DR. R.E. PETER BIOLOGY CONFERENCE 2018

Oral and Poster Presentation Abstract Booklet

Dr. Richard E. Peter Biology Conference

The Dr. Richard E. Peter Biology Conference will be held on March 1 and 2, 2018. This event is organized by the Biology Graduate Student Association in order to showcase the diverse research conducted by Biological Sciences students at the University of Alberta. The event consists of poster and oral presentations by senior undergraduate, M.Sc. and Ph.D. students from each of our six Research Interest Groups (Ecology, Molecular Biology & Genetics, Microbiology & Biotechnology, Plant Biology, Physiology & Cell Biology and Systematics & Evolution).

Dr. Richard Peter

The Conference is hosted every year by the Biology Graduate Student Association at the University of Alberta in honour of Dr. Peter and his contributions to our department. Dr. Peter was born in 1943 in Medicine Hat, Alberta. He obtained his BSc from the University of Calgary in 1965 and his PhD in 1969 from the University of Washington. After his post-doctoral studies, he took up an academic appointment at the University of Alberta. Dr. Peter served two terms as Chair of the Department of Zoology and two terms as Dean of the Faculty of Science. Dr. Peter also served as Vice-President of the Alberta Research Council, and Chief Executive Officer of the Institute for Food and Agricultural Sciences of the Government of Alberta. This was followed by his appointment as Director of Bamfield Marine Station in 2006.

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Conference Schedule

Oral Presentation Schedule

	Thursday Mar 1		**Friday Mar 2**	
ROOM	**BioSci CW 410**	**BioSci CW 313**	**BioSci CW 410**	**BioSci CW 313**
	Set up		Set up	
9:00-9:15	Shane Carey		Natasha Klappstein	Anna Bishop
9:15-9:30	Alyssa Weinrauch		Matthew Rhodes	Julia Shonfield
9:30-9:45	Perrine Delompré		Amanda Martens	Zachary Mueller
9:45-10:00	Curtis Dinn		Darcy Doran-Myers	Elene Haave Audet
	BREAK		BREAK	
10:30-10:45	Amanda Jorgensen		Nathan Grant	Renee Dicipulo
10:45-11:00	Nikki van Klavere		Doaa Waly	Morenike Ajidagba
11:00-11:15	Sean Ritter		Tina Schaefer	Jaclyn McCutcheon
11:15-11:30	Spencer D. Balay		Carley Wall	Logan A. Brand
	Lunch Break/Grad Luncheon		Lunch Break	
	Conference attendees are encouraged to check out posters in CCIS (PCL Lounge - by Second Cup)		Conference attendees are encouraged to check out posters in CCIS (PCL Lounge - by Second Cup)	
1:00-1:15	Emily Durkin	Alyssa M. Bohart	Thomas Brown	Sabrina Fox
1:15-1:30	Mahnoor Riaz	Justin Shave	Erin MacDonald	Kevin Duong
1:30-1:45	Prashanna Pokharel	Alex Beatty	Patrick Neuberger	Mark McAllister
1:45-2:00	Alexandra Grossi	April Robin Martinig	Shibashis Das	Casey Carlisle
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2:30-2:45	Giuditta Migiani	Collin J. Horn	Jamie Stark	Emily Dong
2:45-3:00	Kara MacAulay	Taylor R. Brophy	George Kinley	Zach Dumar
3:00-3:15	Sean Konkolics	Zhuoyan Song	Lee Campbell	Francesca jean
3:15-3:30	Michael Peers	Bianca Sacchi	Nicole Phillips	Abhi Aggarwal
3:45-4:45	Poster Session in **CCIS PCL lounge**		Poster Session in **CCIS PCL lounge**	
5:00-6:00	Keynote Speaker: Dr. Mark Taylor "Science meets management to recover native trout in Banff National Park" **CCIS L2 190**		Keynote Speaker: Dr. Kim Mathot "Understanding consistent among-individual differences in labile traits" **CCIS L2 190**	
6:30-8:00	Pizza and Beer Mixer **BioSci CW 410**		3MT + Mixer **Faculty Club**	

Poster Presentation Schedule

CCIS PCL Lounge (by Second Cup)

*Posters will up for display for the duration of the conference, but presenters will be by their posters during the desginated times below**, posterboard numbers are next to presenter**

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Nora Hussain - Poster #16
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Mahmoud Gheblawi - 11
Min Ku Kang - 22
Monica Takla - 34
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Aradana Muthupandian - 37
Abhi Aggarwal - 1
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Carly M. Davis - 8
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Emily Harvey - 15
Graeme Battigelli - 4
Hae-Won Son - 29
Hayley Todesco - 35

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Sofia Karabatsos - 20
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Helena Magaldi Ribeiro - 24
Keenan Guillas - 13
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Faculty Club, Friday March 2, 6:30pm

Alireza Saidi-Mehrabad

Brooke Biddlecombe
Zach Dumar
Gulnara Tagirdzhanova
Sean Konkolics
Anna Bishop
Nikki van Klavere
Amanda Jorgensen

Opening Keynote Address

Science meets management to recover native trout in Banff National Park

Dr. Mark Taylor (Parks Canada)

5:00pm March 1st, CCIS L2-190

Freshwater fishes are some of the most imperilled taxa worldwide as is evidenced by the number of threatened and endangered species. For example, westslope cutthroat trout (*Oncorhynchus clarkii lewisi*) and bull trout (*Salvelinus confluentus*) have been assessed as “threatened” nationally. Banff National Park is one of the last refuges for these species. Therefore, Parks Canada are developing actions on the ground to meet population objectives. Dr. Mark Taylor will demonstrate how biogeography, genomics and ecology research is helping inform active management of these threatened species.

Closing Keynote Address

Understanding consistent among-individual differences in labile traits

Dr. Kim Mathot (University of Alberta)

5:00pm March 2nd, CCIS L2-190

Behavioural and physiological traits are often inherently flexible and responsive to changes in the environment. However, individuals within populations may exhibit consistent differences in their expression of these traits, referred to as “individual specialization”, “consistent-among individual differences (CIDs)” “niche differentiation” and “animal personality”. Why do individuals differ consistently in their expression of labile traits? In the first part of this seminar, I will outline some of the conceptual and methodological issues that are relevant for the study of CIDs. In the second part, I will present the results of a series of experiments in red knots, *Calidris canutus islandica*, that tested alternative hypotheses for the development of consistent among individual differences in labile behavioural (diet choice, foraging, exploration) and physiological (gizzard mass, pectoral muscle mass, basal metabolic rate) traits. These studies illustrate how studying suites of functionally related traits can provide insights into the mechanisms driving patterns of phenotypic variation that cannot be achieved from a single trait focus.

Oral Presentation Abstracts

1 Engineering Fluorescent Ca2+ Indicators in Zebrafish

Abhi Aggarwal, Landon Zarowny, Tiffany Phan, Richard Kanyo, Michele DuVal, Ted Allison, Robert Campbell

Genetically-Encoded Fluorescent Calcium Indicators for Optical Imaging (GECOs) modulate their fluorescence intensity in response to changes in calcium ion concentration, and are powerful optogenetic tools for the investigation of neuroscience. The focus of this project is engineering a new GECO that exhibits favourable characteristics, such as increased brightness and a higher fold change, and characterizing its utility when expressed in vivo. To develop this new GECO, we started from mNeongreen, the brightest monomeric fluorescent protein currently available. An initial prototype construct was made using rational design, following the precedent of the genetically encoded calcium indicators such as GCaMP. This construct was further improved using directed protein evolution with colony-based screening of libraries of randomly generated variants. We observe the brightness of promising new variants and perform tests to see how new mutations have affected the brightness and the fold change of the variant. After many rounds of screening, our latest variant of mNeonGreen-GECO exhibits a Ca2+-dependent of 12X fold change. When compared to the original construct, this indicator appears significantly brighter with higher contrast between Ca2+-bound and Ca2+-free states. Directed evolution is ongoing and we expect to produce a fluorescent indicator that will be used for in vivo imaging of intracellular Ca2+ dynamics. Once the characteristics of mNeonGreen GECO have been plateaued, we will image its calcium dynamics when expressed as a transgene in the zebrafish CNS. Meanwhile, we are also developing another calcium indicator based on bright monomeric red fluorescent protein, mScarlet and currently working on screening its calcium dynamics when expressed in zebrafish. Doing so will allow us to compare the screening methods for calcium dynamics in-vitro and in-vivo, while producing two calcium indicators that researchers can use to study various disease states.

2 Formation and Assembly of Nucleosome Complex

Morenike Ajidagba, Md Touhidul Islam, Rashmi Panigrahi, and Mark Glover

Aims: DNA structure is vital for maintaining genomic integrity during DNA damage; which if left untreated can lead to the development of cancerous cells. Exposure to ultraviolet and ionizing radiations result in DNA double stranded breaks (DSBs). The basic unit of DNA consists of the nucleoprotein complex called the nucleosome, which has an octamer of core histones wrapped by 146 base pairs of DNA. Four histone proteins, H2A, H2B, H3 and H4, make up this protein core. This compact nature is crucial for regulation of gene expression and prevention of further DNA damage. Our goal is to purify and assemble the nucleosomal complex for future interaction studies with DSB repair proteins.

Methods: The histone proteins were cloned and protein expression studies to determine the best cell line for optimal expression were performed. Expressed proteins were purified on a Ni-NTA affinity column. The purity will be confirmed through SDS- PAGE analysis. The oligomeric state of the protein complexes were analyzed using size exclusion chromatography and native PAGE analysis.

Results: Presently, we have successfully cloned the H2A-H2B and H3.1-H4 histone proteins into pDUET and pACYC vectors respectively. Protein over-expression and purification studies have been performed in BL21DE3 cell lines. The oligomeric state of the complexes have been identified.

Conclusion and Future Directions: Previously, histones were cloned and expressed individually. The expressed histones were recovered from the inclusion bodies using denaturation method. Then further nucleosomal assembly was obtained by dialysing out the denaturant. Our results indicate that a co-expression system can be successfully employed to overexpress and purify the histone partners. In this method, the denaturation step has been eliminated. After successful reconstitution of the nucleosome, its interaction of DSB repair proteins will be analyzed using pull down studies. Structural analysis will be performed using high resolution X-ray crystallography.

3 Finding the magnetoreceptor: Cryptochrome in the zebrafish retina.

Spencer D. Balay and W. Ted Allison

Many organisms use the earth's magnetic field as a navigational cue. Although an ever-growing amount of behavioral evidence exists, the underlying proximate mechanisms of magnetoreception remain unknown. Cryptochrome (Cry), an ancient, light-sensitive protein is a likely molecular candidate. Cry appears to be associated with the visual system as it is co-localized with both short and long wavelength retinal cone photoreceptors in birds. Due to the molecular inaccessibility of the favoured avian model, Cry's association with cones and ultimately magnetoreception has seldom been tested. This project used zebrafish (*Danio rerio*) to test if cry was associated with cones in the fish retina. Zebrafish have six paralogs of cry. While most participate in circadian clock, two genes (cry2 and cry4) appear functionally divergent. We hypothesized that non-circadian cry would be expressed in short wavelength cones. Using fluorescent in situ hybridization we found that cry4 is expressed in larval and adult zebrafish UV cones. Using pharmacogenetic cell ablation and qRT-PCR, we found that cry4 expression dramatically decreased when UV cones were ablated but was unaffected when neighboring blue cones were ablated. This study serves as the first evidence that cry4 is co-localized in fish UV cones and suggests it may play a potential role in magnetoreception Although zebrafish are non-migratory, this system can be used to model magnetoreception in other animals. Migratory salmonids regenerate UV cones as they prepare to migrate back to their natal streams for spawning. Currently, the functional significance of this regeneration remains unknown. These findings could provide a novel explanation of this phenomenon, as UV cones may enable magnetoreception via cry expression.

4 Algal-bacterial interactions simplify lipid extraction for biofuel production through novel extra-cellular lipid bodies

Catherine Bannon, Leen Labeeuw, and Rebecca Case

In nature, bacteria and algae continuously exchange nutrients, vitamins and small bioactive molecules that mediate their interactions and structure marine communities. Consequently, there has been an increase of scientific research focused on interactions in polymicrobial microalgal cultures that promote growth, relieve energy intensive harvesting and potential to stimulate the accumulation of valuable bio-products, such as algal lipids. Neutral lipids in green algae are represented largely by triacylglycerol that are the fundamental molecule for algal biofuel production as well as being of commercial interest for high value speciality oils. We investigated the effect of growth and neutral lipid accumulation during the co-cultivation of green microalgae, *Dunaliella tertiolecta*, with several strains of bacteria. A bacterium was identified to increase the amount of neutral lipid per biomass during co-cultivation, with no effect on growth rate, compared to *D. tertiolecta* grown alone. Mono and co-culture were then monitored for photosynthetic health and growth using pulse-amplitude modulation fluorometry as well neutral lipid content quantified with Nile Red fluorescent dye. We showed that lipid bodies were present in the co-culture during late stationary phase using ImageStream®X Mark II Imaging Flow Cytometer and fluorescence microscopy. This novel physiological response will be advantageous to algal biotechnology as this bacterium could increase lipid production and simplify harvesting and extraction from microalgae during biofuel production.

5 Terrestrial habitat selection by adult female polar bears in western Hudson Bay.

Alex Beatty, Andrew Derocher, and Nick Lunn

The Western Hudson Bay polar bear (*Ursus maritimus*) population spends ice-free summer months on land. While onshore, their movements are low as an energy conservation strategy. As freeze-up progresses, bears migrate from land back on to newly forming sea-ice. Climate change is altering sea ice phenology and resulting in polar bears being forced to spend an increasing amount of time on land. Therefore, understanding the terrestrial habitats utilized by polar bears may become increasingly important for conservation planning. Global positioning system (GPS) collars on >100 adult female bears were used to assess terrestrial habitat use during July through January, 2004-2016. Land cover classes were determined using a high resolution Terrestrial Ecosystem Map, provided by Parks Canada. Resource selection functions were used to assess terrestrial habitat selection and to predict probability of use of different habitats within Wapusk National Park, Manitoba. Preliminary results show adult female polar bears prefer riparian areas and freshwater ponds.

6 Spatiotemporal variability of stream DOC and CO_2 in the high-carbon region of the pacific coastal temperate rainforest

Anna Bishop, Suzanne Tank, Ian Giesbrecht, Maartje Korver, and Allison Oliver

Freshwater streams act as nature's chemistry lab, transporting and transforming carbon between terrestrial, marine, and atmospheric stocks. Streams in British Columbia's Pacific Coastal Temperate Rainforest (PCTR) export globally significant amounts of dissolved organic carbon (DOC) to the ocean, which impacts in-stream production and is a major energy source for coastal marine ecosystems. A proportion of in-stream carbon is also released to the atmosphere as carbon dioxide (CO_2), which has implications for the global carbon cycle and climate change. Using automated, in-situ sensors combined with field-based sampling, DOC and CO_2 are being assessed to determine spatiotemporal variation and controls in four PCTR watersheds over a two-year period. The relationship of peak discharge to peak DOC (hysteresis) and its variability over time will be analyzed according to process-based models, where potential controls will be input to multivariate statistical approaches (PCA and GLM) to test model assumptions of DOC dynamics. Using standard flux equations, CO_2 efflux will be calculated at various locations within each watershed to assess the influence of local conditions such as turbulence and slope. Understanding freshwater carbon dynamics in this high-carbon region has critical implications for coastal marine ecology, stream ecology, and the global carbon cycle, and improves our ability to predict how these systems may be affected by environmental and climatic changes in the future.

7 Migration dynamics of polar bears (*Ursus maritimus*) in western Hudson Bay

Alyssa M. Bohart, Nicholas J. Lunn, and Andrew E. Derocher

Migration cycles of animals are often predictable with seasonal changes as they depend on ephemeral resources such as food. Polar bears (*Ursus maritimus*) migrate onto sea ice as it forms because they depend on ice to access prey. This seasonal feeding is required for survival during the onshore fasting period when ice is absent and prey are unavailable. Climate change is altering the sea ice phenology within Hudson Bay, with break-up occurring earlier and freeze-up later, decreasing the overall ice period. Because polar bears do not migrate gregariously, compared to other migratory species, it is expected that there is great variation between individual migration patterns. The objective of my research is to determine if bears demonstrate different migration patterns influenced by biological and environmental variables and if these patterns have changed with altered ice conditions, as no studies have examined these aspects of movement in a migration context. I will use locational data from satellite-linked collars deployed on adult female polar bears in western Hudson Bay between 2004-2017 to determine movement covariates and temporal variation in migration patterns. To determine the effects of biological and environmental covariates on migration patterns, I will use Markov chain Monte Carlo generalized linear mixed models.

8 Coping with change: Regulation of a stress-responsive cyanobacterial RNA helicase

Logan A. Brand and George W. Owttrim

RNA helicases are proteins involved at all stages of RNA metabolism via interaction with, and modification of, RNA secondary structures and ribonucleoproteins. As may be expected by their ubiquitous role in gene expression, their own expression is often altered in order for cells to respond to changing environmental conditions. This is exemplified in the freshwater cyanobacterium *Synechocystis* sp. PCC 6803, which possesses a single DEAD-box RNA helicase, crhR. While many RNA helicases are upregulated in response to a particular environmental stress, crhR responds to a variety of stresses including cold, heavy metals, and osmotic stress. The accumulation of CrhR in response to stress has been well characterized, yet little is known about how its cis-regulatory elements alter its transcription and translation in response to these stimuli.
Deep sequencing suggests that crhR is primarily transcribed as the second ORF within a dicistronic operon. As such, the promoter and 5' UTR of this operon are of specific interest. To this end, the 5' UTR of the operon was inserted downstream of a constitutive promoter in order to separate the potential regulatory effects of the operonic promoter from any mechanism specific to the 5' UTR secondary structure. Under cold stress, this region was found to alter expression in a manner similar to that of a known cyanobacterial RNA thermometer: an RNA regulatory mechanism which controls expression due to temperature-dependent alterations to secondary structures in RNA during transcription. Identifying and characterizing DNA- and RNA-based mechanisms which regulate gene expression in response to environmental changes not only improves our understanding of these natural genetic networks, but may also be utilized in bioremediation and the biotechnological production of biofuels and pharmaceuticals.

9 A Bite While They Breathe: Parasitic Effects on Host Respiration

Taylor Brophy

Parasites by their nature cause damage to their hosts, which can induce perturbations in basal physiological functions such as metabolism and respiration. Host metabolism can vary greatly depending upon a large number of parasitic factors including parasite density. While an extensive amount of research has examined respiration in insects, only a small subset have examined the impact of parasites on their host's respiration and metabolism. Herein we hypothesized that the respiratory rate of *Drosophila nigrospiracula* was dependent upon infection and density of attachment by *Macrocheles subbadius*, a facultative parasitic mesostigmatid mite. We predicted that increasing density of parasite attachment would increase host metabolic rate, and that an individual's metabolic rate would increase after infection by and exposure to mites. We used manipulative laboratory experiments and flow-through respirometry in order to: (1) measure an individual host's CO2 production before and after parasite exposure and infection; and (2) produce a range of infection intensities to determine the relationship between parasite density and host respiration. Our results indicate that an individual fly's respiratory rate increased after mite attachment, but long-term mite exposure did not significantly change their respiratory rate. Similarly we found that higher infection intensities induced higher levels of host CO2 production. Together these data indicate that *M. subbadius* parasitism and density of attachment has major repercussions on its insect host's respiration.

