UNDERGRADUATE RESEARCH IN NATURAL AND CLINICAL SCIENCE AND TECHNOLOGY (URNCST) JOURNAL
Read more URNCST Journal articles and submit your own today at: https://www.urncst.com

CONFERENCE ABSTRACT BOOK OPEN ACCESS

Dr. Richard E. Peter 2023 Biology Conference: Abstract Book

Montana Bobinski, PhD Student [1]*, Leah Jackson, MSc Student [1],
Aaron Boyd, PhD Student [1], Jiahui Wang, PhD Student [1]

[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

*Corresponding Author: repeter@ualberta.ca

Abstract
For the first time in three years; from March 8-10, 2023; the R. E. Peter Biology Conference was held in-person at the Centennial Centre for Interdisciplinary Science at the University of Alberta! This conference was originally organized by the Biology Graduate Students' Association (BGSA) of the University of Alberta to honour Dr. R.E. Peter (1943-2007) and his contributions to – as well as showcase the diverse research conducted by students in – our Department of Biological Sciences. The conference has grown to include students from other research institutions in the Edmonton area and now invites students in any department whose work aligns with the biological sciences, to encourage cross-disciplinary research. The 2023 conference consists of both oral and poster presentations by graduate and senior undergraduate students from the University of Alberta and MacEwan University.

Keywords: University of Alberta; MacEwan University; biology; biological sciences; ecology; evolution; molecular cellular biology; conference; abstract

Table of Contents

Conference Abstracts

Note: These abstracts have been reproduced directly from the material supplied by the authors, without editorial alteration by the staff of the URNCST Journal. Insufficiencies of preparation, grammar, spelling, style, syntax, and usage are the authors.

Oral Presentations in the Biological Sciences

Characterizing novel salmonella AB5 toxins

Adaobi Ojiakor, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Bacterial AB5 toxins are important virulence factors in number of medically relevant pathogens including Vibrio cholerae, Salmonella Typhi and Escherichia coli. These secreted protein complexes are composed of a catalytic A subunit that disrupts essential host cell functions and a pentameric B subunit which facilitates cellular entry of the toxin by binding to specific receptors. Our lab recently uncovered two putative AB5 toxins present in a number of Salmonella strains that have been isolated from various sources including systemic infection sites in humans. Both toxins have A subunits with striking similarities to the A subunits of a group of toxins known to disrupt eukaryotic protein synthesis. However, the B subunits of these toxins are very different, resulting in a hybrid combination that is very unexpected and yet remarkable in the toxin field. My research is focused on studying the biology and functions of these novel Salmonella AB5 toxins. Using molecular cloning and extensive protein purification systems, we have been able to show that both hybrid toxins can assemble into functional complexes capable of intoxicating cells. For further analyses, several clones of both hybrid toxins have been constructed, some of which contain mutations in key amino acid residues postulated to be important for the catalytic and binding activities of these toxins. Currently, we are focusing on evaluating the effects of both toxins on mammalian cells

using cell viability and protein synthesis inhibition assays. Given that the remarkable structure and specificity of bacterial AB5 toxins make them suitable candidates for manipulation in the treatment of non-bacterial illnesses like neoplasia, this research would not only be useful in the development of anti-toxin therapeutic strategies to control the spread of Salmonella but has very promising implications outside the field of microbiology.

Variability in albacore prey nutritional quality indicates trait-based foraging

Alana M. Krug-MacLeod, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Every living organism requires energy and nutrients to thrive. Optimal foraging theory (OFT) suggests that predators will seek the most efficient way to obtain energy and nutrients, selecting prey based on relative profitability or maximal net gain. Prey nutrition is one measurable currency related to optimal foraging. Monitoring the value and circulation of nutrition as a currency influencing foraging decisions can aid in explaining and predicting shifts in species distributions and abundance when the economic system (food web) is in flux. Climate change is affecting distributions of prey and predator species, which may require predators to choose different habitat or different species within their habitats to maximize nutrition as environmental conditions change. I used bomb calorimetry to measure energy density, and proximate composition analysis to measure % lipid and % protein values of representative groups of albacore prey species from the northern and southern areas of the California Current Large Marine Ecosystem. Comparing intra and inter-specific variation in energy density of five species, revealed patterns of variation. Results showed relatively high nutritional variability within species and considerable overlap in nutritional values between species. This combination suggests that species are not reliable indicators of optimal nutritional value. The high nutritional variability among individuals within species indicates that species do not have set nutritional profiles. The small variations between species suggest that different species of albacore prey have relatively similar nutritional traits (for example, generally high energy-density). This research is useful for predicting how albacore may forage when environmental conditions change. Since species do not indicate relative profitability, traits (independent of species identity) may be more predictive of albacore's future foraging as environmental conditions change. This knowledge can be applied to management of albacore fisheries and to conservation strategies. These findings provide further evidence of the value of building trait-based (vs. species-based) food webs.

The use of a split DNAzyme in the creation of an ATP aptasensor

Amanda Kryjak, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

Aptamers are single-stranded DNA or RNA molecules that have a high specificity for their target molecule. Ligands can range from small molecules to entire cells. Thus, aptamers can be used as biosensors, which is where the term aptasensor stems from. We have proposed to create a novel split-DNAzyme aptasensor for ATP, where two halves of a DNAzyme are separated by a conformation switching aptamer. In our design, when the aptamer is bound to ATP the two halves are separated. When the two halves are together, ATP is not bound and the DNAzyme is functional. DNAzymes are DNA molecules that are capable of catalysis. Our design features the peroxidase mimicking enzyme, which requires the DNAzyme to be rich in guanine residues in order to form a G-quadruplex. The G-quadruplex enables the peroxidase activity which can be detected and quantified through a color change using ABTS. To first characterize the conformational change, we have used DMS Footprinting. Different guanine residues are inaccessible for methylation and cleavage depending on what conformation the aptamer is in. Our results throughout the study are compared to an ATP aptamer that does not undergo a conformational change. The ATP aptamer that does undergo a conformational change has an added-on extension containing a flexible end. After confirming that a conformational change in our desired ATP aptamer occurs, the DNAzyme is ligated to both ends of the aptamer. We have chosen to first apply our design concept to ATP, since there are readily available aptamer sequences for ATP that undergo a conformational change. However, this design concept can be applied to detect any target molecule in various fields such as microbiology, pharmacy, medicine, forensics, and agriculture.

Anti-nociceptive effects of cannabinoids and terpenoids on the zebrafish model of nociception and pain

Andrew Mingyu Kim, MSc Student [1]
[1] Faculty of Medicine and Dentistry, Neuroscience and Mental Health Institute, University of Alberta, Edmonton, Alberta, Canada T6G 2R7

With many communities affected by the opioid crisis, it has become of paramount importance to explore methods of pain management outside of treatments with opioids. One alternative that has seen a recent surge in interest is the cannabis- and related phytochemical-based treatments. Some cannabinoids and terpenoids have demonstrated anti-nociceptive effects in various model systems. However, for the vast majority of terpenoids in cannabis, these effects remain unexplored. In this study I used a zebrafish model of nociception to test the anti-nociceptive effects of cannabinoids, terpenoids and their combination. Zebrafish provides a robust and high-throughput model system for such inquiry. Using behavioural assays, we confirmed the ability of acetic acid to elicit a change in locomotion in larval zebrafish. Exposure to low concentrations of acetic acid (0.001% - 0.01%) led to a drastic – a near four-fold – increase in mean activity in the larvae at 5 days post-fertilisation (dpf). Cannabidiol (CBD) at 2.5 mg/L and 5 mg/L and trans-nerolidol and caryophyllene oxide at 10mg/L, when administered to the environment of the larvae, prevented the subsequent acetic acid-induced increase in activity. However, tetrahydrocannabinol (THC) and other tested terpenoids, failed to prevent the effects of acetic acid. Combinations of the terpenoids with CBD did not lead to any additional alterations to the anti-nociceptive effects of each individual compound. By the use of specific blockers, we have determined that the process through which CBD, trans-nerolidol, and caryophyllene oxide displays anti-nociceptive effects involves the transient receptor potential (TRP) cation channels. These findings lay the foundation for a more thorough investigation of the therapeutic effects of cannabinoids, terpenoids and combinations of the two, as well as a mechanistical understanding of how such effects arise at cellular and systemic levels.

Potentiation of the PFOA uptake in pacific oyster (Magallana gigas) by PS-NP nanoparticles

Arian Farajizadeh, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Hydrophobic persistent organic pollutants (POPs) such as polyaromatic hydrocarbons (PAHs) and perfluorinated organic acids (PFOAs) are near-ubiquitous in the environment. They are known to negatively affect living organisms even at very low concentrations. Recently, our lab has demonstrated that certain hydrophobic plastics can adsorb some PAHs and potentiate uptake of these PAHs into the freshwater zebrafish embryo. We also hypothesized that the exponential increases in specific surface area of nanoplastics when compared to microplastics could exacerbate this potentiation of uptake. We hypothesized that similar processes may be occurring in seawater species and that uptake would be increased in the presence of smaller sized plastics. In this research, we used radiolabelled 14C-PFOA to explore the potential for adherence of PFOA to polystyrene nanoplastics. Secondly, we assessed whether the presence of nanoplastics could potentiate the uptake of PFOA into a marine (Pacific Oyster (Magallana gigas)) species. We developed a novel radiotracer-based method to track the uptake of PFOA in the presence or absence of either 500 or 20 nm nanoplastics. Our study demonstrates that the presence of nanoplastics can significantly increase the rate of uptake of PFOA and that smaller 20 nm nanoplastics have higher rates of potentiation when compared to 500 nm nano plastics. We also demonstrate that presence of nano plastics significantly increases thio - barbituric acid-reactive substances (TBARS) as a measure of lipid peroxidization (LPO) and that 20 nm nanoplastic invokes greater increases in LPO compared to 500 nm nanoplastics.

Using digenean trematodes to study the impact of host biodiversity on parasite species richness

Brooke McPhail, PhD Student [1]
[1] School of Public Health, University of Alberta, Edmonton, Alberta, Canada T6G 1C9

All animals in an aquatic ecosystem can be parasitized by a digenean trematode. Their ubiquity allows them to be used as biodiversity indicator organisms due to their connections to other organisms in the environment. Even if their host is no longer present in the area, trematodes can act as a record of its presence. For the last decade, the trematode community of Alberta, Canada has been extensively studied, resulting in the identification of 79 species. It is one of the most studied trematode communities in the world, making it ideal to study the relationship between host biodiversity and parasite richness. Using traditional biodiversity survey methods and trematode/snail sampling, we characterize the host-parasite communities at ponds that differ in age but share many properties. Eight reclaimed wetland sites located in Alberta were chosen for this study. Snail collections occurred biweekly from June to September over 4 years. Snails were assessed for trematode infection and cercariae were identified using DNA barcoding. Traditional biodiversity monitoring tools implemented included

invertebrate tows, benthic kick-netting, field cameras and birdsong recorders. 1979 of 21850 snails were found infected (9.1%). 56 species of trematodes from 9 families were identified, including 12 species that were not previously found in Alberta. We currently know the lifecycles of 27 of these species, meaning many gaps remain. To date, 155 species of potential intermediate and definitive hosts have been detected at the sites.
This research allows us to use a natural system to characterize the relationship between host diversity and trematode species richness on a large scale. We will also continue to improve upon our knowledge of trematode lifecycles in Alberta within the context of aquatic ecosystem biodiversity, which has applications in biodiversity surveillance and wetland reclamation.

Parasitic mites induce non-consumptive effects in cactophilic flies

Caroline Liang, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

When predator-prey interactions end in the predator eating a prey, this can decrease the prey population size. However, the mere presence of predators can have non-consumptive effects on the prey. These effects are known cumulatively as the 'ecology of fear' and can include changes in prey behavior, appearance, and body functions. The ecology of fear can be applied to parasites as well: flies (Drosophila nigrospiracula) exposed to parasites (Macrocheles subbadius), without direct contact or infection, suffered shorter lifespan and lower fertility, but why those decreases occurred is unclear. We explored whether parasite avoidance behaviors such as increased grooming or vigilance trade off with feeding in the fly-mite system. When exposed to mites, flies increase their defensive grooming behavior at the expense of feeding, which may then have impacts on their fitness. I also investigated how previous exposure to parasites (prior to sexual maturity) impacts parasite avoidance behaviors due to learning or habituation. I conducted 2x2 factorial experiments, where previous exposure and current exposure differed. Previous exposure consisted of exposing newly emerged flies to mites for 5 days. Scans to assess behavior were performed every minute for an hour on 8-day-old unmated females. GLMs and negative binomial regression analyses showed that mite presence increased grooming at the expense of feeding. Grooming increased in the presence of mites, as expected, but exposure history did not affect grooming rates. Feeding frequency is affected by a strong interaction between past and current exposure, where previously exposed flies increase their feeding rates. Parasites have a potentially larger impact on host populations than previously documented.

Does copper affect the critical thermal maximum (CTmax) of mangrove killifish (*Kryptolebias marmoratus*)?

Caroline MacDonald, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Biodiversity loss and ecosystem collapse are just some of the threats facing aquatic mangrove forests from climate-related fluctuations. Mangrove forests play a huge role in carbon capture and distribution along coastal zones; however, human activities have left the mangroves and the organisms that inhabit them at risk for extinction from pollution outflows e.g., Copper (Cu). One of the organisms that inhabit these forests is the mangrove killifish - a self-fertilizing amphibious hermaphrodite that has emerged as a unique model to investigate environmental perturbations. Previous research has shown that an exposure to environmentally relevant concentrations of Cu alters the behavioral emersion response in this species – with the fish unable to recognize hypoxic conditions, leading to a lowered response rate. Cu also affected normal metabolism and responses to environmental carbon dioxide levels. Therefore, we sought to investigate how Cu alters the response to temperature, as global climate change is increasing temperatures worldwide. To test this, we will expose fish to an incremental amount of Cu of concentrations (nominal 0 µg/L, 300 µg/L, and 600 µg/L for 24 hours before assessing their critical thermal temperature at which they lose equilibrium (CTmax), a sublethal measure. Results from this study will allow us to start understanding co-exposure studies and reduced the lab-to-field variability. Using non-model organisms will contribute meaningful research in understanding how organisms will cope with climate related changes in a multi-stressor context.

Accumulation and mechanisms of selenite transport in the water flea, *Daphnia magna*

Chantelle Klaczek, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Coal mining has been a global practice for centuries due to its high value and wide use in generating energy and electricity. Recently, the Province of Alberta has proposed to build up to 14 new mines along the North Saskatchewan River, however 5% of the watershed is already covered by coal leases. Coal mine effluents contain multiple metal pollutants such as selenium, zinc, and copper, in addition to increased sediment loads and toxic cationic polymers; however, selenium is of particular concern. Selenium is a trace element essential to all life, however it possesses a very narrow margin between essentiality and toxicity in living organisms. Although it is naturally occurring, toxic concentrations exceeding guidelines have been associated with various mining activities and linked to fish extirpation events, however it's accumulation and mechanistic uptake is severely understudied in aquatic organisms. The objective of the current study was to determine the accumulation and mechanistic uptake of the naturally prominent form, selenite, in Daphnia magna. We hypothesized that selenite would accumulate and compete with water cations for uptake, in particular mechanistic uptake would be coupled with compounds of similar ionic structure. To test this hypothesis, radioactive selenium (75Se) uptake in one hour exposure periods was measured at various selenite concentrations (0, 1, 2, 4, 8, 16, 32 µM). Manipulations to exposure water chemistry were used to interrogate the mechanism(s) of selenite acquisition. Our results indicated that selenite is accumulating in daphnids in a dose dependent manner and there is evidence for both a low and high affinity uptake pathway. We demonstrate that selenite uptake is likely mediated by a phosphate transporter at low concentrations and is enhanced by carbonate/bicarbonate transporters at higher concentrations. This suggests that concentrations of phosphate and carbonate in coal mining affected waters could potentially alter selenite toxicity in aquatic organisms.

Northern nickel: Evaluating aquatic nickel toxicity in the Arctic

Connor Stewart, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Nickel (Ni) is an economically and biologically important trace metal, but due to increased demand globally, environmental contamination may arise. The Arctic is not isolated from these impacts, with substantial Ni production in Northern zones leading to contamination of surrounding environments, with global warming increasing accessibility of reserves and thus risk of continued contamination. Many Arctic freshwaters are predicted to have high Ni bioavailability and thus toxic risk due to their abiotic composition (hardness, pH, DOC), while heterogeneity in marine waters may lead to site-specific increases in bioavailability. Freshwater Ni bioavailability and risk under Arctic exposure scenarios will be evaluated with both acute and chronic Ni exposures in the Arctic relevant cladoceran Daphnia pulex. This study will evaluate Ni toxicity in waters that mimic Arctic chemical parameters (i.e., hardness, pH) and will evaluate how altered temperature may modify sensitivity. Incorporation of both lethal and sublethal endpoints will allow for assessment of both overt toxicological effects and the mechanism of toxic action in D. pulex under Arctic exposure scenarios. Alteration of a single hardness ion (magnesium or calcium) to Arctic observed levels reduced 48-hour median lethal concentrations for D. pulex neonates from 4.90 mg/L in control waters to 3.76 mg/L and 1.57 mg/L, respectively. Simultaneous modification of multiple abiotic parameters will be used to better mimic Arctic waters and is predicted to further increase Ni toxicity. The green sea urchin (Strongylocentrotus droebachiensis) was used to evaluate Ni risk in Arctic marine waters, indicating they are highly sensitive to Ni contamination, with a 96-hour effect concentration (EC50) of 1.38 µg/L for induction of developmental abnormalities. These results taken together provide insight into the mechanism and extent of Ni toxicity under Arctic-specific exposure scenarios for both fresh and marine waters, furthering the understanding of the potential risks of Ni in these unique ecosystems.

The effects of VANISH species of bacteria in a mouse model of multiple sclerosis

Dale Archer, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The gut microbiome has profound effects on the immune and central nervous systems. As such, alterations to the gut microbiome due to modern lifestyle factors, including improved hygiene and decreased fibre consumption, may have contributed to the recent rise in the incidence of autoimmune diseases, including multiple sclerosis (MS), in industrialized societies. However, it is not known whether and how bacteria that are missing in industrialized individuals, including Limosilactobacillus reuteri and Helicobacter species, can modulate MS outcomes. Our objective is to determine the mechanisms by which these bacteria modulate disease severity and pathology in the relapsing remitting EAE (RR-EAE)

mouse model of MS. To address this, we treated RR-EAE mice with one of three strains of L. reuteri or one of two Helicobacter species. We found that L. reuteri had strain-dependent effects on EAE disease incidence and severity. Most notably, L. reuteri PB-W1 (an isolate from a non-industrialized individual) had protective effects, with no mortality in this group compared to the 21% mortality in the PBS-treated control group. The Helicobacter species had contrasting effects on disease severity, with H. macacae being protective, with a mean disease score of 1.2 and 20% mortality, and H. pylori being detrimental, with a mean disease score of 2.19 and 75% mortality. H. pylori-treated mice had a greater proportion of immune cell populations involved in driving disease in EAE and MS, including activated microglia in the hindbrain, and activated CD4+ and CD8+ T cells, and Th1 cells in the spleen, compared to the PBS and H. macacae-treated groups. Despite the strain-specific effects of L. reuteri on disease outcomes we found no differences among the L. reuteri-treated groups for these immune cell populations in the hindbrain or the spleen. Ultimately, these findings may lead to the development of probiotics or microbial-based interventions targeted for MS patients.

