insects, are formulated from microbes such as viruses and bacteria. Biopesticides have been successfully used as a biological control agent of other pests and could be a useful tool to help manage SWD. However, the development of virus-based biopesticides for use against SWD cannot proceed without basic knowledge of what viruses infect this pest and how their microbiome might protect them against virus attack. In this project, using a genomics approach, I will determine what viruses are present in SWD in different fruit crops and natural habitats in BC over the course of the growing season. Additionally, I will investigate whether a symbiotic bacterium known to protect these flies against viruses, Wolbachia, is present in SWD. If Wolbachia is found, I will investigate if there is an impact on locomotor activity in SWD as well as other fitness attributes.

Author: **Planidin, Nicholas**
Degree Sought: MSc
Supervisor: Dr. Thomas Reimchen
Category: Ecology and Evolution

Spatial, sexual and rapid temporal differentiation in neuromast expression on lateral plates of Haida Gwaii stickleback

Lateral lines, a major sensory modality in fishes, are diverse among taxa, but their intraspecific variation has received limited attention. We examined numbers of superficial neuromasts on the buttressing lateral plates (LP) of 1910 threespine stickleback (*Gasterosteus aculeatus* Linnaeus, 1758) from 26 ecologically and morphologically diverse populations on the Haida Gwaii archipelago, western Canada. Extending from previous studies, we predicted that (i) highly stained dystrophic localities would have threespine stickleback with elevated numbers of neuromasts per plate due to a greater reliance on non-visual sensory modalities and (ii) that LP count and neuromast numbers per plate would functionally covary with predatory assemblage. We found that there were no differences in neuromast count across major habitats (marine, lake, stream), but clear-water populations and those with predatory fish had significantly more neuromasts per plate than most populations in highly stained dystrophic lakes, the effects being accentuated on the first buttressing plate (LP4). We also report the first evidence that neuromast counts per plate are sexually dimorphic, with males having a greater density of neuromasts in most populations. Two transplant experiments between ecologically opposite habitats indicate that within 12 generations, neuromast counts per plate can rapidly shift in response to a change in habitat.

Author: **Powell, Candice**
Degree Sought: MSc
Supervisor: Dr. Steve Perlman
Category: Ecology and Evolution

Characterization of a selfish genetic element in *Drosophila testacea*

Selfish genetic elements can cheat Mendelian patterns of inheritance by biasing their transmission, even if this results in negative fitness consequences. Although they are thought to be ubiquitous, selfish genetic elements can be difficult to detect, due to cryptic phenotypes and/or selection on the rest of the genome to suppress them. One of the most powerful and visible selfish genetic elements is X chromosome drive, which is common in *Drosophila*. Males that carry a selfish X chromosome produce a product that destroys Y-bearing sperm, siring only daughters. We recently characterized an X chromosome drive system in a common woodland fly, *Drosophila testacea*. Here, we test whether drive also occurs through females (i.e., whether the selfish X chromosomes show biased transmission relative to non-driving X chromosomes). Following controlled crosses, we genotyped young larvae using markers that can distinguish between driving and non-driving chromosomes. We found that offspring of heterozygous females carried the driving X chromosome more often than the non-driving one. Interestingly, the strength of distortion depended on the father's genotype. It is very unusual for a selfish genetic element to bias transmission in both sexes, as male and female meiosis are very different. Finally, in order to distinguish between true female meiotic drive and differential survival, we compare egg development and fecundity in females that carry driving X chromosomes.

Author: **Christensen, Chloe**
Degree Sought: PhD
Supervisor: Dr. Francis Choy
Category: Neuroscience, Cell and Molecular Biology

Investigating therapeutic applications for lysosomal disease: Gaucher disease and mucopolysaccharidosis IIIB

Rare genetic lysosomal diseases (LD) are characterized by a dysregulation of lysosomal function. Mucopolysaccharidosis IIIB (MPS IIIB) and Gaucher disease (GD) are caused by mutations in *NAGLU* and *GBA1*, which encode enzyme α-N-acetylglucosaminidase (Naglu) and glucocerebrosidase (GCase), respectively. MPS IIIB and GD type II are characterized by neurodegeneration, resulting in early lethality. Recent advances in genome editing technologies allow for precise manipulation of DNA *in*- and *ex vivo*. Genome editing of *NAGLU* and *GBA1* mutations in induced pluripotent stem cells (iPSC) is a putative regenerative therapy for these patients. We have generated iPSCs from MPS IIIB and GD human skin fibroblasts. Early issues arose with reprogramming MPS IIIB patient cells. We hypothesized that insufficient heparan sulfate (HS) turnover, characteristic of MPS IIIB, disrupts HS and fibroblast growth factor (FGF)-2 interactions that are necessary for cell signalling and pluripotency maintenance. We sought to overcome this hurdle by supplementing MPS IIIB iPSCs with additional FGF2. FGF2 supplementation (100 ng/mL) resulted in a significant increase in MPS IIIB iPSC confluency after 48 hrs ($p \leq 0.01$), persisting at 72, 96 ($p \leq 0.01$), and 120 hours ($p \leq 0.05$). Healthy and disease control iPSC cultures were not significantly impacted. Pluripotent MPS IIIB iPSC lines (2) and GD iPSC lines (1) were used in genome editing experiments. We designed, delivered and assessed the genome editing outcomes for three single nucleotide polymorphisms in *NAGLU* and *GBA1*. Genome editing in patient iPSCs has applications for future regenerative medicine for patients with neurodegenerative LDs.

