

**Ottawa-Carleton Institute of Biology  
22nd Annual Symposium  
April 28-29, 2025**

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**Adapting to Change and Challenges**

**Abstract Booklet**

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## 3 Minute Thesis Presentations

Involvement of dl3 neurons in spinal motor learning

Emam Khan, Sarah Chiasson, Sarah Goltash, Lauren Couvrette, Alex Laliberte, Tuan Bui

The nervous system integrates sensory input from the environment with motor output to muscles. This enables adaptive muscle activity based on external stimuli—for example, adjusting leg movements when running on uneven terrain. This adaptation of motor output in response to sensory information is referred to as ‘motor learning’. Motor learning is a complex process governed by the nervous system, and its mechanisms in advanced motor behaviors such as locomotion remain poorly understood. Moreover, the extent to which the spinal cord itself contributes to motor learning is only beginning to be explored.

Investigating spinal motor learning will deepen our understanding of the spinal circuits responsible for integrating sensory input and motor output. Our aim was to develop a simplified model of spinal motor learning. Using stationary, spinalized mice, we assessed their ability to modify hindlimb vertical position in response to electrical stimulation of a hindlimb nerve. Specifically, we recorded video and electromyographic activity of the

hindlimb and stimulated the nerve if the toe dropped below a defined vertical threshold. We then examined the spinal circuits involved in this learning process, focusing on a specific class of excitatory spinal interneurons—the dI3 neurons—which are known to receive sensory input and project to motor neurons. We therefore hypothesized that dI3 neurons are necessary for motor learning to occur without connections from the brain, which we tested by inhibiting dI3 neural activity. Our results will serve as a foundation to study motor learning in more complex behaviors, such as locomotion.

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## The Evolutionary Dynamics of GBM and Intra-tumor Heterogeneity as a Potential Predictor of Tumoral Fitness

Hussein Omran, Andrew Simons, Bruce McKay

Glioblastoma multiforme (GBM) is a highly aggressive primary brain tumour that primarily affects adults. The prognosis is very poor, with a median survival time of 14–15 months after diagnosis. The specific cell of origin responsible for initiating GBM pathogenesis reflects its diverse molecular and phenotypic profiles. As a result, GBM tumours are highly heterogeneous, posing a significant barrier to targeted therapeutic efforts. In this experimental evolutionary study, the therapeutic resistance of two GBM cell lines was evaluated in response to two selective pressures: the targeted therapeutic drugs Taxol and Affinitor. The two cell lines used were an isogenic pair of U-87MG wild-type and U-87MG mutant cells. The mutant line was engineered to express the R132H mutation, which is associated with increased production of the oncometabolite 2-HG. A cumulative value representing intratumoral heterogeneity (ITH) was derived mathematically using morphometric measurements obtained from fluorescent micrographs analyzed in Fiji. The relationship between ITH and therapeutic resistance was examined to determine whether a statistically significant correlation exists between the two variables. Preliminary studies conducted on the isogenic pair have revealed insights into growth dynamics and therapeutic response.

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## Phylogenetic evolution of the actinodin (and) and augurin (ecrg4) genes

Atho Jeremy

Actinodin genes encode proteins involved in the formation of fin fibers called actinotrichia. Like fins, these actinodin genes have not been found to date in tetrapods. We believe that the loss of these genes this during evolution allowed the transition from aquatic life to terrestrial life. On the other hand, in tetrapods, there is the augurin gene ECRG4, a