10 Seasonality of mountain zooplankton communities

Thomas Brown

Zooplankton community assemblages have shown to vary throughout the growing season especially in complex, dynamic lakes at low elevations. However, lakes situated in montane and alpine regions, which have shorter growing seasons and lower diversity, may exhibit less seasonal variability. Using species turnover rate as a proxy for changes in zooplankton community composition, the aim of this study is to determine if single sampling event effectively captures seasonal variability in these regions. Four limnologically comparable lakes, two alpine and two montane, were sampled in the early, mid and late growing season of 2017 in Banff National Park. Preliminary analysis indicates that turnover rates are insignificant in alpine lakes and high in montane lakes. Additionally, it was found that most individuals in the in early and mid sampling events the alpine lakes were impossible to identify and difficult to identify in the montane sites because they had not yet reached maturity. This can be attributed to the shorter growing season in these regions. In conclusion, it is suggested that single sampling events done in the late growing season of alpine regions sufficiently capture seasonal variability of zooplankton whereas montane regions will require more then one sampling event

11 Investigating TRIM27.1 and TRIM27-L innate immune pathway modulation

Lee K. Campbell and Katharine E. Magor

Ducks are the natural host and reservoir of avian influenza virus and show remarkable resistance to morbidity and mortality of viral infection when compared to other species such as humans or chickens. I am studying tripartite motif (TRIM) proteins in ducks as these proteins have been shown to play important roles in species specific antiviral defenses through either direct antiviral recognition or innate immune pathway modulation. Here I investigate the antiviral roles of TRIM27.1 and TRIM27-L, two TRIM proteins found on the avian MHC B locus. TRIM27-L is found only in ducks, while TRIM27.1 is found in both ducks and chickens. Both proteins are upregulated in response to influenza infection. TRIM27-L was found to highly upregulate type I interferons downstream of the RIG-I pathway while TRIM27.1 slightly downregulates it. Confocal analysis of TRIM27 proteins overexpressed in DF-1 chicken fibroblasts showed that each protein altered mitochondrial dynamics in different ways. TRIM27.1 forms round sac-like structures surrounding hyperfused mitochondria while TRIM27-L aggregates with mitochondria. In the future I will perform mass spectrometry analysis on TRIM27.1 and TRIM27-L to determine which components of innate immune signaling pathways they are interacting with. I will also use an inducible expression system to create stable cell lines expressing these proteins to determine if either can directly restrict viral replication. By investigating this family of proteins, we can gain a better understanding of which innate immune pathway modulations help protect the duck from the detrimental effects of influenza virus infection.

12 Transcriptomics of Heteroarthrocarpic Fruits from *Erucaria erucarioides* and *Cakile lanceolata* Suggests Proximal Conservation of Valve Margin Pathway

Shane Carey, Kerrin Mendler and Jocelyn Hall

Understanding how genetic pathways are recruited and altered to diversify fruit structures elucidates the ecological importance of those structures. Insight into the genetics of fruit diversity directly impacts our understanding of plant fitness, because fruits are the vehicles for seed dispersal and their morphology determines how offspring are distributed to the environment. The Brassiceae is an ideal tribe to study complex fruit morphology, because it is home to a unique fruit type known as heteroarthrocarpy. This complex fruit type is defined by variable dehiscence in the proximal region of the fruit and indehiscence in the distal region. Additionally, heteroarthrocarpic fruits are bisected laterally by a variably abscising joint, further facilitating two dispersal types in one fruit. The joint is the novel and unifying feature of heteroarthrocarpy, because it is present in all subtypes. One way of understanding heteroarthrocarpy and the joint is through comparative gene expression between different subtypes considering what is known about the valve margin pathway in *Arabidopsis*. This has been accomplished through transcriptomics in *Erucaria erucarioides* and *Cakile lanceolata*, two well studied representatives for heteroarthrocarpy. It was shown that the distal segments of both species share similar expression profiles, as was expected due to their lack of distal valve tissue. Correspondingly, the proximal segments from both species have distinct expression from their distal segments and from each other, as was expected due to variable proximal dehiscence. Most interestingly, joint abscission in *C. lanceolata* is likely due to a co-option of a portion of the valve margin pathway, as is shown with upregulation of INDEHISCENCE and SPATULA , two key downstream genes of this pathway.

13 Myosin proteostasis in zebrafish muscle mutants.

Casey Carlisle, Kendal Prill, and David Pilgrim

The precise organization and alignment, and turnover of muscle proteins into its smallest functional unit, the sarcomere, is essential for muscle function. In skeletal muscle, failures in this process can lead to a variety of incurable muscle diseases (myopathies), many of which are fatal. A limiting factor in developing cures for myopathies lies in our lack of understanding of how sarcomere assembly and maintenance occurs normally. Zebrafish make an excellent model system to study muscle development due to their ability to survive with myopathies that are fatal in other organisms, and many zebrafish with muscle mutations are available for study. One such mutant, herzschlag, shows disorganized muscle myosin due to a mutation in the protein Titin a. However, unlike our other zebrafish muscle mutants, the early stages of muscle assembly in herzschlag appears normal, and myosin disorganization appears after sarcomere assembly. We hypothesize that the Titin a mutation interrupts a sarcomere bracing function of titin, and the disorganized myosin in herzschlag is a result of contraction induced damage. Supporting this hypothesis, chemically paralyzed herzschlag mutants devoid of skeletal muscle contractions show reduced sarcomere damage. Furthermore, we propose that the herzschlag mutation exacerbates muscle atrophy primarily in slow twitch muscle, which is supported by transmission electron microscopy. By screening though various protein quality control factors, we aim to uncover the mechanism controlling this selective protein turnover, and highlight potential targets for myopathy therapies.

14 Shedding light on hydraulic fracturing fluid toxicity: the effects of flowback and produced water on phototactic behaviour in *Daphnia magna*.

P. Delompré, C. Glover, T. Blewett, and G. Goss

Hydraulic fracturing (HF) allows the improved extraction of gas or oil from the deep sedimentary deposits. To release hydrocarbons, a solution of chemicals and proppants is injected into the wells at high pressure to fracture the rocks. The fluid brought back to the surface after the extraction (termed Flowback and Produced Water; FPW) is a highly saline solution containing both petrogenic and anthropogenic organic and inorganic constituents. Recent research has studied FPW lethality and demonstrated its sub-lethal impact on the aquatic biota at biochemical and physiological levels. For instance, acute toxicity studies elucidated a 48h-LC50 of 0.75% and 0.19% of total FPW, respectively for adult and neonate Daphnia magna, a key toxicity model species. The goal of this research was to examine the sublethal behavioural effects of FPW on *Daphnia*. We found that FPW induced changes in the positive phototactic response of *D. magna* and the effects on behaviour were dependent on dose and length of exposure. A strong dose-dependence effect was observed in the presence of FPW in naively-exposed organisms with an increase of the organisms' speed in response to light. On the contrary, positive phototaxis was inhibited after both acute and chronic pre-exposure to FPW. This is the first study to investigate the impact of FPW on the behaviour of *D. magna*.

15 The role of Cecr2 in eye and bone development

Renee Dicipulo, Kacie Norton, and Heather McDermid

Chromatin remodellers have significant impacts on gene expression through modification of chromatin architecture and accessibility to transcription factors. Cecr2 acts in a chromatin remodeling complex, and is known to have impacts on brain development, as mutants show the lethal neural tube defect exencephaly. In the Cecr2 exon 4 mutation, where exon 4 is deleted in the C57Bl/6 genetic background, I have shown that mice have eye defects (coloboma and micropthalmia), and polydactyly (extra digits) on both front and hind paws. This implies that loss of Cecr2 produces a syndrome with defects in multiple tissues. I have also examined a Cecr2 deletion mutation in a Balb/c genetic background, where the promotor and first exon of Cecr2 was deleted. Only the novel phenotype polydactyly was present. My research asks whether the mutation, background, or both are responsible for variation in the defects. Therefore, I am studying four lines, two mutations on two backgrounds. Preliminary studies have shown that the exon 4 mutation on the Balb/c background has polydactyly. However, the deletion mutation on C57Bl/6 background has polydactyly as well as coloboma and micropthalmia, suggesting genetic background is the cause. Observation of coloboma suggests a link to Cat Eye Syndrome (CES), a human genetic disorder characterized by duplication of a region of chromosome 22 that contains CECR2. CES is highly variable, and coloboma is seen in half of affected individuals. Although CES is caused by a duplication, rare incidences occur where microduplications and microdeletions of the same region have overlapping phenotypes. Therefore, we are sequencing CECR2 for deleterious mutations in patients with CES-like symptoms but without a the duplication. I seek to understand the role of CECR2 in development and the critical role of genetic background, as well as provide a possible explanation for the phenotypes seen in CES.

16 Development of a Methanotroph Chassis: Genetic engineering of Methylomicrobium album BG8 for production of value-added products

Shibashis Das, Marc Waddingham, Dominic Sauvageau, and Lisa Y. Stein

Methylomicrobium album BG8 is a methanotrophic bacteria notable for a rapid growth rate utilizing single carbon (C1) compounds, i.e. methane and methanol. This trait, along with its rich genetic potential, makes the strain a candidate for the development of an industrial biological chassis for the conversion of C1 compounds into value-added products such as biojet fuel and biopolymers. This requires the development of new functional genetic tools to enable a larger library of value-added products from *M. album* BG8. This will allow the manipulation of the organism into a suitable platform that efficiently directs carbon flow into products and away from storage or oxidative fates. Products of interest include isoprene, a valuable platform chemical and precursor to many advanced biofuels. Here, we describe a plasmid-based expression system and a marker free deletion system developed to transform BG8 and achieve increased levels of isoprene production. Experiments are also described to determine optimal conditions for expression of isoprene pathway genes already present in *M. album* BG8

17 Sponge (Porifera) Biodiversity in the Eastern Canadian Arctic

Curtis Dinn, Xinyue Zhang, and Sally P. Leys

Benthic habitats in Canada have been well-sampled since the annual groundfish survey commenced in 1970. However, trawl surveys only cover non-rocky sediments and many species collected are not identified to lower taxa, leaving large gaps in our understanding of benthic biodiversity. Sponges are a prime example. These ecologically important filter-feeding animals preferentially attach to hard substrates; therefore, trawls do not sample the most sponge rich habitats. Further, the identification of sponge species requires extensive comparative taxonomy that cannot be performed in the field. While almost 9000 sponge species are known globally, relatively few are described in the Eastern Canadian Arctic, which is an area opening to increased human activity and potential exploitation. As part of the ArcticNet HiBio (Hidden biodiversity and vulnerability of hard-bottom environments in the Canadian Arctic) project, sites along the eastern Canadian shelf were studied using remotely operated vehicle (ROV), box core, and Agassiz trawl from the CCGS Amundsen. Skeleton morphology and DNA barcoding were used to develop a new view of sponge community structure and habitat types in the Eastern Canadian Arctic and Subarctic. Through these identifications, 61 distinct sponge species have been identified from the Eastern Canadian Shelf, one of which could potentially be a new species. Only 8 of the identified species were previously recorded from the region. These findings have been compiled into a guide of sponges living in the region to be used in future biodiversity studies in Eastern Canada. From limited sampling over a wide geographic area using a targeted approach, it is clear that there is a hidden biodiversity of benthic organisms to be discovered in Canada.

18 Exploring the Evolutionary Origins of Vertebrate Vision in the Degenerating Eye of Pacific Hagfish

Emily Dong and W. Ted Allison

"The eye is a precise and complex organ which has remained remarkably conserved despite changes in morphology as vertebrate lineages adapted to diverging life histories. The same distinguishing eye characteristics found in humans are also found in zebrafish and lamprey, implying that our eye (as it first arose) has remained nearly unchanged since at least the time that lamprey diverged, nearly 500 million years ago. Though development and structure have been well defined across vertebrates, our understanding of how the eye evolved remains poorly understood. Pacific hagfish (*Eptatretus stoutii*) are in the unique position of straddling the boundary between eyed vertebrates and non-eyed chordates. Likewise, their eyes are difficult to categorize as they lack many of the diagnostic features shared by vertebrates including a lens, ocular musculature, and a 3-layered retina. These relatively simple features lead us to question, is the hagfish eye representative of a transitional species in the evolution of vertebrate eyes, or is it degenerate?
We hypothesize that the lack of observable vertebrate-like organization in the adult hagfish retina may be due to a degeneration or re-distribution of retinal cell types during maturation and growth. Preliminary evidence suggests that juvenile hagfish show layering of the retina that more closely resembles that of vertebrates in comparison with adults. Using RNAseq, protein and gene expression assays, this project aims to further explore retinal cell-types and their organization within the hagfish retina in order to better interpret their morphology in the greater context of vertebrate eye evolution. We will capture any characters that aid us in revealing the hagfish eye as degenerate or ancestral, allowing us to place the hagfish in the context of the evolution of the vertebrate eye."

19 Comparative methodology of Canada lynx density estimation

Darcy Doran-Myers

Reliable population density estimates are critical for ecological research and species management but can be difficult to obtain. Recent technological and statistical advances have made estimating density easier for researchers, less invasive for the study species, and has allowed for improved estimates for a variety of data types. Canada lynx are a species of ecological, economic, and intrinsic interest, but studies seeking density estimates are few and have been slow to adopt advances. Non-invasive sampling methods, including genetic sampling and remote camera traps, have potential to improve density estimates of lynx and to increase the efficiency, effectiveness, and precision of estimates. I applied and compared methods for estimating lynx density over two years in southwestern Yukon Territory. I collected data on lynx using hair snares, camera trapping, and snow tracking, then applied and compared statistical analyses across the data types. Comparisons across methods are essential to improve investigations of lynx density. More reliable density estimates resulting from this work can be used in studies investigating numerical responses of lynx to fluctuating prey densities and to provide fundamental data for wildlife management decisions. Results also have clear applications to research, management, and conservation for functionally similar wildlife species.

20 Is non-nervous behavior in sponges modulated by amino acids and nitric oxide?

Zach Dumar and Sally Leys

All animals coordinate their cells to respond to environmental stimuli. Rapid responses are performed by the nervous and neuroendocrine systems. Sponges lack nerves, and so coordinate behavior in other ways. The demosponge *Ephydatia muelleri* expands and contracts its canals to get rid of irritants that may clog its filters; this behavior has been likened to a sneeze. It is hypothesized that small molecules are involved in the spread of the response throughout the body of the sponge. A previous study found that glutamate application triggers the sneeze behavior, but it is expected that other molecules are involved in transmission of the signal along tissues. Analysis of the amino acids in *E. muelleri* showed high concentrations of glutamate, and of several different D-amino acids, including D-serine and D-aspartate. In other organisms D-amino acids are used in both neurotransmission and reproductive functions. In another sponge nitric oxide (NO) was shown to modulate contractions. NO is an ancient widely used gaseous signaling molecule used in a variety of processes including vasodilation and establishment of circadian rhythms. NO synthase appears to be present in *E muelleri*, but whether it is involved in coordinating contractions remains unstudied. Sponges treated with D-aspartate and its isomer L-aspartate do sneeze, suggesting that these amino acids may act as triggers of the sneeze response. The sneezes triggered by these amino acids match those triggered by glutamate in both the time required to trigger the sneeze and the extent to which the diameter of the sponge canal changed. This study will provide insights into the signaling toolkits used by modern day sponges to avoid filter clogging, as well as some insights into the possible types of signaling used by the earliest animals.

21 Characterizing the Role of Cecr2 in Male and Female Mouse Subfertility

Kevin Duong

Chromatin remodelers modify the ability of transcription factors to access chromatin. Thus, as a chromatin remodeler, Cecr2 may influence transcription regulation and impact gene expression. Exencephaly, a lethal neural tube defect, is a phenotype of Cecr2 mutants. However, not all mice exhibit exencephaly. Instead, certain mice are affected based on their genotype. The unaffected mice often exhibit other defects, including subfertility. As a result, we compare Cecr2GT/Del mice, that do not exhibit exencephaly yet exhibit subfertility, with Cecr2 wild-type (Cecr2+/+) mice.

In Cecr2GT/Del males, subfertility defects start at 24 days-post-coitum (dpc) and peak at sexual maturity (42 dpc), through abnormal spermatogenesis. However, at 100+ dpc, testis defects are less severe and litter sizes are larger. I am currently analyzing genes obtained from an RNA-seq using 24 dpc Cecr2GT/Del and Cecr2+/+ male testis, which indicates genes differentially expressed between the samples. From the list, 53 genes were located on the X chromosome and all were upregulated in Cecr2GT/Del males. As a result, I am studying Hormad2 and Scml2, genes involved in meiotic sex chromosome inactivation (MSCI), a process that silences the X and Y chromosomes during meiosis.

Subfertility in Cecr2GT/Del females is well-documented. When crossed to wildtype males, Cecr2GT/Del females give birth to half as many pups, take twice as long between litters and display fewer uterine implantations compared to Cecr2+/+ females. However, no differences in fertilization rate has been observed between Cecr2+/+ and Cecr2GT/Del females. Currently, we are searching for uterine implantation abnormalities through artificial decidualization. This procedure involves injecting sesame oil into a mouse's uterine horn at 4 days after mating with a vasectomized male to stimulate decidualization of the pseudo-pregnant uterine lining. Blinded samples could not be distinguished upon morphology, thus if a difference exists, it is subtle. This investigation continues to further our understanding of Cecr2's role in development and fertility in male and female mice.

22 Evolutionary Ecology of Parasitism

Emily Durkin

Parasitic strategies are ubiquitous in nature and parasites make up a substantial proportion of biodiversity. Although parasites evolved from free-living ancestors, empirical evidence for how and why parasitism evolved is limited. Commonly proposed hypotheses posit that intermediate strategies, such as phoresy and facultative parasitism, served as stepping-stones towards the evolution of more obligate strategies. The fitness benefits gained from those intermediate associations allowed some symbioses to evolve towards more obligate relationships by means of natural selection. First, to support the hypothesis for facultative parasitism as a stepping-stone towards obligate parasitism, we used artificial selection to calculate the additive genetic variation in the infectious behaviour of the facultatively parasitic mite *Macrocheles muscaedomesticae*. Mites responded positively to selection for increased infectivity; realized heritability of infectious behaviour was significantly different from zero and estimated to be 16.6% (±4.4% SE). We then investigated why *M. muscaedomesticae* exhibit a facultative association despite their potential to evolve more parasitic associations. We hypothesized that evolutionary trade-offs associated with increased infectivity constrain the evolution of more obligate associations. After comparing the longevity, fecundity and infection plasticity of infectious and control mites, we found no support for the presence of evolutionary trade-offs. We propose that facultative parasitism is maintained in *M. muscaedomesticae* by the constantly variable and unpredictable nature of their habitats or perhaps through the utilization of a bet-hedging strategy. Our study is the first to provide an estimate of additive genetic variation for infectious behaviour in a facultative parasite and provides insight into their life history, with important implications for the evolution of parasitism.

23 Heart, Kidney and Palate Defects in Cecr2 Mutant Mice

Sabrina Fox, Kacie Norton, and Heather McDermid

Cat Eye Syndrome (CES) is a rare genetic condition characterized by coloboma (a gap in the iris of the eye), polydactyly (multiple digits), kidney defects, cleft palate, and heart defects. CES is most commonly caused by a duplication of a critical region on chromosome 22. Cecr2, a gene encoding an ATP-dependent chromatin remodeler, maps to this critical region. Mice homozygous for a loss-of-function allele of Cecr2 display exencephaly, an inability of the neural tube to close during development, resulting in a lethal brain defect. Mutants that show full neural tube closure have fertility defects. Neither of these phenotypes have been connected to CES.
Recently, a new mutation, Cecr2Ex4, was isolated in both the Balb/c and C57Bl/6 mouse strains. Cecrc2Ex4 mutant mice develop exencephaly with ~86% penetrance in the C57Bl/6 genetic background and almost 100% penetrance in the Balb/c genetic background. In addition to exencephaly, the novel phenotypes of iris coloboma and polydactyly were also detected in C57Bl/6 Cecr2Ex4 mice. Since both phenotypes are characteristic of CES and Cecr2 is in the CES critical region, it is reasonable to predict that the Cecr2Ex4 mutation may give insight into the development and progression of CES. By analyzing other structures that are commonly malformed in patients with CES including hearts, kidney, and palates, we wish to determine whether CES features are commonly seen in our Cecr2Ex4 mice. Additionally, DNA samples have been collected from human patients that show CES-like symptoms but do not contain a microduplication or microdeletion. By sequencing the exons of the Cecr2 gene, detrimental variants that may be responsible for the CES-like symptoms in these patients will be found. This, taken together, could facilitate our understanding of how CES causes specific deformities and symptoms.