Memory regulation through the trafficking of dopamine receptors

Dana Guhle, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Memory flexibility, the ability to both learn and forget, is an essential feature of the brain. Dopaminergic signaling through two receptors, Dop1R1 and Dop1R2, highly expressed in the memory center of Drosophila melanogaster, are critical for learning and forgetting, respectively. However, it remains unclear how these receptors are trafficked to and from the cell membrane and how changes in trafficking impact the ability to learn or forget. To advance our understanding of Dop1R1/2 signaling, we utilized TurboID proximity labeling proteomics and RNAi screening to identify Dop1R1/2 interactors that regulate memory. Proximity labeling in cell lines expressing Dop1R1/2-Turbo-V5 constructs identified candidate proteins significantly more abundant around one or both receptors. Disruption of candidate proteins in mushroom body (MB) memory circuits leads to significantly altered memory functionality. Several candidates are predicted to either transport GPCRs to, or remove from, the plasma membrane, including the Sec24AB COPII protein, predicted to bind and transport GPCRs from Endoplasmic Reticulum to Golgi. Interestingly, loss of Sec24AB decreases memory formation while increasing stability. Immunostaining and in vivo imaging experiments will reveal if these candidates change Dop1R1/2 receptor expression at synapses, downstream secondary messenger signaling, and synaptic memory trace formation/stability. Altogether, our study will identify and characterize novel pathways regulating dopaminergic signaling and illuminate how the brain genetically fine-tunes memory.

The effect of alternative protein diets on zebrafish (*Danio rerio*) growth, behaviour, and gene expression

Emilie Torwalt, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

In the context of global climate change, the need for sustainable alternative protein sources has risen while the effects of alternative protein sources on human health remain uncertain. Alternative proteins derived from milk, pea, soy, and cereals are frequently used as substitutes for traditional meat and fish products. In this study, we used zebrafish (Danio rerio) to model the effects of vegetarian diets on growth, muscle development, behaviour, and gene expression. Standard fishmeal (FM) was used as a control diet and two different pea-proteins blends, a wheat protein/pea protein hybrid, a milk protein/pea protein hybrid, and a milk protein diet were used as experimental groups. Zebrafish from each tank were randomly selected at six points throughout the study and their body length was monitored; after termination, muscle tissue was extracted from the caudal region of two fish in each tank to measure the surface area (μm) of each muscle cell. A behavioural assay was also conducted to measure the response of each treatment group to a physical stimulus. We are currently conducting further research on molecular parameters using qPCR and 16s rRNA to investigate the differences in the gut microbiome and the expression of genes important for muscle growth, neurological development, and disease between the diets. We found that there was no significant difference in mean muscle cell size, growth over time, response to physical stimuli, or survivorship between both pea protein treatments and the control, but a significant difference between the milk protein treatments and the control was detected. These results, which use zebrafish as a model, suggest that pea protein may be a viable substitute for traditional protein sources and that milk protein should not be used exclusively as a replacement when implementing a vegetarian diet in humans.

Investigating the toxicity of copper nanoparticles to *Daphnia magna* within the context of agricultural pesticide runoff

Fleur Issac, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Many pesticides for the use of agricultural pest management have the potential to leach into the environment and cause detrimental effects on surrounding aquatic biota. Nanoformulations or nanopesticides (e.g., Copper nanoparticles (CuNPs)) are becoming increasingly popular as they are cost-effective, have improved solubility, and provide a greater surface area for application ensuring a more targeted mode of pesticide delivery. While useful for reducing pests in agriculture, nanoformulations exhibit novel properties that have unknown effects compared to their conventional counterparts as a result of their reduction in size. However, NPs are relatively unstable, aggregate, and fall out of solution, raising concerns about the long-term effects of their deposition in the environment and their effects on aquatic organisms. We aimed to compare and contrast the already established impacts of both acute and chronic toxicity of dissolved Cu to those of the CuNPs found in agricultural pesticides, as the toxicity of CuNPs is currently unclear. The 48-hour lethal median concentration (LC50) of Cu and CuNPs will be tested using the freshwater crustacean Daphnia magna, as they represent a critical species in many food webs. Then, chronic 21-day exposures will be used to understand the sub-lethal mechanisms of toxicity of these novel formulations allowing us to understand long-term exposure effects exposure. Understanding the potential toxicity posed by nanopesticides will allow for proper risk assessment and mitigation of any aquatic environmental exposure.

Contributions of custom fever responses to animal health

Haddad Farah, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Fever is one of the cardinal signs of infection in animals and humans, recognized for over 2500 years. Yet, there are still debates whether it is positive or negative for health. This is because current models are very limited in their capacities to show this value. Herein, I will take advantage of a cold-blooded teleost fish model to understand a fever response's attributes and assess whether specific responses are induced against different immune challenges. Our data demonstrate how even in these primitive animals, there are custom fever responses following different immune challenges. This further highlights the level of sophistication even at this early level of evolution. We took advantage of high-resolution behavioural tracking, molecular techniques, and functional assays in the utilized model. Using a validated Annular Thermal Preference Tank (ATPT) comprising different temperature zones maintained by water flow, we characterized these custom fever responses. A zymosan-induced peritonitis and a live Aeromonas veronii cutaneous infection models were used to study the behavioural response using the ATPT as a high-resolution custom setup. We found that the zymosan challenge led to an increase in temperature preference simultaneously with two lethargy behaviours indicated by a decrease in swimming velocity and migration rates across different thermal zones. Meanwhile, the behavioural thermoregulatory response against A. veronii was distinct from that against zymosan in terms of a longer duration of fever window and later timing of fever induction. These custom behavioural fever responses were paired with increased efficiency of leukocyte recruitment to the immune challenge site, early expression of proinflammatory cytokines, promotion of antimicrobial responses, rapid resolution of inflammation and bacterial clearance compared to control fish held at standard housing temperatures. These findings suggest essential benefits of fever to host survival and immune response.

Is habitat placement of ramat daughters in clonal smooth brome (*Bromus inermis*) based on mother plant growth

Heather Anderson, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Smooth Brome (Bromus inermis) is a grass species that will reproduce sexually and asexually through rhizomes creating clones/ramets. It is understood that these species will use “clonal integration” to differentially allocate resource acquisition roles in ramets. For example, one ramet focuses on soil resources while another acquires light. However, few studies have used an evolutionary-behavioural approach to investigate clonal plant growth patterns. Specifically, how the original “mother” plants' growth conditions would impact ramet placement when choosing between new conditions and the “mother” conditions. In our study, we grew B. inermis in three fertilizer levels (high, medium, and low). Pots were divided into four sections of equal volume, with a circular central patch containing the “mother” and one of the three fertilizer levels. Surrounding the central patch were three patches, two of different fertilizer levels and one matching the “mother“ conditions. Pending results, we anticipate that if ramet placement favoured the “mother's” birth conditions due to trait plasticity optimizing for certain conditions, the “mother” would be exhibiting imprinting. This is due to the “mother’s” experience

causing physiological changes that favour birth conditions over other ones. Clonal plants like B. inermis are invasive species that modify plant community structures. Understanding how the proliferation of clones changes with abiotic conditions experienced by founding "mother" plants may allow for better predictions of how these invasives impact ecosystems.

Functional characterization of goldfish (*Carassius auratus*) leukocyte immune-type receptors: Examining the effects of cytoplasmic tail region splicing events

Hussain Al-Rikabi, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Innate cellular defence mechanisms such as phagocytosis are in part mediated by the actions of conserved immunoregulatory receptors-types and their intracellular signaling networks. The evolutionary conserved nature of many of these receptors across vertebrates provides an opportunity to understand vertebrate immunity by allowing us to study such processes within a range of model systems, including fish. In 2006, a novel and diverse family of leukocyte immune-type receptors (LITRs) in channel catfish (Ictalurus punctatus) were identified. Phylogenetic and sequence analyses showed that LITRs belong to the immunoglobulin superfamily (IgSF) and they are related to mammalian Fc receptors (FcRs) and FcR-like protiens. For my research, two LITRs of interest are the goldfish (Carassius auratus) CaLITR2.0 and CaLITR2.1. These receptors are identical except for a 30-amino acid deletion in the cytoplasmic tail (CYT) region of CaLITR2.1, which includes a specific tyrosine (Y) motif potentially involved in cell signaling. This deletion is due to an alternative splicing event and implicates targeted changes in LITR CYT regions for the fine-tuning of immune cell effector functions. Using our established ImageStream-based phagocytic assay as a model for examining LITR immunoregulatory potential(s), functional characterization and comparisons of CaLITR-types was investigated. This presentation will showcase the effects of CYT region motif splicing events on the functional capacity of fish LITRs.

Optimization of bioautography in screening antimicrobial phytochemicals from *Origanum vulgare* and *Eugenia caryophyllus* steam distilled extracts

Inder Singh, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

As multidrug-resistant bacteria increase in prevalence, alternatives to traditional antibiotics are needed to mitigate health and economic burdens. Plants are a possible source of new compounds since they represent chemical libraries containing many effective antimicrobial phytochemicals. However, high cost and time burdens are associated with traditional bioassay-guided isolation of plant phytochemicals, delaying breakthroughs. Bioautography, a highly customizable technique that combines agar diffusion assays with thin-layer chromatography (TLC), significantly reduces shortcomings associated with traditional bioassay-guided isolation. This study investigated the application of bioautography in screening for antimicrobial phytochemicals using steam-distilled oil mixtures of Origanum vulgare and Eugenia caryophyllus as models of phytochemical extracts. Oil mixtures were spotted onto TLC plates, separated using ethyl acetate and hexane solvent systems, and overlayed with Mueller-Hinton (MH) agar streaked with Escherichia coli. Following incubation, inoculated agar plates were examined for zones of inhibition (ZOI), indicating the antimicrobial activity of phytochemicals separated from oil mixtures. TLC solvent systems, the volume of poured MH agar overlay, triphenyl tetrazolium chloride (TTC) application, and oil mixture concentrations were examined to optimize the production of discernible ZOI on agar plates. Discernable ZOI were obtained using TLC plates spotted with 1:10 oil to acetone solutions developed in 3:8 ethyl acetate to hexane. Optimal ZOI were obtained using these developed TLC plates when overlayed with 40mL MH agar and pre-sprayed with 2% TTC before bacterial streaking. Overall, bioautography represents a promising alternative to traditional bioassay-guided isolation, but additional work must be done to optimize this technique for use with other plant-derived extracts and bacterial species.

Understanding the mechanism of toxicity from naphthenic acids in oil sands process-affected water in *Daphnia magna*

Jenelle McCuaig, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The waste by-products of oil and gas extraction have the potential to be environmentally devastating. Oil sands process-affected water (OSPW) is generated from bitumen extraction in the oil sands region of Northern Alberta and is stored in large human-made tailings ponds that contain many different contaminant by-products, such as naphthenic acids (NAs). The NA fraction has been identified as the most toxic component, and there is very little understanding of the chronic effects of these

slowly degrading compounds. Acute 48-hour lethal concentration studies were assessed to understand the sensitivity of Daphnia magna to NAs. The calculated LC50 was 70.4 mg/L (95% CI 42.2-100). Chronic, multigenerational studies will follow using environmentally relevant concentrations of NAs, which may occur from OSPW spills, potential seepage or release. Overall, it is expected that chronic exposure to NAs will negatively impact growth, survival, and reproduction in D. magna, as well as alter key proteins needed for oxidative metabolism. Molecular analyses (qPCR and proteomics) will be conducted to identify the mechanisms of toxicity. This research will help define and implement remediation timelines, priorities, and policy pertaining to tailings pond management while providing insight into potential ecosystem recovery.

Quantifying the impacts of wildfires on drinking water quality in forested watersheds on Vancouver Island, BC

Jeremie Mahaux, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Many communities in western Canada rely on forested surface waters for access to clean drinking water. However, forested watersheds are very susceptible to disturbances like wildfire, which are predicted to increase by 50-118% in Western Canada over the next century. Wildfires have a major influence on forested watersheds, altering ecosystem processes that can directly impact water quality. Subsequent precipitation events can transport the products of wildfire into streams, causing altered loads of sediments, key nutrients (e.g., nitrogen and phosphorus), and dissolved organic carbon – all of which can be problematic for water treatment. The water quality consequences vary greatly depending on landscape characteristics (watershed hydrology, vegetation, and soil type) and fire behaviour (intensity, area burned, patchiness). It is therefore crucial to build resilient systems and develop comprehensive source water protection plans that take climate change and its consequences into account. I am investigating the water quality impacts from 8 wildfires that occurred in central/southern Vancouver Island and span a range of ages, sizes, and burn intensities. Using a combination of synoptic and targeted sampling, I sampled 40 streams, including 22 burn-affected streams and 18 unburnt reference streams between May 2022 and January 2023. These samples will allow me to track the origins of the in-stream material and describe fire-driven changes in water quality, with a particular eye towards drinking water treatment. I hope to help answer questions like how do the consequences of wildfires of different size and severities compare to one another? How do those effects change over time? Does natural landscape/seasonal variation overwhelm the impacts of wildfire? This will help local water purveyors better understand and overcome the wildfire consequences unique to their environment so they can continue delivering safe high-quality drinking water.

Toxicological effects of artificial sweeteners on embryonic and larval zebrafish

Jillian Sims, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Artificial sweeteners (ASWs) are emerging contaminants that have poor metabolism in the human body and persist in our environment after excretion into our wastewater. ASWs are highly integrated into human food consumption in low-calorie diets, as well as in veterinary pharmaceuticals, personal care products, and farming. Through wastewater systems, large amounts of artificial sweeteners such as sucralose, cyclamate, aspartame, and acesulfame, are being discharged unchanged into sensitive aquatic environments and groundwater. Additionally, the transformation of ASWs may lead to the formation of toxic substances and adversely affect marine life and aquatic ecosystems. The environmental potential for accumulation or transformation of ASWs and their metabolites into other toxicants is of concern. In addition to their persistence in the environment, ASWs have unique chemical structures that are likely to elicit a chemical response within Danio rerio. ASWs have been shown to impact learning and memory and disturb neurotransmitter functioning in the brain of adult zebrafish. At this time, only adult zebrafish have been exposed to artificial sweeteners to observe toxic effects; however, it is important to consider the impacts at an embryonic and larval life stage, both critical stages of development. In my preliminary research, fertilized zebrafish embryos will be exposed to varying concentrations of artificial sweeteners and observed up to 7dpf. For all artificial sweeteners, toxicity endpoints will include mortality and unstimulated behavioural swim tests. Embryonic and larval development will additionally be recorded and scored on anatomical abnormalities and hatching rate. To examine toxicological effects on neurological profiles, 1-2 sweeteners will be selected for further behavioural swim tests – novel tank test, startle response, and light/dark stimulation.

The potential of canola and field pea intercrops in the management of diamondback moth, *Plutella xylostella* (lepidoptera: plutellidae) in Alberta, Canada

Jose M. Correa Ramos, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The diamondback moth, Plutella xylostella, is a major pest of Brassicaceae crops worldwide including in the Canadian prairies where the moth's larval stage feeds on the leaves of canola and can cause economic damage through yield loss. Current management practices in Alberta include chemical control via insecticides and biological control with hymenopteran parasitoids like Diadegma insulare and Microplitis plutellae. There is room to include cultural management practices in the control of P. xylostella, including intercropping to reduce damage in canola and promote increased biological control services. Intercropping, the planting of more than one crop in a cropping area, has the potential to be a sustainable way to control P. xylostella without using insecticides and limiting the evolution of insecticide resistance. My project focuses on the impact of a canola and field pea intercrop (peola) on the behaviour of P. xylostella and its specialist larval parasitoid, D. insulare. In several laboratory-caged experiments, I am testing the effect of peaola intercrops under different fertilizer regimes on P. xylostella oviposition preference and larval feeding damage. I will further test the host finding and acceptance behaviour of D. insulare in intercropped systems by examining the parasitism rates in these systems. In field trials, I will measure the colonization rate of P. xylostella in intercropped vs. monocropped fields. My results will help inform better-integrated pest management practices for this major worldwide pest and develop long-term sustainable solutions that aim to reduce the reliance on insecticidal applications for management.

Chemical inhibition of novel protein kinases in *Arabidopsis thaliana*

Joselyn Steyer, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Gene expression is an essential process in Arabidopsis thaliana, by which a gene is transcribed then translated to produce a protein needed for a specific function. There are many proteins that are involved in this process, including protein kinases and phosphatases. Protein kinases are enzymes that regulate the function of other proteins by phosphorylating specific amino acids of the target protein, this can induce a change in the target to have an inactive or active form of the protein. The Uhrig lab has recently discovered a novel family of protein kinases responsible for phosphorylating proteins central to the regulation of gene expression. These protein kinases regulate the function of these gene expression proteins by phosphorylating specific amino acids of the target proteins to regulate their intracellular function. The activity of these protein kinases, although well studied in humans, is relatively unexplored in the Arabidopsis plant model system. Using known chemical inhibitors targeting this family of protein kinases, we explore the molecular-cellular effects of disrupting their function using a combination of transcriptomics, proteomics, and phosphoproteomics. Here, we analyze the enzymatic activity of these protein kinases via in vitro kinase assays and compared the activities of the inhibited and uninhibited proteoforms. Correspondingly, data generated here, in conjunction with the on-going research efforts of the Uhrig lab, further our overall understanding of how this family of protein kinases function in plants.

Potential impacts of black bear predation on boreal caribou population dynamics

Liam Horne, *MSc Student [1]*
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Boreal woodland caribou (Rangifer tarandus caribou) populations are declining across their North America-wide range. The most immediate cause of these declines is predation. Black bears (Ursus americanus) can be significant predators of caribou calves, but the extent of predation and whether they actively search for or incidentally encounter calves is poorly understood. In our study system in the western boreal forest, black bear density is estimated to be an order of magnitude higher than caribou density, suggesting that bear predation of calves must be a rare event or else all calves would be predated. In the absence of direct evidence of predation, we used a combination of location data and video-collars to evaluate whether black bears change their habitat use and/or behaviour in response to a pulse of caribou calves. We also used a simulation approach to quantify the probability that calves will be encountered by bears. We found that bears used calving habitat the least during peak calving, and behaved similarly while in calving habitat compared to upland deciduous. Our simulation demonstrated that bears have the potential to encounter most caribou calves, and that calves born after peak calving were more likely to be encountered by bears. Our findings suggest that bears in our study area are not actively searching for caribou calves, which is consistent with caribou-bear systems in the eastern boreal forest. Our simulation suggests that there are potential evolutionary

pressures for caribou to calve early and synchronously. Additional work is needed to understand why most simulated calves were encountered by bears, yet calf predation by bears must be rare to achieve empirical recruitment rates.

Effects of parasite exposure on host reproduction

Lisa MacLeod, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The presence of a natural enemy (predator, parasite) can have non-consumptive effects on organisms in the form of changes in behaviour, physiology or morphology. Non-consumptive effects pertain to the responses when death or consumption does not occur, but there is still a cost associated with the interaction (e.g., reduced mating or foraging success, energy income reduction, etc.). These costs then lead to trade-offs because organisms possess a finite amount of energy that they allocate to various life processes, including immunity and reproduction. While research has focused on the non-consumptive effects of predators on potential prey, parasite-host relationships are also believed to have similar outcomes. Using the Drosophila nigrospiracula – Macrocheles subbadius system, I tested how exposing flies to ectoparasitic mites prior to reproduction affects fecundity during the reproductive period. I hypothesize that non-consumptive effects during pre-copulation exposure will result in a trade-off between parasite defense and reproductive function. I predict this trade-off will result in decreased pupation and adult eclosion rate, as well as decreased body weight for the offspring of females exposed to M. subbadius. Investigating the non-consumptive effects of parasite-host relationships is an important step toward understanding the ecology of fear in the context of infectious diseases.

