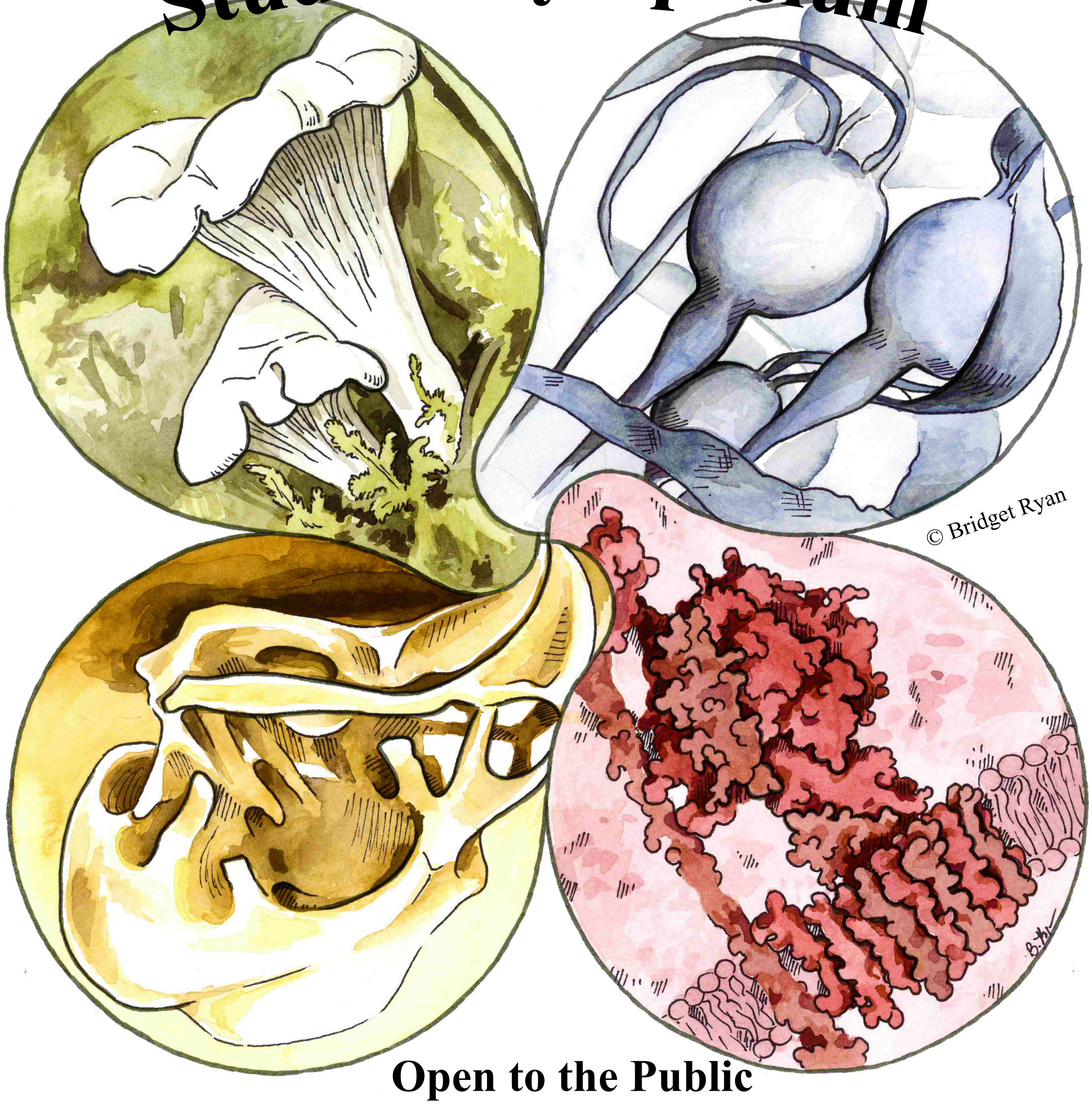
The University of Victoria 29th Annual Biology Graduate Student Symposium



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Open to the Public
Free admission

November 14th & 15th, 2017 · 9:00 am – 5:00 pm
David Strong Building · Room C103

Tuesday **November 14, 2017**

Time	Chair	Name	Supervisor	Title
8:45-9:00	Coffee			
9:00	Dr. B. Hawkins	**Dr. B. Hawkins**	**Opening Remarks**	
9:05		Graeme Keais	Dr. S. Perlman	Maintenance of an ancient selfish X chromosome in a mushroom-feeding *Drosophila* species
9:20		Caitlin Curtis	Dr. S. Perlman	The molecular basis of an extraordinary sex-ratio distortion in booklice
9:35		David Minkley	Dr. B. Koop	Expansion of repeated DNA has differentially shaped the genomes of salmonids
9:50		Nova Hanson	Dr. L. Page	Development and evolution of a derived feeding system in *Amphissa columbiana*
10:05-10:25	Coffee			
10:25	Nova Hanson	Gerry Gourlay	Dr. P. Constabel & Dr. B. Hawkins	Can condensed tannins act as *in vivo* antioxidants and protect poplar against oxidative stress
10:40		Kennedy Boateng	Dr. B. Hawkins & Dr. P. Constabel	Seasonal variation and wounding response in foliar oregonin in red alder (*Alnus rubra* Bong.)
10:55		Jessica Wyatt	Dr. J. Ehlting	Assessing severity of Swiss Needle Cast in a British Columbia Douglas-fir breeding population
11:10		Marie Vance	Dr. P. von Aderkas & Dr. B. Hawkins	Assessing range-wide genetic structure in subalpine larch (*Larix lyallii*)
11:25		Yuriko Carrington	Dr. J. Ehlting & Dr. P. Constabel	The functions of quinate dehydrogenase genes in plants
11:40-12:40	Lunch			
12:40	Malcolm Cowan	Kieran Cox	Dr. F. Juanes	Intertidal resource use over millennia alters marine biodiversity
12:55		Morgan Black	Dr. F. Juanes	The effects of First Nation's clam gardens on fish and mobile invertebrate communities
13:10		Piata Marques	Dr. R. El-Sabaawi	Effects of urbanization on guppy life history traits
13:25		Therese Frauendorf	Dr. R. El-Sabaawi	Climate change and exotic species affect tropical stream nitrogen dynamics
13:40		Danielle Claar	Dr. J. Baum	Symbiotic diversity and coral resilience during an extreme ocean warming event
13:55-14:15	Coffee			
14:15	Yuriko Carrington	Jacob Weil	Dr. F. Juanes	Fine-scale variability in the energy density of prey for juvenile Chinook salmon
14:30		Monique Raap	Dr. B. Koop & Dr. H. Gurney-Smith	Impacts of habitat alteration and microplastic contamination on shellfish physiology
14:45		Malcolm Cowan	Dr. W. Hintz	Summer mortality of Pacific oysters in Baynes Sound
15:00		Lia Chalifour	Dr. J. Baum	Evaluating the use of estuarine habitats by fish communities in the Fraser River estuary
15:15		Jennifer Magel	Dr. J. Baum	Impacts of mass coral bleaching events on coral reef structural complexity
15:30-15:45	Coffee			
15:45	Jenn Magel	Haewon Shin	Dr. S. Perlman	Interactions between microbiota composition and parasite infections in wild flies
16:00		Eric Rondeau	Dr. B. Koop	Genomic diversity in rainbow trout
16:15		Cameron Freshwater	Dr. F. Juanes & Dr. M. Trudel	Individual variation and population-specific strategies shape migration phenologies
16:30		Will Duguid	Dr. F. Juanes	Northern anchovy in the Salish Sea
16:45		Garth Coverton	Dr. J. Dower & Dr. S. Dudas	Microplastics in BC bivalves

Wednesday **November 15, 2017**

Time	Chair	Name	Supervisor	Title
8:45-9:00	Coffee			
9:00	Gerry Gourlay	Michael Minkley	Dr. P. Walter & Dr. R. Nashmi	Systemic biomarkers of disease burden in neurodegenerative disorders
9:15		Rhea Ashmead	Dr. F. Choy	Purification of human recombinant Naglu and uptake studies with MPS IIIB fibroblasts
9:30		Laura Hanson	Dr. G. Awatramani	Silent synapses in the mature DS ganglion cells in the mouse retina
9:45		Anastasia Litke	Dr. R. Chow	Investigating the pathogenicity of *VSX1* P247R and its role in corneal dystrophies
10:00-10:25	Coffee			
10:25	Geoff deRosenroll	Amanda McLaughlin	Dr. J. Taylor	Fine scale correlations in coupled retinal ganglion cells
10:40		Farnoosh Farhoomand	Dr. K. Delaney	Long term cortical plasticity in male Rett mice model
10:55		Chloe Christensen	Dr. F. Choy	Gene-editing of *NAGLU* mutations in mucopolysaccharidosis IIIB patient-derived iPSCs
11:10		Bridget Ryan	Dr. R. Chow	MicroRNA regulation of Pax6 expression
11:25-13:00	Lunch			POSTER SESSION (see below)
13:00	Katie Harms	Kyle Beer	Dr. T. Lacourse	Peatland carbon accumulation over the last 10,000 yr on central Vancouver Island
13:15		Matthew Adeleye	Dr. T. Lacourse	Changes in forest composition on central Vancouver Island over the last 14,000 years
13:30		Rande Kanne	Dr. G. Allen	The phylogenetic relationships and phylogeographic patterns of Garry oak
13:45		Jillian McAllister	Dr. P. Gregory	Seasonal movements and hibernation ecology of common gartersnakes
14:00-14:25	Coffee			
14:25	Dr. D. Varela	Amy Teffer	Dr. F. Juanes & Dr. S. Hinch	Relationships among stressors and infections affect salmon survival and migration success
14:40		Geoffrey Osgood	Dr. J. Baum & M. McCord	Shark community composition and abundance in a South African warm-temperate bay
14:55		Mauricio Carrasquilla	Dr. F. Juanes	Yelloweye and Quillback association with benthic habitat
15:10		Rhonda Reidy	Dr. F. Juanes & Dr. L. Cowen	Investigating the foraging ecology of humpback whales in British Columbia
15:25		**Dr. D. Varela**	**Closing Remarks**	