putative tumor suppressor gene whose N terminal part is partly similar to that of the actinodin genes . How does the phylogenetic analysis of actinodin genes elucidate their evolutionary trajectory, from origin to loss in certain lineages? This is the main question of our research. In summary, I can say that my research has three short term goals: The first is to perform a phylogenetic analysis of the actinodin and *ecrg4* genes by considering only the N-terminal part of and which has some similarities with *ecrg4* to date and estimate the appearance and disappearance of actinodin genes during evolution. The second objective is to do the synteny of the actinodin genes in different species of vertebrates in order to confirm the loss of the gene in tetrapod but also to confirm the results of my phylogenetic analysis. I will also do an analysis of the synteny between different species of teleost in order to observe the divergences that could exist in acantomorphs due to the presence of spinous rays. The third objective will be to make a prediction of the three-dimensional structure of proteins allowing the formation of ceratotrichia in chondrychians to compare them with those of actinotrichia in osteichthyes such as zebrafish and acantomorphs. This prediction will allow to understand the morphological difference at the level of the fin rays of different species of fish. The long-term goals of this study are to understand the evolution of actinodin genes and their role in the formation of fish fin rays, by exploring the morphological differences between soft and spiny rays.

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## Evaluation of the Impact of Environmental Antimicrobial Residues on the Gut Microbiome and Resistome Using a Mouse Model

Amer Abdelgany, Tamara Morrill, Alex Wong, Catherine Carrillo, and Jiewen Guan

Antimicrobial resistance (AMR) is a growing public health concern, driven by the spread of antimicrobial-resistant bacteria (ARB) and resistance genes (ARGs) in environments such as farms and water systems. This study investigates the effects of environmental and clinical antimicrobial exposures specifically ampicillin and tetracycline on ARB colonization, microbial dysbiosis, and horizontal gene transfer in the gut microbiome. Using a mouse model, Enterobacteriaceae conjugation experiments were performed under various antimicrobial exposures. Ampicillin was administered at a clinical dose, while tetracycline was tested at subclinical, MIC, sub-MIC, and clinical levels. Fecal samples were collected at multiple time points and analyzed through culture, 16S rRNA sequencing, qPCR, and colony PCR. Donor *Salmonella* Heidelberg, isolated from farm chicken and carrying a multidrug-resistant *IncA/C* plasmid, persisted in all antimicrobial-treated groups. It temporarily disappeared after initial ampicillin treatment but re-emerged following repeated exposures. Transconjugant *E. coli* were detected in most antimicrobial groups, confirming in vivo plasmid transfer. Plasmid transfer to recipient *S. Heidelberg* was

also confirmed. These findings highlight the persistence and transferability of ARB and ARGs under environmental antimicrobial exposure. The results underscore the role of antimicrobial residues in promoting resistance gene spread and the potential for zoonotic transmission. Ongoing work includes whole-genome sequencing and analysis of host immune responses and *Salmonella* colonization mechanisms to further explore AMR dynamics.

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## Undergraduate Session

How Long Are Shorebirds Retaining Ingested Microplastics?

Brooke MacIsaac, Reyd Dupuis-Smith, Jessie Wilson, Marshall Ritchie, Scott Flemming, Morag Dick, Christopher Guglielmo, and Jennifer Provencher

Microplastics are ubiquitous across the globe, yet plastic use continues to rise, increasing ecosystem-wide contamination. Microplastics can absorb harmful toxins and heavy metals, which can cumulatively affect bird health and development. While microplastic ingestion in wild birds is well documented, retention time remains understudied. The retention time of ingested

microplastics is crucial for using microplastics collected in the feces of wild shorebirds as an environmental-monitoring tool. To assess microplastic retention in shorebirds, nine wild-caught Western Sandpipers (*Calidris mauri*) originally obtained for a flight-study, were selected for this secondary experiment. The sandpipers were fed wet dog kibble, mealworms, and 100 $\mu$ m polyethylene beads for 96 hours, with fecal samples collected at 3, 6, 9, 24, 48, 72, and 96 hours. Five of the sandpipers were euthanized after this period, while the remaining four immediately underwent a 96-hour recovery period, where they were fed only kibble and mealworms. Fecal samples were taken at the same interval, after which the remaining four sandpipers were euthanized. Results suggest that the majority of microplastics were excreted within 24 hours after ingestion of the plastics ceased, with some breakdown of the microplastics during digestion. The presence of microplastics in the recovery period suggests trace retention longer than 24 hours, however, further analysis of the digestive tracts is ongoing to examine any possible long-term retention.