Multilocus DNA barcoding in identifying unknown soft coral species of anthelia (*Octocorallia*)

Mannraj Pataria, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

There are an estimated 1-9 million species of corals yet to be discovered. Anthelia is a species of soft coral that belongs to the Xeniidae family within Octocorallia. The Xeniidae family of soft corals are of interest due to their ability to rapidly recolonize disturbed reefs, which have become more prevalent with global warming. Octocorallia also contains some of the most valuable corals used in jewelry. Identifying corals not only contributes to its conservation and our knowledge of its evolution, but also prevents fraudulent coral jewelry and the overharvesting of coral beds. However, morphologically identifying corals is very difficult and is further exacerbated when it is polished and carved into jewelry. Instead, multilocus DNA barcoding can utilize the genetic material of corals to reveal an accurate classification of species. Specifically, genetic loci in the mitochondrial or nuclear genes can be used to tag and classify corals, with referencing done to genetic databases such as GenBank or NCBI.

Ferritin assembly dynamics

Mariane Khoury, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Iron is an essential micronutrient for nearly all organisms. In pro- and eukaryotes alike, highly regulated molecular pathways ensure that iron is incorporated into protein cofactors such as heme or iron-sulfur clusters. Iron overload or deficiency contributes to the development of harmful free radicals; therefore, iron levels must be tightly regulated on both systemic and cellular levels. Ferritin is the primary iron-storage molecule, it is a heteropolymer composed of H (heavy chain) and L (light chain) subunits. In Drosophila, ferritin is encoded by the ferritin 1 heavy chain homolog (Fer1HCH) and ferritin 2 light chain homolog (Fer2LCH). In insects, ferritin is secreted from cells and predominantly found in the hemolymph (“insect blood”), whereas most vertebrate ferritin is found intracellularly. As such, ferritin may also systemically deliver iron, but details are lacking. While the molecular function of ferritin nanocages is to store iron, many aspects of how ferritin is assembled remain unclear. We hypothesize that assembly is highly regulated and a previous report suggested that the subunits are kept separated before assembly is initiated. To study assembly dynamics, I will use two fly lines, each carrying a tagged version of either the H or L chain instead of the endogenous gene (“knock-in”). Specifically, Fer1HCH carries a GFP reporter (green) whereas Fer2LCH is tagged with mCherry (red). This allows me to generate flies with both reporter knock-ins and map the distribution and appearance of the GFP and mCherry signals in the developing animal (tissue and cellular level). In addition, I will carry out experiments to test whether the tagged ferritin nanocages assemble into functional units and capable of

storing iron. These studies will allow me to examine whether the two genes are co-regulated and whether the assembly of the two subunits underlies temporal control.

Evaluating the Agena MassARRAY technology for characterizing CYP2C19 and CYP2D6 haplotypes

Megana Thamilselvan, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Pharmacogenomics (PGx) aims to use the genetic information of an individual to personalize drug prescribing. There are studies that show that PGx testing before prescription may increase efficacy and cost-effectiveness of treatment. When considering psychiatric drugs, CYP2D6 and CYP2C19 are the two most well-studied enzymes for their associations with clinical effects; both are cytochrome P450 enzymes that are involved in drug metabolism. CYP2D6 metabolizes up to 20% of all licensed medications and CYP2C19 metabolizes up to 7%. Different people have different strings of variants, or haplotypes, of these genes, which affect drug metabolism. Therefore, when prescribing drugs metabolized by CYP2D6 or CYP2C19, adjusting the dose and choice of drug according to the patient's haplotypes can lead to better treatment outcomes. CYP2D6 is one of the most variable human genes, with haplotypes including SNPs and a variety of structural variants. CYP2C19 has fewer haplotypes, comprising SNP variants, with structural variants just beginning to be studied. The degree of variability and the nature of the structural variants makes it highly challenging to accurately characterize CYP2D6 haplotypes. Agena MassARRAY determines haplotypes using PCR amplification and mass spectrometry. In this project, we used DNA samples for which we already had data, to evaluate the ability of MassARRAY to accurately detect haplotypes. MassARRAY was able to accurately call CYP2C19 haplotypes for 98% of the analyzed samples, but only 34% had accurate calls for CYP2D6. This work is important because in order to implement PGx in a clinical setting, we need methods of genotyping that are rapid, accurate and cost-effective. As such, it is an ongoing effort to evaluate different methods to see which ones are suitable for different clinical uses. Our results show that Agena may be used for genotyping CYP2C19, but needs to be improved for CYP2D6 haplotype detection.

Optimizing trapping strategies to reduce ecosystem impacts of European green crab (*Carcinus maenas*)

Milène Wiebe, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Invasive species have continued to spread globally over the past decade, potentially damaging habitats and increasing competition and predation on native species. These impacts are not only felt within the system itself but can result in losses to human populations if the habitat supports species of cultural or commercial importance. The European green crab (Carcinus maenas) is a particularly concerning invader impacting coastal natural systems and communities and is expanding northward on Canada's Pacific coast. In collaboration with the Heiltsuk (Haíłzaqv) Integrated Resource Management Department of the Haíłzaqv First Nation, this project focuses on determining the effort necessary to reduce the adverse effects of green crabs on clam populations within the Territory. Specifically, we aim to determine the removal effort necessary to decrease green crab below abundances that deplete clam populations in the region. Removal is being conducted via trapping, with trapping efficacy quantified by tracking green grab catch per unit effort, size structure, and sex ratios in relation to the density of clams at invaded beaches over time. Monitoring size structure also allows us to evaluate if an increase in population abundance is occurring due to the removal of cannibalistic adults that suppress the growth of juveniles from the population, an unintended consequence that has been found in other trapping efforts. We predict that a catch of 20 rate crabs per trap will be sufficient to prevent further declines in clam populations. Our results will inform efforts by communities along North America's Pacific coasts who are investing considerably in controlling green crab populations by optimizing trapping that will support the efficient allocation of resources.

Rolling in the dumpy: Developing *Caenorhabditis tropicalis* as a molecular model system

Montana Bobinski, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The Pilgrim laboratory has demonstrated that the species Caenorhabditis elegans is robust for studying the function and evolution of genes that regulate developmental decisions. In C. elegans, the number of sex (X) chromosomes determines the observable sex of the organism, either male (XO) or hermaphrodite (XX). However, mutations in key genes result in animals that ignore this chromosomal signal in sex determination. For example, both XX and XO animals with mutations in the fem-2

gene develop as female. Furthermore, molecular analysis of the sex determination genetic pathway in C. elegans and C. briggsae, a second male/hermaphrodite species, has shown that many orthologous sex determining genes are not significantly similar in DNA sequence. Utilizing the assumption that high DNA/protein sequence conservation will identify genes possessing similar developmental roles to those in C. elegans and C. briggsae, my current graduate research project entails the use of a third closely related male/hermaphrodite Caenorhabditis species, C. tropicalis, chosen due to its currently undefined sex determination pathway. This provides an opportunity to identity the species' sex-determining genes and their functional and evolutionary relationships to orthologous genes found in C. elegans and C. briggsae. To induce mutations in these C. tropicalis sex determining genes, CRISPR/Cas9 was adapted for novel use in C. tropicalis. However, with most mutations being recessive in a heterozygote, effective use of CRISPR/Cas9 in C. tropicalis required the development of a dominant co-transformation marker. This was developed via a dominant missense mutation in the C. tropicalis homologue of dpy-10 which produces obvious rolling and dumpy phenotypes in heterozygous and homozygous organisms, respectively. This mutation was confirmed through sequencing and will be instrumental in the effective use of CRISPR/Cas9 in C. tropicalis as an emerging model of studying developmental biology and genetics in metazoans.

Sty1874, a novel lipoprotein, activates typhoid toxin expression through PhoPQ in *Salmonella typhi*

Paris Brown, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

This project identifies a novel lipoprotein predicted to play a key role in bacterial gene regulation, including that of the deadly typhoid toxin, by modulating Salmonella Typhi's two-component system PhoPQ. Bacteria utilize host cues in their environment to sense information about their surroundings and regulate internal processes important for survival, replication, and virulence. They often do so using two-component systems, including PhoPQ. For Salmonella enterica, PhoPQ regulates responses to external changes by altering gene expression for many cellular functions, including production of the typhoid toxin upon infection. Typhoid toxin, produced by S. enterica serovar Typhi, is the causative agent of the severe and often fatal typhoid fever. A genetic screening of S. Typhi mutants identified a putative lipoprotein that upregulated typhoid toxin expression via stimulation of the PhoPQ system. We show here that this lipoprotein, named Sty1874, can stimulate typhoid toxin genes in a PhoPQ-dependent manner. However, Sty1874 is not required for PhoPQ functionality, suggesting that Sty1874 may act to turn on PhoPQ genes under specific circumstances. Because the sty1874 gene is downstream of a predicted RpoE promoter, we predict that activating conditions for the alternate stress factor sigmaE (σE) will cause σE to bind to the promoter and turn on expression of Sty1874. This could represent a pathway S. enterica has adopted to tune its PhoPQ regulon to the alternate stress response. To elucidate the mechanism behind Sty1874 interaction with PhoPQ, we are currently working to determine the cellular location of Sty1874. We hypothesize that it embeds itself in the outer membrane of the bacterium to stimulate PhoPQ. As Sty1874 is found only in S. enterica and not in other PhoPQ-expressing enterobacteria, characterization of this lipoprotein will expand our understanding of the evolutionary adaptations of the PhoPQ system and typhoid toxin expression within Salmonella.

Development of agricultural & clinical phage therapy against the emerging pathogen *Burkholderia gladioli*

Philip Lauman, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The increasing global spread of antimicrobial resistance is an imminent danger to public health worldwide. One multidrug resistant species of particular concern is Burkholderia gladioli, which has historically been identified primarily as a devastating pathogen of several plant species - but has been increasingly recognized in recent years as a severe, opportunistic, nosocomial human pathogen which is associated with particularly poor prognosis among patients afflicted with cystic fibrosis and chronic granulomatous disease. Although B. gladioli's pathogenicity in both agricultural and clinical settings makes it an excellent candidate for phage therapy, few phages targeting this organism have been identified and characterized. Although B. gladioli is genetically distinct from the members of the Burkholderia cepacia complex (Bcc), we identified several Bcc-targeting phages which are nevertheless able to infect both clinical and environmental strains of B. gladioli. We therefore optimized these phages against B. gladioli in vitro with the aim of investigating the ability of these phages to control B. gladioli infections in two experimental models: ex planta in onion bulb slices of Allium cepa and in vivo in larvae of the greater wax moth Galleria mellonella. Since existing descriptions of the agricultural virulence of B. gladioli are limited to qualitative observations which are impractical for assessing the therapeutic effectiveness of phages, we devised a novel quantitative parameter, the ex planta virulence index (xPVI), for evaluating the virulence of pathogens such as B. gladioli in A. cepa - and we are currently investigating the generalizability of this approach. We then tested several Bcc phages targeting

B. gladioli in both ex planta and in vivo settings, and found that these phages are able to both prevent and treat B. gladioli infections in these model organisms - implying that Bcc phages may be suitable for agricultural biocontrol and clinical therapy against the emerging pathogen B. gladioli.

Evaluation of capture methods and seasonal movement of alfalfa weevil in alfalfa fields grown for seed in Alberta

Priyatha Chennamkulangara, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The alfalfa weevil (Hypera postica (Gyllenhal), Curculionidae: Coleoptera) is major pest of alfalfa (Medicago sativa L., Fabaceae) that feeds on foliage during the pre-bloom to the early bloom stages. High density larval populations can cause significant damage through leaf skeletonization and adult weevils also feed on foliage. This study examines adult weevil movement in the field at various times throughout the growing season. The study was conducted in five alfalfa fields grown for seed in southern Alberta in 2021 and 2022 which were monitored weekly using various capture methods including sweep samples, soil samples, malaise traps, yellow sticky traps, and pitfall traps. Alfalfa weevils were recovered from sweep and soil samples and pitfall traps. Sweep samples caught a significant number of the adult weevils in both the years. Pitfall traps positioned on the edge of the field, captured equal numbers of adult alfalfa weevils as traps positioned in the interior of the field. On the other hand, more individuals of other weevil species were captured in pitfall traps placed on the edge of the fields.

Evidence of hierarchical adoption of provisioning tactics in peregrine falcons (*Falco peregrinus tundrais*)

Rebekah Alice McKinnon, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Adult birds should increase investment in parental care in response to increasing nestling demand (i.e., older nestlings, larger broods). This may be achieved by increasing provisioning rate at the expense of self-care, and/or reducing prey selectivity. When these tactics prove insufficient to satisfy demand, parents may strategically shift their preference or aversion for variable foraging options. This is termed variance-sensitivity and is vastly understudied to date. Evidence for strategic behavioural shifts in existing studies varies across years suggesting an influence of year-specific environmental conditions. It is suggested that adoption of tactics to cope with increasing brood demand is hierarchical, with variance-sensitivity being a 'last resort' when parents are faced with challenging conditions. Parents should have plastic provisioning behaviour within the confines of year-specific conditions. Thus, in years where parents are exerting more energy to meet the demand of an average sized brood (intercept), they should be less able to reduce the time between successive provisioning visits (inter visit interval, or IVI) with increasing demand (slope) resulting in higher residual variance i.e., there should be negative among-year covariance between intercept and slope, intercept and variance, and positive covariance between slope and variance. We monitored breeding Peregrine falcons using motion-sensitive cameras at nest sites. Provisioning data, primarily IVI, was then extracted from collected images for 7 study years (2013-2019). We found parents decreased IVI with increasing nestling demand across all study years. We also found that intercept, slope and variance differed across study years. However, we did not find evidence in support of the anticipated covariances between intercept, slope, and variance. We discuss explanations for this lack of support, particularly in reference to difficulties associated with modelling heterogeneous residual variance and provide suggestions for how researchers addressing similar questions in future may overcome these challenges.

Anti-pyresis during infection induces molecular changes in goldfish thrombocytes

Reema Joshi, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

White blood cells are fundamental to host defense against pathogens. We have recently shown that fever impacts recruitment and functional phenotypes of white blood cells throughout the acute inflammatory process (Peisler and Kubes 2019;Havixbeck et al 2016; Haddad et al, submitted 2023). Furthermore, we have shown that antipyretics (drugs frequently administered in response to fever or wound pathophysiology) disrupt benefits of the natural fever response. Recently, thrombocytes in goldfish (Carassius auratus) demonstrate functions beyond the canonical roles of coagulation and wound healing pathways (as seen in mammalian platelets). Goldfish thrombocytes have shown to hold phagocytic capabilities, and release key molecules involved in pro and anti-inflammatory pathways (Nagasawa et al, 2014).While some primordial functions of thrombocytes have been identified, their contributions to the induction and control of acute inflammation are unknown. Due to the potent capabilities of thrombocytes such as modulation of host response and pathogen survival, it is

essential to investigate their role in infection, particularly during antipyresis. This project elucidates the involvement of thrombocytes in the acute inflammation and fever processes via qPCR techniques. Overall, fever modifies the genetic expression of thrombocytes along key time points during infection. The administration of antipyretics results in slower wound healing and prolonged upregulation of thrombocytic genes.

Trend analyses on cyanobacteria community in three Albertan lakes

Renz Layugan, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

A key challenge of freshwater sciences is to better identify and predict trends in harmful algal blooms (HABs). Public perception is that HABs have worsened despite scientific knowledge gaps concerning the environmental drivers of their overall intensity and taxonomic composition. We compiled cyanobacterial data generated for three Albertan lakes over the past 10 years. Then, we performed trend analyses to identify the best suite of environmental variables that explained temporal variance in total cyanobacterial abundance and its taxonomic composition. Univariate trend analyses revealed that cyanobacterial abundance had declined significantly in Pigeon Lake between 2012 to 2022, while it remained relatively unchanged in Wabamun Lake and Lac La Biche. Nitrogen and underwater light availability best-explained variance in HAB intensity in Pigeon Lake, while phosphorus and redox potential best captured its taxonomic variance. In contrast, ammonia, phosphorus, and redox potential were identified as predictors of HAB intensities in Wabamun Lake. Our findings indicate that HABs have not increased in these three Albertan lakes despite increased public concern over these events. We also conclude that HAB dynamics are highly lake-specific and likely controlled more by local rather than regional factors.

Viral variance: QTL screening for variation in virus susceptibility in honey bees

Robert X. Lu, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

As in many other organisms, viruses have been linked to serious illness in honey bees (Apis mellifera), and thus significantly contribute to ongoing worldwide colony losses – a major threat to agricultural pollination. Israeli acute paralysis virus (IAPV) is a particularly virulent pathogen of honey bees, able to infect all castes and life cycle stages. While it has been observed that individual susceptibility toward IAPV infection varies across different genetic lineages, little is known about the underlying causes of these differences. This study sought to identify quantitative trait loci (QTLs) for survival following an acute IAPV infection. Experimentally, two lines differing in IAPV susceptibility were backcrossed and resulting worker offspring were tested for IAPV susceptibility. This was done via IAPV inoculation followed by monitoring for survival over a 3-day period. From this screening, the 129 most and least susceptible individuals were selectively genotyped by marker sequencing and assessed for the natural presence of other viruses. Survival following IAPV treatment and natural viruses titres were then related to the approximately 54,000 variable SNP markers in the mapping population. I will report my findings on the genetic architecture of IAPV susceptibility and discuss the locations of candidate causative genes in honey bees. I will also discuss the prospect of breeding virus-resistant honey bees for sustainable beekeeping and expound on how this analytic process can be applied to the management of other honeybee viruses.

Developing a detection assay to quantify polysialic acid expression in mice

Ronak Patel, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Polysialic acid is a complex carbohydrate structure composed of alpha 2,8-linked sialic acid monomers. The attachment of this glycan to proteins of certain cells following translation has been shown to hinder immune responses through influencing migration, maturation and cell-to-cell signaling processes. Previous studies have indicated expression of Polysialic acid in immunocompromised populations including cancer patients is positively correlated with progression of the disease. The mechanism through which glycosylation of proteins causes immunosuppression is not well understood and further research into identifying which proteins are glycosylated is required. The development of a reliable and sensitive method for measuring Polysialic acid expression in biological samples such as serum is needed to further our understanding of its effects. Currently, there is no known method to accurately quantify Polysialic acid in mice. This aim of our project is to develop such a detection method using an ELISA assay. We are in the process of constructing a single-chain variable fragment primary antibody against Polysialic acid. This antibody has been expressed in E.coli which allows it to be used as a substitute for

commercially available antibodies produced in mice which cannot be used to conduct studies involving mice serum. The development of this detection assay will sever as valuable tool to study the role of Polysialic acid in mice and will enhance our understanding of its involvement in immunosuppression.