Wednesday **November 15, 2017** **Poster session**

Time		Name	Supervisor	Title
11:30-12:15				
1	Foyer of DSB	Juan Aldana	Dr. B. Hawkins & Dr. J. Russell	Histological, chemical and gene expression aspects of the resistance to CLB in *Thuja* spp.
2		Geoff deRosenroll	Dr. G. Awatramani	Context-dependent scaling by NMDARs in direction-selective ganglion cells
3		Katie Harms	Dr. L. Page	Developmental modularity of the foregut in a gastropod mollusc: *Evalea tenuisculpta*
4		Dawei Ma	Dr. P. Constabel	Characterization of (-) condensed tannin and flavonoid MYB transcription factors in poplar
5		Luci Marshall	Dr. D. Varela	Investigating the meltdown in the coastal Arctic: phytoplankton and environmental dynamics
6		Deb Wertman	Dr. S. Perlman & Dr. K. Bleiker	Photosensitivity in developing mountain pine beetle (*Dendroctonus ponderosae*)

Biology Graduate Symposium
Social Event 2017

BARD & BANKER
PUBLIC HOUSE

Come join us for appetizers and drinks at **Bard & Banker,** 1022 Government Street, starting @
7:00 pm on Wednesday Nov. 15th '17

Graduate students: **Free food and a drink ticket**

Additional tickets: Faculty, staff and guests are **$15** (includes appetizers)

Tickets can be picked up/purchased at the Biology Main Office (CUN 202) **starting Monday, October 30th**
Ticket Deadline: Tuesday, November 14, 3:30pm

https://www.facebook.com/events/186124538622178/

Biology Graduate Student Presentation Abstracts 2017

Author: **Adeleye, Matthew**
Degree Sought: MSc
Supervisor: Dr. Terri Lacourse
Category: Forest Biology

Changes in forest composition on central Vancouver Island over the last 14,000 years

A paleoecological study is being carried out on a 4.7 m peat core from a wetland on central Vancouver Island, BC, using fossil pollen and spores to document changes in forest composition on long timescales. Pollen analysis reveals that willow tundra prevailed after deglaciation about 14,000 years ago. Then, as temperatures rose, lodgepole pine forests became established. About 12,900 years before present (yr BP), green alder shrubs and mountain hemlock and fir trees expanded, marking a brief return to cool conditions. Thereafter, lodgepole pine forests return as temperature again increased. Open Douglas-fir forests dominated between 10,600 and 7000 yr BP, when climate was warmer and drier than present. Closed coniferous rainforest dominated by western hemlock has prevailed over the last 7000 years. Relatively stable forest composition over the last several thousand years reflects a stable climate of moist, cool conditions.

Author: **Aldana, Juan A.**
Degree Sought: PhD
Supervisors: Dr. Barbara Hawkins and Dr. John Russell
Category: Forest Biology

Histological, chemical and gene expression resistance mechanisms against *Didymascella thujina* in *Thuja* spp.

Thuja plicata (western redcedar, WRC), an important timber species in British Columbia, is susceptible to *Didymascella thujina* (cedar leaf blight, CLB). Resistance to CLB was first studied in 1956 using *Thuja standishii*, WRC and hybrids. It was proposed that an *R* gene from *T. standishii* was responsible for CLB-resistance, however the molecular mechanisms are still unknown. Here, the results of one study exploring the differences among *Thuja* spp. plants with dissimilar CLB resistances are presented.

Two WRC seedling lines, and *T. standishii* and *T. standishii* × *plicata* clones were included. Leaf anatomy was assessed, and a time-course experiment comparing real and mock CLB-infections was carried out. Samples were collected within 8 days and used for chemical composition and *RNA*-Seq analyses. Disease resistance was evaluated as severity.

CLB was significantly less severe in *T. standishii* and the hybrid than WRC, and both had thicker cuticles. Aluminum (Al) was the only element that showed significant differences. Stability selection analysis using Al as a target revealed up-regulation of calcium signalling and the phospholipid pathway. Grade of Membership analysis showed that bark storage proteins (BSPs) were highly expressed only in the hybrid and *T. standishii*. This is the first report of an increase in Al in leaves associated with a defense response although Al is toxic to plants. BSPs are known to respond to pathogens, but they have never been reported in the studied species. Al and BSPs may play important roles in CLB defense. Further studies to dissect their specific roles are required.

Author: **Ashmead, Rhea**
Degree Sought: MSc
Supervisor: Dr. Francis Choy
Category: Neuroscience, Cell, and Molecular Biology

Purification of human recombinant α-N-acetylglucosaminidase from Sf9 cells and uptake studies on diseased human fibroblasts

Mucopolysaccharidosis IIIB (MPS IIIB) is a lysosomal storage disease that occurs with a prevalence of approximately 1:250,000 live births. This disease results from deleterious mutations in the α-N-acetylglucosaminidase (*NAGLU*) gene, which encodes for the lysosomal enzyme, Naglu. These mutations result in limited Naglu activity in the lysosome, which leads to the toxic accumulation of Naglu's substrate, heparan sulfate. Patients with MPS IIIB experience progressive central nervous system degeneration and die within their first two decades of life. Presently, there is no treatment for this disease. The goal of our research is to improve enzyme replacement therapy so it could be a viable treatment option for MPS IIIB. The major obstacle for enzyme replacement therapy is the delivery of functional enzyme across the blood-brain barrier. Protein transduction domains are capable of transducing active enzymes across biological membranes, including the blood-brain barrier. Previous research in our lab has fused a synthetic protein transduction domain–PTD4–to human recombinant Naglu and stably expressed this fusion enzyme in a Sf9 cell line. Currently, the focus of our research is to purify the fusion enzyme–Naglu-PTD4–to homogeneity from Sf9 media using column chromatography. Following purification, we will conduct uptake studies with Naglu-PTD4 on MPS IIIB fibroblasts, and eventually on a MPS IIIB mouse model for therapeutic study.

Author: **Beer, Kyle**
Degree Sought: MSc
Supervisor: Dr. Terri Lacourse
Category: Ecology and Evolution

Peatland carbon accumulation over the last 10,000 yr on central Vancouver Island

Peatlands are an integral part of the global carbon cycle due to their vast accumulation of below-ground organic material. The strong influence of climate along with similarities in carbon (C) accumulation among peatlands suggests that the study of past environments will aid in the prediction of peatland response to current and future climate change. Though peatland dynamics have been a focus in the Arctic and Europe, there have been few studies of long-term C dynamics in the peatlands of coastal British Columbia. I will present C accumulation rates for the last 10,000 years for a wetland complex on central Vancouver Island. The mean accumulation rate was 25.2 g C/m^2/yr, with a maximum of ~100 g C/m^2/yr during the early Holocene, between about 9750 and 8500 years before present, when summers were warmer and seasonality was higher than present. High early Holocene C accumulation is typical of northern peatlands and reflects the importance of climate in controlling C accumulation on long timescales.

Author: **Black, Morgan**
Degree Sought: PhD
Supervisor: Dr. Francis Juanes
Category: Marine Biology

The effects of First Nations’ clam gardens on fish and mobile invertebrate communities

Project Garden Fish aims to assess the fish and mobile invertebrate communities of ancient First Nations’ clam gardens. Clam gardens are impressive man-made features in the inter-tidal where huge numbers of rocks were piled strategically at the low tide mark creating a wall or terrace. This changed the slope and composition of the beach making it more suitable for clams to grow and then be harvested. They are at least several hundred, if not a few thousand years old. Habitat modifications caused by humans are extensive the world over. Coastal habitats are among the most modified. Clam gardens provide a unique example of a very long-standing human caused habitat modification, and therefore an excellent opportunity to research the effects on the ecosystem. Preliminary evidence suggests clam gardens support higher abundance and diversity than non-walled beaches, and may serve as nursery habitat. This project is generously supported by Hakai Research Institute, EIRP Lab (VIU), and the Juanes/Baum Lab (UVIC).

Author: **Boateng, Kennedy**
Degree sought: PhD
Supervisors: Dr. Barbara Hawkins and Dr. Peter Constabel
Category: Forest Biology

Seasonal variation and wounding response in foliar oregonin in red alder (*Alnus rubra* Bong)

Oregonin is a diaryheptanoid xyloside that occurs naturally in the bark, wood and leaves of *Alnus* species. It has been shown to be a significant deterrent to cervid feeding on red alder because of its antinutritive properties. The effects of oregonin on insect feeding were unknown until my recent study on red alder defense mechanisms. My work showed a significant negative correlation between foliar oregonin concentration and tent caterpillar feeding. If oregonin is a defensive compound against insects in red alder, its foliar concentration might be expected to vary during the growing season or upon attack by insects. My objective was to measure the seasonal variation and wounding response of oregonin and total phenolics in red alder leaves. To assess the seasonal variation of foliar oregonin and total phenolics, leaves from three-year-old red alder trees from five different families were harvested and analyzed on eight dates from early April to mid-October, 2016 to quantify oregonin and total phenolics concentrations. Wound induction experiments were conducted outdoors in 2016 and in a greenhouse in 2017, using four-year-old trees. Foliar oregonin, condensed tannin and total phenolics concentrations were measured. Results showed that concentrations of all the measured compounds were generally stable over most of the growing season and there were no significant responses to wounding. The results suggest that red alder foliar oregonin, condensed tannin and total phenolics are constitutive defenses and are not wound-induced.