24 Species-specific Glass Sponge Behavioural Responses to Suspended Sediments is seen in Four Glass Sponges

Nathan Grant and Sally Leys

Glass sponges form unusual deep-water reefs in Hecate Strait and Queen Charlotte Sound, Canada. In February 2017, they were established as a Marine Protected Area (MPA). This MPA is buffered by an adaptive management zone closed to bottom trawl fisheries established on the precautionary principal that sediments resuspended by trawls may affect sponge feeding. In May 2017, in situ experiments in Hecate Strait assessed whether increased suspended sediment concentrations (SSCs) cause glass sponge species to arrest filtration. The data show that not all reef sponge species respond equally to sediment and threshold SSCs that triggers arrests vary among species. Filtration activity was negatively correlated with increased SSC ($r = -0.84$, $p < 0.01$) in two species whose pumping arrests were triggered at SSC thresholds of 4 - 10 mg l-1, well below those generated by trawling. Another species did not arrest filtration in response to elevated SSC. In these experiments, SSCs were 10-fold higher (50 mg l-1) than natural Hecate Strait SSCs, 2-3 mg l-1, but still below bottom trawling levels (20-550 mg l-1). Understanding the range and extent of responses to disturbance seen in glass sponges will help guide future management decisions regarding the Hecate Strait MPA.

25 Ectosymbionts of Pigeons in North America, did they miss the boat?

Alexandra Grossi and Heather Proctor

Rock Pigeons (*Columba livia*) were introduced to North America in the 1600s and are now found in almost all urban centres. In addition to birds themselves being introduced, their ectosymbionts were also introduced. The ectosymbionts associated with pigeons are chewing lice (Insecta: Phthiraptera: Menoponidae and Philopteridae) and feather mites (Acariformes: Astigmata: Analgoidea and Pterolichoidea), both of which are permanent symbionts and therefore complete their entire life on their host. In order for a ectosymbiont to be present in a location its host must be there, but the presence of a host does not guarantee the presence of the ectosymbiont. To investigate if the presence and intensity of ectosymbionts infesting pigeons changes based on location, pigeons from across Canada were collected and their ectosymbionts were examined. Ectosymbiont assemblages varied greatly in both species present and intensity of individuals based on location, with locations on east and west coasts having a species of feather mite, *Pterophagus columbae* that did not occur elsewhere and had higher intensities of ectosymbionts. Warmer and more humid coastal climates may have allowed persistence of this species, or its presents may be from independent introductions of pigeons and their ectosymbionts in these areas.

26 Environmental factors driving avian community assemblages in Alberta's boreal wetlands

Elene Haave Audet, Julia Shonfield, Daniel Yip, and Erin Bayne

The boreal forest represents critical breeding habitat for many migratory birds, and much of Alberta's north plays host to this diverse array of species. Further, Alberta's boreal region is characterized by highly heterogeneous habitats, encompassing a range of environments, from treed upland areas to lowland wet habitats. Within these wetland regions, there exists further heterogeneity. However, there is little information describing which environmental factors may be important drivers of avian species assemblages in boreal wetlands. A lack of understanding of the factors that may be critical to supporting species diversity prevents wildlife managers from making informed decisions regarding which habitat types and environmental characteristics to prioritize for conservation. My study attempts to fill this knowledge gap by providing a quantitative measure of the relationship between avian species assemblages and environmental factors characterizing boreal wetlands. I have used acoustic recordings of bird vocalizations collected using autonomous recording units (ARU), deployed in Alberta's Lower Athabasca region over four years. I targeted sampling sites that were stationed in areas that were characterized by at least 50% wetland land cover area within a 300 m radius of the ARU, as determined using a Geographic Information System (GIS). Overall, 240 stations were used for analysis, located in bog, fen, marsh, and swamp wetland types. The resulting recording data were processed by trained listeners to identify any birds, of which a total of 131 species were detected. To study patterns of community assemblages, I conducted Canonical Correspondence Analysis (CCA) to partition the variation explained by the differences in environmental covariates between wetland types, including water flow, nutrient content, moisture level, and vegetation type. Preliminary analyses suggest that bogs and fens are characterized by different avian communities, providing support for the need to maintain habitat heterogeneity in the boreal region.

27 Exposure to parasites reduces host fitness independent of infection in a *Drosophila-Macrocheles* system

Collin J. Horn and Lien T. Luong

Parasites are known to have direct negative effects on host fitness; however, the indirect effects of parasitism on host fitness sans infection are less well understood. Hosts undergo behavioural and physiological changes when exposed to parasites. Yet, there is a lack of experimental evidence showing that these changes lead to long-term decreases in host fitness. Our aim is to test if parasite exposure affects host fitness outside of infection, because current approaches to parasite ecology may underestimate the effect of parasites on host populations. We assayed the longevity and reproductive output of *Drosophila nigrospiracula* exposed or not exposed to a natural parasite, *Macrocheles subbadius*. To ensure infection did not occur, mites and flies were permanently separated with a mesh wall. We found that exposed flies had shorter lives, and produced fewer offspring compared to unexposed flies. As far as we know, no prior research has shown a decrease in host fitness due simply from exposure to parasites. Our findings mirror the non-consumptive effects observed in predator-prey systems, in which prey species suffer reduced fitness even if they are not predated upon. We show that there are analogous effects in parasite-host systems, and suggest new directions for research in parasite-host relationships.

28 Investigating unc119 genes in zebrafish for retinal disease phenotypes affecting photoreceptors

Francesca Jean and Dave Pilgrim

In humans, two different mutations in the gene UNC119A cause cone-rod dystrophy – a disease characterized by progressive photoreceptor degeneration, eventually resulting in blindness. The cellular defect underlying the retinal degeneration in these individuals is not understood, although several possibilities are plausible, based on work on the gene product in cell culture. A tractable model, where eye development can be followed at cellular resolution in an animal that can be genetically manipulated, will be necessary to test these hypotheses, and the zebrafish is ideal. Zebrafish have two copies of the human UNC119A gene (known as unc119a and unc119b). Both of the paralogues are transcribed in the photoreceptor layer, consistent with a role in photoreceptor function. I have generated loss-of-function mutations in both of these genes using CRISPR-Cas9 technology; neither single- or double-mutants show gross morphological phenotypes. However, I am examining whether there are any degenerative effects caused by loss-of-function of these genes at 4.5 days post fertilization, 1 month, and 6 months of age using an antibody specific to photoreceptors. Additionally, I am also studying photoreceptor cell ultrastructure to determine whether single- and double-mutants have any cellular phenotypes that may explain why retinal degeneration occurs in the human patients.

29 The smell of success: evaluating pheromone monitoring tools for wheat midge in the Peace River region

Amanda Jorgensen, Jennifer Otani, and Maya L. Evenden

The orange wheat blossom midge, *Sitodiplosis mosellana* Géhin (Diptera: Cecidomyiidae) is an invasive pest on wheat (Triticum spp.) in Canada. The objective of this research is to assess monitoring tools for wheat midge in the most northern part of its expanded range in the Peace River region of Alberta. Season-long flight activity was monitored with pheromone-baited traps. We compared trap capture of male midge in green and orange delta traps baited with pheromone released from flex lures (Scotts™), or rubber septa lures (Scotts™ or Great Lakes IPM™) to that in unbaited control traps. Traps were monitored weekly during wheat midge flight. In 2016, significantly more wheat midge were captured in pheromone-baited traps compared to unbaited traps, but there was no difference in the number of midge attracted by the different lures tested. Seasonal activity peaks varied by four weeks among sites. The results from this study will help us understand wheat midge flight activity and develop monitoring tools for this pest within its relatively 'new' northern distribution.

30 Different classes of PI3K regulate Basal and Ghrelin-stimulated LH and GH release in *Carassius auratus*.

George Kinley, Federico Sacchi, and John Chang

Growth hormone (GH) and Luteinizing hormone (LH) are central regulators of growth and reproduction in vertebrates. LH and GH are constitutively released at a basal level from pituitary gonadotroph and somatotroph cell types respectively. LH and GH release is also regulated by a variety of factors, including the orexigenic gastric peptide Ghrelin (GRLN), which potentially links energy homeostasis to growth and reproduction. Previous work suggests phosphoinositide 3-kinases (PI3Ks) are involved in basal and/or GRLN-stimulated LH and GH release, but isoform-specific functions are unknown. In the present study we investigated the involvement of multiple PI3K isoforms in basal and GRLN-stimulated LH and GH release using selective PI3K inhibitors in perifusion studies. We demonstrate that class I PI3Ks are necessary for GRLN-stimulated LH and GH release, and that class II/III PI3K isoforms negatively regulate basal LH and GH release. This implicates the enigmatic class II/III PI3K isoforms in LH and GH release for the first time. This research provides insight into the function of lesser studied PI3Ks as well as conditions involving GRLN and LH/GH dysregulation such as anorexia nervosa, Prader-Willi syndrome, obesity, and type 2 diabetes.

31 Going against the flow: sea ice drift and polar bear population decline in western Hudson Bay

Natasha J. Klappstein, Ron R. Togunov, Nicholas J. Lunn, and Andrew E. Derocher

Animals in dynamic habitats face unique energetic challenges, as movement with or against the environment may be necessary and therefore the velocity of the medium affects the energy expenditure of individuals. Sea ice is highly motile and drift speeds in much of the Arctic have been increasing due to climate change, which presents new challenges for pagophillic specialists that rely on the ice. Polar bears have been shown to move counter to ice drift in high Arctic seas, and in recent years, the increasing drift rates have been linked to increased energetic demands. However, this has not been evaluated in an landlocked, low-latitude, seasonal system; our study is the first to do so in the Hudson Bay. We examined spatial and temporal ice drift patterns, and compared these to polar bear movement. We found a significant negative long-term trend in ice drift in Hudson Bay, however, low predictive power of the models indicates this may be of little ecological importance. Bear movement was approximately perpendicular to ice drift during freeze up, counter to ice drift in early winter, and highly dispersed in late winter and break-up. Models are currently under development to assess the variation of ice drift experienced between individuals and the direct effect of ice drift speeds on bear movement. However, in contrast to other systems, the trends in ice drift suggest that even if ice drift affects bear movement, this not be an increasing threat to western Hudson Bay bears. The causes of observed population decline are more likely associated with other factors, such as prolonged melt season and decreased foraging opportunities. This exemplifies the importance of population-specific research, as risk factors cannot always be accurately extrapolated between populations.

32 A burning question: How do woodland caribou use post-fire habitat in northeastern Alberta?

Sean Konkolics and Boutin, S.

In recent decades woodland caribou in northeastern Alberta have experienced population declines due to habitat alteration from industrial development and climate change. These declines prompted the 2012 Canadian Federal Recovery Strategy for woodland caribou, which states that areas burned by wildfire in the last 40 years are disturbed habitat. This delineation of disturbed habitat has major economic and social implications across boreal Canada. Caribou have been shown to avoid young seral stage forests in recently burned landscapes due to a decrease in lichen resources and increase in predators. Yet detailed research about the relationship between post-fire forest regeneration and caribou habitat selection in areas of high anthropogenic disturbance is lacking. Additionally, fires have been mapped using coarse polygons, with little consideration of unburned residual forest patches that commonly constitute large percentages of the burn. Using caribou radio collar GPS locations and detailed maps of wildfires from the past 40 years, generated with the Normalized Burn Ratio (NBR), we developed multi-scale selection ratios to detail the degree to which burned areas and fire skips are selected by caribou. Preliminary results suggest that caribou avoid burned landscapes at the home range scale but show selection for unburned residual patches when inside the boundaries of a fire. With the Recovery Strategy obligation to reach 65% undisturbed habitat in herd ranges and the projected increase in the severity of wildfires, understanding the relationship between caribou and burned landscapes is imperative to effectively conserving a species with limited conservation dollars.

33 Spatial mortality risk for elk in a multi-predator community

Kara MacAulay, Eric Spilker, Jodi Berg, and Evelyn Merrill

There is evidence that prey perceive the risk of predation, as they navigate a "landscape of fear" and alter their behaviour in response. Previous approaches to mapping spatial risk use predator and prey distributions to estimate potential encounters, yet this approach does not account for attack success resulting in mortality. Locations of prey kill sites represent mortality in space, but obtaining kill site data can be cost intensive and require time to accumulate adequate sample sizes. I address an alternative to these approaches for mapping predation risk based on mortality by relating features within a buffer to contents of predator scats in Ya Ha Tinda (YHT), a multi-predator community along the eastern slopes of the Rocky Mountains. Scats collected from four carnivores from summer 2013-2016 have been analyzed for presence of elk. The objectives of this study are to: (1) compare diets of large carnivores through microhistological and DNA methods, (2) determine whether % elk in scat be predicted by elk use and/or landscape features, and (3) validate risk predictions with known elk kill sites. Preliminary results suggest that cervids (elk and deer) comprise a large part of wolf, cougar and coyote diets, while vegetation dominates bear diets. Within cervids, juveniles occur more frequently in all predators except cougars. My project is part of a 16-year study investigating the role of predation in the changing migratory behaviour of the YHT elk, and will provide baseline data on predation in the Panther-Dormer region before the bison reintroduction into Banff National Park.

34 Carbon composition and microbial communities in permafrost-affected terrains

Erin MacDonald and Suzanne Tank

Increasing temperatures from climate change are enhancing permafrost thaw that can make the carbon currently "locked-up" in permafrost become available for release. Once this organic carbon is exposed, it is decomposed by microbes through biodegradation, a key mechanism that controls the release of organic carbon to the atmosphere. The rate of biodegradation is codependent on the composition of the carbon substrate and the microbial community preferences to decompose certain substrate types. Both of these factors can vary greatly between different landscapes and depths, but little is known about the link between these components in permafrost deposits in northwestern Canada. Thaw slumps are a destructive geomorphic result of permafrost thaw that transport massive amounts of material, often into nearby streams. The Peel Plateau, NT, has a high abundance of thaw slumps that are known to alter the quantity and quality of dissolved organic carbon (DOC) in streams, but no studies to date have determined if there are impacts to the microbial communities responsible for biodegradation of this released DOC. My research will first characterize the composition of DOC from permafrost cores collected along a latitudinal gradient in northwestern Canada and use this DOC in an incubation experiment to measure the rate and extent of biodegradation for different compositions of DOC. Secondly, I will investigate the effects of DOC compositional change on microbial community diversity within thaw slump-impacted streams relative to unimpacted, upstream conditions. I will use next-generation sequencing techniques to identify the Operational Taxonomic Units that make up the microbial community structure and diversity in various stream conditions. The results of my project will fill part of the knowledge gap on the link between composition of DOC and microbial communities in northwestern Canada, to better predict potential release of DOC from permafrost thaw across diverse landscapes in the Arctic.

35 The Lost Creek Wildfire: Long-term Impacts on Aquatic Ecology in Rocky Mountain Streams

A.M. Martens, U. Silins, H.C. Proctor, E. Luchkow, C.H.S. Williams, and M.J. Wagner

Wildfire is an important natural disturbance on forested landscapes influencing physical and biological processes. The 2003 Lost Creek wildfire was one of the most severe on Alberta's eastern slopes. The Southern Rockies Watershed Project (SRWP) was established to document the effects of the fire on hydrology, biogeochemistry and aquatic ecology. Eleven years of continuous monitoring in reference (unburned), burned and burned & salvage logged watersheds has shown the effects of the wildfire on water quality and biogeochemistry to be persistent.

Macroinvertebrates were sampled eight years after the wildfire to assess the long-term impacts on aquatic fauna. Invertebrates were identified to the finest practical taxonomic level and enumerated. Ordinations performed using non-metric multidimensional scaling (NMS) indicated distinct macroinvertebrate assemblages in reference, burned, and burned & salvage logged watersheds ($p < 0.01$). Burned watersheds had the greatest abundance of macroinvertebrates and were characterized by greater abundance of chironomids and caddisflies. Burned & salvage logged watersheds supported high numbers of riffle beetles and crane flies. Reference watersheds were characterized by more stonefly taxa and had the lowest abundance of macroinvertebrates. Greater invertebrate productivity in burned watersheds has been attributed to increased utilization of periphyton (instream) energy sources. Analysis of carbon isotopes was utilized to compare resource use between burned and reference watersheds. Two source mixing models using $\delta 13C$ ratios indicated increased (6 to 58% greater) utilization of instream energy sources in burned watersheds for all but one macroinvertebrate taxon. This research demonstrates that wildfire can have long lasting effects on macroinvertebrate assemblages. These effects are driven by changes in habitat quality and resource availability.

36 Analysis of altered blood metrics and erythropoietic regulator gene expression in goldfish during infection with *Trypanosoma carassii*

Mark McAllister and Miodrag Belosevic

Trypanosoma carassii is a flagellated bloodstream parasite of cyprinid fish. Pathogenesis of *T. carassii* infection manifests primarily as anemia in experimentally infected fish. The anemia is characterized by a substantial decrease in the number of circulating red blood cells (RBCs) during peak parasitemia; indicated by significant drop in the packed cell volume and total RBC counts. This anemic state induces a process known as erythropoiesis, which triggers the production of RBCs and restoration of blood homeostasis. Erythropoietin (EPO) and its associated receptor (EPOR), along with members of the GATA family, are important regulators of erythropoiesis and have been implicated in the resolution of anemia in other model systems. Related Trypanosome species have been implicated in the alteration of erythropoiesis; leading to increased morbidity and delayed recovery from infection. The role of erythropoiesis in recovery, and mechanism through which *T. carassii* induces anemia during infection remain unclear.

Our lab has previously characterized the hematopoietic pathway in goldfish, including these key regulators and how differential expression leads to expansion of critical cell populations during times of need. In this study, we describe the changes in the expression of genes predicted to be important in the resolution of the anemic state and analyze changes in hematological indices of the host during infection.

37 Identification of a Shared Receptor between Broad Host Range Bacteriophages DLP1 and DLP2

Jaclyn G. McCutcheon, Danielle L. Peters, and Jonathan J. Dennis

The emerging bacterial pathogen *Stenotrophomonas maltophilia* is rapidly increasing in prevalence in nosocomial infections. Treatment of *S. maltophilia* infections is difficult due to its innate resistance to a broad range of antibiotics. A possible alternative treatment is phage therapy, the clinical application of bacteriophages to eradicate target bacteria. Two phages previously isolated in our lab are capable of infecting across taxonomic orders, lysing strains of both *S. maltophilia* and *Pseudomonas aeruginosa*, another highly antibiotic resistant bacterial pathogen. DLP1 and DLP2 are closely related phages, however they have significantly different host ranges. To explain their unique cross-order infectivity and differences in host range, we have identified and are characterizing the primary receptor and mechanism of attachment to both host species by DLP1 and DLP2. Screening of a 2,242 member *P. aeruginosa* PA01 mutant library, a host that is susceptible to DLP1 but not DLP2, identified DLP1-resistant mutants with disruptions in pilus structural and regulatory components. Subsequent complementation of the disrupted pilin subunit genes in PA01 restored DLP1 infection, indicating that DLP1 uses the type IV pilus, a virulence factor on the surface of the bacterium, as its primary receptor for adherence. Clean deletion of the major pilin subunit, encoded by pilA, in the *S. maltophilia* strain D1585, a shared host between DLP1 and DLP2, prevented phage binding and lysis by both phages and complementation restored both DLP1 and DLP2 infection. These results suggest that both phages use the type IV pilus as the first point of contact with their hosts. Future research will mutagenize the pilA gene in D1585, and resulting changes in phage susceptibility will aid in differentiating the phage binding sites. This research will further characterize DLP1 and DLP2 as phage therapy candidates for the treatment of multidrug resistant bacteria from multiple genera.