Author: **deRosenroll, Geoff**
Degree Sought: PhD
Supervisor: Dr. Gautam Awatramani
Category: Neuroscience, Cell, and Molecular Biology

Applying artificial neural networks and other machine learning techniques to decode retinal ganglion cell activity to see what they saw.

The retina is the part of the brain inside the eye. Many are surprised to learn that the retina, rather than simply acting as a *"dumb"* camera collecting photons, and sending this data on to the rest of the brain to be processed, performs a substantial amount of filtering and computation on the light information coming in from the outside world. It does so with a feed-forward neural network, ending with the ganglion cell layer, whose axonal projections make up the optic nerve. There are reportedly greater than 30 functional types of these ganglion cells in the highly studied mouse retina, ranging from cells that simply prefer increases and decreases in light level or contrast, to cells that only respond when objects move through their receptive fields in particular directions. By combining 2-photon laser scanning microscopy and a genetically encoded fluorescent calcium indicator (GCaMP) we are able to capture the activity of hundreds of these ganglion cells simultaneously as they respond to light stimuli projected on to the retina *in vitro*. In order to better understand how the visual scene is encoded into these diverse information channels before being sent down the optic nerve, I am constructing a data processing pipeline ending in a generative artificial neural network to reconstruct the stimuli shown to the mouse retina by decoding the Ca^{++} responses of populations of retinal ganglion cells. Preliminary results using simulated ganglion cell responses suggest this approach is viable for stimuli such as moving spots and bars.

Author: **Farhoomand, Farnoosh**
Degree Sought: PhD
Supervisor: Dr. Kerry Delaney
Category: Neuroscience, Cell, and Molecular Biology

Sensory-evoked activity in somatosensory cortex as a model to probe cortical plasticity in a mouse model of Rett syndrome

Rett syndrome (RTT) is one of the most severe autism-like disorder affecting 1 in 10,000 female birth. RTT is caused by mutation of X-link Methyl CpG-binding Protein 2 (*MECP2*) gene. *MECP2* is highly expressed in neurons. RTT is characterized by severe cognitive and intellectual deficit also sensory and motor impairments.

To better understand the consequence of MeCP2 loss of function for neuronal circuit, we evaluate activity dependent plasticity in somatosensory cortex of symptomatic (4-6 weeks old) male Rett mice model, which lack *MECP2*. Normally, sustained stimulation of a sensory organ leads to a reduction (adaptation) in cortical response which goes back to baseline level after a recovery time. Data collected by Intrinsic Optical Signal Imaging (IOS) technique showed reduction in cortical response due to 1hour stimulation of HL in both wild type (n=6) and Rett (n=6) animals but recovery was faster in Rett animals ($p<0.001$, t-test). Current data assessed by Local Field Potential Recording (LFP), a method to record neuronal activity directly, confirmed the result from IOS.

This data suggesting a quick recovery in Rett male mice model and long-lasting adaptation in wild type animal. Further investigation is needed to identify the location of the adaptation in sensory pathway (from mechanoreceptors in skin to somatosensory cortex layers). In the next step, we will measure the sensory nerve conduction velocity in male mice HL (both Rett and wild type) and apply the same protocol to discover if any adaptation would occur in peripheral part of the sensory pathway.

Author: **Hanson, Laura**
Degree Sought: PhD
Supervisor: Dr. Gautam Awatramani
Category: Neuroscience, Cell, and Molecular Biology

"Silent" synapses in the mature mouse retina and their response to graded signaling

Synapses lacking the function expression of AMPA receptors are often considered 'silent' as glutamate binding to NMDA receptors alone does not substantially activate them (due to the voltage-dependent magnesium block). The direction-selective ganglion cells of the mouse retina have been shown to express silent, NMDA only synapses, however, the synaptic organization resulting in this silencing effect and how these synapses respond across a range of stimulus contrasts remains unknown. Here, I utilized a combination of patch-clamp and 2-photon imaging techniques to first identify silent synapses in the mature mouse retina and secondly, discover that these synapses exhibit graded responses to increasing contrasts at the individual synaptic level. Together, these findings show that synaptic NMDA receptors in a subtype of ganglion cells in the retina do not saturate to single vesical release as previously believed.