Understanding microplastic retention time, particularly in highly mobile species like Western Sandpipers, is crucial for examining avian environmental microplastics transport and the potential health effects of microplastics on migratory birds.

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Acute oxygen-dependent epigenetic regulation in rainbow trout liver: Is H3K4me3 linked to induced metabolic genes?

Sally Adil, William Johnston, Dr. Jan Mennigen

Environmental hypoxia in freshwater systems is increasing, even more so with climate change. Among freshwater fishes, some are relatively more tolerant to hypoxia, like the goldfish (*Carassius auratus*); others, such as the rainbow trout (*Oncorhynchus mykiss*), are intolerant. Physiological responses to acute hypoxia exposure vary, among them is metabolic plasticity. At least in part, metabolic plasticity is mediated via transcriptional changes in rate-limiting enzymes of metabolic pathways involved in glucose and lipid metabolism. Transcriptional responses are well-known to be mediated via the Hypoxia-Inducible Factor oxygen sensor system. Recent *in vitro* evidence revealed that oxygen-dependent epigenetic machinery may also be involved in direct regulation of transcripts. Here, we probe whether the activating histone modification, H3K4me3, enhanced in hypoxic condition *in vitro*, is linked to metabolic transcript induction by acute 4h hypoxia exposure (50% and 25% O<sub>2</sub> saturation) in the trout liver. Contrary to prediction, results show 25% O<sub>2</sub> saturation induced transcripts involved in gluconeogenesis (*pck1*) and fatty acid synthesis (*fasn*) exhibit a decrease in H3K4me3 modification in the upstream putative promoter region. These observations suggest that under the experimental conditions tested, other O<sub>2</sub> dependent (epigenetic) molecular mechanisms are involved in the induction of these enzymes. Additional studies looking at different hypoxia regimes and O<sub>2</sub> sensitive epigenetic markers are warranted to further address the role of epigenetic regulation on metabolic pathways in hypoxia response in fish.

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Using Microsatellite Markers to Investigate Genetic Diversity in Kaladar's Disjunct *Opuntia fragilis* Population

Shelby Atkinson, Melanie Beaudin, Root Gorelick, Catherine Cullingham

*Opuntia fragilis*, commonly known as the brittle prickly pear cactus, is one of four cactus species native to Canada. A disjunct population of *O. fragilis* located just outside Kaladar, Ontario, is notable for being over 800 km away from its nearest neighbouring population. This has drawn the attention of many scientists over the years, but none have taken a genetic approach to studying this population. Our objective is to apply a population genetics approach to investigate the genetic diversity of the Kaladar *O. fragilis* population to determine whether the population is clonal. To do so, we will perform microsatellite marker analysis on *O. fragilis* samples from Kaladar and other locales across North America. To date, we have tested sixteen microsatellite primers designed for use in *Opuntia*

species. We have confirmed the efficacy of these primers and have optimized nine that we are using to assess genetic diversity. Results from two of these microsatellite primers indicate that there is no genetic variation among the Kaladar *O. fragilis* samples, which suggests that the population is clonal.

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## Talk Session 1

### Session 1: Quantifying Flowering Bias in Community Science Data

Matthew Coffey, Andrew Simons

Community science platforms like iNaturalist—typically used to document species ranges—are increasingly being used to study more complex phenomena including plant phenology. However, community science data is generally comprised of casual observations rather than targeted field sampling, and the extent to which observations may be biased toward specific plant life-stages is unknown. For example, in a previous study of *Lobelia* species using iNaturalist data, we found most observation photographs to be of flowering individuals. In addition, a preliminary analysis of observations of eudicot species in Ottawa, found that woody species were significantly less likely to be observed in flower relative to forbs; suggesting that the period of the year a species is observable (which is shorter in temperate forb species) might influence flowering observation frequency. In this study, we explore whether iNaturalist observations are biased toward flowering while accounting for differences in species' observable periods. Here, we use phenological data from National Ecological Observatory Network sites (NEON) to define the expected proportion of flowering observations, for 543 plant species, based on the number of weeks a species is flowering out of the total weeks it is observable. Then, iNaturalist records from a 20km radius around each NEON site are scored for the presence of flowers. By measuring the extent to which a species' observed proportion of flowering observations deviates from the proportion expected based on the species' phenology, we can quantify the magnitude and direction of flowering bias and explore how bias is influenced by species-level traits.