Author: **Carrasquilla-Henao, Mauricio**
Degree sought: PhD
Supervisor: Dr. Francis Juanes
Category: Marine Biology

Yelloweye (*Sebastes ruberrimus*) and Quillback Rockfish (*S. maliger*) presence and abundance in association with benthic habitat parameters in the Strait of Georgia

Marine ecosystems are threatened due to anthropogenic activities such as pollution, habitat degradation and overfishing. Yelloweye and Quillback Rockfish are particularly vulnerable to overfishing due to their long life span, late age at maturity, and association with specific rock reef habitats. Studies relating habitat characteristics with the distribution and presence of rockfish at large scales remain scarce. The purpose of this study is to investigate the relationships between benthic habitat characteristics with presence and abundance of two rockfish species (Yelloweye and Quillback) caught in longline research surveys in the Strait of Georgia. Depth, slope, rugosity, curvature, TPI, distance to rock, distance to mixed substrate, and latitude were calculated from a 20 m resolution bathymetry layer as habitat parameters. Area of rock, mixed, mud and sand substrate was also calculated. Presence and absence of the two species were determined at each individual site and habitat parameters between presence and absence compared. Abundance was also modeled with respect to habitat parameters. Both species presented a clumped distribution, which was more evident in northern latitudes. Abundance was positively correlated to slope, curvature, and latitude, whereas distance to rock was negatively correlated. The differences in slope and rugosity demonstrate the importance of complex rock reef habitat for the conservation of these two species. While ROV data offer valuable visual habitat and fish information, longline surveys may be a more inexpensive and appropriate method for large-scale studies.

Author: **Carrington, Yuriko**
Degree Sought: PhD
Supervisors: Dr. Juergen Ehlting and Dr. Peter Constabel
Category: Forest Biology

The functions of quinate dehydrogenase genes in plants

The shikimate pathway leads to the production of aromatic amino acids in plants, bacteria and fungi. In plants, these are used to synthesize proteins and diverse aromatic secondary metabolites for reproduction and defense. Plant dehydroquinate dehydratase/shikimate dehydrogenase (DQD/SDH) catalyzes the formation of shikimate, the central intermediate of the shikimate pathway while 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 are yet 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-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: **Chalifour, Lia**
Degree Sought: MSc
Supervisor: Dr. Julia Baum
Category: Marine Biology

Evaluating the use of estuarine habitats by fish communities in the Fraser River estuary

The Fraser River feeds the largest estuary on Canada's west coast, and its many kilometers of delta support numerous fishes, including some of the most abundant salmon runs in the world. Despite its importance, the Fraser River estuary has had few fish surveys since the 1980s, save for specific small-scale studies done for the purposes of industrial expansion.

We surveyed salmon and associated fishes at 17 sites across the Fraser River estuary, which encompassed three habitat types: eelgrass, marsh, and sand flat. Sites were sampled biweekly from March - July, 2016 using beach and purse seine methods. All fish were identified to species and enumerated. All salmon were measured (forklength and depth), and hatchery markings (clipped adipose fin) were noted if present. Non-lethal fin clips were taken from juvenile Chinook for genetic stock identification, and a subsample were retained for otolith growth analysis. Seasonal shifts in fish community structure were captured by repeating the sampling once in September and October, 2016 following the same methods.

Data will be used to assess the relative abundance and diversity of resident fish communities across habitats and seasons, and to quantify the use of estuarine habitats by juvenile salmon in relation to fitness measures. Results from this field study will inform habitat and fisheries management decisions via the Salish Sea Marine Survival Project, and will support a Marine Environmental Observation Prediction and Response (MEOPAR) Network visioning and management project for the Lower Fraser region.

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

CRISPR/Cas9-mediated gene editing of *NAGLU* in mucopolysaccharidosis IIIB patient-derived induced pluripotent stem cells

Mucopolysaccharidosis IIIB (MPS IIIB) is a rare autosomal recessive lysosomal storage disease that lacks therapeutic treatments. Affected individuals experience progressive neurodegeneration, which is fatal within the first three decades of life. Mutations in *NAGLU* result in non-functional N-acetyl glucosaminidase (Naglu), the enzyme that is responsible for breaking down heparan sulfate. When Naglu is non-functional, heparan sulfate accumulates within lysosomes, leading to disease manifestation. The lack of treatment options for MPS IIIB is due to the inability of recombinant Naglu to cross the blood-brain barrier. CRISPR/Cas9, a recent tool in biotechnology with myriad applications, allows for precise gene editing driven by homology directed repair following Cas9-induced double-stranded cleavage. This technique has been used for targeting and correction of patient-specific mutations in a number of cell types. In induced pluripotent stem cells (iPSCs), CRISPR/Cas9 has been explored as a regenerative medicine for genetic disease. To determine if this method is feasible for mutation correction in the *NAGLU* gene, we have employed CRISPR/Cas9 using a liposome transfection approach in iPSCs derived from a patient with MPS IIIB ($NAGLU^{Y140C/\mathrm{R297X}}$). Monoclonal iPS colonies were found to be corrected for the p.R297X (c.889C>T) mutation with a 0.3% correction efficiency as confirmed through restriction fragment length polymorphism and Sanger sequencing. We have expanded our study to further target three other mutations in the *NAGLU* gene. This work will allow for a better understanding of the applications and limitations of this technique as a potential tool in regenerative medicine for MPS IIIB.

Author: **Claar, Danielle**
Degree Sought: PhD
Supervisor: Dr. Julia Baum
Category: Ecology and Evolution

Symbiotic diversity and coral resilience during an extreme ocean warming event

Coral reefs, the most biologically diverse marine ecosystems on the planet, are threatened due to climate change, which exposes corals to increasingly severe and prolonged episodes of heat stress. The response of corals to these disturbances is critically modulated by the structure and function of their diverse algal symbiont communities (*Symbiodinium* spp.), with some coral-*Symbiodinium* partnerships being much more heat tolerant than others. Identifying the mechanisms that underpin these functional differences may help us understand the capacity of corals to adapt to increasingly severe climate disturbances. To this end, we studied *Symbiodinium* communities in corals during an extreme climate disturbance (2015/16 El Niño) at Christmas atoll, which experienced some of the most severe temperature anomalies ever recorded. We collected tissue samples from ~1,000 tagged corals before, during, and after recovery, and analyzed their symbiont communities. Although bleaching was severe and mortality high, some corals recovered remarkably quickly, regaining symbionts even before the heat stress subsided. This resilience was associated with directional changes in symbiont community structure and increased survivorship of individual coral colonies. These findings indicate that, even under unprecedented thermal stress, resilient coral-symbiont interactions allowed some corals to survive, providing some hope for coral reef persistence in the Anthropocene.

Author: **Covernton, Garth**
Degree Sought: PhD
Supervisors: Dr. John Dower and Dr. Sarah Dudas
Category: Marine Biology

Microplastic concentrations in wild and cultured clams and oysters in British Columbia, Canada

Microplastic contamination is an emerging threat to marine ecosystems. Many aquatic animals – ranging from mammals to invertebrates – have been shown to ingest microplastics. These particles can disrupt digestive and reproductive processes, act as vectors for harmful chemical pollutants, and reduce overall animal health. As relatively non-specific filter feeders, bivalves are susceptible to ingesting microplastics from the water column. In southern British Columbia (BC), shellfish aquaculture is an important industry, and Manila clams (*Venerupis philippinarum*) and Pacific oysters (*Crassostrea gigas*) are the dominant culture species. Shellfish aquaculture often uses plastic infrastructure (anti-predator netting, fencing, rope, cages, trays, floats) that may degrade and release secondary microplastics. We quantified the microplastic content of these two species in southern BC by transplanting an initial population of adult individuals to shellfish farms and nearby non-aquaculture intertidal areas in 6 regions important for shellfish aquaculture with varying degrees of farming intensity. The bivalves were collected after 2-3 months, chemically digested with 10% KOH to remove tissue, filtered, and their microplastic content visually quantified against procedural blanks using a compound microscope. Water samples were also collected and analyzed for microplastic content. Results suggest that shellfish grown on aquaculture sites do not contain significantly more microplastics (majority microfibres) than those grown at non-aquaculture sites. The average number of microplastic particles found in BC shellfish (0.98 ± 1.42 and 1.38 ± 1.92 [SD] for clams and oysters respectively) are similar to microplastic concentrations reported for these species by other studies.

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

Summer Mortality of Pacific Oysters (*Crassostrea gigas*): The Role of Environmental Variables, Pathogens, and Spawning

Shellfish aquaculture has been an important industry and cultural component in British Columbia for over a century and Baynes Sound is a major region for the cultivation of Pacific oysters (*Crassostrea gigas*). The area has experienced periodic mass mortalities of oysters that are similar to mortality events reported around the world. Globally, Pacific oyster summer mortalities have been linked to elevated temperatures, reduced salinity, spawning events, nutrient levels, decreased food supply, harmful algal blooms, and suspended sediments.

The objectives of the present study are to: (1) identify the environmental variables correlated with Pacific oyster mortality, (2) determine the roles that pathogenic bacteria and reproduction play in mortality, and (3) create a predictive model for Pacific oyster summer mortality in Baynes Sound. To address these objectives, we set up wracks of adult oysters at five commercial oyster aquaculture sites throughout Baynes Sound. Over the summer/fall seasons, these sites were monitored to track oyster mortality events, environmental parameters (*i.e.* temperature, light, turbidity, salinity, dissolved O_2, chlorophyll-a, pH, and sediment grain size/organic content), and the diversity of phytoplankton and zooplankton. Oysters were also collected weekly to examine the resident bacterial populations and to complete histological analyses of gamete development.