38 Assessing the interactions between personality, population density and food availability and their influence on the reproductive success of female American red squirrels (*Tamiasciurus hudsonicus*)

Giuditta Migiani

Animal personality can be defined as the repeatable and moderately heritable differences in the behaviour of individuals. Personality is retained across various ecological contexts, unlike plasticity, defined as the ability of individuals to alter their behaviour within their lifetime to cope with changing environmental conditions.

During the past decade, the study of animal personality has been gaining increasing attention amongst ecologists, as the results of multiple studies suggest that personality can be expected to have a significant influence on the fitness of individuals and species. New analyses have revealed that the interaction between behavioural, genetic, physiological and life-history traits can lead to the coevolution and coadaptation of diverse suites of correlated traits, creating variability at the intra- and inter-population level. However, how this variability is maintained and why it is not selected against by natural selection is still subject of debate.

Environmental factors have been shown to contribute to the emergence of such suites of traits. Fluctuations in population density and food availability levels are highly likely to impact on the selection of personality, and differences in how personalities perform under various conditions may explain some of the variability discussed above.

My research will investigate the interactions between personality, food abundance and population density in a population of American red squirrels (*Tamiasciurus hudsonicus*) and the effects of these factors on the reproductive success of the females. An understanding of how personality is related to changing environmental conditions is critical for future ecological and evolutionary studies, as it would allow for more accurate predictions on population and ecosystem dynamics.

39 The salt and metal components of oil sands process affected waters (ospw) effects on metabolism and swimming ability in rainbow trout (*oncorhynchus mykiss*)

Zachary Mueller and Keith Tierney

Oil sands process affected (OSPW) is created as a by-product of bitumen extraction in Athabascan region of Alberta. Given that demand for oil is increase and OSPW has a shelf life for oil extraction, tailing ponds containing OSPW has vastly increased in the previous decade. Herein we investigate how the metals and salts similar to that found in OSPW may alter swim performance and metabolic rate in rainbow trout (*Oncorhynchus mykiss*). Three salts (Na, Ca, & Mg) and five metals (Al, Mo, Cu, Ni, & Zn) were selected and fish we exposed for 96 hr with a 48 hr static refresh. Fish were swam swim tunnel respirometer pre and post exposure. We found that metal and salts similar to OSPW decreased the repeatability of swim performance after exposure. Metals and salts at twice the concentration of OSPW decreased swim performance. Those same fish also had a decrease in maximum metabolic rate. Carbonic anhydrase and sodium/potassium ATPase activity within fish gills were significantly decreased. Prolonged exposure to metals and salts similar to OSPW may have profound effects on the activity and metabolism in rainbow trout. Although metals and salts in OSPW are not the primary driver of toxicity, they may impact fish physiology. Whether, OSPW has convergent results with the metal and salt mixture used here needs to be assessed. Futures studies should examine how exposure period and methods of OSPW impacts swim performance, osmoregulation, and metabolism in rainbow trout.

40 Changes in microbial community composition in response to permafrost thaw

Patrick Neuberger, Duane Froese, and Brian Lanoil

As northern Canada warms, permafrost thaw can lead to dramatic ecosystem changes, including the formation of thermokarst ponds. The potential for microbial degradation of organic carbon increases with thermokarst development, resulting in increased flux of the greenhouse gases CO2 and CH4. In laboratory experiments, the composition and gene expression of the permafrost microbial communities shift rapidly upon thaw, however, there have been few studies examining thaw under field conditions. To examine the effect of anthropogenically-induced permafrost thaw on living microbial communities, we examined a site where thaw was induced by stripping of the area's vegetation and one meter of surface soil in preparation for goldmining at a site near Dominion Creek, Yukon, Canada. We examined three cores to a depth of 100cm across a permafrost thaw gradient. Three subsamples were taken within active layer cores (when applicable) at depths of 15cm, 30cm, and 45cm as well as two permafrost subsamples at depths of 75cm and 90cm. An additional eight surface soil samples were collected across the same gradient from undisturbed forest active layer to disturbed soils composed of newly thawed permafrost to newly formed thermokarst pond sediments. DNA was extracted sent for targeted amplicon Illumina sequencing of the V4 region of the 16S rRNA gene for community analysis. Findings indicate that the soil physicochemical parameters do not change rapidly under field conditions following permafrost thaw. Cluster analysis of the total assemblage identified three distinct clusters within the community dataset: (1) undisturbed active layer (2) lower active layer and disturbed permafrost, and (3) intact permafrost. Diversity, evenness, and richness of disturbed permafrost all increased in relation to undisturbed permafrost. This study suggests there is a clear microbial community response to rapid permafrost thaw under field conditions.

41 Quantifying fear effects on prey demography in nature

Michael Peers

In recent years it has been argued that predator fear exacts a higher demographic toll on prey populations than the direct killing of prey, with far-reaching impacts on ecosystems. However, efforts to quantify the effects of fear have primarily relied on experiments that replace predators with predator cues. Interpretation of these experiments have two important caveats: 1) The magnitude of experimenter-induced predator cues may not realistically compare to those of the prey's natural sensory environment, and 2) without functional predators, fear effects observed may be largely compensatory with consumption in the wild if the cue applied rarely occurs naturally without resulting in prey mortality. It is our contention that demographic consequences of fear in natural populations may have been overestimated because the intensity of predator cues applied by experimenters in the majority of studies has been unnaturally high. We describe an alternative treatment design that does not utilize predator cues, and better isolates the demographic effect of fear from predator caused mortality. Rather than manipulating the type and amount of cues applied, this treatment would remove them completely, and shift to simulating the consumptive effects of predation. This simple change substitutes the traditional cue experiment where consumptive effects are eliminated and fear is simulated, for a design where fear is removed and consumptive effects are simulated through the removal of prey by the experimenter. Comparison to a natural population would isolate the effect of fear on the demographic variable of interest. This approach represents a critical advance in quantifying the mechanistic pathways through which predation structures ecological communities. Discussing the merits of both treatments will motivate researchers to go beyond simply describing the existence of fear effects and focus on testing the true magnitude of this phenomenon in wild populations and natural ecosystems.

42 Impacts of in vitro exposure to oil sands process-affected water and its fractions on mammalian immune cells.

Nicole Phillips, Li Fu, James Stafford, and Miodrag Belosevic

Any water which contacts oil sands is defined as oil sands process-affected water (OSPW) by Natural Resources Canada. Therefore, recovery of unconventional crude oil sources such as the Alberta oil sands produces large volumes of OSPW which must be stored on-site due to a zero-release policy in the Alberta Environmental Protection and Enhancement Act of 1993. Characterization of OSPW and its associated toxicity is challenged by its complex nature, as it is composed of over 400 chemical constituents. Most broadly, OSPW components can be physically separated into the organic and inorganic fractions. Naphthenic acids (NAs), phenols, and polycyclic aromatic hydrocarbons are major components of the organic fraction, while heavy metals including mercury, lead, and arsenic, as well as salts are contained within the inorganic fraction. Most research examining OSPW toxicity has focused on the organic fraction and NAs indicating them as the major toxic component and saturating OSPW research in this direction. Comparatively, little is known about the contribution of the inorganic fraction to the toxicity of OSPW. Previous research by our lab has found that at the same NA concentrations whole OSPW, and not the organic fraction, causes significant toxicity in vitro as measured by cellular viability, proliferation, and function. The focus of my research is to compare toxic effects of both fractions, and unfractionated (whole) OSPW with a focus on the influence of the inorganic fraction components to whole OSPW. This work suggests that the inorganic fraction is a major contributor to toxicity of OSPW in vitro.

43 Behavioural consistency in juvenile North American red squirrels (*Tamiasciurus hudsonicus*)

April Robin Martinig, Prashanna Pokharel, Kimberly J Mathot, and Stan Boutin

Consistent individual differences in behaviour are repeatable and consistent across time and contexts. This has important ecological implications for life history events, however, the ontogenetic explanations behind behavioural consistency remains unresolved. Here we studied behavioural consistency in juvenile North American red squirrels (*Tamiasciurus hudsonicus*) in a population near Kluane, Yukon where consistency has been successfully documented in this population post-weaning (75 days old). We aimed to determine the repeatability (proportion of behavioural variation due to among-individual differences; r2) of aggressive and active behaviour post-emergence (between 50-75 days old) in juvenile red squirrels. The average repeatability for among-individual behavioural differences across taxa has previously been documented as 0.37. We measured repeatability by subjecting each individual to two standardized behavioural assays (once post-emergence and another post-weaning). Activity and aggression scores were extracted using principal component analysis and were used as response variables in linear mixed effects models to test for the effects of factors such as sex, treatment (radio-collar or control), and natal location on behavioural score. We found that aggression had higher repeatability (r2 = 0.41, 95 % Credible Interval (CI): 0.312, 0.496) than activity (r2 = 0.159, 95 % CI: 0.106, 0.207). There was no effect of an individual's sex, natal location, or the presence of a radio collar on an individual's aggression or activity score. These results indicate that in juvenile red squirrels, active and aggressive behaviours are repeatable among-individuals in the post-emergence period.

44 Pelvic myology of caenagnathid dinosaurs and its implications for locomotion

Matthew Rhodes, Gregory Funston, and Philip J. Currie

Dinosaur locomotion studies offer insight about how these animals were adapted to their environment and tend to focus on limb anatomy. The locomotion of non-avian theropods is particularly interesting due to the evolutionary constraints inherited by their avian descendants. Among theropods, caenagnathids are closely related to birds and believed to be highly cursorial (adapted for running) based on limb anatomy. Furthermore, caenagnathids are phylogenetically bracketed by clades that show disparate arrangements of locomotory muscles; ancestral clades rely heavily on tail muscles, but derived clades employ more hip and knee muscles. For this reason, caenagnathids may occupy a crucial transition point on the evolutionary line to birds. However, their musculature has not yet been examined, which may offer a new perspective on locomotory adaptations. Comparison of caenagnathid pelvic material reveals little variability across the family. Pelvic musculature is reconstructed based on soft tissue attachment sites identified through extant phylogenetic bracketing and direct observation of fossil material. The first reconstruction of caenagnathid locomotory muscles sheds light on the stepwise transitions towards bird-like muscular configuration and tracks the progressive change from tail-driven to knee-driven locomotion. Notably, expansion of the preacetabular and reduction of the postacetabular portion of the ilium, loss of the supraacetabular crest, and lateral migration of some pubic muscles suggests reorganization with increased reliance on hip and knee flexors. The reduction in hip extensors compared to ancestral taxa captures a transitional stage in the decoupling of tail and hip musculature, additionally casting doubt on highly cursorial abilities of this family.

45 Do wildlife passages negatively affect prey? Evaluation of the prey-trap hypothesis

April Robin Martinig, Mahnoor Riaz, and Colleen Cassady St. Clair

Wildlife passages are intended to mitigate the negative effects of roads on habitat connectivity and wildlife mortality. However, mitigation may not be possible if wildlife passages have detrimental effects on the species that use them. The prey-trap hypothesis posits that predators can take advantage of how wildlife passage structures funnel individuals into confined spaces, which could make prey easier to detect and capture. Using infrared cameras, we examined how 7 prey species and 3 predator species used 17 wildlife passages along a four lane divided highway in the Laurentian Wildlife Reserve, Quebec, Canada from 2012-2015 to test the prey-trap hypothesis. We predicted that predators should use passages more frequently following prey use, while prey should use passages less frequently following predator use. Using Markov chain models, we tested the probability of four possible events occurring in wildlife passages: prey following prey, predator following prey, prey following predator, and predator following predator. Our results indicated that prey following prey events and predator following predator events occurred more frequently than expected; conversely, predator following prey events and prey following predator events occurred less frequently than expected. We found no evidence to suggest that wildlife passages acted as prey traps for predators to exploit. These findings support the continued use of wildlife passages as mitigation tools.

46 Evidence for a Convergent Sensing Mechanism in Cyanobacteria.

Sean Ritter and George Owttrim

In order to respond to stressful conditions presented by their environment, bacteria typically utilize two-component signal transduction pathways to alter gene expression. These consist of sensory histidine kinases and corresponding response regulators which facilitate signal transduction. Responses are typically very stress specific and modular with little crosstalk between signaling pathways. Despite the model cyanobacteria *Synechocystis* Sp. PCC 6803 encoding 47 histidine kinases and 45 response regulators, a large number of stress responsive genes do not appear to be regulated by any one two-component system. One such gene is crhR, a redox-regulated RNA helicase which facilitates post-transcriptional regulation through both RNA unwinding and annealing activities. Expression of CrhR is induced by the seemingly unrelated stresses of cold-shock, osmotic pressure and exposure to heavy metals. Importantly, all changes in expression follow similar kinetics in the presence of various inhibitors of the electron transport chain, such as DCMU, DBMIB and Methyl Viologen. We propose the presence of a convergent sensing mechanism by which the redox potential of the electron transport chain specifically between Photosystem II and cytochrome-b6f is altered by divergent abiotic stresses. This triggers a signaling pathway by which genes required for response to multiple abiotic stresses can be controlled. In the case of crhR, this provides the cell a rapid way to couple transcriptional regulation of specific mRNAs with current levels of photosynthetic efficiency. More broadly, this research answers an outstanding question of how a variety of two-component nonspecific genes are regulated in prokaryotes. Evidence for related systems in Staphylococcus aureus and higher plants suggest that convergent sensing mechanisms may be evolutionarily conserved and occur more widely than anticipated.

47 Causes and timing of juvenile mortality during dispersal

April Robin Martinig and Stan Boutin

While movement takes many forms, dispersal, the movement from a natal site to new site, is a crucial life-history response by which individuals can react to their environment. For those that do ultimately disperse, the act of dispersal is presumed to entail costs mainly relating to survival. By following 67 juvenile North American red squirrels (*Tamiasciurus hudsonicus*) in southwestern Yukon, Canada, I investigated the outcome of dispersal for this cohort from May to August 2017. Juveniles were radio-collared at 25 days old and tracked twice daily post-emergence (50 days old) until 80 days old or death. In 2017, 40 (out of 67) juveniles were subjected to behavioural (assays and focal) measurements, of which 24 survived until collar removal. Mortality due to natural causes (excluding predation) was most common (65.7 %), with 14 juveniles being recovered body intact, followed by fecal impaction (n = 5), conspecific injuries (n = 2), and weather (n = 2). Mortality due to predation (n = 9) or predator related injuries (n = 1) accounted for 28.6 % of the mortalities. Unnatural deaths (n = 2) accounted for 5.7 % of mortalities. Behavioural type (activity and aggressiveness) did not affect the probability of survival, nor did sex or growth rate.

48 Genomic signatures of mountain pine beetle resistance

Bianca Sacchi, Rhiannon Peery, Kate St. Onge, and Janice Cooke

Lodgepole pine is the primary host of the mountain pine beetle (MPB). The latest MPB outbreak resulted in mortality of approximately 19 million hectares of mainly lodgepole pine forests in British Columbia and Alberta. Mountain pine beetles overcome tree defenses through a mass attack strategy: trees are killed when numbers of attacking beetles are greater than the tree can defend against. Even when MPB populations are extreme, some lodgepole pine individuals survive the outbreak by evading detection, resisting beetle attack, or preventing colonization. My goal is to determine whether trees that survive an epidemic have a genetic makeup that helps them resist MPB detection and attack. Based on previous studies, I predict that there is a genetic basis to surviving extreme MPB outbreaks. To test this hypothesis, I am conducting analyses on a unique genomic dataset representing thousands of single nucleotide polymorphisms (SNPs) collected from the offspring of beetle-killed and surviving trees from central British Columbia. I have performed population structure analyses to inform my later analyses and gain a better understanding of the underlying genetic variation in this group of trees. These results, coupled with other population genetics analyses such as principle component and Fst outlier analysis suggest that some genetic differences exist between the offspring of killed and surviving trees. My next objective is to conduct a genome wide association study (GWAS) to identify specific SNPs that are associated with the trait of parental survival. SNPs associated with survival to MPB attack may be located in or close to genes that improve the tree's ability to defend itself or evade detection.

49 Does feeding alter enzyme activity along the alimentary canal of the Pacific hagfish (*Eptatretus stoutii*)?

Christina M. Schaefer, Alyssa M. Weinrauch, and Greg G. Goss

Hagfish represents one of the oldest basal lineages of extant vertebrates evolving over 550 million years ago. Their phylogenic position allows them to be a model organism for comparative environmental vertebrate physiology. Hagfish have four very unique feeding habits including opportunistic scavengers, predation, encounter competition and passive feeders. The hagfish's capacity to switch between living and dead prey expands the flexibility of their feeding and has likely contributed to their evolutionary success. Past research in bony fish has shown digestive enzymes to be indicative of feeding ecology, correlating well with diet but data for digestive enzyme activity is limited in hagfish. Thus, we measured the activity of seven different enzymes along the length of the intestine, looking for higher activity in the hindgut due to the presence of digestive zymogen granules, between fasted and fed hagfish. We hypothesized that feeding would upregulate the activity of proteases, lipases and amylases, if present, along the entire length of the intestine. This research will demonstrate the enzymatic activity for the most primitive members of vertebrates and will be useful for studies of evolutionary comparison.

50 Diet composition and prey selectivity of gray wolves (*Canis lupus*) in Prince Albert National Park, Saskatchewan

Justin Shave and Andrew Derocher

Few studies have investigated the direct role of gray wolves (*Canis lupus*) in predator-prey dynamics with the plains bison (*Bison bison bison*). This project aims to study wolf predation on plains bison and other ungulates in the southwest corner of Prince Albert National Park (PANP), Saskatchewan. The Sturgeon River plains bison (SRPB) population is one of only a few remaining wild populations of plains bison in their historical range in Canada, and has experienced a decline of over 50% in the last eight years. We investigated to what extent wolves are contributing to the decline of the SRPB population using direct observation of wolf kill sites and stable isotope analysis (SIA). We determined kill sites via spatially- and temporally-clustered data points obtained from GPS-collared wolves over four consecutive winters (2014-2017). We collected samples used for SIA opportunistically during wolf kill site visits. Overall, both methods indicated that white-tailed deer (*Odocoileus virginianus*) were consumed most frequently, followed by moose (*Alces alces*) and plains bison. We also examined levels of hair cortisol concentration (HCC) and marrow lipid percentage among wolf-killed prey, as measures of chronic stress and body condition respectively. Plains bison killed by wolves had significantly higher HCC than harvested bison. In addition, there was a negative relationship between HCC and marrow lipid percentage in wolf-killed bison. Our next step is to examine HCC and marrow lipid in moose and deer, to investigate if there is evidence for any inter-species variation. The results of this study will quantify the contribution of wolves to SRPB mortality, and support the long-term viability of plains bison in this region.

51 Morphology and gene expression associated with dispersal capability in mountain pine beetle (*Dendroctonus ponderosae*)

Victor Shegelski, Maya Evenden, Dezene Huber, and Felix Sperling

The mountain pine beetle, *Dendrochtonus ponderosae*, has become a major forest pest in Western Canada, causing immense economic losses in forestry. Dispersal by mountain pine beetle is poorly understood and increasing our knowledge of its dispersal capabilities would improve predictive modelling, allowing more efficient allocation of management resources. While some flight morphology (primarily wing size and body weight) is correlated with flight capacity, there is still a large amount of unexplained variation in flight performance that is likely genetic. This study aims to identify genes associated with differential flight capacity in mountain pine beetle. Beetles were flown on flight mills to collect flight data, and RNA-seq was used analyze gene expression levels relating to flight. So far, patterns of differentially expressed genes indicate a reallocation of resources to maximize flight capacity. Some of the systems associated with the differentially expressed genes include: muscle function, metabolism, immune response, reproduction, and detoxification.