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### Session 1: Soybean Cell Wall Development is Microbiome-Responsive

Alicia Halhed, Isabel Molina, Owen Rowland

Plant stress response mechanisms allow these species to be resilient in the face of environmental stress. Plant-associated microorganisms (i.e., the microbiome) contribute

to this stress tolerance, including outcompeting pathogens. To further tolerate stress, plants naturally reinforce the cell walls of some tissues with suberin, a hydrophobic polymer. Suberin can limit root pathogen colonization in agricultural crops like soybeans. The primary objective of this research was to identify whether root suberin determines root microbiome colonization in early soybean development.

Three soybean cultivars with varying degrees of pathogen tolerance were grown with and without microbiome treatment. The total suberin content was measured for each cultivar at three time points in early develop. Next, root and rhizosphere microbiome composition will be analyzed to identify suberin associated microbiota across these soybean cultivars.

Current results suggest that only soybean cultivars with high pathogen tolerance increase suberization in response to microbiome treatment early in plant development.

Transcriptome analysis suggests that these plants undergo cell wall remodification with microbiome treatment. Continued research on plant-microbe interactions contributes to efforts in sustainable agriculture to feed a growing global population.

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Session 1: The importance of germplasm collections: a case study in soybean protein and amino acid content

Simon Lackey, Siwar Haidar, Mohamad Elian, Jakob Bruggink, Ashkan Golshani, Elroy Cober, Bahram Samanfar

Germplasm collections of crop plants are maintained throughout the world as a source for genetic variability that can be used to modify existing cultivars for novel purposes. Things like stress resistance, regional adaptation, and seed composition characteristics will need to be continually fine tuned to mitigate against climate change and satisfy the needs of industry and consumers in the current era and beyond. In this case study, a novel panel of soybean germplasm was assembled to investigate seed protein and amino acid content differences between eastern and western growing regions of Canada. Field trials of 206 cultivars were grown across Canada in 2021 and 2022, from which 31362 single nucleotide polymorphisms were used to detect 370 marker trait associations. Phenotypic data was assessed to determine the heritability and correlation of the traits studied, finding that this newly assembled panel was less susceptible to the commonly reported western Canada protein deficit. After consolidation into 175 quantitative trait loci (QTL), commonly reported major QTL for seed protein content on chromosomes 14, 15, and 20 were validated. QTL detected using only eastern or western datasets independently suggest that different genes (as well as mutations in those genes) can impact seed composition characteristics differently in different environments. This case study reinforces the utility of maintaining



more regionally centric germplasm collections, such as Plant Gene Resources of Canada, and demonstrates that important cultivars harboring rare alleles are often maintained in these critically important resources for plant breeding goals both now and into the future.

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Session 1: The first steps towards population genomic research in arbuscular mycorrhizal fungi

Kevin MacColl, Nicolas Corradi

Population genomic analyses have been crucial for expanding our knowledge of fungal biology, however, such analyses have never been attempted on arbuscular mycorrhizal (AM) fungi, which are the most abundant and taxonomically widespread plant mutualists in nature. Population genomic analyses in fungi require dozens to hundreds of single-strain cultures, however, starting such cultures with AM fungi is notoriously difficult due to their dependence on a plant host. Here, we present a protocol that allowed us to isolate dozens of new strains of two AM fungal species isolated from multiple field plots. Spores isolated from these cultures will be subject to low-coverage whole-genome Illumina sequencing, allowing for the first genomic analysis of AM fungal population structure, for example, determining rates of sexual versus asexual reproduction, estimating within-population genetic diversity and measuring gene flow between populations. These analyses should be ready for publication later this year.