Factors associated with coyote dens and scats could be used to mitigate human-coyote conflict

Sage Raymond, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Urban coyotes (Canis latrans) are associated with both physical conflict (e.g., attacks) and zoonotic disease risk, which include the zoonotic tapeworm Echinococcus multilocularis that sheds eggs with coyote scats. Both forms of conflict might be mitigated with more understanding of how the unique ecology of coyotes in urban areas causes humans and coyotes to overlap. We advanced this information by identifying locations of coyote dens and scats in Edmonton, Alberta where the tapeworm is especially prevalent, and comparing both to environmental predictors and reports of coyote conflict submitted by members of the public. We also tested a subset of scats for infection with the tapeworm. Among 120 detected dens, we found few broad scale environmental predictors, but a preference for dense vegetation on east-facing slopes, often with surprising proximity to buildings, and a higher prevalence of reports by the public. Among 1263 scats, deposits were common near human residences, often contained anthropogenic food, and were sometimes fed upon by magpies (Pica hudsonia), which may redistribute microscope tapeworm eggs in their own feces. Among 269 scats we tested, infection was more common in scats that contained anthropogenic food or were deposited near compost. Our results provide environmental predictors that might be used to mitigate risk of conflict associated with urban coyotes, such as by thinning vegetation that could attract denning coyotes near residential areas, securing compost associated with infection and other coyote attractants, and educating the public about the potential for tapeworm eggs to accumulate in locations frequented by coyotes.

Prophylactic treatment with anticonvulsants in a zebrafish model of post traumatic seizures, demonstrates seizure and tau pathology reduction

Sam Tan, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Traumatic brain injury (TBI) is a common affliction found from mild to severe levels in millions of individuals worldwide. It is also a known risk factor for tauopathies, dementia, and other neurodegenerative diseases. Tauopathies in particular describe a family of neurodegenerative diseases characterized by the abnormal formation of tau aggregates like chronic traumatic encephalopathy (CTE) and Alzheimer's. Seizures have also been shown to be a mechanistic link between the prion like spreading of tau and cell death surrounding neurodegeneration. We have utilized a novel TBI method, replicating blast induced TBI and a tauopathy reporter in zebrafish, able to effectively report the presence of human tau aggregates. With these tools, we have determined that anticonvulsant treatment of zebrafish with post traumatic seizures after TBI, reduces tau aggregates, cell death, and seizure activity. We have developed and applied a manual scoring technique to quantify seizures and it has helped demonstrate that anticonvulsants reduce behavioural seizure activity in TBI treated fish. A goal of this project, is to test further anti-epileptic drugs (AEDs) and their synergistic effects with other AEDs, where we will examine reduction in tau inclusions and seizures. Calcium imaging of brain activity (CaMPARI) is another tool we are continuing to optimize for imaging brain activity during seizures and after anticonvulsant treatment. Future work includes removal of the receptors that bind to these AEDs with CRISPR gene editing to further elucidate the drugs' specificity and receptor necessity for the post-traumatic seizure phenotype in zebrafish. Treatments with the AEDs removal and TBI will demonstrate receptor importance in antiepileptic treatments. This investigation will allow us to build on ideas to further refine clinical treatment aspects of post traumatic seizures. In particular, this contributes to work seeking better clinical outcomes concerning Alzheimer's and other related neurodegenerative diseases.

Clonal imprinting behaviors in *Bromus inermus*

Samantha Sech, BSc Student [1]
[1] Faculty of Agricultural, Life & Environmental Sciences; University of Alberta, Edmonton, Alberta, Canada T6G 1C9

This presentation focuses on part two of a collaborative experiment with Heather Anderson. The research is conducted within the field of plant ecology focusing on intra-species plant behavior. Specifically, it studies whether Bromus inermus exhibits choice in optimizing clonal kin fitness and whether these choices may be likened to kin imprinting behaviours in some

animals. Part one measures the presence of kin fitness optimization using measurements of clonal kin placement in differing nutrient patches (low, medium, and high) which equally surround parents grown in a central plot core (low, medium, or high). Part two examines whether severing underground ties between parents and kin in each nutrient patch alters kin fitness by blocking their access to shared root networks that span across all nutrient gradients. It also tests whether B. inermus plants that are initially grown in one of the 3 nutrient gradients are primed to exhibit greater fitness when transplanted into soil of the same nutrient content or if higher nutrient levels are consistently preferred. This transplant study gives us greater perspective in examining why we might see certain patterns of kin placement in part one of the experiment. Optimization of kin fitness in part two is measured by analyzing kin placement among nutrient patches (angle and distance of kin from parent) as well as tiller growth from time of severing (severed and control tiller height). This research may help us gain greater insight into the relationships between clonal plants and their kin which have implications for the use and growth of B. inermus in rangelands as a forage crop.

The role of movement-dependent sensory feedback in post-embryonic neurogenesis

Shelby Sherlock, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Physical movement is a sensory experience that generates feedback which stimulates brain growth via neurogenesis, though how this feedback reaches the forebrain to stimulate this process is unknown. In zebrafish, the feedback generated by swimming/tail movement is transported via the peripheral nervous system through the dorsal root ganglion (DRG) to the hindbrain brain, however, this input alone cannot explain the mechanism by which sensory feedback drives neurogenesis. I hypothesize that bodily movement/tail displacement in post-embryonic zebrafish larvae generates sensory feedback that modulates developmental neurogenesis. To address this hypothesis, I have begun validating models of immobilization through behavioural monitoring that prohibits larval tail movement during development, including the use of both CRISPR/Cas9 mutants targeting the chrna1 gene, and a viscous methyl cellulose media. Once these paradigms have been validated, I will then test the effects of immobilization on neurogenesis primarily through histology-based analysis, looking for changes in the proportion of cell proliferation markers indicative of brain growth, such as phosphohistone 3 (PH3), between immobilized and control groups. Preliminary results suggest that larvae immobilized with methyl cellulose do exhibit a reduced amount of actively dividing neural cells compared to control larvae, and I expect to see similar results for larvae immobilized with the CRISPR/Cas9 knockout of the chrna1 gene. Because neurogenesis and physical movement are shared by all vertebrates, I expect these findings to be applicable beyond zebrafish and represent a shared mechanism through which the environment contributes to brain structure and function. It can also contribute to advances in non-invasive interventions based on sensory/physical therapies or environmental enrichment to improve brain developmental outcomes early in life.

Sperm-derived signals regulate female meiosis in the fertilized embryo

Shreyosi Bose, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The fusion of gametic cells is a fundamental process that ensures the survival and propagation of all sexually reproducing species. Gametes are produced when male and female germline cells undergo meiosis to form haploid sperm and oocytes, respectively. The fusion of sperm and oocyte (fertilization) gives rise to the diploid zygote, which eventually divides to form a multicellular embryo. Fertilization involves complex signalling pathways and strict regulation of the cell cycle. In most metazoans, oocytes arrest at multiple stages of meiosis to coordinate maturation with fertilization. In vertebrates, oocytes arrest at metaphase of meiosis II, and only complete division after fertilization. This indicates the presence of sperm-derived signals that trigger the completion of meiosis in oocytes, though little is known about such a mechanism. C. elegans is a microscopic hermaphroditic nematode, where spermatogenesis and oogenesis take place within the same germline. Due to this unique property and its short life span, C. elegans poses an ideal model to study sperm-oocyte signalling and post-fertilization development. The Srayko lab identified oocyte-specific proteins MEMI-1,2,3 (meiosis to mitosis), involved in the completion of female meiosis after fertilization. Loss of MEMI proteins causes embryonic lethality due to “skipped meiosis II”, a phenotype also observed when sperm fail to fertilize the embryo. This indicates the involvement of MEMI proteins in receiving a post-fertilization sperm signal. Supporting this hypothesis, a suppressor screen of a gain-of-function mutant, memi-1(sb41), identified multiple sperm components. Interestingly, sperm PP1 phosphatases and GSK3-like kinases, required for sperm development and motility, have been implicated in this pathway. This study provides substantial evidence

that paternal components play a crucial role in post-fertilization embryo development. In my talk, I will discuss the function and regulation of sperm components and their effect on post-fertilization embryonic development.

Sunscreens are better together: Understanding the differences in whole sunscreen mixture toxicity in *Daphnia magna* compared to isolated ultraviolet filter toxicity

Sidney Martin, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Ultraviolet filters (UVFs) are the primary active ingredients in sunscreen and skin care products that we use to protect ourselves from the sun's harmful UV rays. Their common use and introduction to the environment has made them a compound of interest for previous toxicological research, which has indicated that UVFs can have negative effects on aquatic organisms. Although individual UVFs have been extensively studied, information is lacking regarding the exposure of organisms to whole sunscreen mixtures. To address this, five different commercial sunscreen mixtures were acquired & tested with Daphnia magna to determine acute (48 h) and chronic (21 d) toxicity. The results from this study indicate that the toxicity of whole sunscreen mixtures does not match the expected toxicity of each individual UVF present within the mixture, as Daphnia survived long term exposure to sunscreen mixtures containing UVF concentrations far in excess of what has previously demonstrated to be lethal. Along with the altered toxicity, sunscreen mixtures reduced growth and molting, outcomes not observed with individual UVFs, indicating a different mechanism of action for sunscreen mixtures. This suggests that there are mixture effects associated with whole sunscreen products, leading to changes in the overall toxicity in these aquatic systems. Our results demonstrate that studies observing isolated UVF do not accurately reflect the toxicity of whole sunscreen mixtures that contaminate aquatic ecosystems.

How does the social context influence the sublethal toxicity of copper in threespine stickleback (*Gasterosteus aculeatus*)?

Sienna L Overduin, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Many animals, particularly fish species, take advantage of the benefits provided by group living including increased foraging, decreased predation, and social buffering. Social buffering is the reduction in stress experienced by individuals when in a group of the same species. However, sociality is not the only factor fish deal with on a daily or seasonal basis; changes in environmental variables due to climate change and anthropogenic stressors are leaving aquatic environments vulnerable. Up to date, minimal research has been performed to expand our understanding of the nexus between social standing and anthropogenic toxicity. Therefore, we sought to test the effects of copper (Cu), a common aquatic toxicant, under different social contexts in Swedish marine threespine stickleback (Gasterosteus aculeatus). We hypothesized that stickleback exposed to sublethal concentrations of Cu in isolation would experience a higher metabolic rate, critical thermal maximum (CTmax), and Cu accumulation as compared to stickleback exposed to Cu in pairs. To test this, fish were randomly placed in one of four experimental treatment groups: isolated control (single fish, no added Cu), paired control (two fish, no added Cu), isolated Cu (single fish, 300 µg/L of Cu), and paired Cu (two fish, 300 µg/L of Cu) for the duration of the experiment. Half the fish were measured for oxygen consumption (proxy for metabolic rate, MO2), whilst the remaining fish had their critical thermal maximum (CTmax) assessed. All fish were then euthanized and dissected with the organs (gill, intestine, liver, carcass) assayed for Cu accumulation. Overall, no difference was observed with respect to CTmax, while MO2 was altered as a function of sociality. The importance of understanding how sociality in fish alters the response to a given toxicant is rarely if ever investigated, but the social structure, and its role in fish metabolic rate and homeostasis cannot be dismissed.

Predicting reef fish abundance on coral patch reefs in the Florida keys, USA

Sofia Panzetta, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Patch reefs are small, isolated coral reef structures and are ecologically important habitats for coastal reef fishes and invertebrates in tropical and subtropical regions. In the face of worsening global and local stressors (e.g., climate change and pollution), they have become increasingly important as a pathway between juvenile and adult coral reef fish habitats. This study investigated the effects of biotic and abiotic factors on the abundance of two significant reef fish species: gray snapper (Lutjanus griseus) and bluestriped grunt (Haemulon sciurus). We partitioned the sub-adult L. griseus and H. sciurus patch

reef abundance records into model calibration and validation subsets using a random 70-30% train-test split. We then fit species-specific negative binomial regressions to the calibration data. We evaluated their predictive performance using the withheld species validation records. Using the models, we predicted species-specific abundances at validation sites where the fitted negative binomial model for sub-adult L. griseus had an overall predictive accuracy of 18.92%. However, when the predicted abundance was allowed within ± 5 of the observed fish count, the predictive accuracy of the fitted L. griseus model increased to 78.38%. Similarly, the sub-adult H. sciurus model had an overall predictive accuracy of 8.11% when used to predict the known fish counts. When held instead to a ± 5 fish range, the model's predictive accuracy increased to 67.57%. We hope this research will enable a more thorough investigation of the drivers of coral reef fish residency on patch reefs in the subtropical seascape of the Florida Keys, USA, where multi-scale interacting stressors continue to threaten the stability and functioning of coastal marine communities. Identifying the biogeophysical attributes of coral patch reefs that most strongly influence their use by migrating reef fishes is a critical step in planning effective habitat management and conservation programs.

Developing a method to immobilize Endo-N for studying polysialic acid

Sogand Makhsous, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Polysialic Acid (PolySia) is a glycan and linear homopolymer of Neu5Ac residues that are connected via α-2,8 linkages. In healthy human adults, polySia expression is limited to the nervous, immune, and reproductive systems and is upregulated in cancer and mental health disorders. However, the role of polySia in regulating systems during health and diseases is poorly defined. Endoneuraminidase-N (Endo-N) is the endo-sialidase that solely hydrolyzes α-2,8 linkages and is an important tool for studying polySia. We found that Endo-N is hard to wash out and stays associated with the cells. This could confound the results of previous and future studies on polySia. We have developed a protocol for immobilizing Endo-N using magnetic beads. In this method, we constructed and expressed recombinant Endo-N with an N-terminal Avi-tag. The Avi-tagged Endo-N was biotinylated with Bir-A and was immobilized by conjugating the enzyme with streptavidin-coated magnetic beads. For the proof of this study, we used NK-92 cells, which express a high level of polysialylated NCAM. The cells were incubated with the magnet-conjugated Endo-N and the enzyme was removed from the cells using a magnet. The immobilized enzyme was shown to be highly active in hydrolyzing polySia and getting removed from the cells. Magnet-conjugated Endo-N can be an effective mean to reveal the role of polySia in the biology of different systems as well as molecular mechanisms by which polySia participate in diseases.

Genetic engineering of M.album BG8 for pinene production

Umut Oktay, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Methanotrophs are bacteria that consume methane, a potent greenhouse gas, as their source of carbon. These bacteria hold the potential to convert methane to high-value products such as monoterpenes. Genetic engineering is a method to specifically enhance the production of such molecules from methanotrophs. Pinene is a monoterpene naturally produced by certain plants, yet its extraction from these plants can be labor-intensive. We are therefore aiming to provide an alternative method of pinene production by genetically engineering Methylomicrobium album BG8 with the ultimate goal of producing pinene from methane. This project involves two parts: The first include the demonstration of successful expression of exogenous genes in M. album BG8 and investigating the enzymatic activity of their gene products and the second step involves the cloning of Abies grandis pinene synthase gene into M. album BG8 with the ultimate aim of converting methane to pinene. Our results showed that xylE gene of Pseudomonas putida and PFE gene of Klebsiella pneumoniae were successfully cloned into BG8 and we successfully purified proteins encoded by these genes using His-tag protein purification method. We also determined that these enzymes are functional in BG8. We are currently trying to clone pinene synthase gene into M. album BG8 and this cloning step will be followed by the purification of pinene synthase and the determination of pinene synthesis capabilities of the engineered bacterium. Consequently, our results will demonstrate whether it is possible to exploit methanotrophs for the conversion of greenhouse gasses into valuable products.

ATP signaling in sneezing sponges and the evolution of coordination
Vanessa Ho, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Sponges (phylum Porifera), one of the earliest diverging metazoan lineages, lack a nervous system, yet they are able to sense and respond to their environment with coordinated contractions that expel water from the whole body. Contractions can be triggered by neuroactive molecules such as glutamate. Purinergic signaling often works together with glutamatergic signaling in the nervous systems of many animals, leading us to ask whether ATP also works with glutamate to coordinate contractions in sponges. Genes for glutamate receptors, as well as for ATP-activated purinergic P2X receptors, are found in several sponge transcriptomes & genomes. Using pharmacological approaches on the freshwater sponge Ephydatia muelleri - an emerging model system that can be easily cultured in the lab - we show that ATP triggers the expansion of excurrent canals, but prevents them from returning to their initial resting state. When incubated with apyrase, an enzyme that hydrolyzes ATP, sponges can undergo complete contractions when ATP is added, however when glutamate is added instead, the excurrent canals become constricted. Blocking purinoceptors with PPADS prevents glutamate-triggered contractions entirely. These data suggest an essential role of ATP in coordinating contractions, and that ATP and glutamate work in a balanced feedback loop to regulate sponge behaviour. Furthermore, our phylogenetic analysis of protein sequence alignments show that P2X receptors are highly conserved in metazoa and beyond. Our findings contribute new knowledge in understanding the physiology of sponges, and provide new insight into the evolutionary origins of the nervous system.

Poster Presentations in the Biological Sciences

Coyote-related experiences, knowledge, and perceptions among residents of Edmonton, Alberta
Abby Keller, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Coyotes (Canis latrans) are adaptable generalist carnivores that have expanded their range across much of North America and now thrive in many urban areas. In cities, abundant resources and a lack of persecution can lead to coyotes losing their fear of humans and becoming involved in conflicts with people and pets. Coyote sightings and human-coyote conflicts have increased over time, including in Edmonton, prompting a need for management strategies that reduce conflicts. Understanding the public's experiences with and perceptions of coyotes, coyote management, and factors that contribute to conflict can help inform identify areas of need for education. We conducted a survey of Edmonton residents (N=5926) in Spring 2022 to determine resident experiences, knowledge, and perceptions of coyotes. Most respondents (88%) had seen coyotes in the last year, and 45% of sightings occurred at close range (<50m). Anthropogenic food resources that attract coyotes were seen in neighbourhoods (87%) and greenspaces (52%). Respondents had generally positive attitudes towards coyotes, though concerns for children and pet safety were prevalent and perceptions of disease transmission risk were divided. Most respondents would report a coyote that was sick, injured, or being fed by humans to the City of Edmonton, and most respondents knew not to run from a coyote. Education was the most supported management option (89%), while lethal control was the least supported (8%). Additionally, most respondents were familiar (62%) and comfortable (52%) with using hazing tactics to deter a bold coyote. These findings provide valuable insights about the experiences with and perceptions of coyotes among Edmonton residents, which will inform ongoing education efforts. Further, the survey data will be used to investigate topics such as the potential for conflict over different management actions and the factors that predict whether an individual reports a coyote to the City of Edmonton.

Colorimetric analysis of L-carnitine: A biomarker for sheep pregnancy status and other human disease
Abby Kropielnicki, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

L-carnitine has been identified as a useful metabolite biomarker. In literature, it is reported that changes in serum/plasma L-carnitine levels along with other metabolite markers can be used to detect pregnancy in animals including sheep as well as various diseases in humans. The development of a portable carnitine detection system could be particularly useful for on-farm or in-clinic applications. There are several manufacturers that sell carnitine assay kits, but they are expensive and require multiple pipetting steps that are difficult to perform outside of a lab. Further, they are not designed for easy-to-use, one-step testing in a dry assay format stored at room temperature. Here, we describe a new carnitine assay that overcomes all mentioned challenges. This new carnitine acetyltransferase assay, which uses 5,5′-dithiobis-(2-nitrobenzoic acid) (DTNB) as

the colorimetric reagent, has been developed to provide an easy-to-handle, inexpensive colorimetric assay for carnitine detection and quantification in serum or plasma. Chromogen DTNB reacts with Coenzyme A (CoA) produced from the carnitine acetyltransferase reaction with the substrate L-carnitine to form a strong yellow color that can be spectrophotometrically measured at 450 nm. In addition, an economical method of deproteinization which utilizes a specialized polymer to rapidly precipitate proteins has been developed which is used in combination with the one-step L-carnitine assay when testing sheep serum samples. The dry reaction L-carnitine assay has a dose-response curve in both Milli-Q water and sheep serum with a coefficient of determination of 0.99 and performs 79% more effectively than the liquid assay. Reaction mixture and carnitine acetyltransferase enzyme were prepared separately with 25% w/v sucrose added to the reagents for lyophilizing. We believe this new, simplified carnitine assay has the potential to be taken to the field as a pen-side instrument that could be used by farmers, veterinarians, physicians, and even the general public.