To date, we have recorded 20–37% mortalities at the five sites and have identified 120 bacterial isolates – including *Vibrio aestuarianus*, *V. splendidus* related strains, and *Shewanella* spp. – all known pathogens of Pacific oysters. Preliminary results have also detected a correlation between the timing of oyster spawning and mortalities.

Author: **Cox, Kieran**
Degree Sought: PhD
Supervisor: Dr. Francis Juanes
Category: Marine Biology

Intertidal resource use over millennia alters marine biodiversity

Shellfish aquaculture has played a key role in coastal ecosystems for the past 10,000 years and is currently increasing annually at a rate of 8%, making it one of the fastest growing food industries globally. Historically, First Nations clam gardens were constructed during the late Holocene by building rock walls in the low intertidal, which added structural complexity, stabilized sediments and enhanced shellfish productivity. Currently, shellfish aquaculture is associated with similar environmental modifications and plays a key role in meeting the global need for seafood, while alleviating pressure on declining wild populations. The extent to which these aquacultural practices impact marine ecosystems remains unknown but is a critical issue for mitigating potential environmental impacts, ensuring sustainable food security and habitat protection. In an attempt to determine the effects shellfish aquaculture has on marine biodiversity, we evaluated 12 current and historical shellfish aquaculture sites and 12 control sites within three distinct regions (Baynes Sound, Quadra Island, and Calvert Island) along British Columbia's coast. Initial findings suggest that species diversity and abundance varies locally, regionally and in relation to aquacultural practice. Biodiversity, species abundance and non-native species abundance increased pole wards, while species diversity and species abundance were strongly correlated. These findings further our understanding of how shoreline modifications affect marine biodiversity and community structure. As this project is one of the first large-scale assessments comparing current and historical shellfish aquaculture, our findings will lead to further insight into First Nations cultural practices, ecosystem management, and the long-term implications of shellfish aquaculture.

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

The molecular basis of an extraordinary sex-ratio distortion in booklice

Many genetic elements, including genes, chromosomes or endosymbionts, have been found to dramatically affect sex-ratios in a number of species. The distortion of sex ratios can have profound effects on the ecology and evolution of a species. A recently discovered species of *Liposcelis* booklice is polymorphic for two female types, one of which produces exclusively female offspring (distorter females), while the other produces both male and female offspring (normal females). The molecular and genetic basis of this sex-ratio distortion remains unclear. Remarkably, recent genomic and transcriptomic work has revealed a horizontal transfer event in this species of booklice, whereby genes from *Wolbachia*, a known sex-ratio distorting endosymbiotic bacteria, have been transferred to the genome of the distorter females. This represents one of the few differences between distorter and normal female genomes. These data suggest that the horizontally transferred *Wolbachia* DNA could be underlying the sex-ratio distortion exhibited by distorter females, and is therefore a promising candidate for functional characterization. We have validated the integration of the *Wolbachia* DNA through the use of targeted primers, sequencing, and the discovery of introns. Earlier transcriptomic work showing that *Wolbachia* DNA is expressed exclusively in distorter females has been validated with qPCR. Ongoing work is being done to express this candidate gene in the model yeast system which could allow us to examine the potential functional role of the transferred bacterial gene within a eukaryotic system.

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

Context-dependent additive and multiplicative neuronal arithmetic by NMDA receptors in direction-selective ganglion cells

Neural circuits often combine multiple sensory features through ‘additive’ and ‘multiplicative’ scaling operations to compute their outputs. For example, responses of monkey visual cortical neurons can be both ‘additively’ scaled (shift in x-axis) or multiplicatively scaled (y-axis expansion) according stimulus size. The synaptic mechanisms that enable these arithmetical scaling operations remain to be fully determined.

Here we examine arithmetical operations mediated by NMDA receptors in the direction-selective ganglion cell (DSGC) circuit in mouse retina. Using a simple two-compartment neuronal model built in the NEURON simulation environment with synaptic inputs based on conductances measured from DSGCs *in vitro*, we tested how NMDARs affect the output of these cells. Then, we employed multi-electrode array recordings of ON-OFF DSGCs to test our models’ predictions.

We found the relative contribution of NMDA receptor-mediated inputs was maximal at the lowest contrasts, and decreased with increasing contrast. As a result, the contrast response function in the absence of NMDA receptors was rightward shifted (C_{50}: 26.5% Weber contrast in control; 32.5% without NMDA receptors). However, as this increase in sensitivity has a post-synaptic locus and directly modulates the DSGCs spiking response amplitude (y–scaling), this operation can be considered ‘pseudo-additive’, to distinguish it from x–scaling operations that result from input modulation. In spite of their additive effect on contrast, NMDA receptors performed multiplicative scaling on directional responses of DSGCs, amplifying their output while preserving their DS tuning properties.

NMDA receptors can mediate additive and multiplicative scaling operations in the DS circuit in a context-dependent manner.

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

Northern Anchovy in the Salish Sea

Many small pelagic fish species exhibit dramatic fluctuations in abundance and range. The location and extent of suitable habitats may also shift in response to both short-term variability and long-term trends in climate. Near the margins of a contemporary range, trends in abundance may reflect a continuation of historical variability or foreshadow future changes in distribution. Understanding mechanisms of change is often challenging due to a lack of stock assessment data for species with little or no prior importance to fisheries. Northern Anchovy (*Engraulis mordax*) have been scarce in the Salish Sea for most of the 20th century, and are not generally considered as an important component of the ecosystem. Since 2014, there has been an increase in the frequency and abundance of Northern Anchovy catches in monitoring programs. Atypical observations of Northern Anchovy have also been reported by members of the public, with accounts of anchovy appearing in the diets of valuable and depressed salmon stocks. We synthesize a diverse, but patchy, collection of datasets bearing on the biology and dynamics of Northern Anchovy in the Salish Sea. Our results suggest that recent increases in Northern Anchovy abundance may be related to elevated ocean temperatures. If warmer temperatures become the new normal, Northern Anchovy have the potential to restructure Salish Sea food webs.

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

Reorganization of Cortical Somatosensory Map (Barrel cortex) Imaged Through Long-Term Sensory Deprivation in Rett Mice Model

RTT, mutation of MeCP2, is a postnatal neurodevelopmental disorder occurring in 1-10,000 girls worldwide. Patients develop normally until 6 to 18 months old and then start showing the symptoms, including loss of speech and purposeful hand use, stereotypical movements, acquired microcephaly, seizures, autistic features, and mental retardation.

Here, I evaluate sensory deprivation dependent plasticity in barrel cortex in male Rett mice model to better understanding the consequences of MeCP2 loss of function for neural circuit function. Cortical plasticity happens during learning, development, brain injury or somatic injury including denervation. Previous studies showed, when a sensory input removes, the receptive field corresponding to that particular area is shrieked.

I hypothesized that Sensory cortical map plasticity in Rett mice is less than plasticity in wild type mice. Animal mouse model is Mecp2$^{-/Y}$ (1month old) with lack of exon 3. Trim C1 whisker to 5mm, and whisker B2 as non-trim (control). Two days after implanting cranial window, stimulate whiskers with 20Hz amplitude for 1 second, image (for 14 days) the brain surface with intrinsic optical imaging technique. Data have shown that the activity of whisker B2 corresponding barrel cortex stays the same during time but the activity of C1 whisker corresponding receptive field is reduced. This reduction between day 7 and day 0 for wild type is 21.66% ± 4.7 and for Rett animal is 16.94%± 8.2.

This project works towards addressing the fundamental question: “How are MeCP2-mutant neurons wired into, and performing within circuits in the Rett brain?” to guide strategies for developing therapeutic interventions.

Author: **Frauendorf, Therese**
Degree Sought: PhD
Supervisor: Dr. Rana El-Sabaawi
Category: Ecology and Evolution

Combined effects of climate change and exotic species on tropical stream nitrogen dynamics

It is important to understand how multiple human impacts affect freshwater ecosystems. Climate-driven changes in rainfall are predicted to decrease streamflow and increase flash flooding in tropical streams. Increased flooding can give exotic species access to new habitats and increased drought events can enhance competitive effects on native species. I investigated how climate-driven changes in flow and the exotic guppy fish alter nutrient dynamics in Hawaiian streams. I measured stream nitrogen demand and supply via excretion of three resident invertebrates and the non-native guppy fish. We estimated these variables in three guppy-free and three guppy-invaded streams across a rainfall gradient on Hawaii Island that mimicked predicted changes in stream flow. Climate-driven changes in flow decreased the amount of nitrogen exported by guppy-free streams. However, when streams are invaded, guppies and climate change have synergistic effects on nutrient dynamics. Nitrogen demand was up to 3x lower in guppy-invaded streams, but did not change significantly with stream flow. Guppy population nitrogen excretion increased with climate-driven changes in flow. Native insect populations excreted up to 4x less nitrogen in guppy-invaded streams, but this difference decreased to 1.5x in drier streams. Total community excretion in guppy-free streams supplied 20% of the nitrogen demand, which decreased to 5% with lower flow. In guppy-invaded streams total community excretion supplied 40% of the nitrogen demand under current climate conditions and increased to 180% with predicted changes in flow. Climate change appears to enhance effects of guppy introductions, and the combined effects increase nutrient export in tropical streams.