Author: **Le Gratiet, Keyrian**
Degree Sought: MSc
Supervisor: Dr. Raad Nashmi
Category: Neuroscience, Cell, and Molecular Biology

Spatial profiling of co-transmitted acetylcholine and GABA inputs onto substantia nigra dopaminergic neurons

Neuronal communication in the mammalian brain relies on the presynaptic release of neurotransmitters which bind to ligand-gated ion channels found on postsynaptic neurons and modulate neuronal excitability. My lab studies a specific class of ligand-gated ion channels, nicotinic acetylcholine receptors (nAChRs), which are involved in motor control, sensory modulation, and higher executive functions. For my research, I focus on ACh-mediated neurotransmission onto dopaminergic (DAergic) neurons in the mouse substantia nigra (SN), a brain region important for reward-coding of motor behaviors and found to be critically impaired in Parkinson's Disease (PD). While a great amount research has been done to define the characteristic synaptic currents that SN DAergic neurons receive, very little is known about their local subcellular microcircuitry. Understanding local subcellular neuronal circuits requires mapping the connections between the neurons and their synaptic partners, as well as determining the location where the synapses occur along the somato-dendritic extent of the neuron. We have discovered a population of DAergic neurons in the medial SN that receive co-transmitted ACh and GABA. The goal of my research is to examine in detail how cholinergic and GABAergic inputs modulate neuronal excitability in SN DAergic neurons by determining the spatial subcellular localization where these fibers functionally synapse onto the soma and dendrites of neurons and what are their pre- and postsynaptic physiological properties. The localization and timing of converging synaptic inputs on the dendritic tree defines the excitability of neurons and this research aims to understand how cholinergic and GABAergic inputs can differentially shape dopaminergic output from the SNc.

Author: **Vance, Marie**
Degree Sought: PhD
Supervisor: Dr. Patrick von Aderkas
Category: Forest Biology

Population genomics of a high-elevation conifer, subalpine larch (*Larix lyallii*)

Subalpine larch (*Larix lyallii*) is a deciduous conifer that only grows at timberline in the Cascade Range and Rocky Mountains of the Pacific Northwest. Predicted climate change could further reduce available habitat by increasing the frequency of late-summer drought events and/or by encouraging the upward migration of more competitive timberline species. To cope with its changing environment, subalpine larch will be required to adapt *in situ* or face maladaptation and eventual decline. Demographic factors such as a relatively long generation time (average 500 years) and late arrival at sexual maturity (100 – 200 years) will slow adaptation. Low levels of genetic diversity could further limit the magnitude of a potentially adaptive response to selection. To assess patterns of genetic variation in this species, I sampled 61 populations distributed across the species' natural range and used restriction associated DNA sequencing (RAD-seq) to generate single nucleotide polymorphism (SNP) data. Four genetic clusters were identified. Intensive sampling within a subset of 15 populations revealed high levels of inbreeding, moderate genetic diversity, and strong genetic differentiation between populations. Coalescent simulations detected a strong signal of post-glacial expansion. Among northern populations, phenotypic clines in cold tolerance indicate that local adaptation has also played an important role in structuring genetic variation in this species. This research should provide the basis for future management and conservation efforts for this species.

Author: **Carrington, Yuriko**
Degree Sought: PhD
Supervisor: Dr. Jürgen Ehlting
Category: Forest Biology

The functions of QDH genes in plants

The shikimate pathway leads to the production of aromatic amino acids in plants, bacteria and fungi. These aromatic amino acids are used by plants for synthesizing proteins and diverse aromatic secondary metabolites, functioning in reproduction and defense against environmental stresses. Plant dehydroquinate dehydratase/shikimate dehydrogenase (DQD/SDH) catalyzes the formation of shikimate, the central intermediate of the shikimate pathway. On the other hand, the structurally similar quinate, is a secondary metabolite synthesized in a side-branch of the shikimate pathway by quinate dehydrogenase (QDH). Previously, it was discovered that poplar has five *DQD/SDH* genes, two of which has been shown to encode QDH activity *in vitro*. This marks the first genetic characterization of *QDH* genes. However, the *in vivo* functions of these putative *QDH* genes in plants remain unknown. To investigate the *in vivo* functions of poplar *QDH* genes, CRISPR technology will be used to knock-down expression of *QDH* genes in poplar whole-plants. HPLC-MS analysis will be used to determine whether decreased *QDH* gene activity leads to decreased concentrations of quinate or quinate derived compounds, thus confirming their role in quinate biosynthesis.