Using behavioural neuroscience tests in zebrafish to quantify effects of the terpene, alpha-pinene, and its enantiomers
Andréa Johnson, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

Research into the effects of terpenes has been on the rise as a result of the recent Cannabis legalization in Canada. Cannabis terpenes have been shown to possess a wide range of medicinal properties and may be promising therapeutics for a variety of pathological conditions. This study investigated the acute effects of α-pinene on zebrafish locomotion and anxiety-like behaviour using the open field exploration test. α-pinene was administered in 0.01%, 0.02%, and 0.1% doses. As α-pinene is a racemic compound, we also tested its (+) and (−) enantiomers to observe any differential effects. α-pinene demonstrated differential dose-dependent effects on anxiety-like and motor variables. Specifically, (+)-α-pinene and (−)-α-pinene had significant effects on anxiety measures at different doses in the open field test (time spent in the thigmotaxis and center zone), as well as locomotor variables (swimming velocity and immobility). (+/−)-α-pinene showed only a small effect on the open field test on immobility at the 0.1% dose. This study demonstrates that α-pinene can have a sedative or anxiolytic effect in zebrafish and may have different medicinal properties when isolated into its (+) or (−) enantiomers.

Uncovering how short chain fatty acids improve antitumor immunity in colorectal cancer
Angela Hamie, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Colorectal cancer (CRC) is the second biggest cause of cancer deaths worldwide. While 85% of CRC display the chromosomal instability (CIN) phenotype, 15% of CRCs display microsatellite instability (MSI) due to numerous DNA mutations, which is known to improve the anti-tumor immune response. Preliminary data shows that short-chain fatty acids (SCFAs) produced by microorganisms in the colon microbiota also have a role in CRC's ability to stimulate the immune system. The objective of this study is to investigate how SFCAs stimulate a better immune response. We hypothesize that these SCFAs help CRC, especially MSI CRC, to activate CD8+ T cells. A mouse cell line or human MSI or CIN CRC organoids will receive SCFAs and then CD8+ T cells. The typical signs of immunological activation of CD8+ T cells will be evaluated utilizing a variety of experimental techniques including flow cytometry, immunofluorescence microscopy, and western blotting. If a difference is observed, then blocking specific steps in SCFA signaling will reveal how the SCFAs modulate immune activation. This research will determine at least one mechanism through which SFCA activates intracellular signaling pathways in CRC that mediate CD8+ T cell activation, and thus result in the enhanced immune response. The pathways identified in this project can be used to design potential treatments to increase antitumor immunity, particularly in CIN CRC patients.

Mitochondrial DNA as a key stimulant for cGAS/STING in colorectal cancer subtypes
Angie Chen, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Colorectal cancer (CRC) is the third leading cause of cancer death in Canada. CRC is characterized by genetic instability with two subtypes called chromosome instable (CIN) and microsatellite instable (MIN). Patients with CIN subtypes have lower survival compared to patients with MIN subtypes due to an increased immune response in MIN CRC patient. The cGAS/STING pathway, a cytosolic DNA sensing system, may be responsible for the increased immunity through mitochondrial DNA (mtDNA) detection in the cytoplasm. MtDNA release in MIN may be caused by a truncation of

mitochondrial transcription factor A (TFAM), a protein which helps mtDNA repair, stability, and transcription. Due to this truncation of TFAM in MIN, we hypothesize that mtDNA release into the cytoplasm is a key player in cGAS/STING activation within MIN CRC. Using MIN and CIN variants of MC38 mouse CRC cells, we reduced mtDNA content in our cells using ethidium bromide (EtBr). Results on Western blots show decreased cGAS/STING activation through reduced levels of pTBK1, pSTAT6, and pIRF7 after EtBr treatment, indicating the importance of mtDNA in cGAS/STING signalling in CRC. Flow cytometry measurements of various immune factors, such as CCL5 and CXCL10, further demonstrate the reduced cGAS/STING activation upon EtBr treatment. Treating cells with a cGAS or STING inhibitor decreased immune factor release to similar levels in both the EtBr treated and untreated conditions. In future, we hope to further investigate why mtDNA is important in cGAS/STING activation in MIN CRC by determining the role of TFAM truncation in MIN CRC on mtDNA. This includes investigation into changes in mtDNA release, structure, and transcription which may affect the generation of reactive oxygen species and metabolism. We hope to understand the mechanism behind the enhanced immunogenicity of MIN cells to aid in developing immunotherapy treatments for CRC patients.

Alternative typhoid toxin assembly in *Salmonella bongori*

Antonio Chemello, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Bacteria of the Salmonella genus cause many diseases including gastroenteritis and typhoid fever. An important virulence factor of Salmonella enterica subspecies Typhi is a holotoxin, typhoid toxin. Typhoid toxin is an A2B5 toxin, composed of 2 distinct active subunits (PltA and CdtB) and 5 identical binding subunits (PltB). However, in S. Typhi the toxin not only assembles with the binding subunit within the toxin islet, PltB, but also with an isolated and unrelated binding subunit, PltC. Therefore typhoid toxin exists in two different subtypes that exhibit different characteristics. S. bongori, a related species, contains the typhoid toxin and an unrelated B subunit, PltD. It is hypothesized that PltA and CdtB assemble with PltD to form a unique TT subtype. The genetic expression of relevant genes was analyzed via qPCR and western blotting strains with FLAG/histidine-tagged proteins. Conditions tested include those known to induce toxin expression in S. Typhi. TT genes and PltD are both expressed under conditions that mimic intracellular infection. Additionally, an important regulating system of the TT in S. typhi, PhoPQ, is shown to regulate TT genes and pltD in S. bongori. Immunoprecipitation and protein purification via nickel columns conducted in S. bongori and recombinant E. coli reveal that PltD and PltB are both associated with CdtB and that their interaction is mediated by PltA. ArtB also appears to associate with CdtB and PltA in recombinant E. coli. This emphasizes the versatility of B subunits with pertussis toxin homology. Future experiments will determine if other B subunits from other toxins like pertussis toxin can associate with CdtB and PltA. Finally, S. bongori's PltD toxin will be compared to its PltB toxin in how they affect human epithelial cells. This will determine the functional difference between the two toxins in terms of their cytotoxicity.

Effects of embryonic exposure to artificial sweeteners in zebrafish (*Danio rerio*)

Anwyn Neraasen, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Artificial sweeteners (AS) are used as sugar replacements in foods, pharmaceuticals, and personal care products. AS enter aquatic environments from wastewater, and have been detected in surface waters at concentrations in the µg/L range. For this reason, they have been labelled as emerging contaminants of concern. Prior studies have investigated the effects of AS exposure on aquatic animals using zebrafish (Danio rerio) as a model. However, most studies have focused on toxicity of a small number of AS to adult fish only. This work investigates the effects of exposure to various AS on zebrafish embryos and larvae. Zebrafish were continuously exposed to AS (acesulfame-K, aspartame, cyclamate, and xylitol) until 7 days post-fertilization (dpf). Toxic effects were measured by scoring survival, hatching rates, and the presence of developmental abnormalities in exposed larvae. Following exposure, physiological stress levels will be evaluated by qPCR measurement of stress response gene expression. So far, we have found that embryonic exposure to acesulfame-K and aspartame increases mortality, delays hatching, and increases the prevalence of developmental abnormalities in zebrafish. Similar results are expected for cyclamate but remain to be confirmed. We expect this to be reflected at the molecular level by the upregulation of stress response genes following AS exposure. Our findings will advance understanding of the effects of AS in aquatic environments by considering a wider variety of AS than previous work. Our focus on embryonic and larval life stages is also significant, as sensitivity to AS may differ from adults at these stages. Finally, our study evaluates toxicity of AS using alternative endpoints to lethality, a key consideration since environmental levels of AS are not sufficient to induce mortality. Together this will contribute to a more environmentally relevant understanding of the impact of AS in aquatic environments.

Chronic effects of new generation organophosphate flame retardants to juvenile rainbow trout (*Oncorhynchus mykiss*)

Ashley McCullough, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Hydraulic fracturing is a type of well stimulation technique that consists of fluids and proppants being injected into bedrock through a highly pressurized liquid, referred to as "fracking fluid." This technique is used in the petroleum industry to extract oil and gas from subsurface geological reservoirs, and it is responsible for the production of hydraulic fracturing flowback and produced water (FPW), which is stored in large quantities above surface. It has recently been discovered that FPW contains novel organophosphate compounds including diphenyl phosphate (DPP) and triphenyl phosphate (TPP), both of which have various industrial uses, including as flame retardants. One of the main concerns regarding FPW and its constituents is that they are stored close to public drinking water sources and may be contaminating these areas as well as leaking into aquatic ecosystems. Recent studies have determined that organophosphates may cause acute and chronic toxicity to fish including endocrine disruption; therefore, the goal of this study was to determine the mechanisms by which chronic waterborne exposure to TPP and DPP affect the physiology of a model organism, rainbow trout (Oncorhynchus mykiss). In this experiment, tissue and plasma samples were collected every 7 days for a total of 28 days. Plasma vitellogenin (VTG) was measured in this experiment due to its reliability as a biomarker of endocrine disruption in juvenile fish and to evaluate estrogenic activity. Lipid peroxidation was also measured to determine potential oxidative damage to tissues. We hypothesized that chronic exposure to DPP and TPP would lead to an increase in VTG in the plasma of rainbow trout. Preliminary data has suggested that plasma VTG levels increase over exposure time to TPP and DPP, more prominently with exposure to TPP.

Isolation and characterization of phages for biocontrol of bacterial phytopathogens

Ashlyn Waters, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Over 150 species of bacteria are estimated to be capable of causing plant disease, which has vast consequences, especially to agricultural yield and food security. The pathovar Xanthomonas axonopodis pv. vasculorum causes gumming disease in sugarcane, with infection also observed in maize, Guatemala grass, broom bamboo, and certain palm species. Erwinia amylovora is known historically as the first bacterium identified to cause plant disease, however it is more commonly known for causing fire blight in orchard trees of the Rosaceae family, such as apples and pears. Fire blight can cause complete necrosis of the host via bacterial migration from the site of infection, risking severe, prolonged economic loss for an orchard. Predominant measures against these pathogens rely on antibiotic treatments and prevention. A proposed new measure is the revived use of bacterial viruses, known as bacteriophage (phage). Phage treatment has many advantages, including host specificity, ability to evolve, and ability to overcome antibiotic resistance by using different targets than antibiotics. In this study, soil samples collected from Alberta and British Columbia were screened for bacteriophage activity against these pathogens. Four potentially novel bacteriophages were isolated: AW1, AW2, AW3 and AW4. Two phages, AW1 (isolation host Xanthomonas axonopodis pv. vasculorum) and AW3 (isolation host Erwinia amylovora) were prioritized for characterization. Transmission electron microscopy revealed that AW1 is of Siphoviridae morphology, while AW3 is of Podoviridae morphology. Host range analysis of AW1 further revealed that AW1 is additionally capable of infecting various strains of Stenotrophomonas maltophilia, a multi-drug resistant pathogen involved in potentially fatal nosocomial and community-acquired infections. Future work of this study would be to continue characterization of these phages, including genome sequencing, host range analysis, and investigating possible depolymerase activity observed in AW3. This characterization may enable these phages to be suitable candidates for future treatment against their pathogenic hosts.

Signalling of human neuraminidase enzymes in the proliferation of cancer

Benjamin Bekkema, BSc Student [1,2]
[1] Department of Chemistry, MacEwan University, Edmonton, Alberta, Canada T5J 4S2
[2] Department of Chemistry, University of Alberta, Edmonton, Alberta, Canada T6G 2G2

The human neuraminidase enzymes (NEU; also called sialidase) are glycosyl hydrolase enzymes that modify glycoprotein and glycolipid substrates. These enzymes cleave terminal N-acetyl-neuraminic acid (also known as sialic acid), leading to modified glycan epitopes. Sialic acids are common features of membrane glycoproteins and often act as important recognition elements in protein-protein and cell-cell interactions. Our group has been investigating the role of NEU in

regulating cell migration and adhesion, processes that are critical for understanding immune response and cancer. We have observed that inhibition or knock-down of expression of human NEU can have dramatic effects on the migration of endothelial and leukocyte cells in vitro. This project has worked to characterize the processes involved in these changes by knocking out individual NEU enzymes using CRISPR-Cas9. We used leukocytes and endothelial cells (Jurkat and HEK), which are sensitive to changes in NEU activity. Cultured cells were transfected with lentiviral CRISPR vectors. Knockouts were achieved through the creation of indels in NEU genes through errors in the repair of DNA using non-homologous end joining repair systems as a result of CRISPR-Cas9 cleavage. Cell colonies were screened using PCR amplification and T7 endonuclease mismatch assay. Following screening, mutations were confirmed using sanger sequencing. These Knockout cell lines will help to further explore the specific biochemical changes for which NEU enzymes are responsible and will enable future work to investigate applications of these results in inflammation and other diseases.

Habits, habitats, and host specificity of burying beetle-associated mites (*Mesostigmata*: *poecilochirus* and *macrocheles*) in Alberta

Bennett Grappone, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Burying beetles (Nicrophorus spp.) are a group of carrion-feeding beetles that bury small carcasses before laying eggs on them. These beetles carry several species of mites that help the beetle by feeding on fly eggs and maggots that would otherwise compete with the beetle larvae for food. Currently, most of these mites are placed into a single species (Poecilochirus carabi) that is found around the world and on dozens of species of beetle. Recent analysis of genetic differences within this "species" have shown that it is likely a cluster of many distinct species, each of which may have different preferences for host beetles, habitats, and prey species of fly. My work will begin in the spring of 2023 and will involve year-long trapping of beetles and mites at Elk Island National Park in a variety of habitats and carrion types. I hope to find distinct habitat, food, and host preferences for the distinct genetic lineages of mites. Furthermore, once these differences are established, I hope to formally describe several of these lineages as new species. Carrion-feeding arthropods are important ecosystem members, but the species that are not found on human corpses remain understudied. My project aims to improve our knowledge of these mites and their beetle hosts in order to better document the biodiversity and ecology of Alberta, and to promote further research into the ecological and evolutionary relationships within the burying beetle-mite complex.

Novel jumbo phage offers a potential antimicrobial and anti-virulence strategy against *Burkholderia glumae*

Brittany Supina, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The genus Burkholderia includes a diverse array of Gram-negative pathogens causing devastating infections in both humans and plants. One member of this genus, Burkholderia glumae, is a pervasive phytopathogen that causes bacterial panicle blight in rice, reducing rice yields and threatening crop security. Control strategies for B. glumae are limited to the use of partially resistant rice cultivars or the agricultural antimicrobial, oxolinic acid. However, oxolinic acid resistance has emerged in certain populations of B. glumae, challenging the usefulness and sustainability of this chemical. Combined with the growing economic impact of bacterial panicle blight, this resistance highlights need to develop new treatment strategies to control B. glumae. As an alternative to chemical control options, Bacteriophages (phages) have gained interest. Phages are bacterial viruses that recognize specific pathogens and be used to target and kill resistant bacteria. Phages are abundant in nature and can control pathogens with minimal environmental impact. In this study, we isolated a novel phage, Surprise13 (S13) with strong potential against B. glumae and a range of agricultural and clinical Burkholderia species. Genomic and structural characterization of S13 revealed a large genome of ~220 kb and a contractile tail, classifying it as a jumbo myovirus. Preliminary characterization of S13-resistant bacterial mutants suggests that S13 may impact bacterial motility, highlighting the potential of S13 as both an antimicrobial and anti-virulence agent. Future work will include the characterization of the bacterial surface structure recognized by S13. This receptor identification will provide information about the molecular interaction between S13 and B. glumae, aiding the design of multi-phage treatments aimed at both directly killing bacteria and attenuating their ability to cause infection.

Tiny plants, big impact? An assessment of invasiveness in small-sized, exotic annual forbs in the interior pacific northwest

Britton McNerlin, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

While there is a large body of research looking at the invasiveness of small-sized exotic annual grasses in western North America, there is little known about the invasiveness of small-sized exotic annual forbs in the same regions. My research project aims to understand the effect of small-sized exotic annual forbs on the growth of native perennial seedlings and annual plant species in the interior Pacific Northwest. In order to measure that, I will set up a competition experiment at the Plant Growth Facilities on the University of Alberta's North Campus. Specifically, I will cross one of four small-sized exotic annual forbs with a competition partner species in a pairwise manner, using ten replicate pots per species combination and ten replicate control pots for each study species grown without a competitor (total n = 390 pots). The results of my study will help to fill a gap in our understanding of the invasiveness of small-sized exotic annual forbs in Alberta and western North America.

Identification of potential paralysis proteins in the tick *Dermacentor andersoni*

Caleb Odegard, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

Ticks transmit a vast array of bacterial and viral pathogens; the most of all blood feeding arthropods. Additionally, many species of ticks can induce host paralysis during feeding. Ticks act as disease vectors to humans and other animals, resulting in a threat to public health and economic burden within the agricultural sector. Furthermore, the range of many ticks is expanding due to changes in landscape, and climate change. Dermacentor andersoni an ixodid tick found throughout western Canada can induce potentially lethal host paralysis during feeding. Salivary gland (SG) paralysis proteins have been identified and isolated in several tick species. However, in D. andersoni little is known about these proteins and mechanisms of action. This project attempts to elucidate possible candidate paralysis proteins within the SG of D. andersoni. Analysis of the recently published D. andersoni genome using genomic and protein data from other tick species has been implemented to detect potential paralysis proteins. Additionally, analysis of non-annotated genes with open-reading-frames that correlate to the suspected paralysis proteins may be implemented. When candidate genes are detected, appropriate primers will be developed and tested against cDNA produced from SG RNA using both paralysis virulent and avirulent D. andersoni. Preliminarily results are limited at this time. However, a histamine binding salivary protein from D. andersoni shares homology with the SG protein TSGP4 from the soft-shell tick Ornithodoros savignyi which is known to be toxic and implicated with paralysis. Additional research will be conducted to determine if this gene is more strongly expressed in the virulent strain of D. andersoni, and if so, will be flagged as a potential paralysis protein. The identification of paralysis proteins may lead to novel treatments in preventing paralysis in affected animals. Additionally, tick SG proteins are suspected to have pharmacological value. Thus, providing data for future research.

Looking at the rate evolution of different components of the C. elegans sex determination pathway using genetic and bioinformatic methods

Chloe Cettiga, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

C. elegans, C. briggsae, and C. tropicalis are the only male/hermaphrodite species of the Caenorhabditis genus. When studying the evolution of the C. elegans sex determination pathway the question for this project is how the cells signal in this pathway for a hermaphrodite fate and whether the rapid evolution of this pathway promotes this. In my project I am using genetic methods to look at the ed24 mutation in the C. briggsae sex determination pathway that causes a pseudo male, TRA-3 phenotype. The goal of this component of the project is to confirm whether this mutation is in TRA-3 and the effects it causes at different conditions. This will indicate the type of mutation, and other pathways that the gene is involved in. The results are that the ed24 homozygous C. briggsae animals were seen to be temperature sensitive and that this phenotype was also in C. briggsae animals homozygous for a TRA-2 mutation called nm1. As well, the development of the ed24 strain was slower than wild type and the nm1 strain at 20 degrees, but not at 16 degrees. However, at 25 degrees half of the adults had died. The second area of this project is developing bioinformatic models that look at the evolution of certain genes and the conserved nature of these genes between C. elegans, C. briggsae, and C. tropicalis. The purpose of these models is to gain insight into the possible function of specific areas in genes that have a role in the signaling of the sex fate, and that may be

conserved. We are interested in their regulation, whether certain motifs are conserved, and the speed a gene evolved at in comparison. The models for FEM-1, FEM-2, and FEM-3 have been completed and include multiple sequence alignments, phylogenetic trees, and predicted protein structures.