Author: **Freshwater, Cameron**
Degree Sought: PhD
Supervisors: Dr. Francis Juanes and Dr. Marc Trudel
Category: Ecology and Evolution

Individual variation, population-specific strategies, and stochastic processes shape marine migration phonologies

Migration phenology can influence individual fitness, moderate population dynamics, and regulate the availability of ecosystem services to other trophic levels. Phenology varies within and among populations, and can be influenced by conditions individuals experience both prior to departure and encounter en route. Assessing how intrinsic and extrinsic factors interact to influence variation in migratory phenologies across ecological scales is often limited due to logistical constraints associated with tracking large numbers of individuals from multiple populations. We used two natural tags, DNA and otolith microstructure analysis, to estimate the relative influence of individual traits (life history strategy, body size at departure, and growth during migration), population-specific strategies, and interannual variability on the phenology of marine migrations in juvenile sockeye salmon *Oncorhynchus nerka*. We show that the timing and duration of juvenile sockeye salmon migrations were correlated with both life history strategy and body size, while migration duration was also correlated with departure timing and growth rates during migration. Even after accounting for the effect of individual traits, several populations exhibited distinct migration phenologies. Finally, we observed substantial interannual and residual variation, suggesting stochastic environmental conditions moderate the influence of carry-over effects and population-specific strategies. Given evidence that intraspecific diversity can stabilize ecological systems, conservation efforts should maintain migratory variation among populations by preserving locally adapted phenotypes, while also regularly assessing variation within populations, which may buffer systems from environmental stochasticity.

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

Can condensed tannins act as *in vivo* antioxidants and protect poplar against oxidative stress?

Condensed tannins are polyphenolic compounds synthesized from the flavonoid pathway and the most abundant plant secondary metabolites. They accumulate to high concentrations in trees and are often considered to be plant defense compounds, but they may have additional functions. In poplar, tannin biosynthesis is stimulated by high light intensity and UV-B irradiation, which suggests they may be important in resistance to abiotic stresses. Condensed tannins have potent antioxidant capacity *in vitro*, but it is not known if they have this function *in planta*. This project tests the hypothesis that condensed tannins can act as *in vivo* antioxidants and therefore help to protect poplar leaves against reactive oxygen species (ROS) that accumulate during stress. To achieve this, transgenic poplar saplings engineered to accumulate high concentrations of condensed tannins were challenged with drought stress, a stress treatment that causes an accumulation of reactive oxygen species. For drought stress, water availability to saplings was reduced for three weeks. Chlorophyll fluorescence measurements showed that high-tannin transgenic poplar lines retained greater photosystem II operating efficiency (Fq'/Fm', φPSII, or $\Delta F/Fm'$) compared to control plants. By contrast, low-tannin RNAi plants were more susceptible to damage by drought. These results suggest that condensed tannins help to protect against oxidative damage caused by these abiotic stressors. We speculate that tannins may also be important for tolerance to other abiotic stresses that generate ROS, such as UV-B or heat stress.

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

AMPA-lacking silent synapses in the mature direction-selective ganglion cells in the mouse retina

Synapses lacking the functional expression of AMPARs are often considered ‘silent’, as glutamate binding to NMDARs alone does not substantially activate them (due to the voltage-dependent block of NMDARs by external Mg^{2+} ions). While silent synapses have been studied extensively throughout the central nervous system, whether they arise presynaptically through the ‘whispering synapses’ and/or glutamate ‘spill-over’ hypothesis, or post-synaptically by the lack of AMPAR expression still remains unclear. Here we use electrophysiological patch-clamp and 2-P imaging techniques to investigate the synaptic mechanisms underlying silent synapses in the direction-selective ganglion cell (DSGC) circuit of mature mouse retina, where these synapses play an important role in E-I coordination. NMDAR-mediated miniature-like events could be detected in DSGCs under pharmacological isolation (0 Mg^{2+}, NBQX), suggesting that NMDARs were located at synaptic sites and were able to respond to quantal glutamate release. These events could be distinguished from AMPA EPSCs based on their slower kinetics. Under control conditions, analysis of sEPSCs reveals two distinct populations of AMPA and NMDA-like sEPSCs, suggesting that the receptors are spatially segregated at individual synapses. Consistent with these findings, NMDAR-mediated ‘optical quantal’ activity could be detected at discrete dendritic sites using 2-P Ca^{2+} imaging techniques. These results indicate that silent synapses in mature DSGCs represent synapses lacking the postsynaptic expression of AMPA receptors.

Author: **Hanson, Nova**
Degree Sought: MSc
Supervisor: Dr. Louise Page
Category: Marine Biology

Development and evolution of a derived feeding system in *Amphissa columbiana*

Evolutionary developmental biology focuses on how development has changed through time. Studies have shown that development is modular, meaning that groups of traits develop together as a module, and modules develop independently of other modules. Modularity promotes evolvability, the capacity of a developmental system to evolve, because change can occur in one module without having deleterious effects on other modules. This can foster a surge of phenotypic variants, such as the diverse feeding systems of predatory marine snails (neogastropods). While the ancestral mode of feeding in gastropods is herbivorous grazing, neogastropods have become predators that feed with a highly derived proboscis. Remarkably, the morphologically complex foregut of neogastropod predators has evolved within a life history that begins with a larval stage that feeds on microalgae. Studies have shown that the developing foregut of neogastropods is modular and the modules have been uniquely modified during development of buccinoidean and conoidean neogastropods. However, further comparisons between ancestral herbivorous grazers and derived predatory gastropods are needed to discern the foregut morphogenesis process. This comparative study of foregut development in a predatory neogastropod, *Amphissa columbiana*, and a herbivorous gastropod, *Crepidula fornicata*, will reveal how the unique foregut of this derived neogastropod predator develops. Preliminary results indicate that the foregut of *A. columbiana* is composed of a dorsal and ventral module, enabling the adult feeding apparatus to differentiate throughout larval development (ventral module) without obstructing the necessary conduction of microalgae that is required to fuel development (dorsal module).

Author: **Harms, Kathrina**
Degree Sought: MSc
Supervisor: Dr. Louise Page
Category: Marine Biology

Developmental modularity of the foregut in a gastropod mollusc: *Evalea tenuisculpta*

Phenotypic variation among offspring is the raw material that natural selection works on, and development may play an important role in creating this variation. Developmental organization may therefore be a key factor for explaining differences in the 'evolvability' of a lineage. Recent research on gastropods has identified two developmental modules for the foregut: a dorsal and ventral module. The dorsal module becomes the dorsal food channel of the post-metamorphic foregut, but it also serves as the esophagus for the feeding larval stage. The ventral module becomes the buccal cavity, radula and salivary glands of the post-metamorphic stage. In neogastropods, a very large clade of gastropods that are predators following metamorphosis, temporal and spatial dissociation of the two foregut modules during their development may have promoted evolvability of the post-metamorphic foregut, because the ventral module of the foregut can develop a plethora of diverse morphologies without interfering with larval feeding. Pyramidellids are a group of gastropods that are not closely related to neogastropods, but they, like the Neogastropoda, include a very large number of species and have an extremely complex and highly derived, post-metamorphic foregut for predatory feeding. If modularity and spatial separation of foregut modules during development has contributed to the observed evolvability of neogastropods, then modularity and spatial separation of the modules during development might also be expected for the pyramidellid foregut. I will use histological sections and 3D reconstructions to document the development of the foregut in the pyramidellid gastropod, *Evalea tenuisculpta.*

Author: **Kanne, Rande**
Degree sought: MSc
Supervisor: Dr. Geraldine Allen
Category: Forest Biology

Utilizing sequence data to examine the phylogenetic relationships and the phylogeographic patterns of Garry oak (*Quercus garryana*)

Garry oak (*Quercus garryana*) is the single native oak species in British Columbia and Washington, with a geographic range extending south to California. Within this distribution, three varieties of Garry oak are commonly recognized: var. *garryana* in the north, and var. *breweri* and var. *semota* further south. I am using chloroplast and nuclear sequence data to investigate patterns of infraspecific variation across the geographical range. I have sampled uniformly throughout this range, as well as sample of several outgroup species. In this study I address the following questions. 1) How are populations of *Q. garryana* related to one another and to other white oaks in western North America? 2) How did Garry oak come to occupy its current geographical range. To date, my analyses of sequence data from two cpDNA regions have revealed 19 plastid haplotypes, showing a strong north-to-south gradient in haplotype variation. Most samples in the northern part of the range belong to a single widespread haplotype. My results also suggest that Garry oak is hybridizing with two other white oak species that have overlapping distributions, *Q. lobata* and *Q. douglasii*. Presently, I am sequencing three additional DNA regions (two plastid and one nuclear) to further refine these results and to determine the phylogenetic position of Garry oak in relation to other white oaks.

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

Maintenance of an ancient selfish X chromosome in a mushroom-feeding *Drosophila* species

Driving X chromosomes (X^D) are selfish genetic elements that bias their transmission relative to the Y chromosome in a number of organisms. These selfish chromosomes are widespread in nature and can have important effects on a species' ecology and evolution. Individuals that carry an X^D transmit almost exclusively X^D-bearing gametes, and therefore sire predominantly female broods. Once they arise, X^Ds are predicted to spread deterministically, eventually driving a species to extinction due to a lack of males. Despite this prediction, many X^Ds are found at intermediate frequencies in the wild, raising the question of how X^Ds are maintained in species over time. Here, we investigate the evolutionary maintenance of an ancient X^D in a common woodland fly, *Drosophila testacea*. We provide evidence that the origin of the X^D in *D. testacea* pre-dates the split of *D. testacea* and its sister taxa, *Drosophila neotestacea* and *Drosophila orientacea*. We are investigating the evolutionary forces allowing the persistence of this selfish chromosome by comparing the fitness of X^D-carriers to individuals carrying the wild-type X. So far, we have found that the X^D causes major fertility defects in males, but does not affect their longevity. Ongoing work is investigating the effect of the X^D on female fitness.

Author: **Litke, Anastasia**
Degree Sought: MSc
Supervisor: Dr. Robert Chow
Category: Neuroscience, Cell, and Molecular Biology

Investigating the pathogenicity of *VSX1* P247R and its role in corneal dystrophies

Despite the association of missense mutations in the transcription factor-encoding gene, *Visual System Homeobox 1 (Vsx1),* and two corneal dystrophies, the role of *Vsx1* in these diseases is controversial. To address this issue, we utilized *in vitro and in vivo* approaches to determine the pathogenicity of *Vsx1* P247R, a change that is found in disease populations and is located in the highly conserved CVC domain.