52 Investigating effects of industrial noise on small mammal abundance and activity

Julia Shonfield and Erin Bayne

Research on the effects of anthropogenic noise has primarily focused on species that rely heavily on vocal communication (e.g. songbirds, squirrels, frogs, bats, and cetaceans) for important components of their life history (e.g. defending a territory, attracting a mate). Many species of small rodents, such as mice and voles, rely mostly on olfactory communication. Though we would not expect them to be directly impacted by noise, they could be indirectly impacted through altered predation dynamics. Small mammals could become distracted by the noise and thus be more vulnerable to predation, or could find refuge if predators avoid noisy areas. We investigated whether the abundance and activity of small mammals was affected by anthropogenic noise. We set up grids of live-traps at forested sites in northeastern Alberta in 2014 and 2015, with one side adjacent to a forest edge that differed in the presence or absence of a noise source. Sites were selected based on three noise categories: chronic noise (adjacent to a compressor station), intermittent noise (adjacent to a road) and no noise (adjacent to a forest clearing). We estimated abundance of small mammals using mark-recapture methods. The maximum distance moved between traps by individuals during a trapping session was used as a measure of spatial extent of activity. We found no difference in abundance of small mammals, and no difference in small mammal activity between the three noise categories. We also did not detect an edge effect on small mammal abundance within sites, regardless of the presence of a noise source at the edge. This is the first study to look at impacts of industrial noise on small mammals and our results suggest noise has minimal effects on small mammal abundance and activity.

53 Parasite prevalence increases with common-final-host abundance and waterbody age in a trophically transmitted parasite system

Zhuoyan Song and Heather Proctor

In freshwater ecosystems, parasite prevalence can vary between different water bodies at fine spatial scales. These spatial variations in parasite prevalence can be influenced by waterbody age (a proxy of colonization times for host and parasite) and host abundance. However, empirical evidence remains scarce regarding how these biotic and abiotic factors interact to influence parasite prevalence in natural systems. We use a six-field-season dataset (from 2015 to 2017) from a waterfowl-Muskrat-Gammarus-acanthocephalan system to test the effects of waterbody age, common/rare/non-final-host abundance and intermediate host abundance on parasite prevalence in intermediate host. We found that the acanthocephalan prevalence in Gammarus increased as the abundance of common final host increased while the abundance of intermediate and rare/non-final host were not significant across the four-field seasons from 2015 to 2016. In three of the four field seasons, acanthocephalan prevalence in Gammarus was highly related to the waterbody age. To further test the association of acanthocephalan prevalence with waterbody age and abundance of common final host, we selected 10 of the 36 water bodies in May and August 2017, with two different age groups (5 young and 5 old) but being similar in terms of environmental conditions and waterbody size. We found that both waterbody age and common final host were significant correlates of acanthocephalan prevalence in 2017. These results support the importance of host specificity, host commonness and amount of time available for colonization by intermediate hosts and parasites in determination of prevalence of freshwater parasites.

54 Investigating the role of Active Beta-Catenin in tumour progression and metastasis in Neuroblastoma.

Jamie Stark, Noureen Ali, Elizabeth Garcia, and Sujata Persad

Neuroblastoma or NB is a childhood cancer that develops from neuroblasts, immature nerve cells in the sympathetic nervous system, derived from neural crest cells. Of cancer deaths in children, about 15% are due to NB. Identifying and understanding proteins in pathways that contribute to the initiation and progression of NB can provide potential drug targets for NB treatment. One such protein Beta-Catenin, the primary effector of the Wnt signalling pathway. This pathway plays an important role in normal neural crest stem cell proliferation and differentiation, but is involved in the development of neuroblastoma when deregulated. β-Catenin is a transcription factor for genes involved in proliferation, it therefor has oncogenic activity when deregulated. The Wnt pathway regulates β-Catenin through phosphorylation/de-phosphorylation of 4 amino acid residues. Therefore, we hypothesize that higher levels of the transcriptionally Active β-Catenin (ABC), which has two amino acids phosphorylated, likely contributes to higher levels in aggression, invasion and metastasis of certain NB tumours. The goal of this study is to determine whether upregulation of ABC is involved in the progression of NB and if it can be used as a prognostic marker. To test this hypothesis, several NB cell lines were arranged into panel in order of least to most aggressive. This was done by measuring migratory and invasive abilities of cell lines using migration and invasion assays. The amount of ABC in each cell line was determined via Western Blotting. Preliminary results indicate a correlation between aggressiveness and ABC levels. Causation will be tested by over expressing an ABC reporter protein in a parental (isolated from patient before therapy) cell line, to determine if this in fact causes it's progression to a more aggressive form of NB, resembling it's daughter cell line (taken after therapy).

55 Evolution of lichen morphology

Gulnara Tagirdzhanova

For a long time, lichens have been regarded as a symbiosis between fungi and algae, where the fungal partner is the key part, alone determining the overall symbiotic outcome. However, recent studies show that lichen biology is more complex than was believed. Lichen morphology often does not correspond to the genomic evolution of the fungus. Since in some cases it also correlates with the composition of microbiota of lichen cortex, it can be argued that the symbiotic outcome is a result of complex interactions of symbionts.

Lichen morphology varies in terms of complexity of the structure. Microlichens forming thin crusts closely attached to a substrate are simple and two-dimensional, while macrolichens form more complex 3D structure. Macrolichens have evolved from microlichens several times independently. The majority of macrolichens belong to Parmeliaceae (Lecanorales), the most diverse lichen family. However, macrolichens are also present in some other taxa. The morphology of macrolichens is diverse. It includes many different life forms, which can be divided into two groups: leaf-like foliose lichens and fruticose lichens. The latter group includes hair lichens, a group of phylogeneticaly unrelated macrolichen genera characterized by a specific morphology resembling hair. What has driven the rise of complexity in the lichen evolution? In order to answer this question, one can study processes which have accompanied the transition between the lichen life forms. Understanding how lichens of different morphologies differ in terms of thalli composition and genomics of symbionts, can provide insights into the evolution of lichens as a whole. Combined with revealing the mechanisms of integration of symbionts within a lichen thalli, it may bring us closer to the understanding the nature of lichen symbiosis.

56 Assessing algal community structure and stream functional responses across a nutrient gradient in agricultural streams

Nikki van Klaveren, Suzanne Tank, Rolf Vinebrooke, Gregory Piorkowski, and Madison Kobryn

Streams provide important ecosystem services such as organic matter transformation, nutrient uptake, provision of water for livestock and irrigation, and fish habitat. Anthropogenic activity including urbanization and agriculture can affect in-stream nutrient status through point and non-point source inputs. When large quantities of nutrients enter streams, nutrient cycles can become impaired, leading to increased transport to downstream systems with consequent effects for eutrophication. Two potential metrics for quantifying stream health and function are algal taxonomic composition and nutrient uptake potential. Algal community structure is being investigated at fifty-five streams within the agricultural regions of Alberta, half in the Grassland and half in the Parkland ecoregions. Periphyton samplers were left in each stream for one-month periods in late-spring and mid-summer, to collect and identify algal communities to genus. These data will be analyzed using NMDS ordinations and threshold analyses to determine how algal community structure relates to nutrient concentrations. Nutrient injections using Cl^-, NH_4-N, and PO_4-P tracers will be used to calculate mass transfer coefficients (vf) in up to 20 of the selected streams. This will indicate the limiting nutrient and an information theoretic approach will be used to evaluate which stream characteristics best explain variation in vf across streams. This presentation will provide preliminary results, including an overview of stream water chemistry across the study systems. The results of this research are intended to guide watershed management programs in Alberta's agricultural region by suggesting nutrient endpoints that maintain aquatic ecosystem services in streams.

57 Filling the evolutionary gap: Zinc uptake across the hindgut and skin of the Pacific hagfish

Carley Wall, Alyssa Weinrauch, Greg Goss, and Tamzin Blewett

Zinc (Zn) is a trace metal used as an essential co-factor for more than 300 enzymes, many of which are required for biomolecule synthesis and whole-body homeostasis. Hagfish (of the family Myxinidae) are an extant group of ancient fishes which diverged from the vertebrate lineage over 500 million years ago. They are neither invertebrates nor true vertebrates, and therefore make an excellent evolutionary and physiological model to study. Hagfish exist as benthic scavengers, burrowing into dead and decaying flesh of other animals when available. This unique lifestyle leads to nutrient acquisition not only from dietborne sources across the intestine, but also possibly from the surrounding nutrient-rich water using skin as a transport surface, as has been found for other nutrients. Zinc uptake experiments using the Pacific hagfish (*Eptatretus stoutii*) were completed using an in vitro gut sac and skin chamber techniques. Within the hindgut, Zn uptake followed a saturable, sigmoidal relationship with an apparent Km of 65.48±14.70 µM and Jmax of 0.1504±0.02 nmol/cm2/h. In addition, the skin also demonstrated Zn uptake following a sigmoidal relationship but with a higher affinity for Zn (apparent Km of 25.11±3.92 µM) and higher Jmax (1.229±0.1247 nmol/cm2/h). A range of metal competitors (Pb, Cd, Ni, Cu, La) were used to elucidate the cellular proteins involved in hagfish Zn transport. At 2X and 5X the concentration of Zn present in solution, none of the metal treatments had any effect on Zn uptake in either the hindgut or skin. The ability for hagfish to use their skin as a transport surface for metals has only been demonstrated in invertebrates, and so this gives insight into the evolution of Zn transport and helps our understanding in the evolutionary transition from invertebrates to vertebrates.

58 Antibody affinity maturation in fish (Primordial germinal centers)

Doaa Waly and Brad Magor

Affinity maturation is the process to improve antibody affinity for an antigen during an immune response. This process is mediated by activation-induced cytidine deaminase (Aicda) and it occurs in distinct structures called germinal centers (GCs). Fish were thought to lack affinity maturation, in part because they lack histologically distinct GCs. Previous research showed that Aicda expressing cells co-exist with a population of pigmented cells called melano-macrophages. These aggregates are associated with IgM+ B-cells, and CD4+ T-cells, which are considered to be essential components of GCs. We propose that these aggregates in fish are functionally analogous to mammalian GCs.
GCs in mammals are nucleated by up to 6 activated B-cells each with its' own unique antigen binding site (VDJ sequence), which then proliferate and acquire Aicda mediated mutations within the VDJ exon. If these aggregates are acting as a primordial GC the immunoglobulin VDJ sequences from B-cells within a single cluster should trace back to a few parental cells, which can be identified by comparing the unique complementarity determining region 3 (CDR3) at the V-D-J junction that forms as the gene is recombined during development.

We used high throughput sequencing to determine if B-cells within melano-macrophage clusters (MMΦCs) are derived from limited activated B-cells. Between 45,000 and 65,000 useful reads were obtained per cluster, and we focused our analysis on the CDR3. Each cluster was found to be colonized primarily by 5-6 parental B-cells and these clonally expand while acquiring mutations. MMΦCs appear to be continually evolving structures, this can be inferred from the latter entry of few more activated B-cells. These results support the hypothesis that these clusters are the sites where affinity maturation occurs in fish. Determining if MMΦCs are functionally analogous to GCs will allow further studies into the different cell types involved in affinity maturation in fish.

59 Metabolic responses of two Pacific sea cucumber species, *C. miniata* and *P. californicus*, to low oxygen environments

Alyssa Weinrauch and Tamzin Blewett

Hypoxia and anoxia are naturally occurring challenges faced by marine organisms, particularly those in the intertidal zone that experience daily tidal fluctuations. During reduced oxygen conditions marine invertebrates modify physiology to maintain metabolism or instead attain energy from anaerobiosis. We sought to quantify whether a differential tolerance to low oxygen persists in two species of sea cucumber, the Pacific Northwest (*Cucumaria miniata*) and the giant California (*Parastichopus californicus*) given their differing habitats. *C. miniata* inhabits the rocky intertidal and thus experiences daily oscillations in oxygen content, whereas *P. californicus* inhabits the more stable, low intertidal zone. We hypothesized therefore, that *C. miniata* would have pre-existing adaptations enabling a higher tolerance to both anoxia and emersion when compared to *P. californicus*. We observed a higher basal metabolic rate in *C. miniata* likely owing to their continuous filter-feeding nature in comparison to the periodic sediment-feeding *P. californicus*. Regardless of species or oxygen content, the coelomic fluid glucose concentrations remained unchanged (66.2 ± 10.5 μM) however, *P. californicus* liberated

~6-fold more tissue glucose when faced with low oxygen to maintain metabolism. Lactic acid production, a marker of anaerobic metabolism, was significantly elevated when *P. californicus* underwent emersion, yet was unaltered in *C. miniata* in all conditions tested. Overall, we illustrate that habitat can influence hypoxia tolerance as the intertidal *C. miniata* is more tolerant to low oxygen conditions in comparison to the low intertidal, *P. californicus*.

Poster Presentation Abstracts

1 Engineering Fluorescent Ca2+ Indicators in Zebrafish

Abhi Aggarwal, Landon Zarowny, Tiffany Phan, Richard Kanyo, Michele DuVal, Ted Allison, Robert Campbell

Genetically-Encoded Fluorescent Calcium Indicators for Optical Imaging (GECOs) modulate their fluorescence intensity in response to changes in calcium ion concentration, and are powerful optogenetic tools for the investigation of neuroscience. The focus of this project is engineering a new GECO that exhibits favourable characteristics, such as increased brightness and a higher fold change, and characterizing its utility when expressed in vivo. To develop this new GECO, we started from mNeongreen, the brightest monomeric fluorescent protein currently available. An initial prototype construct was made using rational design, following the precedent of the genetically encoded calcium indicators such as GCaMP. This construct was further improved using directed protein evolution with colony-based screening of libraries of randomly generated variants. We observe the brightness of promising new variants and perform tests to see how new mutations have affected the brightness and the fold change of the variant. After many rounds of screening, our latest variant of mNeonGreen-GECO exhibits a Ca2+-dependent of 12X fold change. When compared to the original construct, this indicator appears significantly brighter with higher contrast between Ca2+-bound and Ca2+-free states. Directed evolution is ongoing and we expect to produce a fluorescent indicator that will be used for in vivo imaging of intracellular Ca2+ dynamics. Once the characteristics of mNeonGreen GECO have been plateaued, we will image its calcium dynamics when expressed as a transgene in the zebrafish CNS. Meanwhile, we are also developing another calcium indicator based on bright monomeric red fluorescent protein, mScarlet and currently working on screening its calcium dynamics when expressed in zebrafish. Doing so will allow us to compare the screening methods for calcium dynamics in-vitro and in-vivo, while producing two calcium indicators that researchers can use to study various disease states.

2 Formation and Assembly of Nucleosome Complex

Morenike Ajidagba, Md Touhidul Islam, Rashmi Panigrahi, and Mark Glover

Aims: DNA structure is vital for maintaining genomic integrity during DNA damage; which if left untreated can lead to the development of cancerous cells. Exposure to ultraviolet and ionizing radiations result in DNA double stranded breaks (DSBs). The basic unit of DNA consists of the nucleoprotein complex called the nucleosome, which has an octamer of core histones wrapped by 146 base pairs of DNA. Four histone proteins, H2A, H2B, H3 and H4, make up this protein core. This compact nature is crucial for regulation of gene expression and prevention of further DNA damage. Our goal is to purify and assemble the nucleosomal complex for future interaction studies with DSB repair proteins.
Methods: The histone proteins were cloned and protein expression studies to determine the best cell line for optimal expression were performed. Expressed proteins were purified on a Ni-NTA affinity column. The purity will be confirmed through SDS- PAGE analysis. The oligomeric state of the protein complexes were analyzed using size exclusion chromatography and native PAGE analysis.
Results: Presently, we have successfully cloned the H2A-H2B and H3.1-H4 histone proteins into pDUET and pACYC vectors respectively. Protein over-expression and purification studies have been performed in BL21DE3 cell lines. The oligomeric state of the complexes have been identified.
Conclusion and Future Directions: Previously, histones were cloned and expressed individually. The expressed histones were recovered from the inclusion bodies using denaturation method. Then further nucleosomal assembly was obtained by dialysing out the denaturant. Our results indicate that a co-expression system can be successfully employed to overexpress and purify the histone partners. In this method, the denaturation step has been eliminated. After successful reconstitution of the nucleosome, its interaction of DSB repair proteins will be analyzed using pull down studies. Structural analysis will be performed using high resolution X-ray crystallography.

3 Algal-bacterial interactions simplify lipid extraction for biofuel production through novel extra-cellular lipid bodies

Catherine Bannon, Leen Labeeuw, and Rebecca Case

In nature, bacteria and algae continuously exchange nutrients, vitamins and small bioactive molecules that mediate their interactions and structure marine communities. Consequently, there has been an increase of scientific research focused on interactions in polymicrobial microalgal cultures that promote growth, relieve energy intensive harvesting and potential to stimulate the accumulation of valuable bio-products, such as algal lipids. Neutral lipids in green algae are represented largely by triacylglycerol that are the fundamental molecule for algal biofuel production as well as being of commercial interest for high value speciality oils. We investigated the effect of growth and neutral lipid accumulation during the co-cultivation of green microalgae, *Dunaliella tertiolecta*, with several strains of bacteria. A bacterium was identified to increase the amount of neutral lipid per biomass during co-cultivation, with no effect on growth rate, compared to *D. tertiolecta* grown alone. Mono and co-culture were then monitored for photosynthetic health and growth using pulse-amplitude modulation fluorometry as well neutral lipid content quantified with Nile Red fluorescent dye. We showed that lipid bodies were present in the co-culture during late stationary phase using ImageStream®X Mark II Imaging Flow Cytometer and fluorescence microscopy. This novel physiological response will be advantageous to algal biotechnology as this bacterium could increase lipid production and simplify harvesting and extraction from microalgae during biofuel production.

4 Downstream of the Oil Sands: The effects of various metals and salts in oil sands process-affected water on the metabolism of Rainbow Trout

Graeme Battigelli

The extraction of bitumen from oil sands requires treatment with large amounts of water. After treatment, the water is contaminated with both hydrocarbons and various cations. Although hydrocarbons may be easily separated, the cations are difficult to effectively remove. Water with cation concentrations similar to oil sands process-affected water (OSPW) was created in the laboratory. *Oncorhynchus mykiss* were treated under the following conditions: 1x, 2x and 5x OSPW concentrations, as well as exclusive NaCl, high Cu and low Cu. Fish swam before and after a 96 hour exposure to the treatment. Cost of transport increased in *O. mykiss* exposed to the 2x and 5x treatment, even though swim performance decreased. This reduction in swim ability may have originated from an increase in metabolic processes related to loss of osmolites and accumulation of ammonia. Glutathione, an antioxidant found in the liver, could play a role in reducing reactive oxygen species generated by these metabolic processes. When under increased oxidative stress, the ratio of reduced glutathione (GSH) to oxidized glutathione (GSSG) decreases as it reacts with reactive oxygen species. In order to manage the decreasing GSH to GSSG ratio, glutathione-disulfide reductase (GSR) activity needs to be upregulated. This increase in GSR activity could be resulting in the increased cost of transport (COT) observed in the 2x and 5x OSPW conditions. A glutathione assay will be performed on liver tissue samples. If the 2x and 5x OSPW treatments result in greater concentrations of oxidized glutathione, then this may explain the mechanism behind the increased metabolic cost of higher metal and salt concentrations on *O. mykiss*.

5 Mating ecology of polar bears in the Beaufort Sea, Canada

Brooke Biddlecombe, Andrew Derocher, and Evan Richardson

Mating ecology is determined by a combination of factors, such as access to females, resource availability, and spatial patterns of conspecific distribution. The mating ecology of polar bears (*Ursus maritimus*) differs from terrestrial ursids due to the dynamics of their sea-ice habitat that affect the distribution of mates and prey. Pronounced sexual dimorphism and clumped resources of polar bears suggests a polygynous mating system, whereby intrasexual competition between males affects access to females. The objective of this study was to examine the mating ecology of polar bears in the Beaufort Sea, Canada over 1970 to 2014. Data were available from 135 mating pairs observed from March to May, with a mean date of April 21. Paired females had a mean age of 9.7 years (range 3 – 31 years) and paired males had a mean age of 11.5 years (range 5 – 31 years). Paired males were older (by 2.2 years) and had significantly higher mass (by 70.9 kg) than unpaired males.