TLR signalling at the site of schistosome invasion in biomphalaria snails

Christina Bowhay, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The tropical freshwater snail Biomphalaria glabrata has become an important model organism as it is the obligate intermediate host of Schistosoma mansoni, a trematode parasite which impacts millions of people annually by causing intestinal schistosomiasis. Although 56 full or partial TLR proteins have been found in the B. glabrata genome, one has been found to be prominently upregulated during schistosome invasion in snails resistant to infection. We show here that TLR+ granulocytes are largely newly divided and more effective at encapsulating and killing invading parasites. However, it remains possible that engagement with the parasite through a TLR occurs first through cells other than circulating haemocytes. Mucosal and epithelial innate immunity are known to be ancient critical defense mechanisms in animals, making them markedly underexplored in relation to molluscan trematode infections. I will be presenting an initial study of TLR expression and cell proliferation throughout sectioned snail tissues to demonstrate the importance of the systemic immune response, whereas other studies of molluscan PRRs have only examined isolated haemocyte populations.

Sensory and motor neural correlates for seed husking in songbirds

Clara Vicera, *BSc Student [1]*
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Birds possess a wide range of behaviours which are reflected in their neural system. Behaviours that require increased sensory input may be related to an increased volume of neural tissues processing this action, a phenomenon known as Jerison's Principle of Proper Mass. Previous studies have shown that there is an enlargement of the principal sensory nucleus of the trigeminal nerve (PrV) in the brainstem, which receives inputs from touch receptors in the orofacial region (i.e., the beak and tongue) in bird species with complex feeding behaviours that heavily rely on tactile information from the beak, like active filtering in some waterfowls. A notable feeding behaviour that also requires a variety of tactile input from the tongue, and upper and lower jaws is seed husking, which has evolved repeatedly among songbirds (Passeriformes), particularly in the superfamily, Passeroidea. In this study, we measured the volume of PrV, as well as the trigeminal (MV), and the facial motor nuclei (MVII) in 25 species of songbirds, including several granivores from the superfamily, Passeroidea. Our preliminary results suggest that PrV, but not the trigeminal or facial motor nuclei, is enlarged in seed-eating songbirds from the superfamily, Passeroidea. This suggests that seed husking requires enhanced sensory inputs, but not specialised motor control. Future research aims to compare the relative size of PrV and other areas of the brain involved in the processing of tactile information in a larger sample of species, in order to better understand the influence of diet and phylogeny in the evolution of neural circuits that control feeding behaviour in birds.

Does rapid growth of perennial cool-season grasses drive invasion in Canadian grasslands?

Cole Vandemark, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Plant invasion biology represents an important, yet complex discipline that aims to understand core components of global environmental change in terms of the biological, environmental, and economic consequences of non-native plant invaders. In Canadian northern prairie grasslands, the Eurasian perennial cool grass species Smooth brome (Bromus inermis), Kentucky bluegrass (Poa pratensis subsp. angustifolia), and Crested wheatgrass (Agropyron cristatum) have been identified as particularly invasive, leading to the question of what exactly is driving these species' invasiveness. The Evolution of increased competitive ability (EICA) suggests that exotic populations with few specialized enemies in a non-native range will allocate more resources to growth or reproduction instead of defense against enemies. Following this theory, cool perennial grass-species obtained from Canada should grow larger and have a higher competitive ability compared with native con-specifics from Eurasia, leading to a potential mechanism for invasion success of B.inermis, A.cristatum, and P.angustifolia. To test this, seeds are obtained from Ukraine, Hungary, Germany, and Kazakhstan for these three species to represent native populations; and seeds are obtained from Alberta, Manitoba, and Saskatchewan to represent the non-native populations. A

greenhouse experiment is set up to experimentally observe if Canadian populations are larger and more competitive than Eurasian populations. Above and belowground biomass are harvested after 2 months and size and competitive abilities are compared. The results of this study should show that Canadian populations grow larger above/below ground and have a higher competitive ability following predictions from EICA. This project is important as these species are commonly used as turf-grass and forage species which has reduced native biodiversity and plant abundance. A better understanding of what makes these species successful at invasion here in Canada may lead to better management practices or the elimination of using this species for economic purposes.

Interactive effects of glacial flour and dissolved organic carbon on mountain lake ecosystems in a changing climate

Colleen Dawson, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Climate warming in mountain regions is causing the rapid melting of glaciers and upward advancement of alpine tree lines. These landscape changes can affect inputs of glacial flour and terrestrially derived dissolved organic carbon (tDOC) to mountain lakes, altering aquatic environmental conditions. Individually, glacial flour and tDOC have been found to affect abundance and composition of plankton communities; however, their cumulative impact is not well understood. Limited evidence suggests that in glacially fed lakes tDOC does not impact environmental conditions, potentially due to adsorption that results in removal of tDOC from the water column. Therefore, I plan to test the hypothesis that the impacts of tDOC on plankton communities will be suppressed in the presence of glacial flour. This interaction will be studied in the context of expected ecosystem and diversity changes as continued climate warming shifts mountain lakes from turbid to more translucent, nutrient-rich conditions. To test this interaction, I propose a two-factor (glacial flour x tDOC) outdoor mesocosm experiment that will measure the response of phytoplankton and zooplankton communities to individual and combined experimental treatments. Four crossed treatment combinations (two glacial flour levels x two tDOC levels) will each be replicated five times for a total of twenty 1000L tank mesocosms. Plankton will be sampled throughout the experiment and processed to determine key ecological response variables of total phytoplankton and zooplankton biomass along with taxonomic and functional (e.g., body size, feeding group) community composition. Understanding the cumulative impact of these disturbances will aid in accurately predicting freshwater ecosystem responses to future climate change impacts and may be used to inform management protocols for aquatic systems in mountain regions.

Conservation optimism in MacEwan undergraduate students

Cora Kaplan, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

Many studies in other disciplines support the value of optimistic messaging but there is a lack of empirical evidence proving the positive correlation between this form of messaging and an engaged behavioral response in conservation studies. No studies have taken place testing the effects of optimistic messaging in an academic setting so we will be focusing on MacEwan University undergraduate students. The students will provide survey responses that can be used to run a t-test to compare the changes in emotional responses after different forms of messaging; optimistic, pessimistic, and neutral. We acknowledge there may be other variables that influence the emotional response of individuals and consider this in our Principal Components Analysis (PCA). Results that support the most engagement from a specific presentation type will show it may be a more effective presentation method to encourage support for conservation efforts.

Investigating the role of polysialylation on QSOX2 function in breast cancer cells

Dania Al-Rimawi, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Introduction: Recent studies show that elevated expression of the newly discovered enzyme Quiescin Sulfhydryl Oxidase 2 (QSOX2) is involved in metastasis and tumour progression in certain cancer subtypes. However, further aspects about QSOX2 function and the mechanism by which it influences cancer progression requires further investigation. Interestingly, our preliminary data show that QSOX2 in breast cancer cells is glycosylated with polysialic acid (polySia), which is highly expressed in cancer cells and inhibits the immune response. We hypothesize that QSOX2 is a key player in a molecular pathway involved in cancer growth, in part driven by suppressing the immune response. We aim to elucidate the function of QSOX2 in breast cancer and investigate how polysialylation influences its biological effects.

Methods: To examine QSOX2 and polySia expression in different cell lines, a panel of cancer cell lysates were subjected to immunoblot analysis. To further characterize the glycosylation of lymphoblast cells, lysates were treated with polysialyltransferase and CMP-sialic acid prior to immunoblot analysis.
Results: Immunoblots showed that QSOX2 was only polysialylated in breast cancer cells between the different cell lines. Further data collection and analysis suggested that QSOX2 in lymphoblast cells may possess short polySia chains, which has not been previously characterized.
Discussion: Our data suggest that QSOX2 is polysialylated in breast cancer cells and may possess short polySia chains in lymphoblast cells. Our next steps consist of purifying QSOX2 in breast cancer cells for in-depth structural analysis of its glycans. We will also inhibit a domain of QSOX2 which we hypothesize is necessary for its polysialylation to examine if this alters breast cancer cell growth. Further data may ultimately provide insight regarding the role of QSOX2 in cancer progression. This could lead to the identification of novel therapeutic targets to improve the outcomes of individuals with cancers associated with increased QSOX2 expression.

Identifying the role of mitochondrial DNA in the immune activation of MSI colorectal cancers

David Doell, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Cancer is the leading cause of death in Canada with colorectal cancer (CRC) causing the second most deaths of all cancers. Traditional treatments for cancer, including chemotherapy and radiotherapy, have significant adverse effects to patient health. In contrast, immunotherapy treatments cause fewer side-effects since they aim to stimulate the patient's own immune system to target cancer cells. Recent research has shown that certain CRC subtypes characterized by their microsatellite instability (MSI) respond better to cancer immunotherapy treatments than other chromosome unstable (CIN) subtypes. The underlying mechanism for this is currently unknown. Preliminary data suggests that mutations in important mitochondrial proteins due to the higher instability of MSI cancers relative to CIN cancers could explain their higher immunogenicity relative to CIN cancers given that mitochondrial DNA (mtDNA) released by unstable mitochondria holds more similarities to immunogenic bacterial DNA than nuclear genomic DNA. We hypothesize that if mtDNA stimulates a stronger immune response than genomic DNA, we should observe higher immune activation in CRCs that release more mtDNA relative to genomic DNA into the cytosol and that this occurs most often in MSI CRCs. This project aims to stimulate two key cells in the immune system, Dendritic cells (DC) and T cells, with varying ratios of mitochondrial to genomic DNA from MSI and CIN cancer cell lines. At various time points following these stimulations, we measured cytokine production using flow cytometry, cell migration using a T cell migration assay, and inflammation markers using western blotting to determine whether the effect of cancer cell mtDNA is significant to the anti-cancer immune response of DCs and T cells. Understanding how MSI CRCs respond better to immunotherapy than CIN CRCs will allow future research to better tailor immunotherapy to MSI cancer targets or possibly promote changes in CIN cancers to increase their susceptibility to immunotherapy.

The effects of low temperature incubation and benzalkonium chloride addition to water samples permeated with *Thymallus arcticus* eDNA on degradation rates of DNA

Edward Na, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Environmental DNA (eDNA) refers to DNA present in the environment without a proximal organismal source. The persistence of eDNA in natural waters offers a mechanism for detecting the recent presence of an organism through a simple water sample, rather than intensive and invasive traditional biomonitoring approaches such as electrofishing. Our laboratory has recently developed an eDNA assay for the detection of the iconic fish species Arctic grayling (Thymallus arcticus). In order to properly validate this assay and to adequately interpret results from field sampling, it is necessary to understand Arctic grayling eDNA degradation rates and examine means of preserving eDNA in water samples after collection. This research focuses on the preservation efficacy of benzalkonium chloride (BAC), a cationic surfactant which binds to DNA, slowing its degradation significantly. We added BAC to water samples containing Arctic grayling eDNA and compared these samples to controls over a number of different temperatures (0, 20, 30 degrees) covering the range of likely to be encountered in the field, over the course of a week (0H, 24H, 72H, 144H). Following filtration and eDNA extraction, the persistence of eDNA signal was assessed using qPCR. Ultimately, we hope that this research will help us to establish a sensitive and robust eDNA collection method that can be applied to the field surveillance of Arctic grayling across northern Canada. Critically, an effective preservation method may represent a significant time and cost saving for the collection of waters in areas accessible only through long distance transport or via helicopter where immediate filtration may not be possible.

Avian responses to fire, insects, and harvest along elevational gradients

Emily Swerdfager, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The Canadian Rocky Mountains and Foothills are experiencing unprecedented ecological consequences of climate change, such as the increased frequency and severity of forest disturbances; including wildfire, mountain pine beetle outbreaks and salvage logging practices. These disturbances alter the vegetation structure and composition of the forest, which presumably results in changes to avian communities in response. This research aims to compare avian community responses across elevational gradients (foothills, montane and subalpine) to three different forest disturbance types; post-fire stands, post-mountain pine beetle attacked stands, and post-harvested stands. We will compare the resilience of avian communities across elevation gradients by testing for the effects of time since disturbance on the following community metrics; community composition, species richness, and functional diversity. We will use bioacoustic data collected with Automated Recording Units from over a thousand locations in the Canadian Rocky Mountains and Foothills from zero to 20 years post-disturbance, to investigate avian community change over time as part of the forest recovery trajectory. The findings of this research will provide new insights on the cumulative impact of forest disturbances and management interventions for biodiversity conservation and inform future forest management practices.

Antibody affinity modification in the gut of zebrafish

Emmanuel Alimo, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

For a long time, the process of Antibody Affinity Maturation (AAM) has been poorly understood in humans with autoimmune diseases. However, recent studies indicate that sites of affinity maturation in autoimmune individuals occurs in sites outside of the known germinal centers and these areas where the autoantibodies produced by B-cells affinity mature may be analogous to Melanomacrophage Clusters (MMCs) in early vertebrates. This study will provide more insight into where these MMCs may be located in the gut of early vertebrates, like Zebrafish. Fluorescence microscopy will be used to detect and isolate the MMCs from the gut which autofluorescence due to the presence of melanin, hemosiderin and lipofuscin. B-cells expressing IgM and IgZ which are prominent in the gut will be targeted with specific primers and then amplified with PCR. Following the confirmation of the transcript size with gel electrophoresis, it will then be sequenced through next generational sequencing. This will give us an idea if the B-cells within the MMCs are undergoing Clonal expansion, Somatic Hypermutation and antigen driven selection which are classical hallmarks of B-cells undergoing antibody affinity maturation in germinal centers and this can be traced back to the parental cells that are have antigen bound to them before entering the site. This work will not only have implications on vaccine use in aquaculture, but also help us better understand antibody affinity maturation processes in autoimmune disorders.

Natural fever as a protective factor against disease transmission in teleosts

Ethan Proctor, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Fever has been conserved over 600 million years of vertebrate evolution yet is classically treated as a symptom of infection rather than an adaptive player in the innate immune response. Ectotherms exhibit fever through their behaviour, selecting for warmer regions in the environment. The Barreda lab has used an ectothermic teleost model to show that fever contributes to enhanced selective leukocyte recruitment, inflammation control, and wound healing. I hypothesize that in an environment where fish are free to select their desired temperature, disease transmission will be dampened due to a reduction in individual infectiousness through natural fever. To test my hypothesis I developed the Rectangular Thermal Preference Tank (RTPT) which is able to maintain a stable >8℃ temperature differential across its surface without barriers and can be set to a static temperature to mimic afebrile conditions. I also developed a protocol using the machine learning software TRex to visually identify and track the motion and posture of >20 individuals in a group simultaneously without tagging. I injected cohorts of goldfish with the non-transmissible fungal mimic zymosan and established behavioural fever as a robust indicator of fever at every cohort size, although small cohorts had to expend more energy to maintain their desired temperature due to disruption by healthy conspecifics. To evaluate transmission I will inoculate a small cohort of goldfish with GFP-transfected Aeromonas veronii and use both behaviour and nascent fluorescence as markers of transmission in dynamic and static temperature conditions. I will then examine the implications of inhibiting fever with an antipyretic drug during a transmission

scenario. This research will contribute to our fundamental understanding of innate immunity and its evolution, provide the basis for novel vaccination strategies for aquaculture, and inform more responsible clinical antipyretic use.

The effect of movement on the development of the peripheral nervous system in zebrafish

Gabriel Dillenburg, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Sensory feedback associated with movement impacts early brain development. In zebrafish, movement has been shown to stimulate neurogenesis in the forebrain via sensory feedback sensed by dorsal root ganglia (DRG), the peripheral sensory cells in the larvae body that detect bodily movement during swimming. However, the previous work ignores that DRG themselves also develop, including through neurogenesis, during postembryonic development. Therefore, I hypothesize that DRG development is affected by movement during postembryonic development. To teste this hypothesis, I will rear zebrafish under restraint conditions, in which they swim less during postembryonic development and compare to fish reared in control conditions. I will monitor DRG development through repeated, in vivo imaging of genetically modified zebrafish that express a fluorescent protein in their DRG, and will complement the in vivo approach with traditional histological staining to label DRG. I predict that fish in the restraint treatments will develop fewer DRG cells in comparison to the controls, similar to what was observed in the forebrain. This in turn would allow a deeper understanding on how the sensory feedback shapes the development of the sensory system that senses it, and may indicate that the effects observed in the forebrain are downstream consequences of underdeveloped dorsal root ganglia.

Mineral-organic interactions as a determinant of DOM quality in the western Canadian Arctic

Gabrielle Hatten, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Permafrost soils are a large reservoir of Earth's carbon, storing thousands of years' worth of organic material at varying stages of decomposition. Interactions between organic matter (OM) and mineral surfaces in permafrost soils, facilitated by mass thawing events, may dictate the concentration and composition of dissolved organic matter (DOM) in aquatic ecosystems. In particular, the chemical bonding of OM to minerals (mineral sorption) reduces the availability of the carbon in OM for mineralization to CO2 by microbes. In this study, I will link compositional variation in permafrost with mineral sorption potential across the western Canadian Arctic, and the resulting availability of DOM for microbial mineralization. First, I will characterize samples from across a series of permafrost "end-member" types with different parent material and modification histories across the Peel Plateau and Sahtu regions in the Northwest Territories and the Klondike region in central Yukon Territory. I will then tie compositional variation to each sample's mineral sorption capacity, which will be assessed by adding DOM derived from active layer soils to permafrost materials and measuring changes in DOM concentration and composition. Finally, I will evaluate the impact of sorption on the mineralization of OM into CO2 via an incubation experiment. Pre- and post-sorption leachates from the first experiment will be mixed with a microbial inoculum from the Mackenzie River (i.e., a downstream location), and the decomposition of this DOM to CO2 will be measured. As mineral sorption processes contribute to the regulation of dissolved carbon in aquatic ecosystems, there are implications for rates of carbon decomposition by microbial communities and resulting CO2 emissions.

Effect of ORF10 on CUL-2/ZYG-11 and MEMI in *Caenorhabditis elegans*

Hayley Jackson, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The protein encoded by ORF10 from the SARS-CoV-2 virus has been shown to enhance symptoms of COVID-19 upon infection through interaction with the CUL-2/ZYG-11 E3 ubiquitin ligase complex. This interaction results in increased ubiquitination of another complex (IFT46), subsequently impairing cilia biogenesis and maintenance. In the nematode C. elegans, the CUL-2/ZYG-11 complex is required for the degradation of oocyte-specific MEMI-1/2/3 (meiosis-to-mitosis) proteins shortly after fertilization of the oocyte. MEMIs are required for entry into female meiosis II, but protein perdurance is associated with embryonic death. For example, a temperature-sensitive mutation memi-1(sb41) causes a failure to exit female meiosis II properly due to the persistence of MEMI-1 into mitosis. Loss of zyg-11 results in very similar phenotypes and persistence of MEMI-1/2/3 into mitosis. My research is focussed on testing if expression of the ORF10 protein in C. elegans has an effect on the CUL-2/ZYG-11 complex and the MEMI pathway. To accomplish this, ORF10 will be cloned

with a 6xHIS purification tag and expressed in bacteria. Purified ORF10 protein will be tested for a physical interaction with ZYG-11 and functional assays will assess a possible role for ORF10 in upregulating C. elegans ZYG-11 in vivo. According to our model, upregulation of CUL-2/ZYG-11 might rescue the mutant phenotype of memi-1(sb41) by increasing MEMI protein degradation rates, thus, memi-1(sb41) worms will be fed bacteria that express ORF10 or injected with the purified protein, to test for suppression of embryonic lethality. Alternatively, ORF10 might result in embryonic lethality due to premature degradation of MEMI (or other proteins); in order to test this, wild-type C. elegans will be similarly treated with the ORF10 bacteria and purified protein. Results from this experiment could help further our understanding of MEMI function and provide a basis for future drug studies relating to COVID-19 through small molecule drug screens.
Poster 13, Wednesday, March 8th.