Various *in vitro* techniques were used to examine transcriptional activity, protein stability and localization. Transcriptional activity was investigated using an UAS-luciferase reporter assay. Protein stability and localization were addressed with western blotting and immunohistochemistry respectively. To investigate pathogenicity *in vivo*, stable mouse lines were generated harboring the mutation. Immunolabeling and histological analyses on *Vsx1 P247R* mice were performed on retinal and corneal tissue.

The *in vitro* luciferase reporter assay supported previous findings that wild-type Vsx1 can function as a transcriptional repressor. In addition, Vsx1 P247R, showed a 50% increase in transcriptional repression when compared to wild-type Vsx1 ($P < 0.001$, $n=9$). No significant differences were observed with respect to protein stability and subcellular localization.

Investigating whether a unique mutation is truly pathogenic for a disease is important in determining the cause, treatment and prevention of a disease. Our analysis showed that Vsx1 P247R increases transcriptional repressor activity which indicates a previously uncharacterized role for the CVC domain in regulating transcriptional activity. The increase in activity indicates that Vsx1 P247R may in fact be pathogenic and requires further investigation into the retinal and corneal phenotypes *in vivo.*

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

Characterization of Negative Condensed Tannin and Flavonoid MYB Transcription Factors in Poplar

Condensed tannins, or proanthocyanidins, are one of the most important secondary metabolites in plants and can constitute up to 25% dry weight of leaves of trees such as poplar. They are a major end product of the flavonoid pathway, which is regulated transcriptionally by a MYB, bHLH and WDR transcription factor complex. Previously, we identified the poplar R2R3 MYB transcription factor MYB134 as a key positive regulator of tannin biosynthesis in poplar. We have now identified two additional R2R3 MYB transcription factors, MYB165 and MYB194, which are predicted to act downstream of MYB134 and have strong sequence similarity with negative regulators (MYB-like repressors). Promoter activation assays showed that both negative regulators could repress the activation of flavonoid gene promoters by MYB134, which suggests they could play a role in tannin biosynthesis. To test this idea, we overexpressed MYB165 and MYB194 in transgenic poplars. These plants showed a strong reduction of tannin accumulation, in particular in roots which constitutively contain concentration of tannins. In addition, the accumulation of other secondary metabolites in the flavonoid pathway was also reduced, including anthocyanins and the salicinoid phenolic glycosides. This could indicate a broad function for the negative regulators. RNA-seq analysis of the transgenic poplars showed downregulation of known genes involved in tannin, anthocyanin and phenolic biosynthesis, as well as reduced transcripts encoding other MYB transcription factors and bHLH cofactors. The interaction of both positive and negative MYB regulators with the bHLH cofactor was confirmed by yeast two-hybrid analysis. The negative regulators may compete with positive regulators for the bHLH cofactor as the repression mechanism. This work will lead to a better understanding of the regulation network of flavonoid biosynthesis in poplar.

Author: **Magel, Jennifer**
Degree Sought: MSc
Supervisor: Dr. Julia K. Baum
Category: Marine Biology

Impacts of the 2015-2016 El Niño and global coral bleaching event on the structural complexity of coral reef ecosystems

Habitat complexity plays an important role in structuring natural communities, particularly in highly-complex coral reef ecosystems. Rising sea surface temperatures are expected to lead to an increased frequency of severe coral bleaching events, which may threaten the structural integrity of reefs by increasing the amount of dead coral substrate available to bioeroding organisms. However, this proposed consequence of climate change remains largely untested – few studies to date have attempted to examine changes in reef structural complexity related to severe coral bleaching. In the wake of the recent El Niño and mass coral bleaching event, we aim to quantify the effects of bleaching-induced coral mortality on the structural complexity of reefs around Kiritimati (Republic of Kiribati), the world's largest coral atoll. Using diver-held cameras, we took high-resolution photos of the reef substrate in 23 permanent mega-photoquadrats (MPQs) around Kiritimati before and after the 2015-2016 El Niño. Through structure-from-motion photogrammetry, we constructed detailed 3D models of the reef from these images and quantified structural complexity metrics by integrating the models into geospatial software. We document a decline in structural complexity in the MPQs less than a year after the onset of the El Niño, likely due in part to the almost complete loss of soft corals throughout the warming event. This study increases our understanding of the effects of severe bleaching on the structural foundation of coral reef ecosystems, which is critical to the future preservation of these important but fragile habitats in the face of accelerating climate change and reef degradation.

Author: **Marques, Piata**
Degree Sought: PhD
Supervisor: Dr. Rana El-Sabaawi
Category: Ecology and Evolution

Effects of urbanization on fish life history traits: lessons from guppies

Currently, 3.9 billion people lives in cities worldwide, and the urban population is expected to increase to 6.4 billion people by 2050. This trend suggests increases in the magnitude of threats to urban ecosystems in the near future. In stream ecosystems, urbanization is known to degrade the habitat, disrupts ecosystem processes, and alters biological interactions. When facing impacts deriving from urbanization, organisms are forced to change their characteristics (ie. traits) in order to thrive in urban environments. In this study, we assessed the effects of urbanization on life history traits of guppy fish, *Poecilia reticulata*. Female guppies were caught in urban and non-urban streams in the city of Rio de Janeiro, Brazil. The number of mature eggs and embryos per fish were counted (N_t). Individual body weight (W_b, mg) and gonad weight (W_g, mg) was used to estimate reproductive investment per fish ($R_i = W_g/W_b$). Differences on R_i and N_t among urban and non-urban streams were tested using body size as a covariate. The results indicate urbanization increases the number of eggs/embryos (p<0,01 F=15,5) and reproductive investment (p=0,04; F=2,77) in female guppies. This suggests that urbanization drives changes in guppy life history traits, increasing guppy fitness which is important for thriving in urban streams.

Author: **Marshall, Lucianne M.**
Degree Sought: MSc
Supervisor: Dr. Diana Varela
Category: Marine Biology

Investigating the meltdown in the coastal Arctic: progression of phytoplankton blooms and environmental dynamics from sea ice coverage to open waters

Phytoplankton studies in the Arctic Ocean have been historically limited to summer when sea ice cover is reduced or absent. Despite recent work showing spring phytoplankton blooms developing under ice, little is known about pelagic production before sea-ice break-up and less about changes in phytoplankton and nutrient dynamics occurring from under-ice to open-water conditions. We will present experimental data results from a 2016 study spanning from a period of ice cover (mid-June) to open waters conditions (early-August), alongside automated data collected by the Ocean Networks Canada (ONC) marine observatory in Cambridge Bay (Nunavut) in the Canadian Arctic Archipelago. We measured biogenic particles (chlorophyll *a*, silica, carbon, nitrogen), dissolved nutrients, phytoplankton taxonomic composition and utilization rates of carbon (^{13}C) and nitrate ($^{15}NO_3^-$), and silica production. Primary production peaked (0.55 μmol C L^{-1} d^{-1}) during ice break-up, dominantly flagellated cells <5 μm. Another peak occurred in July-August in open waters and had a larger contribution of cells >5 μm (*Chaetoceros* diatoms). ONC data shows a yearly shift from net community respiration to production prior to sea-ice melt indicated by changes in the supersaturation of O_2 (‘delta O_2’), here we link delta O_2 changes to surface primary production (^{13}C utilization rate). Parameters measured by the observatory (e.g. temperature, ice thickness) will also be evaluated as drivers for variations in phytoplankton taxa over time. This study provides a comparison between experimentally measured phytoplankton production and cabled observations in the Arctic, critical for testing the validity of automated long-term data collection in a marine setting.

Author: **McAllister, Jillian**
Degree Sought: MSc
Supervisor: Dr. Patrick Gregory
Category: Ecology and Evolution

Seasonal movements and hibernation ecology of Common Gartersnakes (*Thamnophis sirtalis*) near the northern extent of their range

Because essential resources may be physically separated on the landscape, mobile animals often move from one location to another as needs change and may exhibit seasonal movement or migration. Ectothermic vertebrates, such as amphibians and reptiles, do not generate their own body heat and therefore cannot sustain activity in freezing temperatures. Therefore an essential requirement of these animals at high latitudes is a place to overwinter, a hibernating site or hibernaculum. Although Common Gartersnakes (*Thamnophis sirtalis*) are well known for their large-scale communal hibernation in the northern part of their range, in my study area their hibernacula had neither been described nor located. I used radiotelemetry at two sites in east-central British Columbia to determine movement patterns of adult female garter snakes and locate their hibernacula. I estimated the cumulative distance travelled during the active season and calculated movement rate, maximum displacement, and tortuosity ratio. I also compared movement, timing, and duration of hibernation of gravid and non-gravid snakes. Instead of hundreds to thousands of snakes in communal hibernation, the individuals I tracked hibernated with fewer than 10 other snakes and one even hibernated individually. The most common hibernacula I located were inconspicuous underground hollows created by water. Studying animal movements and critical habitat such as hibernacula contributes to conservation decisions and increases the ease with which these populations can be studied in the future given snakes are more easily observed and/or captured during spring and fall at communal hibernacula.

Author: **McLaughlin, Amanda**
Degree Sought: PhD
Supervisor: Dr. John Taylor
Category: Neuroscience, Cell, and Molecular Biology

Fine scale neural correlations are driven by non-linear integration of chemical and electrical input

All information about our visual scene must be transmitted from the retina to the brain via a limited number of ganglion cell axons. Much work has been done to ascertain how such a wealth of information is encoded using a limited bandwidth. Our lab has recently identified a population of electrically coupled ganglion cells in the mouse retina, and gap junctions throughout the CNS often exhibit fine-scale correlated activity, which might endow the system with an additional layer of information processing power. Using multi-electrode whole-cell electrophysiology, we demonstrate that electrically-coupled ganglion cells exhibit synchronous (population level) activity, which is gap-junction dependant. In addition, the strength of synchronous activity varied inversely with spike rate. Together, these features allow synchronized activity to encode information about the spatial distribution of a light stimulus, which would be ambiguous based on the spike rate of single cells alone; therefore endowing the retina with an additional layer of processing power.