Paired males had a mass 1.99 (SD = 0.46; range 1.1 to 3.0) times the mass of the paired females. Differences in age and size of paired and unpaired males supports a polygynous mating system. Neither age or annual timing of pairing changed significantly over the study despite a significant decline in population abundance since 2001 and change in sea-ice.

6 Spatiotemporal variability of stream DOC and CO_2 in the high-carbon region of the pacific coastal temperate rainforest

Anna Bishop, Suzanne Tank, Ian Giesbrecht, Maartje Korver, and Allison Oliver

Freshwater streams act as nature's chemistry lab, transporting and transforming carbon between terrestrial, marine, and atmospheric stocks. Streams in British Columbia's Pacific Coastal Temperate Rainforest (PCTR) export globally significant amounts of dissolved organic carbon (DOC) to the ocean, which impacts in-stream production and is a major energy source for coastal marine ecosystems. A proportion of in-stream carbon is also released to the atmosphere as carbon dioxide (CO_2), which has implications for the global carbon cycle and climate change. Using automated, in-situ sensors combined with field-based sampling, DOC and CO_2 are being assessed to determine spatiotemporal variation and controls in four PCTR watersheds over a two-year period. The relationship of peak discharge to peak DOC (hysteresis) and its variability over time will be analyzed according to process-based models, where potential controls will be input to multivariate statistical approaches (PCA and GLM) to test model assumptions of DOC dynamics. Using standard flux equations, CO_2 efflux will be calculated at various locations within each watershed to assess the influence of local conditions such as turbulence and slope. Understanding freshwater carbon dynamics in this high-carbon region has critical implications for coastal marine ecology, stream ecology, and the global carbon cycle, and improves our ability to predict how these systems may be affected by environmental and climatic changes in the future.

7 Development of a Methanotroph Chassis: Genetic engineering of Methylomicrobium album BG8 for production of value-added products

Shibashis Das, Marc Waddingham, Dominic Sauvageau, and Lisa Y. Stein

Methylomicrobium album BG8 is a methanotrophic bacteria notable for a rapid growth rate utilizing single carbon (C1) compounds, i.e. methane and methanol. This trait, along with its rich genetic potential, makes the strain a candidate for the development of an industrial biological chassis for the conversion of C1 compounds into value-added products such as biojet fuel and biopolymers. This requires the development of new functional genetic tools to enable a larger library of value-added products from *M. album* BG8. This will allow the manipulation of the organism into a suitable platform that efficiently directs carbon flow into products and away from storage or oxidative fates. Products of interest include isoprene, a valuable platform chemical and precursor to many advanced biofuels. Here, we describe a plasmid-based expression system and a marker free deletion system developed to transform BG8 and achieve increased levels of isoprene production. Experiments are also described to determine optimal conditions for expression of isoprene pathway genes already present in *M. album* BG8

8 Effects of Phage Antibiotic Synergy (PAS) on Pseudomonas aeruginosa Strain PA01

Carly M. Davis and Jonathan J. Dennis

Chronic Pseudomonas aeruginosa infections in the lungs are characterized by biofilm formation. Cystic fibrosis (CF) patients are highly susceptible to P. aeruginosa lung infections, with around 70% of CF adults being affected. This bacterium is known for having innate multi-drug resistance (MDR) and incredible adaptive abilities within its environments; given this, a call for better treatments is imperative. Phage therapy, which was generally abandoned in the West in the 1940's due to the rise of antimicrobial agents, is starting to resurface as a potential treatment for MDR bacterial infections. Bacteriophage (or phage) are viruses that exclusively attack and lyse bacteria. It has been shown by a variety of studies that the presence of some antibiotics can induce increased phage activity. This effect was coined phage antibiotic synergy (PAS) after the discovery that some phage plaques increase in size in the presence of sub-inhibitory levels of antibiotics. Some phage also have the ability to break down biofilms, which are well known to have an increased resistance to antibiotics. In this study we hypothesized a synergistic effect between the lytic jumbo phage phiKZ and the prescription inhaled aztreonam antibiotic Cayston™ on Pseudomonas aeruginosa strain PA01. Results confirm phiKZ plaque size increases in diameter in the presence of Cayston™. TEM images show sub-inhibitory concentrations of Cayston™ cause PA01 to take on an aberrant filamentous morphology. Due to their new morphology, pili growth is affected, causing twitching mobility to decrease substantially. The results suggest a synergistic effect may exist between Cayston™ and phiKZ on the eradication of Pseudomonas aeruginosa PA01 biofilm growth. Further studies include quantifying phiKZ phage production in the presence and absence of Cayston™, and establishing both static MBEC and in-vivo-like biofilm growth to further show the synergistic ability to eliminate biofilm growth.

9 Comparative methodology of Canada lynx density estimation

Darcy Doran-Myers

Reliable population density estimates are critical for ecological research and species management but can be difficult to obtain. Recent technological and statistical advances have made estimating density easier for researchers, less invasive for the study species, and has allowed for improved estimates for a variety of data types. Canada lynx are a species of ecological, economic, and intrinsic interest, but studies seeking density estimates are few and have been slow to adopt advances. Non-invasive sampling methods, including genetic sampling and remote camera traps, have potential to improve density estimates of lynx and to increase the efficiency, effectiveness, and precision of estimates. I applied and compared methods for estimating lynx density over two years in southwestern Yukon Territory. I collected data on lynx using hair snares, camera trapping, and snow tracking, then applied and compared statistical analyses across the data types.

Comparisons across methods are essential to improve investigations of lynx density. More reliable density estimates resulting from this work can be used in studies investigating numerical responses of lynx to fluctuating prey densities and to provide fundamental data for wildlife management decisions. Results also have clear applications to research, management, and conservation for functionally similar wildlife species.

10 External variation of the miniature characiform fish *Hemigrammopetersius barnardi* (Alestidae)

Dueck, M.

Hemigrammopetersius barnardi (Herre, 1936) is a miniature fish species of the family Alestidae, one of only four African families in the order Characiformes, a group of approximately 2000 species, most in South America, which include diverse forms such as neon tetras and piranhas. The Alestidae contains a wide variety of species ranging from 21 mm to 1300 mm standard length. Although an abundance of information is available on fish of a medium to larger size, there is still much to be understood about miniature species. Miniature fish are classified as fish that reach sexual maturity below 20 mm standard length or never exceed 26 mm standard length. The objective of this project is to assess the external morphological variation within a population (n = 158) of *H. barnardi*. A series of length and meristic data was collected and summarized. Further analysis on the collected data allowed the overall variation within the data to be visualized. The osteology of the *H. barnardi* population will be examined in future work, to determine how much variation within a population exists, as there are currently few studies that have determined the osteological variation in characiform fishes.

11 Dietary Analysis of Cougars on and off Albertan Reclaimed Mines

Mahmoud Gheblawi, Meghan Beale and Mark S. Boyce

Land reclamation is a key policy point of environmental stewardship. With much of Western Canada having a resource based economy, the sustainability of natural areas for future generations is paramount. In our quest to return disturbed ecosystems to their former pristine states, we question whether our reclamation efforts have introduced unforeseen variables which haven't previously existed. The set up of reclaimed habitats may be exerting environmental stresses that are non-existent in natural surroundings. Changes in predator dietary preference arising from land reclamation may have impactful consequences on prey species conservation. Some reclaimed mine sites in the Western Albertan foothills were established to maintain bighorn sheep populations. Through dietary analysis I aim to investigate whether cougars, generalist predators, feeding on these reclaimed mines have developed a preference for bighorns as opposed to when they are feeding off of the sites.

12 Evaluating the host adaptations of Parasutterella strains to mice

Ashley Gilliland, Tingting Ju, Stephanie Tollenaar, Benjamin Willing

Parasutterella, a Gram-negative bacterium found in the gastrointestinal tract of numerous host species, has been associated with both positive and negative health outcomes in humans. However, very little is known about the host adaptations of this core member of the gut microbiota. To understand the colonization capability of *Parasutterella* and the host adaptations, a highly selective media was used to isolate *Parasutterella* from mouse, human and pig feces. Subsequently, *Parasutterella*-free mice (Swiss Webster, n=4), harbouring a complex microbiota, were exposed to mouse, human or pig strains. The mouse and human isolate shared 93% and 98% 16S rRNA gene sequence identity respectively with the type strain *Parasutterella excrementihominis*. The pig strain, classified as a member of the family Sutterellaceae, shared 88% 16S rRNA sequence identity with type strain *Parasutterella secunda.* The mouse and human *Parasutterella* strains stably colonized the mouse, representing 1.0 – 2.1% 16S rRNA gene copies in fecal contents whereas the pig isolate failed to colonize the mouse; indicating different host-adapted lineages and host-driven diversification of *Parasutterella*. To further investigate the host adaptations of the mouse and human *Parasutterella*, a co-colonization study in mice using a mixture of the mouse and human isolate was conducted. A high resolution melt (HRM) quantitative PCR analysis method was developed to differentiate respective colonization of the human and mouse *Parasutterella* species. In the context of co-colonization the mouse *Parasutterella* outcompeted the human strain. Together these data indicate a shared niche of *Parasutterella* species as well as host specificity. The study provides insight into host adaptations and the evolutionary history of *Parasutterella* species for deepening the understanding of this core microbial genus in the gastrointestinal tract.

13 Settlement of juvenile glass sponges and other invertebrate cryptofauna on the Hecate Strait glass sponge reefs

Keenan C. Guillas, Amanda S. Kahn and Sally P. Leys

As bioherms, the glass sponge reefs of the northeastern Pacific are diverse habitats for a variety of benthic fauna. Though existing knowledge on the diversity of large glass sponge reef-associated organisms is adequate, the difficulties of sampling deepwater reef microhabitats has limited our understanding of the settlement of juvenile glass sponges and other small-bodied invertebrates onto the reefs. Five *Farrea occa* reef-building glass sponges were collected from reefs in the Hecate Strait and Queen Charlotte Sound Marine Protected Area during an expedition in May 2017. Examination of the sponges revealed a surprising density of epifauna, with 108 small-bodied invertebrates or invertebrate colonies found on the largest of the collected specimens alone; 94 of these were found on the attached dead sponge skeleton which forms the base of the reefs. Organisms found on the largest sponge were morphologically identified to comprise phyla Porifera, Bryozoa, Annelida, Foraminifera, Arthropoda, and Mollusca. Porifera (36% of total invertebrates) was the most abundant group of epifauna, followed by Bryozoa (17%). The juvenile sponges found on the largest F. occa specimen represented a variety of ages, with morphological estimates placing the youngest hexactinellid at approximately 6 weeks old. Present findings greatly increase our knowledge of the possible mechanisms of larval dispersal and settlement of the smallest size class of reef-associated invertebrates. The age distribution of epifaunal sponges in this work provides an initial understanding of processes likely to influence reef formation. Invertebrate epibionts associated with the remaining collected sponges are also being identified and enumerated, and this data will be supplemented with previously collected samples of juvenile sponges to further develop our understanding of juvenile glass sponge dispersal and settlement.

14 Studying Myosin in Zebrafish Skeletal Muscle Mutants

Lucy Harris, Casey Carlisle, and David Pilgrim

The sarcomere, the fundamental contractile unit in striated muscle, has a structure that is well understood. However, little is known of the processes involved in sarcomere assembly and maintenance, even though its proper formation and integrity are critical to its function. Zebrafish make a great model to study sarcomere assembly as embryos with sarcomeric mutations can survive for a short length of time. A key component of the sarcomere is myosin, the force-generating protein which allows for muscle contraction. It is currently unclear how non-myosin sarcomeric mutations affect the integrity of myosin in the sarcomere. This project looks at the removal timelines of slow and fast myosin isoforms in both sarcomere assembly and sarcomere maintenance mutant zebrafish. Based on preliminary laboratory data, we hypothesize that in sarcomere maintenance mutants, slow myosin is removed before fast myosin. Using western blotting and densitometry to quantify myosin heavy and light chain protein levels at multiple time points in our two mutants and wildtype fish, we have found that fast myosin appears to still be present in our maintenance mutant at similar to wildtype levels at 48 hours post fertilization (hpf). By identifying variations in myosin integrity across different mutants we hope to gain a better understanding of how these specific mutations affect myosin turnover. A deeper understanding of sarcomere assembly and maintenance can help us better understand fundamental mutations that lead to muscular disorders, known as myopathies, and may hold the potential solutions to prevent or remedy these conditions.

15 E3 Ligases and Muscle Proteostasis

Emily Harvey, Casey Carlisle and David pilgrim

Protein homeostasis, or proteostasis, is critical for cell survival in all tissues. Proteostasis defects are implicated in many well studied neurodegenerative diseases, however, little is known about the role of proteostasis during muscle development and maintenance. When proteostasis is disrupted in striated muscle, diseases like atrophies or storage myopathies result. Currently, there are no targeted treatments for myopathies as the mechanism of protein turnover is not understood. Implicated in the process of turnover is the ubiquitin proteasome system (UPS), which is uses E3 enzymes to specifically target proteins for degradation. It is unclear which E3 enzymes are responsible for this targeting in muscle. Zebrafish make an ideal model for study of muscle myopathies as they can survive several days with fatal defects and can be closely monitored due to the transparency of developing embryos. Using this model, with mutations in either sarcomere assembly (stf) or maintenance (hel), we hope to determine the role of E3 enzymes in proteostasis. Expression of E3 ligases were examined in response to muscle mutations at 24hpf and 48hpf using qPCR. Additionally, overall muscle structure was examined using H&E. We

expect that E3 enzymes involved in UPS degradation will be upregulated in response to muscle mutations, and that there are different enzymes specific to maintenance or assembly mutations.
In support of our hypothesis we observed a subset of E3 ligases were upregulated at 24hpf only in embryos where sarcomere maintenance was compromised. Upregulation of differing E3 ligases was observed in response to assembly mutations at 48hpf. Examination of muscle structure using H&E suggests that degradation of slow muscle occurs in maintenance mutants at 24hpf but is not seen in assembly mutants. Together, this indicates that the mechanism and timing of sarcomere removal differs between un-assembled sarcomeres and un-maintained sarcomeres and highlights potential targets for myopathy therapies.

16 Population Level Comparison of T6SS Mediated Competition

Nora Hussain and Yan Boucher

Vibrio cholerae is the etiological agent of the water-borne diarrheal disease cholera. This diverse species of bacteria exists within brackish waters around the globe, but the pathogenic potential of its various subspecies and their interaction in the environment are poorly understood. Notably, all *V. cholerae* have a Type Six Secretion System (T6SS), which could play a key role in intra- and inter- species interactions. The T6SS produces a molecular poison-tipped spear that is able to pierce adjacent cells to deliver a cocktail of toxins, referred to as effectors, in a contact dependent manner. In order to prevent cell death, recipient cells must have specific immunity proteins required to neutralize oncoming effectors. Cells may outcompete other neighbors by injecting them with incompatible effectors, while encoding the correct immunity genes to survive reciprocal attacks. Two geographically separate strain sets of *V. cholerae* were isolated from coastal Bangladesh, where cholera is endemic, and from the Eastern US coast. Pairwise competition assays against prey Escherichia coli demonstrated all tested isolates were able to kill E. coli using an active T6SS. Within locations, less than 5% of strains are able to cohabit the same environment together with fully compatible EI sets. However, between locations, some strain pairings have congruent EI combinations to allow for coexistence. *V. cholerae* is found at low environmental densities, and 90% of cells have been found to preferentially attach to particles. This may facilitate minimal intra-species competition due to the creation of spatially segregated populations of incompatible *V. cholerae*, suggesting that the T6SS is used more as a defensive mechanism for inter-species interactions.

17 Agronomic and Statistical Aspects of Nitrogen Use Efficiency (NUE) Quantification in Western Canada

Musfira Jamil, Allen Good, Guillermo Hernandez Ramirez

In most cropping systems, nitrogen (N) availability is one of the bottlenecks that reduces crop productivity. Plant N requirement is fulfilled by the addition of nitrogenous fertilizers which results in introduction of massive anthropogenic N in the environment and this results in an increased risk for environmental losses. To increase grain productivity as well as to mitigate potential detrimental environmental effects, 4R Nutrient Stewardship offers a comprehensive set of best management practices (BMP) for nutrient management in particular for nitrogen fertilization. Right fertilization rate is one of the components of this framework and this is also important for improving nitrogen use efficiency (NUE).

To explore the relationship between available soil N and wheat (*Triticum aestivum*) yield, spring soil N and yield data were collected from a field north of Edmonton in fall of 2015. Soil samples were collected at a depth of 15 cm while wheat grain productivity data was recorded with a yield monitor mounted on the combine harvester. Results indicated that quadratic was the best model to explain the relationship between grain yield and available soil N with root mean square error (RMSE) of 347 kg ha-1 and coefficient of determination (R2) of 0.95 (n= 17). This model also showed that the highest grain yield of 4963 kg ha-1 was attained with 25 mg NO3-N kg-1 soil, and beyond this level of available N, the yield plateaued. Piecewise regression proved to be the second best model with slightly larger RMSE (357 kg ha-1) and similar R2 (0.95) as the quadratic approach. According to this model, the yield threshold was 4445 kg ha-1 at 18 mg NO3-N kg-1 soil. Linear and hyperbola models performed relatively poor with RMSEs of 602 kg ha-1 and 585 kg ha-1, respectively. These models can provide useful insights into estimating the optimum rate of nitrogen fertilization for subsequent growing seasons.

Moreover, our results also shed light on some of the statistical challenges involved in measuring NUE. Being a ratio of grain productivity to some measure of N, the validity of NUE analysis, hinges on isometric nature of the two variables. However, our results show lack of isometry in the regression line explaining the functional relationship between soil available N and grain yield, and this entangles the relationship between these two variables.

18 Network and Comparative Genomic Analysis of the Plant Spliceosome

Daniel Jin and Glen Uhrig

The spliceosome is a group of associated protein/RNA complexes, found across all eukaryotes that are responsible for post-transcriptional processing of mRNA. To better understand the function and regulation of the spliceosome in plants we undertook a data and network driven modelling of putative interaction partners of the spliceosome in Arabidopsis thaliana. Using data derived from available systems-level pulldown, localization and gene mutant studies, we generated novel networks depicting how the spliceosome is connected to the greater cellular environment. Additional gene expression and protein localization data assisted in understanding how different subgroups of proteins in the spliceosome likely interact in vivo. The identification of key proteins and loci in the network will serve as a starting point for future experiments characterizing the spliceosome.

This analysis was then used as a framework to identify and compare key genes/proteins of the spliceosome with orthologous systems amongst other plants, green algae and charophytes. Markov modelling and statistical regression is used to quantify phylogenetic differences in the evolution and conservation of genes within the plant spliceosome, with the phylogenetic tree can serving as a basis for future comparative genomics analyses between plants and other eukaryotes. Overall, our bioinformatic analysis has revealed new targets that will serve as a starting point for future experimentation

19 Influence of exposure to host and non-host volatile organic compounds before flight on mountain pine beetle, *Dendroctonus ponderosae* Hopkins, flight propensity and capacity

Kelsey Jones and Maya Evenden

The mountain pine beetle, *Dendroctonus ponderosae* Hopkins (Curculionidae; Scolytinae), is North America's most destructive forest pest. In the most recent outbreak the mountain pine beetle has killed over 18 million hectares of pine in British Columbia, and has begun range expansion towards North-Central Alberta. The recent range expansion presents the threat of the mountain pine beetle moving into Canada's boreal forest, and across the country. Although the mountain pine beetle has been of great interest in the last few decades, much remains to be learned about the beetle's dispersal capabilities. It is unknown whether the presence of host and non-host volatile organic compounds influence the beetle's propensity to fly and/ or flight capacity. Particular importance falls upon understanding how the mountain pine beetle's flight behaviour changes when emerging from trees in forests of historic and novel hosts. Computer-linked flight mills were used to measure the beetle's propensity to fly when exposed to the phloem from host, lodgepole pine (*Pinus contorta*), and novel host, jack pine (*Pinus banksiana*), compared to a clean air control. Measurements of flight propensity, as well as the distance, speed and duration of flight were recorded for individual beetles over the 23 hour flight assay. This data, paired with other research currently ongoing at the University of Alberta will aid in understanding the potential future range expansion of the mountain pine beetle.