Author: **Gourlay, Gerry**
Degree Sought: PhD
Supervisors: Dr. C. Peter Constabel and Dr. Barbara Hawkins
Category: Forest Biology

High condensed tannin levels protect poplar against oxidative damage generated by UV-B exposure or drought stress

Condensed tannins (*syn.* proanthocyanidins) are polyphenolic compounds synthesised from the flavonoid pathway. Although condensed tannins are often considered to be plant defence compounds, they may have additional biological functions. In poplar (*Populus* spp.), condensed tannin biosynthesis is stimulated by multiple stresses including wounding, pathogens, UV-B, high light stress, and nitrogen deficiency, which all generate reactive oxygen species (ROS) and oxidative stress. Condensed tannins have high antioxidant capacity *in vitro*, but whether they protect against oxidative stress *in planta* has not been demonstrated. This work tests the hypothesis that condensed tannins can act as *in vivo* antioxidants. Transgenic poplar saplings engineered to accumulate high concentrations of condensed tannin were challenged with two stresses that induce accumulation of ROS - drought and UV-B exposure. Drought stress was imposed by reducing water availability to saplings for three weeks, and UV-B treatments were carried out in specialized environmental chambers capable of simulating sunlight including UV-B. Chlorophyll fluorescence measurements in both the drought-stressed or UV-B stressed plants showed that high-tannin transgenic poplar retained greater photosystem II operating efficiency (*Fq*'/*Fm*' or *φPSII*) compared to control plants. For both stresses, the high-tannin transgenics had lower hydrogen peroxide and malondialdehyde levels relative to controls. Since the protective effects of condensed tannins were observed with two distinct abiotic stresses, our data suggest that foliar condensed tannins can act as a general defense against stress-induced oxidative damage.

Author: **Lane, Sarah**
Degree Sought: MSc
Supervisor: Dr. Jürgen Ehlting and Dr. Patrick Walter
Category: Forest Biology

The potential of plant root compounds as iron chelators for human medicinal use

Iron overload is a consequence of diseases like thalassemia and neurodegeneration with brain iron accumulation. Excess iron from disruptions in normal iron homeostasis can accumulate in major organs with devastating consequences if untreated. Currently, treatment includes using iron-chelators, which can have serious adverse effects. Alternative iron-chelators with reduced toxicity could be significantly beneficial. Plants growing in alkaline soils may be a good source of these, having evolved mechanisms to overcome decreased iron availability that occurs at high alkalinity. Mechanisms include producing secondary metabolites for exudation into soil that can chelate iron directly, including phenolic acids that may chelate iron at physiological pH in humans. This project is focused on finding bioactive compounds from alkaline tolerant and model plants.

Plants are grown in iron-deficient conditions to stimulate production of secondary metabolites related to iron-deficiency. Plant tissue extracts are collected and isolated to form plant-derived concentrates (PDC), which are analyzed to identify compounds induced by iron-deficiency. PDCs are introduced to cultures of THP-1 cells, a human monocytic cell line, to study their effect on iron homeostasis. Prior to treatment with chelators, cells are cultured under prolonged treatment with Fe-citrate to model chronic iron overload. Chlorogenic acid (CGA), model phenolics, and PDCs are being investigated as potential chelators.

These PDCs contain diverse compounds responsive to iron-deficiency. Treatment with CGA and PDCs moderately reduces intracellular iron in THP-1 cells. Dose-dependency, co-operative effects of treatments, and detailed kinetics of iron-loading during treatment are currently being investigated. Screening plants for novel chelators is providing an abundance of opportunity to study them for potential medicinal use.

Author: **Lea, Carmen**
Degree Sought: MSc
Supervisor: Dr. C. Peter Constabel
Category: Forest Biology

Purification and biological activity of a diarylheptanoid compound found in the leaves and bark of *Alnus rubra* (red alder)