Author: **Minkley, David**
Degree Sought: MSc
Supervisor: Dr. Ben Koop
Category: Ecology and Evolution

Expansion of repeated DNA has differentially shaped the genomes of salmonids

Transposable elements (TEs) are repeated DNA sequences capable of mutagenic proliferation within a host genome and are found in virtually all eukaryotes. Using a variety of complimentary bioinformatics approaches we have characterised the distribution of TEs in the genomes of a number of salmonid species, including Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*) and Arctic charr (*Salvelinus alpinus*). The salmonids are a rapidly-evolving species group whose common ancestor experienced a whole-genome duplication (WGD) event approximately 95 million years ago. WGDs have only rarely been fixed in the vertebrate lineage and are often followed by increases in genetic diversity, novel gene function, gene subfunctionalization and increased regulatory complexity; the processes involved in restoring genome stability following a WGD are only partially understood. We have established that at least 50% of the DNA within each examined salmonid genome is derived from repeated DNA; this is amongst the largest repeat-derived fraction of vertebrate genomes to date. Elements from one major superfamily of TEs, Tc1-Mariner, appear to have been most actively proliferating within the genome of the salmonid ancestor around the time of the WGD. Further, different families of Tc1-Mariner elements were differentially active in different salmonid lineages, contributing to millions of DNA base differences between extant species such as Atlantic salmon and rainbow trout. This work provides insight into key processes of genomic evolution and speciation, and has helped improve the quality and utility of salmonid genome reference sequences.

Author: **Minkley, Michael**
Degree Sought: MSc
Supervisors: Dr. Patrick Walter and Dr. Raad Nashmi
Category: Neuroscience, Cell, and Molecular Biology

Novel clinical findings reveal systemic biomarkers of disease burden in neurodegenerative disorders

Though iron is essential for numerous biological processes in the body, the damaging properties of excess iron accumulation is implicated in a variety of disorders including Neurodegeneration with Brain Iron Accumulation (NBIA) and Parkinson's disease (PD). NBIA is a group of rare genetic disorders characterized by progressive degenerative motor symptoms and the accumulation of iron in the basal ganglia; symptoms which are paralleled in PD. Previous studies of PD have found that a systemic burden of increased oxidative stress and chronic inflammation accompanies the neurological symptoms of the disease. However, current understanding of systemic changes in NBIA disorders is limited, leaving no clear diagnostic biomarkers. My research focuses on identifying novel systemic biomarkers in patients with two NBIA disorders: Phospholipase-A2G6 Associated Neurodegeneration (PLAN) and Pantothenate Kinase Associated Neurodegeneration (PKAN) as well as paired research characterizing a mouse model of early-onset PLAN. These studies expand previous findings of elevated levels of systemic oxidative stress in other neurodegenerative diseases such as PD to include NBIA patients. They provide evidence of significantly elevated levels of free and total malondialdehyde; representative of an oxidative stress burden in NBIA as well as preliminary signs of an accompanying inflammatory burden. The final aspect of this research used proteomics to measure a panel of iron trafficking proteins and other metabolic proteins in patients. Collectively, these findings provide new insights into the systemic burdens of neurodegeneration and reveal potential diagnostic biomarkers for these disorders.

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

Factors influencing the composition of a benthic elasmobranch community in a warm-temperate bay ecosystem

Overfishing has reduced the shark abundance globally, but to assess ecosystem consequences of overfishing, we need information on their ecology to learn how they have been impacted and how they may respond to management. The abundance and distribution of sharks, rays, and skates are influenced by interactions between habitat, prey distribution and fisheries management techniques, such as marine protected areas (MPAs). Walker Bay is a warm-temperate ecosystem in the Western Cape, South Africa with diverse habitats and management paradigms, but with a history of heavy line fishing. Walker Bay's sandy bottom, rocky reefs, and kelp forests are home to a range of species, including catsharks, shysharks, and skates, among other sharks. A whale sanctuary limits boat traffic in parts of the bay from July to December. Mudge Point and Betty's Bay also form nearby MPAs with moratoriums on boat-based fishing. Baited remote underwater videos (BRUVs) were placed at 80 sites in Walker Bay (40 in the whale sanctuary, 40 outside) and at 56 sites in Betty's Bay to evaluate the distribution of shark species in the region in relation to habitat, depth, and management paradigm. Sharks, rays, and skates were widespread across habitats and management zones, but were most abundant in kelp and within protected areas. Different habitat types showed distinct communities with rays and skates preferring sandy habitat within the whale sanctuary and smaller catsharks preferring kelp habitat within MPAs. Species richness did not vary greatly between sites, from 12 in the unrestricted zone to 15 within the MPA.

Author: **Raap, Monique**
Degree Sought: MSc
Supervisors: Dr. Ben Koop and Dr. Helen Gurney-Smith
Category: Marine Biology

Anthropogenic influence of habitat alteration and microplastic contamination on shellfish physiology, growth and survival

Many marine ecosystems have been modified and utilized by humans for food production, industry, land development, transportation, recreation, and waste disposal. This research will examine two different aspects of human impacts in marine ecosystems; the impacts of habitat modification for productivity enhancement and the impacts of anthropogenic debris.

Clam gardens are examples of ancient mariculture beach modifications to increase intertidal habitat and shellfish food productivity. To examine the impacts of habitat alteration, we placed Littleneck clams (*Leukoma staminea*) on clam garden and non-clam garden beaches in Kanish Bay, Quadra Island, for a period of 16 weeks. Clams were sampled for physiological response (transcriptomics) survival and growth. By comparing these metrics we will assess whether habitat alteration promotes optimal conditions for clam growth and function.

Microplastics are pollutants derived from clothing, personal care products and breakdown of primary plastics that are found in sediment, fresh and marine waters worldwide. Concerns have been raised over microplastics in shellfish for human consumption and implications for the marine food web. To assess the impacts of microplastics on the health and physiology of Pacific oysters (*Crassostrea gigas*), we exposed oysters to environmentally relevant amounts of microplastic fibres, alongside controls. The exposure was for 30 days and samples were analyzed for genomic expression, microplastic load, condition indices, and stress (Neutral Red Retention assay). Comparing gene expression patterns of exposed and unexposed groups will determine whether the microplastics are causing stress, which may affect oyster immune function, reproduction, and growth, therefore subsequently affecting productivity and survival.

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

Investigating the foraging ecology of humpback whales in British Columbia

The humpback whale (*Megaptera novaeangliae*) population in the northeast Pacific Ocean is currently recovering from a long period of low abundance caused by commercial whaling. In British Columbia (BC), increasing numbers of whales are found in coastal areas associated with high biological productivity of importance to fisheries. The consumption of juvenile fish and other essential food web resources by this repopulation could be a critical factor in the recruitment and survival of commercially important fish stocks. Key uncertainties include diet composition and prey requirements of the growing feeding aggregations, as well as impacts to fisheries management of ignoring the spatial feeding ecology of humpback whales. My objective is to link humpback whale feeding behaviours to concurrent measurements of prey in BC waters using *i*) a multi-sensor, data-archiving tag designed for large whale deployments, *ii*) concurrent prey mapping surveys from echosounders, *iii*) mid-water prey sampling from tucker trawls, and *iv*) humpback fecal sampling. This study will provide scientists with essential baseline data on humpback whale diet in BC and a model for estimating prey removal by the foraging humpback whales. It will be the first comprehensive analysis of humpback whale diet and foraging ecology in BC waters.

Author: **Rondeau, Eric**
Degree Sought: PhD
Supervisor: Dr. Ben Koop
Category: Ecology and Evolution

Genomic diversity in rainbow trout

Rainbow trout (*Oncorhynchus mykiss*) is a salmonid species native to tributaries of the Northern Pacific Ocean. Life histories in rainbow trout vary widely from small, isolated freshwater populations to an anadromous form known as steelhead. While trout have been successfully introduced worldwide and are a staple in aquaculture, shifting conditions in warmth and acidity in their home range lead to concerns of susceptibility of small, unique populations. Cataloguing genetic variation will allow the development of genomic tools to support management of current populations and to select resilient trout in stocking programs. In this work, we use 54 re-sequenced trout to characterize whole-genome diversity within western Canada. With the addition of 61 re-sequenced individuals from collaborators sampled through the western US, Alaska and Kamchatka, we identify full-genome polymorphism through much of the natural range of the species. Genetic structure is much higher in southern and interior samples relative to coastal populations, with phylogenetics and PCA largely supporting previously described subspecies distributions. The geographic distribution of two large inversions within the genome has been characterized more closely, with chromosomal breakpoints of the inversions identified through comparative mapping. The presence of these inversions follows a largely geographical distribution, low in the southern populations and high in the north but with significant exceptions. Generating the tools with which to genotype trout allows for the development of informed management and stocking strategies to maintain existing genetic pools within natural populations, and to identify rainbow trout most adaptable to a changing climate.