20 How does climate change affect Bighorn Sheep distribution and habitat use in Alberta's Rocky Mountains?

Sofia Karabatsos and David Hik

We are observing a rapidly changing climate, leading to irreparable habitat alterations which are ultimately expected to affect the success of wildlife populations. Mountain ecosystems are particularly sensitive to change; even small fluctuations in temperature or precipitation can lead to significant changes in snow cover depths, vegetation structure and productivity, and ultimately interactions at higher trophic levels. Rocky Mountain Bighorn Sheep (BHS) inhabit high elevations in the Rocky Mountains of Alberta, and have strong ecological, economic and aesthetic value. BHS travel over a large range to forage, with a strong preference for high-elevation grasslands and meadows. As a result, they may be vulnerable to changes in climate (eg. temperature or precipitation) and landscape (eg. shrub encroachment or snow cover depth). My main objective is to create models to determine which, and to what extent, climatic and climate-driven landscape factors affect BHS's distribution across its entire range in the Alberta Rocky Mountains. Using population inventory data dating back to 1971, along with historic climate data for this timespan, I will assess BHS habitat use and distribution in light of historic climate and landscape change. Such a large dataset covering long timescales for alpine species is rare and particularly unique with respect to BHS. My research will enable more accurate forecasts of future habitat use and distribution for BHS, will illustrate the effect of a rapidly changing climate on high-elevation wildlife, and will highlight the steps that we can take to lessen our contributions to it.

21 Characterization of combgap (cg) mutants in *Drosophila melanogaster*

Salina Karpoff and John Locke

Gene regulation is complex and is largely dependent on self-perpetuating chromatin structure. One mechanism for examining the role of chromatin structure in gene regulation is a phenomenon called Position Effect Variegation (PEV). In this model, epigenetic interaction between genes and higher order chromatin state has received extensive investigation in Drosophila melanogaster and has provided insight into parallel systems seen in various other multicellular organisms. By characterizing genes that play a role in the regulation of chromatin structure, we can gain further understanding of the regulation of important developmental processes that are controlled by chromatin state. In this work, a previous genetic screen looking for modifiers of variegation, done by McCracken and Locke, identified over 56 mutants which enhance a variegated eye colour phenotype. One group of these mutants was mapped to the combgap (cg) locus located on chromosome 2, where loss of function of this gene results in a dominant enhancer phenotype. Here I 5will provide quantitative data describing the level of enhancement of four cg alleles and their ability to show enhancement of several variegating alleles of the white locus. I will use standard pigment extraction methods. This characterization will provide a further understanding of the cg gene and its role in gene expression and development.

22 Solving a genetic mystery of a novel immune disorder in the NF-κB pathway

Min Ku Kang, Allison Lewis and Oana Caluseriu

Severe combined immunodeficiencies are genetic disorders marked by complex symptoms and high mortality. We are exploring a new immunodeficiency disorder in a First Nation family in which comprehensive clinical tests have failed to pinpoint the cause. Using genome sequencing, we identified a candidate gene, a crucial molecule activating the NF-κB pathway. Upon infection, this pathway activates various immune genes. We believe this pathway is impaired in the patient as we have observed that patient derived fibroblast cells have decreased NF-κB pathway activation and lower protein level of the candidate gene compared to controls (carrier and wild type sisters' fibroblasts). We then addressed the following: are the candidate gene and other key players in the NF-κB pathway downregulated transcriptionally due to the mutation? Are target genes not activated in patient cells? We used qPCR to measure activity levels of selected key players in the NF-κB pathway and compare this between patient cells and controls. We found that whether stimulated or not, there were no significant differences in the transcript levels of the candidate gene and the selected players indicating they are are not downregulated transcriptionally. The target genes of the pathway involved in immunity were upregulated significantly after stimulation in the controls but not in patient cells. This is the first time we show the functional consequence of our mutation is at a post-transcriptional level which results in perturbed activation of target genes and provide further evidence for how the mutation is contributing to the pathogenesis of this novel human disorder.

23 Transgenic Visualization of the Dorsal Eye

Xaverie MacLennan and Kevin Yoon

'Typical' ocular coloboma is an ocular disease that stems from defective choroid fissure closure with defects that appear on the inferonasal quadrant of the eye (Gregory-Evans et al., 2014). Recently, a second fissure has been noted during eye development and it has been shown that the aberration of a gene or genes leads to the formation of the superior ocular coloboma (Hocking et al., In review). To better understand the 'atypical' coloboma present in patients that exhibit gaps in the tissues of the superior eye, zebrafish models were utilized to determine the role of dorsal ventral patterning in the morphogenesis of the superior ocular fissure (Hocking et al., in review). An in depth investigation of zebrafish eye development made the transient fissure in the superior retina apparent (Hocking et al., In review). A specific transgenic tool would allow better study of this fissure. Although Tbx5 is a classic dorsal marker, questions remain about the regulation of tbx5. Tbx5 is known to express in the lateral plate mesoderm, heart, pectoral fin field, and dorsal eye (Noritaka et al., 2016). CNS (conserved noncoding sequences) around the Tbx5 locus reveal candidate enhancer regions, such as CNS12, a 3,108 base pair sequence downstream of the Tbx5 coding region noted to drive GFP expression in the dorsal eye and pectoral fin (Noritaka et al., 2016). A specific transgenic tool will help shed light on how tbx5 is regulated in the dorsal region of the eye. To create this transgenic tool, we are continuing with our efforts to identify the conserved CNS12 sequence in zebrafish, amplify this sequence in a piecewise fashion, utilize Multi Site Gate Way Cloning for the creation of our DNA constructs, and enlist the Tol2 system to create a novel and more specific transgenic tool for study of the dorsal eye.

24 Microbial Evaluation of Stockpiles in Reclamation Sites at Athabasca Oil Sands Region (AOSR)

Helena Magaldi Ribeiro, Michael D. MacKenzie and Brian Lanoil

Alberta has a history in reclamation policies since bitumen mining in the Athabasca Oil Sands Region underwent its boom in the 60's. For the past decades, it has become a provincial requirement that the amount of land used for mining has to equal the amount of reclaimed land being restored back to its "land capability", and the discrepancy between mined and reclaimed rates remain nowadays alarming. The usual process for reclamation involves the use of direct placement of overburden material, followed by nutrient addition and vegetation planting. Here I study soil material retrieved from stockpiles as a viable approach to be utilized as primary reclamation substrate due to its high availability on mining sites. Time and depth of placement may have deleterious effects on composition of microbial communities of these soils, which play an essential part in ecosystem processes such as biogeochemical cycling and shaping aboveground ecosystems. For that reason, comprehending the processes going within microbial communities in stockpiled soils through time of placement is advantageous in reclamation processes. Molecular surveys using high-throughput sequencing of the 16S rRNA gene and the use of CLPP (Community Level Physiological Profile) plates will allow assessments between microbial communities of the stockpiles and undisturbed sites of the Boreal Forest in order to determine the full use of stockpiles in reclamation processes. In order to use stockpiles to stablish functioning reclaimed ecosystems, an understanding of the microbial processes acting belowground level may break through as an advantage in order to improve restoration in the Athabasca Oil Sands Region.

25 Analysis of O-glycosylation of BCAL1798 in *Burkholderia cenocepacia* K56-2

Shayla R. Mosley and Jonathan J. Dennis

Cystic fibrosis (CF) is an autosomal recessive genetic disorder characterized by a build up of dehydrated mucus in the airways. This leads to coughing, shortness of breath, and chronic lung infections that will eventually lead to death in many patients. Of these infections, the strongly antibiotic resistant opportunistic pathogens of the *Burkholderia cepacia* complex (Bcc) are associated with particularly poor prognosis. Of the Bcc species, one of the most commonly isolated in CF patients is *Burkholderia cenocepacia*, also often associated with epidemic spread between patients. BCAL1798 is one of the 23 glycoproteins targeted by the PgILBC O-glycosylation system in *B. cenocepacia* K56-2. The BCAL1798 glycoprotein possesses an LTXXQ motif domain with characteristic homology to CpxP, a negative regulator of the Cpx stress response pathway in Escherichia coli. This 2 component signal transduction system enhances the virulence of the pathogen by sensing external environment and regulating many structures related to virulence in the gram negative envelope. Targeted deletion of the *B. cenocepacia* K56-2 bcal1798 gene leads to decreased swimming motility and virulence in the *Galleria mellonella* infection model. Site-directed mutagenesis of the BCAL1798 serine residues 43 and 182 to alanine will prevent any possible O-glycosylation at these sites. Once these mutants have been constructed in K56-2, swimming motility and virulence assays in *G. mellonela* will be used to determine whether glycosylation has an activating and/or repressive effect on BCAL1798 function and therefore *B. cenocepacia* virulence levels.

26 Influence of insect marking techniques on noctuid male moths (Lepidoptera: Noctuidae) for mark-and-recapture experiments.

Katrina Neill, Ronald Batallas and Maya Evenden

The true armyworm (*Mythimna unipuncta* [Haworth]) is a sporadic agricultural pest of cereal and pastures in North America. Semiochemical lures that selectively attract the true armyworm can be implemented in monitoring programs to estimate population densities before they reach outbreak levels. Mark-and-recapture experiments are employed to measure the range of attraction of these semiochemical lures to evaluate their effectiveness in determining local pest densities. Glow powder is a standard insect marking tool, although, this technique may negatively affect the performance of the moths and its ability to detect semiochemical lures. An alternative marking method is to rear larvae on artificial diet with oil-soluble colour dyes that internally mark the fat tissue of adult moths. The objective of this project is to assess the effect of different insect marking techniques on the performance and dispersal capability of *M. unipuncta* male moths. Oil-soluble color dyes were dissolved in cottonseed oil and incorporated in the larval diet. Moth marking treatments included: internally- marked with red dye (Sudan Red), internally-marked with blue dye (Sudan Blue), externally-marked with glow powder, and artificial diet with and without cottonseed oil as controls. Moth performance was evaluated through larval developmental time, pupal weight, pupal developmental time and moth longevity. Larvae developed faster when reared on cottonseed oil diet and slowest when reared on red dye. Pupae weighed more when reared on artificial diet alone and developed faster on artificial diet with cottonseed oil. Moths reared on cottonseed oil had longer longevity compared to those reared on dye, or artificial diet alone. Oil-soluble dyes show some effect on pupal weight and longevity of *M. unipuncta*, however cottonseed oil also showed an effect on longevity and pupal weight. Future work will assess the effect of marking techniques on flight dispersal using flight mills.

27 Are There Costs of Shifting Migration Linked to Parasitism?

Jacalyn Normandeau, Evelyn Merrill, Susan Kutz, and Mark Hebblewhite

Most ungulate studies focus on forage-predation interactions, but parasites can be as important in some situations. Parasites can have significant impacts on body condition, reproduction, and longevity in ungulates, but the interaction between migration and parasite levels is not well understood, especially for environmentally transmitted parasites in partially migratory ungulates. Parasite exposure may differ on summer ranges of migratory herd segments for several reasons: (1) early migration from a highly contaminated winter range may provide an “escape” during spring peak infectious period, (2) differences in forage quality on summer ranges may alter susceptibility to parasite infection due to improved body condition, (3) differences in either quality habitat configuration or use of predator refuges may concentrate hosts and increase subsequent transmission, (4) summer ranges may differ in secondary host habitat, or (5) parasite exposure from other ungulate species may differ. This project addresses the above hypotheses in a partially migratory elk (*Cervus elaphus)* herd that winters at the Ya Ha Tinda (YHT), AB, bordering Banff National Park (BNP). The YHT elk herd has been experiencing a population decline and a shift in summer migration from westward into BNP to eastward onto industrial lands along the Red Deer river. Results from a 2017 field season show higher prevalence and intensity of infection by giant liver fluke (Fascioloides magna) in eastern migrant elk of the YHT herd. My study will address changing dynamics among migrant segments and contribute to understanding the trade-offs between forage, predation, and parasite dynamics of a shifting migration strategy.

28 Examining the possibility of modelling retinal degenerative phenotypes caused by UNC119A orthologues in zebrafish

Taral Patel, Francesca Jean, and Dave Pilgrim

Cone-rod dystrophy can be caused by mutations in many genes. One gene found to cause cone-rod dystrophy in humans is UNC119A. UNC119 genes are highly conserved in many organisms and are known to encode for a ciliary trafficking protein, which is critical for photoreceptor function. My project involves investigating the role of UNC119A within photoreceptors, by using zebrafish as a tractable model system. The two orthologues which have the greatest similarity to UNC119A in zebrafish are unc119a and unc119b; due to the possibility of compensation, I am working with wild-type, heterozygous, and homozygous single- and double-mutant zebrafish.

My two focuses are looking for photoreceptor morphology differences at 4.5 days post fertilization between the different genotypes and determining whether there are any visual defects in the mutant fish versus the wild-type. I am looking at photoreceptor morphology using a photoreceptor-specific antibody and will be quantifying and comparing differences in the length of photoreceptor outer segments. Preliminary evidence suggests that the morphology is normal, which is consistent with a degenerative disease. To detect visual defects, I will be using a visual background adaption assay which consists of comparing melanin distribution in the fish after adapting them to dark and bright light. I predict that double mutants will not have normal distribution of melanin in comparison to wild-type fish. The results of this project will lay the groundwork for studying unc119 mutations in a vertebrate model so that we can understand why human mutations in UNC119A cause retinal degeneration.

29 Promoting exon inclusion with LNA/DNA mixmers to ameliorate spinal muscular atrophy

Hae-Won Son, Tejal Aslesh, Aleksander Touznik, Rika Maruyama and Toshifumi Yokota

Spinal muscular atrophy (SMA) is an autosomal recessive disorder that affects approximately 1 in 8000 to 10 000 live births. The disorder is caused by a loss-of-function mutation in SMN1, which results in proximal muscle weakness and respiratory distress. A nearly identical gene, SMN2, only produces ~10% full-length mRNA due to a mutation that excludes exon 7 from the final transcript, leading to an unstable protein that is quickly degraded. The discovery of an intronic splicing silencer (ISS-N1) that presents a strong exclusionary motif on exon 7 of SMN2 introduced antisense therapy as a favourable method of treatment. By blocking the function of this region with antisense oligonucleotides (AONs), a greater percentage of mature mRNA will contain exon 7, subsequently producing higher levels of SMN protein. We developed novel AONs with modifications to bypass key issues of nusinersen, the first FDA-approved AON drug for SMA, such as a high concentration requirement which contributes to an extremely high cost of the drug. We designed AONs composed of locked nucleic acid and DNA molecules (LNA/DNA mixmers) to optimize efficiency and on-target binding, and demonstrated that very low concentrations can initiate a high rate of exon 7 inclusion in SMA patient fibroblasts in vitro. Current in vivo studies in a mouse model are being conducted to determine phenotypic effects of LNA/DNA mixmer injections, as well as to quantify full length and shortened mRNA transcripts in our tissues of interest. Our studies continue to explore the efficacy of using LNA/DNA mixmers to ameliorate the SMA phenotype.

30 Investigating the role of Active Beta-Catenin in tumour progression and metastasis in Neuroblastoma.

Jamie Stark, Noureen Ali, Elizabeth Garcia, and Sujata Persad

Neuroblastoma or NB is a childhood cancer that develops from neuroblasts, immature nerve cells in the sympathetic nervous system, derived from neural crest cells. Of cancer deaths in children, about 15% are due to NB. Identifying and understanding proteins in pathways that contribute to the initiation and progression of NB can provide potential drug targets for NB treatment. One such protein Beta-Catenin, the primary effector of the Wnt signalling pathway. This pathway plays an important role in normal neural crest stem cell proliferation and differentiation, but is involved in the development of neuroblastoma when deregulated. β-Catenin is a transcription factor for genes involved in proliferation, it therefor has oncogenic activity when deregulated. The Wnt pathway regulates β-Catenin through phosphorylation/de-phosphorylation of 4 amino acid residues. Therefore, we hypothesize that higher levels of the transcriptionally Active β-Catenin (ABC), which has two amino acids phosphorylated, likely contributes to higher levels in aggression, invasion and metastasis of certain NB tumours. The goal of this study is to determine whether up-regulation of ABC is involved in the progression of NB and if it can be used as a prognostic marker. To test this hypothesis, several NB cell lines were arranged into panel in order of least to most aggressive. This was done by measuring migratory and invasive abilities of cell lines using migration and invasion assays. The amount of ABC in each cell line was determined via Western Blotting. Preliminary results indicate a correlation between aggressiveness and ABC levels. Causation will be tested by over expressing an ABC reporter protein in a parental (isolated from patient before therapy) cell line, to determine if this in fact causes it's progression to a more aggressive form of NB, resembling it's daughter cell line (taken after therapy).

31 Developing accelerometers as a tool for estimating activity budgets in shorebirds

Abigail Stosky and Kimberley Mathot

Behavioural budgets are an important tool in the field of behavioural ecology. Not only do they improve our understanding of how animals behave, they also help us understand how animals react to changes in their environment, such as increased human activity or rising temperatures. Creating behavioural budgets can be challenging, and are often limited by the researchers' ability to maintain physical or visual contact with the animals. Accelerometers are a tool that helps circumvent this challenge; however, they require the development of classification models which can translate the accelerometer data into behavioural classes. This project investigates if the classification models for accelerometer data which are trained using data from multiple individuals are more accurate at predicting the behaviours of other birds than the algorithms trained using data from single individuals. We tested this using two captive red knots (*Calidris canutus islandica*), and three classification models were developed. One was developed for each individual, and one was developed by combining the data from the two birds. The effectiveness of each of the three learning rules was measured by how well each could interpret the data of both birds. The merged rule was somewhat better at identifying dipping and walking behaviours, but both the merged rule and the individual rules were similarly effective in identifying preening and flying behaviours. All three rules showed significant issues when identifying feeding and vigilant behaviours. Knowing how well merged learning rules preform in comparison to individual learning rules is an important step in understanding how to develop an accurate and generalizable learning rule.

32 Exploring the interplay between diet, gut microbiome, and parasite susceptibility in urban-exploiting coyotes

Scott Sugden, Colleen St. Clair and Lisa Stein

As the human population living in urban areas has increased, urban areas have expanded, substantially impacting surrounding ecosystems. Although the negative effects of human activity on biodiversity are well-documented, many species have become adept at using habitat and other resources created by people. This new coexistence in cities across North America has led to an exponential increase in rates of human/wildlife conflict. In Edmonton, Alberta, urban-exploiting coyotes (*Canis latrans*) eat more anthropogenic food than rural animals, are more likely to be infected with parasites, and exhibit behavioral differences that make them more prone to human conflict. In both humans and animal models, the composition of the gut microbiome has been correlated with diet, mental state, behavior, and intestinal parasites, leaving room to suggest that conflict-prone coyote behavior could be influenced by gut microbiome and, therefore, by diet.
The objective of this ongoing project is to elucidate the relationship between gut microbiome and diet, and its influence on parasite susceptibility, in urban-exploiting coyotes. Urban-exploiting and rural coyotes will be opportunistically collected from the Edmonton area and necropsied to obtain intestinal samples for microbiome characterization using 16S rRNA amplicon sequencing. Microbial community structure will be correlated with stomach contents, parasite load, any known reports of conflict, and diet inferred from stable isotope analysis of hair or toenails. By comparing urban-exploiting coyotes with traditionally “wild” individuals, we hope to develop a preliminary understanding of the structure and function of this previously unstudied microbiome in order to inform future work on the interplay between microbiome and behavior in coyotes and other urban-exploiting species.