Although red alder has historically been considered a weed species, there is renewed interest in alder management due to its ability to fix soil nitrogen in areas of low nutrient bioavailability. Recent studies, however, have highlighted the medicinal value of red alder bark and leaves, including potential antioxidative, antimicrobial, and anti-cancer effects. Chemical analysis has shown that diarylheptanoids, especially oregonin ((5S)-1,7-bis(3,4-dihydroxyphenyl)-5- (β-D-xylopyranosyloxy)-heptan-3-one), are the dominant bioactive constituents. Diarylhepatonoids are bioactive phenolic compounds found in plants, structurally similar to the bioactive compound from tumeric, curcurmin. We recently discovered that high oregonin concentration in alder leaves is associated with enhanced resistance to Western tent caterpillar. My work aims to test the anti-herbivore activity of oregonin directly. A novel purification method was developed for the preparative extraction of oregonin from red alder leaf and bark material to directly test its biological activity. A battery of insect choice and toxicity tests were then carried out against Lepidopterans including several tree-defoliating caterpillars. Oregonin has shown promising insect repellence activity against several generalist Lepidopteran pests including cabbage loopers (*Trichoplusia ni)*, white-marked tussock moths (*Orgyia leucostigma*), and fall webworm (*Hyphantria cunea*), at similar concentrations shown to reduce western tent caterpillar herbivory in alder leaf bioassays.

Author: **Ma, Dawei**
Degree Sought: PhD
Supervisor: Dr. C. Peter Constabel
Category: Forest Biology

MYB transcription factor, MYB117 induces anthocyanin production and increases hydroxylation of flavonoids in poplar

Anthocyanin is an important natural plant pigment and has diverse functions in plants and beneficial health effects. Anthocyanin is one of the end products of the phenylpropanoid and flavonoid pathway. The flavonoid pathway is usually regulated by MYB transcription factors and bHLH cofactors.

Our previous study showed that one poplar MYB transcription factor, MYB117 induced anthocyanin production when it was transiently overexpressed in tobacco. We further overexpressed MYB117 in hybrid poplar. The MYB117 overexpressor poplars show dramatic increase of anthocyanin in various plant tissues. RNA-seq analysis of MYB117 overexpressor poplars reveals upregulation of many flavonoid genes. Interestingly, flavonoid 3’5’-hydroxylase genes which regulate hydroxylation of flavonoids are also upregulated in MYB117 overexpressors. Further analysis of anthocyanin composition in MYB117 overexpressors shows an increased ratio of delphinidin and cyanidin content, which indicates an increased hydroxylation of anthocyanin. We then overexpressed one of the flavonoid 3’5’-hydroxylase in hybrid poplars. Overexpression of flavonoid 3’5’-hydroxylase also leads to increased dephinidin content in hybrid poplars. Future studies will focus on the chemical analysis of other flavonoid hydroxylation in the overexpressors and build a transcriptional regulation network for flavonoid hydroxylation and biosynthesis.

Author: **Duguid, Will**
Degree Sought: PhD
Supervisor: Dr. Francis Juanes
Category: Marine Biology

Regional and seasonal variation in adult Chinook Salmon diets in British Columbia

Adult Chinook Salmon are an important component of coastal ecosystems in the Northeast Pacific. Surprisingly, data on the diets of adult Chinook Salmon in British Columbia are sparse, with no published data since the 1960s and a total lack of information on winter diets. Since 2017 we have been developing a low-cost, citizen science-based program to sample Chinook Salmon diets throughout the year in British Columbia, with a focus on Canadian waters of the Salish Sea. In the short term we are seeking to characterize spatial and seasonal variation in adult Chinook Salmon diets. In the long term we hope to develop this program as a method to monitor changes in the ecosystem from the perspective of the salmon themselves. Size data (including otolith dimensions) for individual prey items are allowing us to infer the seasonal importance of different life-history stages of important prey species. Our results to date suggest spatial and seasonal variation in diet within the Canadian Salish Sea. The mechanisms underlying this variation may have implications not only for growth and fecundity of adult Chinook Salmon, but also for growth and survival of juvenile Pacific Salmon and other species. Adult salmon diet monitoring has the potential to complement existing and future fishery-independent surveys in elucidating natural and anthropogenic changes in the coastal ocean of British Columbia.

Author: **Black, Morgan**
Degree Sought: PhD
Supervisors: Dr. Francis Juanes and Dr. Sarah Dudas
Category: Marine Biology

Marine macrofaunal communities of First Nations' clam gardens

Ancient First Nations’ clam gardens on the west coast of North America provide a unique example of a very long-standing anthropogenic habitat modification in the nearshore marine environment. Clam gardens are a rock wall piled in the low intertidal zone which creates a terrace that changes the beach slope, sediment composition, increases structural complexity, and buffers wave action. These beaches were designed to support clam populations; however, their effects on other organisms have not yet been studied. To assess these effects, we are sampling fish and invertebrates at clam gardens and reference sites. We hypothesize that abundance, richness, and biomass are higher on walled beaches and this is driven by changes to the habitat structure. This research serves to expand our understanding of drivers of diversity, informs on potential restoration of modified coastlines, and supports harmony between indigenous peoples’ land use rights and conservation goals

Author: **Cowan, Malcolm**
Degree Sought: MSc
Supervisor: Dr. Patrick von Aderkas
Category: Marine Biology

Influence of *Vibrio* spp., temperature, reproductive development, and stocking density on Pacific oyster (*Crassostrea gigas*) summer mortality in Baynes Sound, British Columbia.