Author: **Ryan, Bridget**
Degree Sought: PhD
Supervisor: Dr. Robert Chow
Category: Neuroscience, Cell, and Molecular Biology

MicroRNA regulation of *Pax6* expression

PAX6, a gene encoding a dosage-sensitive transcription factor essential for eye, brain and pancreas development, is mutated in the haploinsufficiency disease aniridia. Previous work has implicated the highly conserved microRNA-7 in the post-transcriptional regulation of PAX6 in regions of the brain and in the endocrine pancreas. We identified an 876bp mouse *Pax6* 3'UTR using RNA-Seq, 3' rapid amplification of cDNA ends (3'RACE) and *in silico* approaches, and have identified 55 putative miRNA recognition elements (MREs) in the *Pax6* 3' untranslated region (3'UTR). Many of the miRNAs predicted to target Pax6 were detected in Pax6-expressing cells and tissues by small RNA quantitative PCR (qPCR). We identified 25 miRNAs directly bound to the Pax6 3'UTR in pancreatic α-cells using miRNA trapping by *in vitro* RNA affinity purification (miTRAP). *Pax6* 3'UTR luciferase reporters indicate that some of these sites are functional, raising the possibility that they function in either in parallel or cooperatively to regulate Pax6 levels. To explore the biological relevance of the miR-7 MREs, we generated mice harboring mutations that disrupt one or more of these sites within the *Pax6* 3'UTR using CRISPR/Cas9 technology. Preliminary analysis showed that mice in which a single *Pax6* miR-7 MRE is mutated did not result in elevated *Pax6* mRNA relative to wild type. Our findings suggest that, *in vivo*, microRNA regulation can be mediated through redundant interactions. Since aniridia is the result of insufficient PAX6 protein, understanding how miRNAs negatively regulates *PAX6* may enable the development of therapies to block these interactions and de-repress *PAX6*.

Author: **Shin, Haewon**
Degree Sought: PhD
Supervisor: Dr. Steve Perlman
Category: Ecology and Evolution

Interactions between microbiota composition and parasite infections in wild flies

Microbial symbionts can positively influence host fitness by conferring protection against parasites, either by activating the host immune system, limiting parasite growth via nutrient competition, or by directly attacking parasites. Recent metagenomic studies of wild flies recovered a distinctive group of symbiotic gammaproteobacteria as a major constituent of the gut microbiome, despite their rarity on their food sources. These bacteria are related to a distinct lineage of gut symbionts that were previously implicated in parasite protection in bumblebees. To understand how parasite infections affect the structure of the gut microbiota in wild flies, I surveyed the infection rates of virulent trypanosomatid and nematode parasites in 236 field-collected individuals from two distantly related species (Drosophila neotestacea, Spelobia sp.) that share the same niche. I found a high trypanosomatid infection rate (58.1%) in Spelobia sp., and an infection rate of 10% in D. neotestacea. The infection rates of nematodes were lower; however, 100% of nematode-infected Spelobia sp. individuals were also infected by trypanosomatids, implying a novel interaction between two parasites. As a next step, I will use metagenomics of individual fly guts to determine how community composition responds to the presence of parasites. This work will expand our understanding of defense mechanisms driven by microbiota, and novel interactions between parasites in a host organism.

Author: **Teffer, Amy**
Degree Sought: PhD
Supervisors: Dr. Francis Juanes and Dr. Scott Hinch
Category: Ecology and Evolution

Infections, fisheries capture, temperature and host responses: relationships among multiple stressors influence the survival and behavior of adult Chinook salmon in freshwater

Infectious disease dynamics of wild Pacific salmon are poorly understood and may play a prominent role in recent declines of Chinook salmon populations. Multiple stressors influence the migration success of adult salmon, including rising river temperatures due to climate change and capture and release by fisheries, which likely modulate infection development. To understand how these factors impact survival and migration behavior of adult Chinook salmon in freshwater, we conducted simultaneous holding and telemetry studies with standardized gillnet treatments and nonlethal biopsy. Laboratory fish were held and treated in either cool (9°C) or warm (14°C) water. High temperature reduced survival but did not amplify gillnetting effects. Gillnetting reduced migration rate and distance traveled upriver and amplified bacterial and overall infection burden, but had no effect on longevity. Heavy infections were associated with early mortality of held fish and faster migrations but reduced longevity in the river. Blood properties and immune responses were predictive of survival of held fish, associated with stressors and correlated with infection burden. These results demonstrate multiple impacts of infectious agents on adult Chinook salmon in freshwater, improve our predictive capability regarding how stressors can reduce migration success and longevity, and add to the growing knowledge of disease dynamics in wild Pacific salmon.

Author: **Vance, Marie**
Degree Sought: PhD
Supervisors: Dr. Patrick von Aderkas and Dr. Barbara Hawkins
Category: Forest Biology

Assessing range-wide genetic structure in subalpine larch (*Larix lyallii*)

Subalpine larch (*Larix lyallii*) is a long-lived deciduous conifer with a relatively small range and narrow ecological niche. This species only grows at timberline in the Cascade Range and the Rocky Mountains of the Pacific Northwest. Climate change could further reduce available habitat by increasing levels of late-summer desiccation or by encouraging the upward migration of more competitive timberline species. Understanding the biogeographical history of the species, as well as genetic relationships among populations, will help managers develop a conservation plan for this species. To assess patterns of genetic variation in this species I collected foliage samples from 61 populations distributed across the species' natural range. Five individuals from each population were sequenced using restriction enzyme associated DNA sequencing (RADseq). Single nucleotide polymorphisms (SNPs) obtained from RADseq were analyzed to elucidate the genetic structure of this species.

Author: **Weil, Jacob**
Degree Sought: MSc
Supervisor: Dr. Francis Juanes
Category: Marine Biology

Fine-scale taxonomic and spatiotemporal variability in the energy density of prey for juvenile Chinook Salmon (*Oncorhynchus tshawytscha*)

The growth and survival of juvenile Chinook salmon (*Oncorhynchus tshawytscha*) are determined in part by biotic and abiotic conditions experienced during their first marine summer. Of the biotic conditions, the quality of available prey is integral for optimal growth and survival. Current studies investigating the effect of variable prey quality on salmon growth often approximate energy density using literature values. This approach ignores fine-scale taxonomic as well as spatial and temporal differences in prey quality. To address these possible sources of error, monthly zooplankton tows were performed in Saanich Inlet, Cowichan Bay and Maple Bay off the coast of Vancouver Island in the summer of 2017. Individuals were separated to the species level and wet, dry and ash weights were measured for each zooplankter. Energy density was calculated from an established model, which relates ash-free dry weight: wet weight ratios to energy density measurements. Early results suggested statistically significant differences in energy density between several species of hyperiid amphipods, which represent a large proportion of *O. tshawytscha* diet in some years. Other important species groups such as euphausiids and gammerids differed in energy density from previously reported studies in other locations suggesting spatial variability in energy density may exist. These early results suggest that fine-scale taxonomic variability in energy density exists and that species-specific energy density may vary across space and time. Studies that draw conclusions from literature values of energy density without direct measurement should be cautious in the reliability of these data in relation to their system.

Author: **Wertman, Debra**
Degree Sought: MSc
Supervisors: Dr. Steve Perlman, University of Victoria
Dr. Katherine Bleiker, Pacific Forestry Centre (NRCan, CFS)
Category: Ecology and Evolution

The light at the end of the tunnel: Photosensitivity in developing mountain pine beetle (*Dendroctonus ponderosae*)

This research explores the capacity for functional photoreception in larvae of the mountain pine beetle (*Dendroctonus ponderosae*), an extremely important forest pest insect that is well adapted for development beneath the bark of pine trees. Phototaxis tests, gene expression analysis and development experiments were integrated to assess mountain pine beetle larvae for light sensitivity. When presented with a phototaxis choice test, larvae preferred dark over light microhabitats, revealing that larvae sense and respond behaviourally to light. Long wavelength opsin transcription was identified in all life stages, including eggs and larvae, suggesting that *D. ponderosae* possesses extraretinal photosensitive capabilities across its life cycle. The long wavelength opsin could function in phototaxis or the development phenology of immature beetles, while the ultraviolet opsin, only found to be expressed in pupae and adults, is likely to function in dispersal via the compound eyes. Results from two development experiments reveal an effect of photoperiodic treatment on beetle development rate when reared from the egg stage, but not when reared from mature larvae, indicating that a critical photosensitive life stage(s) must occur in *D. ponderosae* prior to the third larval instar. An effect of photoperiod on adult emergence rates, however, appears to be independent of larval rearing conditions. The discovery of opsin expression and negative phototaxis in eyeless mountain pine beetle larvae, in addition to an effect of photoperiod on immature development and adult emergence rates, suggest that light and photoperiodism likely function in survival and life cycle coordination in this species.

Author: **Wyatt, Jessica**
Degree Sought: PhD
Supervisor: Dr. Jürgen Ehlting
Category: Forest Biology

Assessing severity of Swiss Needle Cast in British Columbia's Douglas-fir breeding population

Swiss needle cast (SNC) is a foliar disease caused by the fungal pathogen *Phaeocryptopus gaeumannii*. This disease is specific to Douglas-fir (*Pseudotsuga menziesii*) and results in decreased needle retention, reduced tree growth, and increased mortality. This economically important disease is endemic to Western North America affecting thousands of hectares of forest in Canada and the United States. Variation of host resistance has been documented in populations of Douglas-fir, however the genetic mechanisms underlying resistance have yet to be identified. This project will first evaluate variation of SNC susceptibility in a Douglas-fir breeding population used widely for reforestation in BC. Disease symptoms across 960 individual trees from a current breeding population grown at two climatically distinct yet geographically close locations, have been screened on the whole tree and branch level for SNC symptom severity. Between family differences in symptom severity are apparent but need further analysis since within family variation is also substantial. Needle level disease phenotyping is ongoing and involves both microscopic symptom severity determination and PCR based fungal load assessment. The results from these analyses will identify potential resistant or tolerant and susceptible families or individuals with which to conduct controlled inoculation trials for RNA sequencing to contrast global gene expression of resistant and susceptible trees in response to *P. gaeumannii* infection in time course experiments. This will characterize induced and constitutive defence responses and identify candidate adaptive genes related to SNC resistance.

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