Chronic social isolation in drosophila: Behavioral effects and underlying neurological mechanism

Heba Mahmood, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Adverse effects brought on by social isolation during the COVID-19 pandemic have become increasingly apparent. In humans, social isolation has been reported to disturb sleep and reduce physical activity. Fruit flies (Drosophila melanogaster) are a social species, demonstrating cooperative behavior and preference for social stimuli over non-social stimuli. Interestingly, social isolation of Drosophila has also been shown to result in sleep loss and impair their locomotor abilities, as assessed using a climbing assay. My project consisted of characterizing behaviors of socially isolated flies and investigating how isolation might alter the brain. Objective one was to test sleep disruption using the DAM system, which records locomotor behavior. Data was analyzed with MATLAB and results showed isolated females slept a fewer number of times per 24 hours compared to grouped females and isolated males slept for shorter periods of time at night compared to grouped males. Objective two was to conduct fly arena experiments where isolated and grouped flies were inserted into an arena, videoed, and analyzed with Ctrax to study social and exploratory behaviors. We hypothesize results will indicate that isolated flies have increased arousal consistent with the sleep data, and that they will demonstrate decreased social interactions with other flies. Objective three was to replicate previous data that identified reduced synaptic proteins in isolated flies. This was done by dissecting, immunostaining, and imaging the brains of isolated and grouped flies. We hypothesize data will replicate initial results, and there will be a reduced number of presynaptic vesicle proteins in isolated fly brains. This research is significant to further understand implications of social isolation on mental health. Investigating cellular mechanisms is critical for mitigating negative effects.

Aging in zebrafish (*Danio rerio*) and copper toxicity to microvillar and ciliated olfactory sensory neurons

Hudson Bovee, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Olfaction in fishes is involved in a network of life-sustaining processes such as predator detection, sex recognition, feeding, and migration. As fish age, their ability to detect these vital oduors decreases. Similarly, neurotoxins like copper have been shown to damage the olfactory epithelium in fishes, as well as disrupt chemical signalling and response, reducing a fish's ability to accurately detect odours. Within the olfactory epithelium of zebrafish, ciliated and microvillar olfactory receptor neurons experience differential copper toxicity. In this study, we exposed middle-aged (1-2yr) and old-aged (>2yr) zebrafish to water with 20 μg/L of copper to determine if copper's differential toxicity to microvillar and ciliated olfactory receptor neurons is influenced by the age of the fish. After copper exposure, sections of the fish's olfactory epithelium are stained with hematoxylin and eosin and will be used to determine cell densities and olfactory epithelium thickness as measures of anatomical damage. Olfactory epithelium thinning is expected with copper exposure and aging. After copper exposure, ciliated olfactory receptor neurons might be more numerous in the middle age fish, and in old age there may be more microvillus cells. Learning more about how copper and age-related olfactory neurodegeneration interact in vertebrates, may aid future research on Alzheimer's and related diseases.

Species distribution and connectivity modeling of reef fishes in the Florida keys reef tract to inform coral restoration design

Isla Turcke, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Due to both natural and anthropogenic disturbances, coral reefs worldwide have undergone drastic degradation. To abate this decline, coral restoration efforts are being made on reefs around the globe to help recover the loss of these invaluable habitats. The functional roles that fishes play on reefs have received relatively little attention in the context of mediating the success of restoration activities. Reefs benefit from the ontogenetic habitat shifts of many fishes, which provide an influx of essential nutrients from nutrient-rich nursery habitats. Herbivorous groups such as parrotfishes play key roles in maintaining coral reef vitality by grazing macroalgae cover, but can also be damaging to coral juveniles, contributing to high mortality rates in newly outplanted coral colonies. The ability to predict the spatial distribution of these interactions, both positive and negative, could aid in the development of ecosystem-based restoration strategies. We examine the potential functional connectivity of reef fish species that undergo ontogenetic habitat shifts along the Florida Keys Reef Tract (FKRT), where degraded reefs are undergoing large-scale restoration. These species fall within two key functional groups of reef fishes: grazers (Scarus coeruleus, Scarus coelestinus, and Scarus guacamaia) and invertivores (Haemulon sciurus and Lutjanus griseus). Using reef and mangrove visual census data for fishes, and environmental predictors including bathymetry, habitat type, and indices of water quality, we construct habitat suitability models (HSMs) for these species. We illustrate how the resulting HSMs can be used to derive cost surfaces, across which least-cost paths are determined using connectivity modeling, leading to ecologically realistic predictions of the species' distributions and movements throughout this heterogenous seascape. Finally, we highlight how metrics of connectivity generated from this modeling framework can be used to identify candidate reefs for coral restoration that are most likely to benefit from ecological interactions with these reef fishes.

Bisabol, a terpene present in cannabis, increases locomotion and has no effect on anxiety-like behaviour or boldness in zebrafish

James Hudson, BSc Student [1]
[1] Department of Biological Sciences, MacEwan University, Edmonton, Alberta, Canada T5J 4S2

Terpenes are aromatic compounds commonly found in many plants, such as chamomile, rosemary, and cannabis. They are thought to possess a variety of medicinal and therapeutic applications, having potential anti-inflammatory, antidiabetic, and anticancer properties. This study investigated the effects of the terpene bisabolol on zebrafish locomotion, boldness, and anxiety-type behaviour at varying concentrations (0.001%, 0.0015%, 0.002%). We used the open field exploration and novel object approach tests and quantified fish location with motion tracking software. Bisabolol did not have a significant effect on anxiety-type behaviour in the open field test or novel object approach test. It did, however, have an impact on locomotion in the open field test at the highest concentration (0.002%), with fish exhibiting an increase in swimming velocity. In conclusion, this study demonstrates that bisabolol has no effect on anxiety-like behaviour or boldness in zebrafish but does alter locomotion at the highest concentration used here.

Evaluating the extent and design of coral reef restoration efforts under climate change

Julia Briand, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The effects of widespread anthropogenic disturbance have resulted in the loss of ecosystem function and, in turn, the reduction of resilience to future disturbance. These effects are particularly apparent in coral reef ecosystems, which have degraded under the increasing threat of climate change. To rebuild coral reef function and resilience, conservation strategies are currently in transition towards restorative management, whereby nursery-reared coral species are replanted in coastal environments. Despite recent advances in the field, coral reef restoration design is largely opinion-based and often monitors metrics unrelated to desired project outcomes (i.e. rebuilding reef function), jeopardizing restoration success. Here, we integrate global datasets of coral cover from >4,700 reefs, restoration design, human pressures, and climatic variables to identify key gaps in restoration efforts and predict the success of current initiatives using quantified metrics for success. Specifically, we quantify variables specific to restoration site and species selection that may be critical to effectively rebuilding reef function. At a regional-scale, we identify and monitor functionally-relevant metrics to measure the success of current restoration projects. Our preliminary findings reveal that future restoration efforts may benefit from targeting sites

isolated from chronic environmental stress, as well as restoring coral species less sensitive to climate disturbance. Results from this study can be applied to a global framework for restoration action that standardizes restoration design and monitoring methods to strengthen coral reef resilience under climate change. In combination with protective management strategies, effective restoration practices could be key to preserving key coastal ecosystem processes and functions.

Abundance, distribution, seasonality and habituation of Roosevelt elk

Kate Rutherford, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Like other elk species and subspecies, Roosevelt elk readily habituate to human activities such as forestry and agricultural operations, transportation infrastructure, and approaches by people. In the southeast area of Vancouver Island near Duncan, British Columbia, many landowners have reported that Roosevelt elk are becoming increasingly abundant and reliant on people, appearing more frequently in and near cropland. Despite the increasing prevalence and sedentary behaviour in these elk, there is little information about their total population size, distribution, abundance, and degree of habituation. To increase information that might support subsequent management, we deployed 35 remote cameras along the edges of crop fields where elk have previously been observed and encouraged landowners to take and share photos of elk sightings. We aim to (1) calculate a minimum population estimate for the monitored region, (2) compare elk visitation rates at cameras to remotely-sensed information about adjacent land cover and human use, (3) model elk distribution based on habitat suitability, and (4) compare elk responses among sites to novel objects and automated deterrents. The first six months of camera deployment yielded 309,927 motion-captured images, of which 25% contained elk. Elk were detected at 31 out of 35 cameras with an average elk group size of 4.8 individuals and a range of 1 to 48. Elk detection rates varied temporally, peaking in September and between the hours of 6 a.m. and 11 a.m. We hope that our results can be used to support subsequent management actions to mitigate human-elk conflict associated with damage to crops, wildlife-vehicle collisions, property damage, and risk of human injury from habituated animals.

Effect of hydraulic fracturing wastewater on brain and behaviour development in zebrafish

Kayla Lottin, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Horizontal hydraulic fracturing is a method to obtain hydrocarbon reserves from geologic formations with low permeability. However, with this technology, a large volume of wastewater is produced, called flowback and produced water (FPW). This wastewater is a heterogeneous highly saline chemical mixture containing hydrocarbon co-contaminants (polycyclic aromatic hydrocarbons), metals, radioactive species, and inorganic ions. Individually fractured wells can produce millions of liters of FPW, resulting in large volume spills that can be devastating to the surrounding aquatic biota. Previous studies have identified sub-lethal toxicity in aquatic organisms following a FPW exposure, and they include xenobiotic metabolism, oxidative stress, and reproductive effects, but little is known about how FPW affects early life stages in species that might be exposed during development. This project aims to investigate the impact of FPW exposure on brain and behaviour development in a model aquatic vertebrate, the zebrafish. Zebrafish will be exposed to either FPW-contaminated, saltwater control, or control water (no contaminants) throughout their first 96h of development. Behavioural data, including distance swam will also be measured during this period. At the end of the exposure, brains are collected and stained for makers of cell proliferation and gross anatomy measurements. Further investigations will include chemical analysis of FPW, physiological measurements (including spine curvature and body length), use of additional immunostaining markers, and the interplay between brain and behaviour. Overall, understanding the risk posed by these complex mixtures will allow us to better inform regulatory bodies and understand the mechanisms of toxicity during early development.

Novel utilization of blood biomarker in sheep for predicting pregnancy and litter size

Leon Naing, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Reproductive management of livestock is highly correlated with sheep farmers' profitability and can jeopardize a farmer's earnings if ineffectively managed. This management is greatly affected by the predicted and detected litter size during ewe gestation, which allows for planning and dictation of feed management, sheep health, and lambing rate. The gold standard of detecting pregnancy and litter size (PLS) is through ultrasonography. However, ultrasonography requires the investment in an

ultrasound machine or trained professionals and is expensive for farms with large flocks or are inconvenient to access. An indirect alternative to ultrasonography is through utilization of molecular biomarkers, such as metabolites or proteins, found in blood, milk, or urine. From a previous large-scale metabolomic study, potential serum biomarkers were determined. L-glutamine was one among the 5 biomolecules found and utilized in PLS detection in sheep. Currently we are aiming to develop a one-step assay by utilizing the transferase activity of glutamine synthetase (GS) as there is no one-easy step for L-glutamine detection. This will be achieved through utilization of GS for glutamine detection. We have designed a plasmid which achieves overexpression of GS, which is highly sensitive towards glutamine with respect to other variants of GS. Once we have the enzyme, all necessary steps and optimization will be completed to develop a dry reaction assay for L-glutamine detection in sheep serum. As one of the several biomarkers discovered and related to PLS detection, this dry assay will significantly aid in the further development of a low-cost and simple blood test to determine PLS and ultimately aid in optimal reproductive management of sheep.

Assessing the diel primary metabolite profile of kale (*Brassica oleracea*) under varying light conditions

Lexyn Iliscupidez, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Generation and accumulation of different metabolites have been shown to be altered under changing light profiles. This does not come as a surprise since light serves as a fundamental energy source and environmental cue for plant life; therefore, the ability to control such light has significant implications for the growth and development of plants. Light-emitting diodes (LEDs) hold great opportunities for horticultural development as they can be programmed under specific schedules to precisely control environmental conditions and thus plant physiology. To examine the impact of light on primary metabolite production, kale cultivars were grown under different light treatment and metabolic analysis was completed through gas chromatography mass spectrometry. Gaining a greater understanding of external influences allows growers to easily introduce genetic modification to achieve desired kale profiles as well as optimize growing conditions for crop production.

The evolution of regulation: How two-component systems diverge in different bacterial lineages

Luke Barretto, PhD Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The acquisition of novel genes is the primary driver of bacterial evolution, a phenomenon which grants bacteria unparalleled access to a wide diversity of niches. However, acquiring ecological innovations from new genes must be tempered by a robust system for integrating these genes into existing regulatory networks. Central to this integration are global regulators, proteins which control the timely expression of horizontally-transferred genes. This research seeks to advance our understanding of how bacteria evolve through the lens of global regulators and their central role in accommodating the acquisition of evolutionary novelties. Through this analysis of global regulators, we hope to gain insight into the mechanisms which cause their divergence among bacteria, and how their differences have fueled bacterial evolution. We hypothesize that global regulators fine-tune their regulation of newly acquired genes to fit the demands of diverse bacterial niches. To characterize the divergence of global regulators, our research examined the mutational consequences of placing Escherichia coli versions of global regulators in a genetically related bacterium, Salmonella enterica serovar Typhi. We focused on the PhoPQ two-component system and moved the E. coli gene sequences of these global regulators into reporter strains of S. Typhi. PhoP and PhoQ control a large set of horizontally-transferred genes and reporter strains with ‘ecoli-cized’ global regulators were shown to have significant phenotypic differences in the expression of genes critical to Typhi’s unique lifestyle, such as pltB, cdtB, and pagC. To expand our analysis beyond these genes, we will use RNA-Seq to acquire a global picture of how the E. coli global regulators have affected regulation in S. enterica with the eventual goal of developing a mechanistic understanding of the evolution of regulation.

Characterizing reovirus Σ1 protein binding domains and their importance on oncolytic properties

Maiah Walters, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Oncolytic reovirus, which preferentially replicates in cancer cells, is undergoing human clinical trials as a potential cancer therapeutic. With the aim of improving the potency of reovirus as a cancer therapy, the Shmulevitz lab discovered virus mutants that can enhance reovirus plaque size on cancer cells which indicates enhanced replication, killing or spread of the

virus. It was previously found that mutations leading to decreased reovirus binding protein, sigma 1 (σ1) relative to parental reovirus (T3wt), resulted in increased oncolytic potency. Using this knowledge, we investigated several more viruses with σ1 mutations, with the goal of characterizing the different σ1 domains. Firstly, we investigated if these mutations resulted in larger plaque sizes using a plaque assay. Second, we investigated if the mutations in the σ1 gene affected the levels of σ1 expressed on each virion by agarose gels. Lastly, we observed if the mutants showed changes in binding to L929 cells using western blots. We found these σ1 mutants had significantly larger plaques than T3wt. Secondly, we found no change in the levels of σ1 protein expressed on the σ1 mutant viruses relative to T3wt, which is different from previously studied σ1 mutants. Furthermore, we saw a significant decrease in binding of the mutants to L929 cells. We are currently further investigating how these binding domains are important for the viruses' oncolytic abilities. By understanding this, we will provide insight into the mechanisms of an oncolytic reovirus that will help us to create a safe and a more efficient cancer therapy

Investigating the organization of forebrain-cerebellar loops in pigeons (*Columba livia*) using retrograde tracing

Mansi More, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Birds and mammals have evolved large brains, with large forebrains and cerebellums. In mammals, these two structures are heavily interconnected through forebrain-cerebellar loops, which are involved in motor and higher cognitive functions. The forebrain-cerebellar loop is a feedback loop where the cortex projects to the cerebellum through the pontine nuclei, and the cerebellum projects to the thalamus, which then projects back to the cortex, particularly the motor and associative areas. In birds, the forebrain sends projections to the cerebellum, but it is unknown whether forebrain cerebellar loops also exist in birds. Previous studies in birds have shown that the cerebellar nuclei project to the dorsal thalamus, but it is unclear if this region projects to the forebrain, and how these projections are organized. In this study, we used neural tracers to study possible forebrain-cerebellar pathways in the Rock pigeon (Columba livia) brain. Retrograde tracers were injected in the motor and associative regions of the forebrain, to reveal which regions of the thalamus project to these areas. Our results show that the associative areas of the avian forebrain receive large and topographically organized projections from dorsal thalamus regions that have been shown to receive projections from the cerebellum. In contrast, motor regions of the avian forebrain only receive projections from the more lateral dorsal thalamus, which do not receive projections from the cerebellum. Our results suggest that the cerebellum of birds provides feedback to the associative, but not motor regions of the forebrain.

Developmental strain variation in zebrafish embryonic development

Maria Sawiak, BSc Student [1]
[1] Department of Psychology, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Variations between genetically modified zebrafish throughout embryonic development provide insight into muscular and eye development because of their similar formations and rapid development. Wild-type (WT) strains of zebrafish, in research, allow these mutations to be compared at baseline to illustrate where significant variations may occur. But what about variation within the wild-type strains? Biological literature surrounding strain variation focuses primarily on behaviour. As a result, there is still little known whether there is a difference in the rate of embryonic development among WT strains. Past experiments have shown that the TL strain displayed smaller morphological measurements, providing some evidence that TL strains develop slower than their counterparts. Despite this evidence, larger sample sizes are critical for conclusive results. The current project investigates the morphological variance between the TL strain and other strains, such as the AB strain and WIK strain, using sample sizes of 30 to allow for normal distribution. We will take morphological measurements of zebrafish embryos at 2DPF, 3DPF, and 4DPF and if the measurements are significant, genetic knockdown techniques will be employed on UNC45B to heighten understanding as to why development is significantly slower in some strains compared to others. Furthermore, focus will primarily be placed in the variation in ocular development in attempts to gain insight into congenital eye diseases. Overall, the study attempts to understand what causes developmental differences across zebrafish strains. Currently, no research explains how to control eye growth in zebrafish during embryogenesis. Genetically unmodified models will help establish a baseline for studies surrounding ocular diseases or other diseases typically studied using zebrafish, closing the gap within biological literature surrounding the genetic lineage of eye development.