Cultured Pacific oysters (*Crassostrea gigas*) in Baynes Sound, British Columbia, have experienced summer mass mortality events in recent years with cumulative mortalities exceeding 90% at some sites in 2015 and 2016. In 2017, we isolated *Vibrio* spp. from oysters and putatively identified potentially pathogenic species, based on *recA* gene sequencing; among the 163 isolates, *V. aestuarianus* and *V. harveyi* were well represented. The objective of the present study was to identify factors influencing the onset of a mortality event in juvenile Pacific oysters during the summer of 2018. We recorded mortality, growth, gonad development, temperature, turbidity, dissolved oxygen, chlorophyll-*a*, plankton assemblages, and bacterial community composition. Our study site contained four replicate trays of four stocking densities: 150, 300, 450, and 600 oysters/tray. Mortality was first observed on July 30, which coincided with a marine heatwave. *Vibrio aestuarianus* and the proportion of *Vibrio* spp., quantified using qPCR and community 16S rRNA gene sequencing, respectively, increased with observed mortality rate. Mortality rates were at their highest on August 12 and we observed systemic mixed microbial infections in histological cross sections of oysters that otherwise appeared healthy. The final cumulative mortalities ranged from 34 to 75%, with the highest density trays having significantly lower mortality than the lowest density trays. Significant density-dependent effects were also observed for oyster size and gonad development. The long-term persistent ocean warming and increased frequency of marine heatwaves associated with climate change are likely contributing to the emergence of summer mortality and pathogenic *Vibrio* spp. in Baynes Sound.

Author: **Cox, Kieran**
Degree Sought: PhD
Supervisors: Dr. Francis Juanes and Dr. Sarah Dudas
Category: Marine Biology

Shellfish subsidies along the pacific coast of North America

Spatial subsidies are associated with pronounced ecosystem responses, as nutrients cross ecological boundaries and cascade through food webs. While the importance of subsidies is known, the role of shellfish, specifically molluscs, as a marine subsidy has not been formally described. Focusing primarily on the Pacific coast of North America, we identify vectors that transport shellfish-derived nutrients into coastal terrestrial environments, including birds, mammals, and over 13,000 years of marine resource use by people. Evidence from recipient ecosystems suggest shellfish drastically influence soil chemistry, forest productivity, and the diversity of primary producers at the regional and landscape level. Responses in higher trophic levels have not yet been investigated, but given documented responses in lower trophic levels, this may be due to a lack of examination. To determine if the processes we describe within the northeast Pacific are pertinent to coastal environments worldwide, we also explore shellfish subsidies globally, with a specific focus on tropical islands. As shellfish are not as spatially or temporally constrained as other subsidies, our examination suggests our findings are applicable to many other geographical regions along the marine-terrestrial interface.

Author: **Dimoff, Sean**
Degree Sought: MSc
Supervisors: Dr. Julia Baum
Category: Marine Biology

Kiritimati's coral reef soundscapes: can listening to the reef inform us about its health?

Underwater acoustics, an exciting new approach being applied in coral reef ecosystems, have the potential not only to assess 'noise pollution' from anthropogenic sources but also provide efficient means of monitoring reef communities. Coral reef soundscapes, the collection of sounds produced by a reef's inhabitants, have recently been used to provide helpful indicators about the health, diversity, and complexity of a reef. One of the next major steps in coral reef acoustics is to determine the effect of specific biogenic noises on recorded frequency bands and calculated indices. In response to this critical information gap, we deployed 5 hydrophones on reefs around Kiritimati (Christmas Island), an atoll in the equatorial Pacific, for field seasons in both 2017 and 2018. I analyzed a subset of these files to determine counts of fish knocks, calls, and snapping shrimp snaps to investigate which sounds were the primary drivers of different frequency bands. This analysis yielded important relationships between acoustic metrics and the biogenic sounds that influence them. These findings help fill a vital gap in understanding how acoustics can serve as a powerful tool for assessing coral reef health.