33 Metabolic Mapping of *Methylomicrobium album* strain BG8 under varying nutrient conditions

Phillip K. Sun and Lisa Y. Stein

Methane is a potent greenhouse gas with 34 times the global warming potential than that of carbon dioxide. Anthropogenic sources of methane from industries such as petroleum and agriculture has increased the methane content in our atmosphere by over 50%, therefore reducing methane emissions is vital in our efforts in combating global climate change. Methanotrophs are bacteria that primarily consumes methane as its' sole source of carbon and energy. Methanotrophs can be exploited to tap into methane waste emissions while simultaneously generate value added products such as bioplastics, biofuels, and high value chemicals. However, our lack of understanding regarding the physiology of methanotrophs remain a barrier to wide scale methane bioconversions, specifically the effects of nutrient sources on the metabolism of these organisms. *Methylomicrobium album* strain BG8 is a candidate methanotroph for methane bioconversions. By measuring gene expression of BG8 grown under varying nutrient conditions, a predictive metabolic map of the organism can be generated for future physiological studies and industrial applications.

34 Analysis of a membrane protein as the bacteriophage DC1 receptor in *B. cenocepacia* strain PC184

Monica M. Takla and Jonathan J. Dennis

For healthy individuals, most bacterial infections can easily be overcome. For those who are immune-compromised however, fighting these infections can be a challenge. Bacteria of the *Burkholderia cepacia* complex (Bcc) pose a serious threat to immune-compromised individuals, such as patients affected with Cystic Fibrosis. Bcc bacteria are highly antibiotic resistant and this makes treatment of their infections extremely difficult. Because bacterial resistance to antimicrobials is on the rise, there is an urgent need to find alternative methods of treating bacterial infections. Bacteriophage (phage) therapy provides one such alternative. Phages are bacteria-specific viruses that have the potential to treat bacterial infections, especially those that cannot be treated using traditional methods. Phages function by attaching to the bacterial host cell via surface structures and injecting their DNA into the cell in order to produce phage progeny. Progeny phages are then released through lysis of the cell. Bacteriophage DC1 is a phage that has been found to infect many species of bacteria within the Bcc. However, its receptor for attachment to the bacterial cell has yet to be discovered. We have screened a random insertion transposon library and have identified a potential receptor as a hypothetical membrane protein in *Burkholderia cenocepacia* strain PC184. We will further characterize this DC1 phage receptor by constructing a clean-deletion of the PC184 gene encoding this membrane protein, and determining whether phage DC1 can no longer adhere to and infect this PC184 mutant. Complementation of the membrane protein gene back into the PC184 mutant should restore the ability of DC1 to cause infection.

35 Outdoor scale-up of a biofilm photobioreactor for cultivation of haloalkaliphilic microalgae

Hayley Todesco, Christine Sharp, Harsimrit Lakhyan and Marc Strous

As a sustainable alternative to conventional fossil fuels, algal biofuels rely on advantageous use of phototrophs' ability to efficiently convert sunlight and atmospheric carbon dioxide into fermentable biomass. Immediate translation of algal biotechnology to commercial biofuel production is limited by unstable outdoor growth, frequent contamination or predation of vulnerable single-species cultures, and high operational costs rendering current efforts economically uncompetitive. Previous laboratory cultures of mixed haloalkaliphilic microalgal biofilms using bicarbonate as a carbon source were able overcome these obstacles as a more resilient, predation-resistant, and cost-efficient culturing strategy. In this project, microbial mats from the soda lakes of the Caribou Plain in British Columbia were used to inoculate a scaled-up outdoor photobioreactor that operated as a continuous closed system. For the duration of a summer, this culture was exposed to natural sunlight, ambient outdoor temperatures, and a regular harvesting cycle. Routine monitoring of weather conditions, biomass productivity, and community composition were used to assess bioreactor performance. Despite exposure to temperatures ranging from 4 to 47 degrees Celsius and daily sunlight exceeding 1000 microeinsteins of photosynthetically-active radiation, this pilot culture maintained moderate areal and volumetric biomass productivities in excess of 200 grams per cubic meter per day during a three-month period. 16S and 18S amplicon sequencing revealed that the outdoor conditions selected for cyanobacteria from the order Oscillatoriales which gradually dominated the community. These results indicate successful establishment of a diverse microalgal community capable of thriving in summer outdoor conditions consistent with a large-scale commercial application. The findings of this outdoor scale-up provides valuable implications and direction for future large-scale culturing strategies necessary to realize the potential of this carbon-neutral energy source.

36 Investigating CrhR degron function in guiding heterologous protein degradation in *Synechocystis* sp. PCC 6803

Sieren Wang

crhR encodes a DEAD box RNA helicase in the cyanobacterium Synechocystis sp. PCC 6803. RNA helicases modify RNA secondary structure, thereby regulating RNA function. Expression of crhR is induced ten-fold by temperature downshift from 300C to 200C, and the resulting CrhR protein level remains stable for as long as the cells are kept at 200C. When experiencing a temperature upshift back to 300C, conditional proteolysis is activated and rapidly returns CrhR abundance back to the basal level observed in cells growing at 300C. A conserved 50 amino acid motif has been previously identified in the C-terminal extensions of 25 cyanobacterial DEAD box RNA helicases which contains a degron: an amino acid sequence which dictates proteolysis by guiding the substrate protein to a protease for degradation upon temperature upshift. In order to observe the effects of the degron-containing region on the proteolysis of a heterologous protein, translational fusions of maltose binding protein (MBP) and an N- or C-terminal CrhR degron will be prepared, under expression of the native crhR promoter. Evidence indicates that without the presence of a degron, MBP accumulates to an elevated level at 300C in Synechocystis 6803 and is reduced gradually upon temperature downshift to 200C. Future experiments will involve producing translational fusions of MBP and the CrhR degron. If the degron is capable of causing the targeted proteolysis of heterologous proteins, MBP abundance would be expected to reduce more rapidly in response to temperature upshift. From the two translational fusion constructs, data could provide information about locational preference of the degron. Recapitulating this experiment in other cyanobacterial strains could further indicate whether the degron functions as a universal cyanobacterial motif.

37 Identification of specific cell types that retain antigen post immunization in fish germinal center reactions.

Brad Magor and Aradana Muthupandian

Our immune system responds to pathogens or vaccine antigens by producing antibodies specific for the antigens. Bound antibodies facilitate the destruction and clearance of the pathogen. During the course of infection the affinity of the antibodies for their antigens is seen to increase. In the initial stage of infection pathogen specific B cells are sequestered to specific tissue regions (Germinal centers) where they proliferate and acquire random point mutations in the exon encoding the antigen recognizing sites of the antibodies. The mutations are generated by antibody gene mutator enzyme AICDA and this may alter the antibody affinity. Mutated B cell now compete for antigen trapped on specific cells within the germinal center. Competitive B-cells receive signal to further proliferate and differentiate into antibody secreting plasma or long-lived memory cells.
The existence of germinal centers and antibody maturation in lower vertebrates is debated. Work done in our lab so far support the existence of these processes in fish cell aggregates called melanomacrophage clusters. There includes in these clusters cells that can trap, but not degrade, foreign antigen. Our approach to establishing the cell type responsible is to immunize goldfish with three different protein molecules (Bovine serum albumin, Keyhole limpet hemocyanin and Phycoerythrin) labelled with florescent dye Alexa fluor 647 (far red). Fish lymphocytes (from blood, spleen and kidney) were harvested at different time points (weeks) after vaccination. Cells with the far red label were FACS sorted and then processed for confocal imaging. Preliminary results show that pigment containing ""melanomacrophages"" are either retaining Ag on their surface or in endosomal compartments containing the pigments. The ability of at least some of the Ag to remain undegraded and 'trapped' on the cell surface is consistent with fish having antibody affinity maturation.

3 Minute Thesis Abstracts

1 Sea-ice fragmentation and polar bear movement in Hudson Bay

Brooke Biddlecombe and Andrew Derocher

Habitat fragmentation is the separation of habitat into smaller more isolated patches, often accompanied by habitat loss, and affects resident species by reducing foraging, dispersal, predation, and breeding abilities. The Arctic is experiencing increased sea-ice fragmentation, decreased sea-ice cover and thickness, and a shorter sea-ice season due to the occurrence of climate warming at twice the rate of the rest of the planet via a process called Arctic amplification. Many organisms in Arctic marine ecosystems rely on the presence of sea-ice to some extent, and as the quality and quantity of sea-ice declines so does the survival ability of these organisms. Polar bears are one such species greatly impacted by sea-ice loss, as the seasonal presence of sea-ice is instrumental in their ability to find prey, migrate, and reproduce. The objective of this study is to examine polar bear habitat quality via the extent of sea-ice fragmentation and connectivity. The focus will be on the three polar bear subpopulations within the Hudson Bay region. Satellite imaging of sea-ice for each month over the study period will be classified in terms of polar bear habitat preference, then the extent of sea-ice fragmentation and habitat connectivity will be determined. GPS movement data from collared bears in Hudson Bay will be analyzed and integrated with sea-ice coverage data to visualize polar bear movement, its comparability to predicted movement models based on sea-ice fragmentation and connectivity, and how movement varies across habitats of various quality. Exploring relationships between habitat fragmentation, connectivity, and polar bear movement will help inform future conservations efforts for this species of Special Concern.

2 Spatiotemporal variability of stream DOC and CO_2 in the high-carbon region of the pacific coastal temperate rainforest

Anna Bishop, Suzanne Tank, Ian Giesbrecht, Maartje Korver, and Allison Oliver

Freshwater streams act as nature's chemistry lab, transporting and transforming carbon between terrestrial, marine, and atmospheric stocks. Streams in British Columbia's Pacific Coastal Temperate Rainforest (PCTR) export globally significant amounts of dissolved organic carbon (DOC) to the ocean, which impacts in-stream production and is a major energy source for coastal marine ecosystems. A proportion of in-stream carbon is also released to the atmosphere as carbon dioxide (CO_2), which has implications for the global carbon cycle and climate change. Using automated, in-situ sensors combined with field-based sampling, DOC and CO_2 are being assessed to determine spatiotemporal variation and controls in four PCTR watersheds over a two-year period. The relationship of peak discharge to peak DOC (hysteresis) and its variability over time will be analyzed according to process-based models, where potential controls will be input to multivariate statistical approaches (PCA and GLM) to test model assumptions of DOC dynamics. Using standard flux equations, CO_2 efflux will be calculated at various locations within each watershed to assess the influence of local conditions such as turbulence and slope. Understanding freshwater carbon dynamics in this high-carbon region has critical implications for coastal marine ecology, stream ecology, and the global carbon cycle, and improves our ability to predict how these systems may be affected by environmental and climatic changes in the future.

3 Sneezing sponges: A view into our past?

Zach Dumar and Sally Leys

When our early single-celled ancestors made the transition to being made of multiple cells, they needed a way to make their cells work together to contribute to a whole organism. Sponges, as one of the earliest diverging groups of animals, can provide some insight into the types of signals that may have been used by early animals to coordinate their cells. My work with modern sponge signaling seeks to provide insights into how early animals made the transition to having multiple cells, one of the first key evolutionary innovations for humans to eventually evolve. Methods: The histone proteins were cloned and protein expression studies to determine the best cell line for optimal expression were

performed. Expressed proteins were purified on a Ni-NTA affinity column. The purity will be confirmed through SDS- PAGE analysis. The oligomeric state of the protein complexes were analyzed using size exclusion chromatography and native PAGE analysis.
Results: Presently, we have successfully cloned the H2A-H2B and H3.1-H4 histone proteins into pDUET and pACYC vectors respectively. Protein over-expression and purification studies have been performed in BL21DE3 cell lines. The oligomeric state of the complexes have been identified.
Conclusion and Future Directions: Previously, histones were cloned and expressed individually. The expressed histones were recovered from the inclusion bodies using denaturation method. Then further nucleosomal assembly was obtained by dialysing out the denaturant. Our results indicate that a co-expression system can be successfully employed to overexpress and purify the histone partners. In this method, the denaturation step has been eliminated. After successful reconstitution of the nucleosome, its interaction of DSB repair proteins will be analyzed using pull down studies. Structural analysis will be performed using high resolution X-ray crystallography.

4 The smell of success: evaluating pheromone monitoring tools for wheat midge in the Peace River region

Amanda Jorgensen, Jennifer Otani, and Maya L. Evenden

The orange wheat blossom midge, *Sitodiplosis mosellana* Géhin (Diptera: Cecidomyiidae) is an invasive pest on wheat (Triticum spp.) in Canada. The objective of this research is to assess monitoring tools for wheat midge in the most northern part of its expanded range in the Peace River region of Alberta. Season-long flight activity was monitored with pheromone-baited traps. We compared trap capture of male midge in green and orange delta traps baited with pheromone released from flex lures (Scotts™), or rubber septa lures (Scotts™ or Great Lakes IPM™) to that in unbaited control traps. Traps were monitored weekly during wheat midge flight. In 2016, significantly more wheat midge were captured in pheromone-baited traps compared to unbaited traps, but there was no difference in the number of midge attracted by the different lures tested. Seasonal activity peaks varied by four weeks among sites. The results from this study will help us understand wheat midge flight activity and develop monitoring tools for this pest within its relatively ‘new’ northern distribution.

5 A burning question: How do woodland caribou use post-fire habitat in northeastern Alberta?

Sean Konkolics and Boutin, S.

In recent decades woodland caribou in northeastern Alberta have experienced population declines due to habitat alteration from industrial development and climate change. These declines prompted the 2012 Canadian Federal Recovery Strategy for woodland caribou, which states that areas burned by wildfire in the last 40 years are disturbed habitat. This delineation of disturbed habitat has major economic and social implications across boreal

Canada. Caribou have been shown to avoid young seral stage forests in recently burned landscapes due to a decrease in lichen resources and increase in predators. Yet detailed research about the relationship between post-fire forest regeneration and caribou habitat selection in areas of high anthropogenic disturbance is lacking. Additionally, fires have been mapped using coarse polygons, with little consideration of unburned residual forest patches that commonly constitute large percentages of the burn. Using caribou radio collar GPS locations and detailed maps of wildfires from the past 40 years, generated with the Normalized Burn Ratio (NBR), we developed multi-scale selection ratios to detail the degree to which burned areas and fire skips are selected by caribou. Preliminary results suggest that caribou avoid burned landscapes at the home range scale but show selection for unburned residual patches when inside the boundaries of a fire. With the Recovery Strategy obligation to reach 65% undisturbed habitat in herd ranges and the projected increase in the severity of wildfires, understanding the relationship between caribou and burned landscapes is imperative to effectively conserving a species with limited conservation dollars.

6 Evolution of lichen morphology

Gulnara Tagirdzhanova

For a long time, lichens have been regarded as a symbiosis between fungi and algae, where the fungal partner is the key part, alone determining the overall symbiotic outcome. However, recent studies show that lichen biology is more complex than was believed. Lichen morphology often does not correspond to the genomic evolution of the fungus. Since in some cases it also correlates with the composition of microbiota of lichen cortex, it can be argued that the symbiotic outcome is a result of complex interactions of symbionts.

Lichen morphology varies in terms of complexity of the structure. Microlichens forming thin crusts closely attached to a substrate are simple and two-dimensional, while macrolichens form more complex 3D structure. Macrolichens have evolved from microlichens several times independently. The majority of macrolichens belong to Parmeliaceae (Lecanorales), the most diverse lichen family. However, macrolichens are also present in some other taxa. The morphology of macrolichens is diverse. It includes many different life forms, which can be divided into two groups: leaf-like foliose lichens and fruticose lichens. The latter group includes hair lichens, a group of phylogeneticaly unrelated macrolichen genera characterized by a specific morphology resembling hair. What has driven the rise of complexity in the lichen evolution? In order to answer this question, one can study processes which have accompanied the transition between the lichen life forms. Understanding how lichens of different morphologies differ in terms of thalli composition and genomics of symbionts, can provide insights into the evolution of lichens as a whole. Combined with revealing the mechanisms of integration of symbionts within a lichen thalli, it may bring us closer to the understanding the nature of lichen symbiosis.

7 Assessing algal community structure and stream functional responses across a nutrient gradient in agricultural streams

Nikki van Klaveren, Suzanne Tank, Rolf Vinebrooke, Gregory Piorkowski, and Madison Kobryn

Streams provide important ecosystem services such as organic matter transformation, nutrient uptake, provision of water for livestock and irrigation, and fish habitat. Anthropogenic activity including urbanization and agriculture can affect in-stream nutrient status through point and non-point source inputs. When large quantities of nutrients enter streams, nutrient cycles can become impaired, leading to increased transport to downstream systems with consequent effects for eutrophication. Two potential metrics for quantifying stream health and function are algal taxonomic composition and nutrient uptake potential. Algal community structure is being investigated at fifty-five streams within the agricultural regions of Alberta, half in the Grassland and half in the Parkland ecoregions. Periphyton samplers were left in each stream for one-month periods in late-spring and mid-summer, to collect and identify algal communities to genus. These data will be analyzed using NMDS ordinations and threshold analyses to determine how algal community structure relates to nutrient concentrations. Nutrient injections using Cl-, NH4-N, and PO4-P tracers will be used to calculate mass transfer coefficients (vf) in up to 20 of the selected streams. This will indicate the limiting nutrient and an information theoretic approach will be used to evaluate which stream characteristics best explain variation in vf across streams. This presentation will provide preliminary results, including an overview of stream water chemistry across the study systems. The results of this research are intended to guide watershed management programs in Alberta's agricultural region by suggesting nutrient endpoints that maintain aquatic ecosystem services in streams.

8 Ancient Storytellers: permafrost microbes tell us about the past climate change

Alireza Saidi-Mehrabad, Patrick Neuberger, Duane Froese and Brian Lanoil

The response of soil microbes to climate change is not well understood, and they might contribute more to release of greenhouse gases. The fingerprints of past climate change since ice age have been preserved in permafrost sediments. By tracing taxonomic and key metabolic changes in the viable portion of the microbial community entrapped in permafrost, we might be able to reconstruct the past, assess the present and predict the future of these microorganisms and the key direct and indirect parameters that might cause them to rapidly respond to climate change as a consequence of increased temperatures.

Information for Presenters

Oral Presenters

1. Presentations are to be 12 min long, plus 3 min for questions
2. Presentations should be provided in electronic format (.ppt preferred).
3. First and second place winners for all levels (Undergraduate, M.Sc., Ph.D.) will be announced during the closing reception.

Poster Presenters

1. Poster size should not exceed 48" x 48".
2. Posters should be hung between 8:30am and noon on Thursday, March 1st, outside of Second Cup in CCIS. Fastening materials will be provided.
3. Posters should be hung on the board corresponding to the number indicated beside the title of your abstract in the "Poster Abstracts" section of this booklet.
4. Please check in at the poster check in table in CCIS before hanging your poster.
5. The formal poster session will be held from 3:30-4:45 pm on Thursday, March 1st and Friday March 2nd. Please stand by your poster during that time in order to have it considered for a presentation prize.
6. First and second place winners for all levels (M.Sc., Ph.D.) will be announced the closing reception.

3 Minute Thesis

1. Presentations should be no longer than 3 minutes. The time begins when the speaker begins to talk.
2. Presenters can only have one static slide, no animations or transitions allowed. All images used must belong to the presenter or be properly credited.
3. No additional media or props will be allowed.

Volunteers and Funding Support

The BGSA is extremely thankful for all who volunteered to make this conference possible and for the support of the students and staff of the Biological Sciences Department. Funding for this event was provided by the Department of Biological Sciences, the Graduate Student Association, the University of Alberta's Student Union, and the BGSA.

Dr. R.E. Peter Biology Conference Volunteers

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