Impact of glacial recession on stream turbidity and algal community composition

Maria Sophia Diluvio, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Glacier recession produced changes in the physical and chemical characteristics of streams, including increased inputs of glacial flour. The increase in glacial flour input has led to increased stream turbidity, which can have profound effects on the algal community composition in affected streams. This study aims to determine how the change in turbidity from increasing inputs of glacial flour affects algal community composition. Periphyton samples collected from streams located in the Rocky Mountains of Alberta, Canada were used to determine algal abundance and overall biomass using high-performance liquid chromatography (HPLC). Additionally, experimental data collected from a mesocosm experiment sampled from artificial substrates were used to compare the effect of varying turbidity levels from an open vs closed environment. This study is ongoing, and data is undergoing analyses to understand the relationship between stream turbidity and algal composition. We would expect a decrease in algal community composition with an increase in turbidity. An increase in turbidity is associated with increased light attenuation which in turn decreases light availability for phytoplankton. This would greatly affect communities, such as green algae, that rely on photosynthesis for food production. Mixotrophs such as diatoms and other species that thrive in low light conditions are expected to increase in abundance, outcompeting autotrophic species. Furthermore, an increase in turbidity also increases scouring of periphytic algae, causing physical damage and abrasion further decreasing algal abundance. This study highlights the importance of monitoring changes in stream turbidity caused by glacier recession and its effects on algal communities in order to better understand the impacts of anthropogenic changes on freshwater systems.

Studying the impacts of plant nutrition through bioluminescence

Maryam Khandani, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Plants use a combination of external receptors and internal signals to respond to environmental cues which help them adapt and grow. These internal and external cues are essential for proper and timely function of essential processes. Plants, being photosensitive organisms, use a complex set of genes to regulate the production or destruction of specific compounds over the course of a day. Macronutrients are necessary for the proper function of these genes, as they make up the building blocks of many essential metabolites. Therefore changes in the bioavailability of these nutrients can affect daily events for plants and thus, the timing of specific plant cell processes. Nutrient stress impacts daily plant metabolism and activity by inhibiting both the synthesis and metabolism of essential compounds. We used a luciferase reporter gene stably inserted into Arabidopsis thaliana plants in order to track real-time activity and changes in the diel biology of plants when grown under nutrient-stressed conditions.

Acute effects of cannabinoid combinations on zebrafish locomotion

Michelle Makila, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Due to its recent legalization, cannabis has become one of the most common recreational drugs in Canada. Two major compounds found in cannabis are the psychoactive component Δ9-tetrahydrocannabinol (THC) and the non-psychoactive component cannabidiol (CBD); both belong to a class of compounds called cannabinoids, which act on cannabinoid receptors 1 and 2 (CB1R and CB2R) and have each been shown to impact early development. While the effects of THC and CBD have been studied in isolation, their combined effects are less understood, and are vital to understanding the impacts of cannabis exposure as these compounds are consumed in tandem. The objective of this study is to measure the acute effects of THC and CBD combinations on the zebrafish (Danio rerio) behavioural escape response to sound. Zebrafish larvae (5 days post-fertilized) were exposed to combinations of THC/CBD, using THC:CBD ratios of 1:1, 2:1 and 1:2, for 30 minutes. Following the exposure period, we delivered an auditory-vibrational stimulus to the larvae-containing petri dish and measured the response rate and latency of their escape response, a reflexive C-shaped turn. Our data show a significant decrease in response rate and increase in response latency in treatments exposed to cannabinoid combinations compared to controls, with the greatest differences in the 1:2 treatment. To understand the mechanism of effect of cannabinoid combinations on the escape responses, we will also investigate the effects of pharmacological blockers of CB1R and CB2R (AM251 and AM630 respectively) in addition to cannabinoid combinations. This study will elucidate the impacts of cannabinoid combinations and their potential synergistic effects on sensory-locomotor behaviour, as well as identify the role of specific cannabinoid receptors on these outcomes.

Space-use of Canadian polar bears (U. maritimus) across the Beaufort sea

Nicholas Paroshy, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Polar bear (Ursus maritimus) subpopulations are delineated using the current, yet potentially outdated, understanding of population-level metrics: genetics, movement, and landscape conditions. The most recent population estimate for the Southern Beaufort Sea (SBS) subpopulation was conducted in 2006, a 16-year timeframe, yet the SBS remains one of the most studied regions across the Circumpolar Arctic. While these long intervals may be adequate in other wildlife species, such as land-dwelling carnivores within a stable environment, they break down in polar bears as individuals experience greater dynamical patterns of sea ice and food availability. This study aimed to review the current boundaries of polar bear subpopulations based on the movement of collared individuals in the Beaufort Sea using modern home-range estimations using data from 78 adult and sub-adult females between 2007-2014. This study also aimed to investigate whether capture location accurately represented an individual's movement. While research has previously focused on individual parameters of movement and habitat selection, understanding how bears move across boundaries would allow for an estimation of migration and dispersal, thereby allowing for the updated development of biologically significant boundaries.

Identifying and characterizing a putative sperm-specific factor in C. elegans involved in the regulation of female meiosis II

Rim Daher, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

In most sexually reproducing organisms, gametic cells fuse via a process known as fertilization. However, in many organisms, the female gamete does not complete the final meiotic cell division until after fertilization. It is still unclear how fertilization triggers the completion of female meiosis, and how the subsequent transition to embryonic development is orchestrated. In Caenorhabditis elegans, fertilization is required for the completion of the female meiosis I (MI) division, and entry into meiosis II (MII). The Srayko lab discovered three paralogous genes, memi-1/2/3 (meiosis-to-mitosis) that are, together, required for completion of MI and entry into MII. The memi genes encode oocyte proteins that are normally degraded soon after the fertilized oocyte enters MII. MEMI proteins are likely involved in the sperm-derived signal required for MII. A hypermorphic, gain-of-function mutation, memi-1(sb41) results in the persistence of MEMI-1 protein, which causes severe MII delays that eventually result in embryonic death. This suggests that MEMI must also be degraded to allow the transition from MII to embryonic mitosis. Previously, gsp-4 and gskl-1/2 were identified as suppressors of memi-1(sb41) using genome-wide RNAi and EMS-based suppressor screens. Interestingly, these genes encode sperm proteins that are essential for processes pertaining to male meiosis, spermatogenesis, and sperm motility. Recently, we identified another gene that suppresses memi-1(sb41), smz-1 (sperm meiosis PDZ domain-containing protein). smz-1 and its paralog, smz-2, encode proteins reported to play a role in spermatogenesis (Chu et al., 2006). However, little is known about their mechanism of action. Herein, we focus on the characterization of smz-1 and how it affects the MEMI pathway in C. elegans. We hope to get more insight into the nature of the molecular signals required for fertilization and the proper transition from female meiosis to mitotic cell divisions of the zygote.

Understanding C. elegans signaling mechanisms through paralysis interactions of the unc-119 gene

Ryan Campbell, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

The unc-119 gene was characterized in C. elegans as a mutation that hinders the movement of C. elegans during its developmental stages and paralyzes them upon reaching adulthood. Although paralyzed, the worms are still capable of eating, breeding and laying eggs, making them an interesting viable model. Studies later showed that the role of unc-119 was in axon branching, where it was required to prevent aberrant axonic branching which would lead to the paralysis phenotype. While we know what the gene does, there is no concrete answer to what pathway the unc-119 gene operates. While there are theories for how it could work, none have yet to be 100% proven. Additionally, the unc-119 gene is heavily conserved in almost all forms of life, however the phenotype varies from species to species. Another question that surrounds this gene is what fundamental purpose does it serve that has made it so vital for all life to keep in their genome. My project was to experiment with genes that could interact with unc-119 by using the harshness of the paralysis as an indicator. I am using movement quantification techniques and GFP reporter strains to identify any changes in C. elegans movement when crossing strains of genes that have potential interactions. While some data has been collected, the evidence is not concrete and more

testing needs to be done with the genes in question. I believe that work on the unc-119 gene is important, as the answers to the questions surrounding the genes functions and conservation could answer questions about how evolutionary pathways diverge, what functions are important for cells to maintain and potential therapies for the human mutation of unc-119 (HRG4) which causes optical degradation.

Investigating the function of a novel typhoid toxin-associated phospholipase in the pathogenesis of *Salmonella typhi*

Sarah Gartly, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Salmonella Typhi is a facultative, intracellular human pathogen, and the causative agent of typhoid fever. Typhoid toxin is a key virulence factor of S. Typhi and is linked to severe disease symptoms. The Fowler lab recently showed that the only uncharacterized gene in the typhoid toxin islet, sty1887, is a phospholipase type A2. Given its strong conservation in the islet, and the function of phospholipases as bacterial virulence factors, we hypothesize that Sty1887 plays a crucial role in S. Typhi virulence. Here, we investigated the regulation of Sty1887, as well as the role of Sty1887 in both typhoid toxin secretion and S. Typhi infection. Guided by the hypothesis that the typhoid toxin islet's cdtB promoter drives sty1887 expression, we performed qPCR using wildtype S. Typhi and a cdtB promoter deletion strain. Additionally, western blotting was used to determine if changes in relative mRNA expression translated into changes in protein expression. Through this research, we confirmed that sty1887 is co-regulated with typhoid toxin via the cdtB promoter, however, protein expression levels of Sty1887 and typhoid toxin differ depending on environmental conditions. Using wildtype S. Typhi and a strain lacking sty1887, we explored the biological role of Sty1887 using typhoid toxin secretion assays. At this point, Sty1887 does not appear to be secreted, nor does it appear to play a role in typhoid toxin secretion in vitro. Research regarding the role of Sty1887 during S. Typhi infection, which will be explored using cell culture, is still underway. Overall, this research allows us to better hypothesize the biological function of Sty1887 and contextualize its role in S. Typhi pathogenesis.

Analysis of cytokine trafficking in airway epithelial cells

Sharanya Das, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Trafficking of newly synthesized inflammatory proteins known as cytokines in epithelial cells is not well understood. Thymic stromal lymphopoietin (TSLP) is an airway epithelial cell-derived master cytokine secreted in response to triggers such as allergens, bacteria, and viruses. Its secretion results in lung inflammation. Preliminary findings show that allergens like cockroach extract (CE) evoke TSLP production in airway epithelial cells. We hypothesize that the exposure of airway epithelial cells to CE induces increased de novo synthesis of intracellular TSLP.
We used airway epithelial BEAS-2B cells to test this hypothesis. Intracellular TSLP was measured using an immunofluorescence assay (IFA) in cells stimulated with an optimal dose of CE (10 µg/ml) or house dust mite (HDM) (10 µg/ml). Protein synthesis inhibitors actinomycin D and verrucarin A (10 µg/ml) were used to determine if TSLP levels were affected upon stimulation with CE. Cells were counterstained with Hoechst nuclear stain and rhodamine phalloidin to detect nuclei and actin cytoskeleton. Images were collected using epifluorescence and analyzed with Volocity software. Cells exposed to CE produced greater intensities of TSLP over a time course, with maximal expression evident at 8 hours. Similar findings were obtained with HDM-stimulated epithelial cells. The addition of actinomycin D and verrucarin A inhibited CE-induced TSLP immunofluorescence to baseline levels. These findings suggest that CE induces de novo synthesis of TSLP in airway epithelial cells. Since CE is a complex mixture of allergens, it likely stimulates cells through multiple Toll-like receptors (TLRs), mannose 6-phosphate receptor, protease-activated receptors (PARs), and others. Future studies will be directed at determining the mechanisms of TSLP release in response to allergens. These results further our understanding of TSLP synthesis, secretion, and trafficking in airway epithelial cells, as well as our understanding of anti-TSLP treatment currently being used to treat severe asthma in Canada.

Development of a simple, one-step colorimetric assay for L-lactic acid detection as a serum biomarker for sheep litter size

Suyenna Huang, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Reproductive and breeding management are key areas in sheep farming to ensure healthy livestock and maximize farm profitability. Early and accurate determination of an ewe's pregnancy and litter size is important to plan the ewe's maternal nutrition, give birth to healthy lambs, and maintain the ewe's health. Currently, ultrasonography is the standard method of determining sheep pregnancy and litter size. However, metabolites as biomarkers offer a promising alternative for cheaper and convenient, on-site testing. L-lactic acid, along with other metabolites, has been recently reported as a serum biomarker for sheep litter size – singlet, twins, or triplets. The main objective is to develop a simple, one-step colorimetric assay to accurately and quickly detect L-lactic acid in sheep serum. In the assay, lactate oxidase (LOX) catalyzes an oxidation reaction to convert l-lactate to pyruvate and hydrogen peroxide. Hydrogen peroxide is further oxidized by Amplex Red, creating a pink-colored product, resorufin, which can be spectrophotometrically detected after a 10-minute incubation period at room temperature. The assay is first optimized in its liquid form. A standard curve in spiked pooled sheep serum yielded a $R2 = 0.99$ and its liquid correlation yielded a $R2 = 0.966$. The reaction mix is lyophilized to create a one-step colorimetric assay which only requires the addition of the serum sample. Importantly, the serum samples do not require pre-treatment to remove other metabolites which also increases the simplicity of this assay. The development of this one-step L-lactic colorimetric assay can be used for detection of sheep serum biomarkers indicative of litter size.

Egg size manipulated by variable honeycomb

Tianna Tanasichuk, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Organisms within social groups, such as social insect colonies, depend on each other and often exhibit division of labor. This labor could not be possible without the Queen constantly laying eggs to turn into fellow contributing members of the colony. The contribution of each member is contingent on their gender which is determined by the Queen. Drone or male eggs are laid in larger honeycomb frames in comparison to the female worker bees although when comparing hive contribution worker bees are far more significant. We hypothesized that the difference in frame size is proportional to the size of the eggs. We tested this by using 3D-printed variable comb and having a Queen lay worker eggs on the comb. The accumulated data was complemented by our findings from the previous summer. The results are discussed in the context of the rules that organize the complex societies of social insects and potentially other systems with efficiency tactics.

Diel modulation of the plant 26S proteasome

Yangyi (Dash) Zhong, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

As sessile organisms, land plants experience constantly changing environmental conditions such as temperature oscillations. To optimize growth and development, plants have evolved with their circadian clock as a molecular timekeeping mechanism that predicts and fine-tunes their daily activities. The 26S proteasome is a proteolytic complex characterized by a combination of 19S and 20S subunits, which assemble into a macromolecular hub responsible for ubiquitin-dependent protein degradation. Previously, the Uhrig lab found that proteasome subunit protein abundance and activity were reduced in the circadian clock gene mutant rve4/6/8. Furthermore, degradation of many clock proteins via the 26S proteasome is found to follow diel trends. Currently, proteasome activity and proteasome subunit genes have been related to plant growth and stress responses, but how the genes encoding these proteins are regulated remains unknown. To decipher the molecular links between the proteasome and diel plant cell regulation, advanced plant phenomics, proteomics, bioinformatic, and molecular biology tools were utilized. Through bioinformatic analyses of the promoter region sequences, we identified transcription factor binding sites in the proteasome genes of Arabidopsis thaliana. We found that removing different circadian clock genes results in varying levels of impairment to mutant growth when proteasome inhibition is applied. Additionally, we analyzed the changes at the RNA and protein levels in different clock gene mutants using in-house transcriptomic and proteomic data and established a more sophisticated understanding of the modulation of proteasome activity by the circadian clock.

Impact of mining development and activities on wolverine (*Gulo gulo*) abundance and distribution in Yukon South Beringia

Zach Fogel, MSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Wolverines/nähträ are a widespread carnivore that are threatened by human disturbance across much of their range. In central Yukon, stewardship of the land and its inhabitants by Hän people has been disrupted by mining, beginning with the Klondike Gold Rush of 1896-1899. Wolverines are a bioculturally important species for Tr'ondëk Hwëch'in First Nation (THFN), who have identified mining as a threat to wolverines and other wildlife in Yukon South Beringia (YSB), which encompasses much of their traditional territory. Academic research indicates that wolverines are affected by industrial activity, with the response varying by intensity and type of activity, but little research has focused on mining. In response to high biodiversity and current landscape change, Environment and Climate Change Canada has identified YSB as the north's first Priority Place. The Priority Place Initiative is a commitment to shift toward collaborative, multi-species, and ecosystem-based management that explicitly includes Indigenous Peoples and Traditional Knowledge. To meet this commitment, we are partnering with THFN, Yukon Government, and other agencies to quantify the relationship between landscape condition and wolverine abundance and distribution. We will deploy trail cameras and autonomous recording units (ARUs) across a gradient of disturbances in regions identified by local knowledge holders as particularly important for both wolverines and traditional activities. Trail cameras will capture images of animals that pass by the camera, and ARUs will record ambient sound. We will estimate wolverine abundance using camera data, quantify industrial soundscape and activity using ARU data and disturbance mapping, and evaluate the relationship between wolverine abundance and industrial activity. We expect that wolverine abundance will be lower in areas of increased disturbance. Our results will inform land use planning, promote compatibility between biocultural and economic interests, and support THFN's ancestral stewardship responsibilities.

Identifying lybatide CRP in solanaceae plants and its potential as small peptide drug

Zimu Zhang, BSc Student [1]
[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9

Lycium barbarum, a long-used traditional Chinese medicine for the treatment of chronic low-grade fever, cough, hemoptysis and hematuria, diabetes mellitus, and hypertension, CRPs <1 kDa have been found to inhibit renin and angiotensin-converting enzymes, and Lycium barbarum is a member of the Solanaceae family. From Dr. Tan and his colleagues' research, a novel CRPs peptide, named α-lybatide 1 and 2 (lyba1 and lyba2), was isolated from the Lycium barbarum roots, displaying a unique C-C-C-C-CC-CC cysteine spacing. They have a unique structure with a dominant cystinestapled -helix and no known plant CRP sequence homologies, giving rise to a new CRP family. Although the new CRP lybatides family has been identified, there is little research on how the lybatides interact with human proteins and whether any peptides show a cysteine pattern similar to that present in lysines in other plants. The purpose of this study is to determine whether lybatidessimilar peptides also exist in other Solanaceae family plants including Solanum ptychanthum, Solanum xanthocarpum, and other closely related species through the 1kp plant database, and to predict the function and intercellular interaction of these peptides.

Conflicts of Interest

The authors declare that they have no conflict of interests.

Authors' Contributions

MB: Primary Event Organizer for the R.E. Peter 2023 Biology Conference whom drafted the URNCST conference abstract book.
LJ: Student Presentations volunteers who primarily drafted the R.E. Peter version of the conference abstract book, whose information was used to draft this document.
AB: Student Presentations and Judging/Prizes volunteer who handled student information and sorted it for ease of use. Also assisted in the creation of the in-house version of the R.E. Peter 2023 conference abstract book.
JW: Logo and Abstract Book design volunteer who assisted with graphical design for the conference and in-house conference abstract book.

Acknowledgements
A big thank you to all the amazing volunteers – including Aaron Boyd, Ade Omorogbe, Christiana Garros, Christine Grams, Dayani Patuwatha Withanage, Ish Jain, Jiahui Wang, Laura Manerus, Leah Jackson, Marlee Kohlman, Meghan Dueck, Montana Bobinski, Sajjad Syed, and Suyenna Huang – that have helped to plan the conference this year. Without all your hard work this conference wouldn't have happened. Thank you for helping navigate all the challenges we faced this year!

Funding
Thank you to our many sponsors for supporting the 2023 RE Peter Conference! This conference was supported (in part) by the Faculty of Science, the Faculty of Graduate Studies and Research, the Graduate Students' Association, and the Department of Biological Sciences at the University of Alberta.

Article Information
Managing Editor: Jeremy Y. Ng
Article Dates: Received Feb 24 23; Published Mar 07 23

Citation
Please cite this article as follows:
Bobinski M, Jackson L, Boyd A, Wang J. Dr. Richard E. Peter 2023 Biology Conference: Abstract Book. URNCST Journal. 2023 Mar 07: 7(3). https://urncst.com/index.php/urncst/article/view/468
DOI Link: https://doi.org/10.26685/urncst.468