Author: **Livingston, Michael**
Degree Sought: MSc
Supervisor: Dr. Diana Varela
Category: Marine Biology

The role of transparent exopolymer particles in the biological carbon pump across environmental gradients in the North East Pacific Ocean

The biological carbon pump (BCP) in the oceans is an important sink for atmospheric CO_2 and provides a critical feedback mechanism between Earth's oceans and atmosphere. Photosynthesis in the upper ocean layers fixes carbon from the atmosphere and stores it in phytoplankton cells, which eventually die and sink to the deep ocean where it may be stored for thousands of years. Transparent exopolymer particles (TEP), produced from the exudation of organic polymers from phytoplankton, form sticky gel matrices in the ocean that play a key role in the formation, aggregation, and sinking of organic matter. Therefore, they are thought to be an important aspect in determining the efficiency of the BCP. The mechanisms behind TEP production in phytoplankton, and its role in the BCP, have not been sufficiently described in the ocean. This research is aimed at examining the relationship between primary productivity and TEP production in the ocean and its potential impact on carbon cycling. TEP production and phytoplankton productivity were compared across gradients in environmental conditions – including both productive upwelling zones and oligotrophic waters. Samples were taken for different size fractions of phytoplankton, which include biomass (chlorophyll, biogenic silica), and productivity (carbon, nitrogen and silica uptake rates) measurements. Bacterial and particulate organic carbon samples were also taken in order to assess any potential contributions to the TEP pool. This research can provide a snapshot as to how primary productivity and carbon gel production are moderating the efficiency of the BCP in different areas of the NE Pacific Ocean.

Author: **Murchy, Kelsie**
Degree Sought: PhD
Supervisor: Dr. Francis Juanes
Category: Marine Biology

Behaviour of Chinook Salmon (*Oncorhynchus tshawytscha*) after acoustic tagging in Cowichan Bay, BC

Chinook salmon (*Oncorhynchus tshawytscha*) stocks have been declining over the last 30 years, resulting in increased research. One area that has not been fully explored is behavioural patterns of adult salmon, due to the challenge of evaluation in a natural environment. However, acoustic tags are increasing in popularity as an effective way to track and evaluate fish movements and behaviour. The traditional method of attaching the tag involves sedating the fish and making a small incision in the abdominal cavity. This method involves exposure to anaesthetics and longer handling time. A minimally invasive alternative is to insert the tag into the fish's stomach but this method introduces a different set of potential complications. To understand post tagging behaviour and potential tagging mortality, 17 adult Chinook Salmon in Cowichan Bay, BC had acoustic tags gastrically inserted. Each salmon was tracked for up to 10 minutes following tagging and their depth and acceleration were compared among individuals. Initial mortality was calculated for up to 24 hours post tagging. Three different depth profiles were observed but all individuals displayed similar accelerations upon release. Mortality due to tagging was low, with 88% of individuals detected at least 24 hours post tagging. Results suggest that gastric tagging might be a plausible alternative for acoustic tagging when traditional methods are not an option.

Author: **Osgood, Geoffrey**
Degree Sought: PhD
Supervisors: Dr. Julia Baum
Category: Marine Biology

Chondrichthyans as an umbrella species complex for conserving South African biodiversity

The use of conservation surrogates such as umbrella and flagship species could help focus South Africa's limited resources into marine protected area designs. Sharks, rays, and chimaeras (Chondrichthyans), which are charismatic and ecologically diverse, are potential umbrella candidates, but tests of the ecological suitability of putative marine umbrella species are lacking. Using baited remote underwater video in and around two MPAs in the Western Cape, we assessed the potential of Chondrichthyes as an umbrella species taxon by quantifying the relationships and co-occurrence patterns between chondrichthyan abundance and diversity and those of other taxa (teleosts, myxinids, crustaceans, cephalopods, birds, and mammals). The abundance and diversity of these other taxa were significantly greater at sites with abundant chondrichthyans. We found habitat associations between chondrichthyans and species of commercial and conservation interest, such as the red roman *Chrysoblephus laticeps*. Notably, endemic scyliorhinids and the broadnose sevengill shark *Notorynchus cepedianus* had many strong positive co-occurrences (28% and 21% of interactions, respectively). The puffadder catshark *Haploblepharus edwardsii* had the highest centrality of any species. Overall, based on co-occurrence and habitat associations, chondrichthyans, especially the *H. pictus, H. edwardsii*, and the broadnose sevengill shark, show strong potential as an umbrella species complex in South Africa.

Author: **Reidy, Rhonda**
Degree Sought: PhD
Supervisors: Dr. Francis Juanes and Dr. Laura Cowen
Category: Marine Biology

Echo sounding humpback whale prey

Developing a cost-effective sampling framework for obtaining time-series data on prey composition and spatiotemporal dynamics of baleen whale feeding remains a major challenge. I investigate a sampling method that measures a variety of surface and deep-water prey characteristics in North Pacific Humpback Whale feeding areas near northern and southern Vancouver Island, British Columbia (B.C.). The vertical distribution of prey is continuously recorded near feeding Humpback Whales from a small vessel using an Acoustic Zooplankton and Fish Profiler (AZFP), following fine-scale transects to map three-dimensional prey fields. The surveys are conducted in daylight hours in regions with and without foraging Humpback Whales to describe prey in the areas used by the whales. Regional mid-water prey sampling informs the species composition of acoustic signal data, while humpback fecal sampling provides information about which prey species are actually consumed. Results show consistent differences between feeding regions, with Humpback Whales targeting shallow Pacific Herring aggregations off northern Vancouver Island but deep layers of fish and euphausiids in southern Vancouver Island waters. Given the current lack of knowledge about Humpback Whale diet and the whales' impact on forage fish in B.C., this combined approach provides a quantitative framework for intensive baseline sampling that is needed in B.C. for accurately estimating diet and regional prey selectivity of Humpback Whales to better inform fisheries decisions.

Author: **Tietjen, Kristina**
Degree Sought: MSc
Supervisors: Dr. Julia Baum
Category: Marine Biology

Coral recruitment on an isolated atoll following mass coral mortality

Global and local anthropogenic stressors that cause coral bleaching or mortality can also compromise both the quantity and quality of coral recruits, thus diminishing a reef's capacity for recovery following disturbance. Whereas in networks of well-connected reefs, if disturbance events decimate adult populations recruits may be sourced from neighboring reefs, on geographically isolated reefs recruitment is reliant on adult corals at that location. Although recruitment success under high temperature stress has been well studied, the effects of combined stressors (e.g., acute El Niño events and local chronic human disturbance) on coral recruitment, and ultimately reef recovery, have not been well characterized. Here, we quantified coral recruitment on settlement tiles at 12 sites that span a local chronic human disturbance gradient, on Kiritimati, a geographically isolated coral reef atoll in the central Pacific, in the three boreal summers following the 2015-2016 El Niño-induced mass coral mortality. We quantified low recruitment rates (mean = 0.2 recruits per tile (± 0.02 SE) or 8.29 recruits/m^2/year (± 1.9 SE); 84% of tiles had no recruits) compared to previous studies. Recruits, which were genetically identified, were primarily from the families Agariciidae and Pocilloporidae. Local human disturbance tended to impair recruitment rates, which were also significantly affected by sampling day and geographic region around the atoll. These results indicate that global and local stressors were interacting to affect the recruitment levels and subsequent recovery of the Kiritimati reefs.

Author: **Wyatt, Shea**
Degree Sought: PhD
Supervisor: Dr. Diana Varela
Category: Marine Biology

Ocean acidification effects on the elemental ratios and nutrient uptake rates of siliceous phytoplankton from the Subarctic Northeast Pacific and Subtropical North Atlantic Oceans

Among planktonic silicifiers, diatoms are responsible for about 20% of Earth's primary production, regulate the marine silica cycle, form the base of efficient food webs, and are a driving component of the biological carbon pump. Despite their biogeochemical and ecological importance, little is known about the effects of ocean acidification on the silica frustule of diatoms and other planktonic silicifiers. We performed manipulation experiments by exposing natural assemblages of phytoplankton from the offshore waters of the Subarctic Northeast Pacific Ocean and from the Bermuda Atlantic Time-series Study site to varying atmospheric CO_2 concentrations. These experiments investigated the effects of the decrease in pH at high pCO_2 on the biomass of diatoms and ratios of particulate carbon, nitrogen, silica and chlorophyll-*a*. Uptake rates of C, N, and Si were measured directly from the incorporation of stable (^{13}C and ^{15}N) and radioactive (^{32}Si) isotopes. Using the fluorescent dye PDMPO, we determined the diatom taxa responsible for the majority of the silica production within the assemblages and assessed frustule integrity. Results from this project will help us understand how ocean acidification affects total phytoplankton and diatom production, and the composition of the phytoplankton assemblages from the vastly different environments of the relatively productive Northeast Pacific and oligotrophic Subtropical North Atlantic Ocean.

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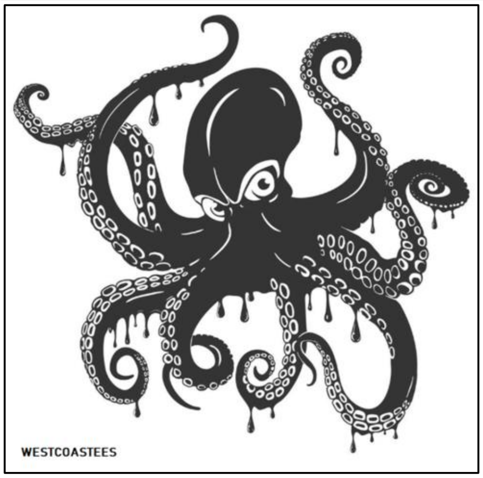

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