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Session 1: Comparison of UAV and ground surveys for the detection of a rare plant in a fragile ecosystem

Ana Hernandez Martinez de la Riva, Murray Richardson, Koreen Millard, Joseph Bennett

Fragile ecosystems require careful monitoring for protection, yet traditional survey methods can inadvertently harm the environments they aim to preserve. In these cases, it might be preferable to use less invasive methods for species monitoring, such as drones. We compared the efficiency of drone and ground surveys for the detection of wood lilies (*Lilium philadelphicum*) at an endangered alvar ecosystem. We found that the drone survey could detect 78% of the plants, including some plants that were beginning to bloom, fading or partially covered by vegetation. Estimating exact plant numbers from the drone survey proved challenging due to the misclassification of closely growing plants as single individuals and plants with multiple flowerheads as separate individuals. However, careful examination of the drone imagery revealed that the ground survey potentially missed 3% of the plants found in the study site. These results suggest that drone surveys have potential

as either a complementary technique to ground surveys or as a standalone method for species detection in fragile ecosystems.

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## Talk Session 2

Session 2: Exploring the functional relevance of stress-induced protein-protein interactions on chromatin remodelling

Ikram Khan

Human cells are regularly subjected to stresses such as low oxygen, lack of nutrients, exposure to harsh chemicals and sub-optimal temperatures that trigger pro-survival stress response pathways. Cancer cells exploit these same stress response pathways to outlast adverse conditions, which makes them excellent targets for primary or adjunct therapies. The integrated stress-response (ISR) is a signalling pathway in cells that is activated in response to various types of stress and promotes cell survival and homeostasis through changes in protein translation and gene expression. A hallmark of the ISR is formation of cytoplasmic stress granules (SGs) that sequester translating mRNA and proteins. Recently, our lab identified a nuclear stress response pathway that is triggered in parallel with the ISR and leads to formation of distinct heterochromatic regions that we termed nuclear stress foci (nucSF). Both nucSF and cytoplasmic SGs assemble and disassemble on similar timescales. The marker protein that first reported the existence of nucSF was RepoMan, a chromatin associated protein that forms a holoenzyme complex with PP1 phosphatase to dephosphorylate substrates such as histone H3S10 and H3T3. Mapping the interactome of RepoMan identified stress-induced interactions with proteins involved in chromatin remodelling and transcriptional repression. Comparison of the stress-induced interactomes of these additional nucSF factors has revealed significant protein overlap and functional enrichment. This suggests an orchestrated response to the remodelling of chromatin.

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Session 2: Developmental genetic endocrinology underlying caste determination and differentiation in ants

Olivia MacMillan, Julia Singer, Sophia Perrakis, Rajendhran Rajakumar

Ants live in societies called colonies that are composed of reproductive and non-reproductive castes. Males in a colony are haploid whereas females in a colony are diploid

and exhibit a great deal of variation. Female reproductive castes (queens) are large, long lived, winged individuals who are responsible for increasing the colony population by laying up to thousands of embryos daily. Non-reproductive worker castes are responsible for non-reproductive tasks and maintaining the colony. Despite being separated by over 100 million years of evolution, ant species of the hyperdiverse genera *Pheidole* and *Camponotus* have independently evolved the ability to sub-divide their non-reproductive worker castes into minors and soldiers. Minors forage for food and take care of the brood while soldiers defend the colony and have a larger head-to-body allometry. Juvenile hormone (JH) is a molecule that mediates gene-by-environment interactions, enabling developing insects to respond to environmental perturbations related to nutrition and temperature. In *Pheidole*, JH is a critical hormone in regulating caste determination and soldier development. Whether this hormone has been independently recruited to regulate soldier development in *Camponotus* remains a mystery. Here we show that ant caste determination in *Camponotus floridanus* is mediated by a JH-mediated minor-soldier switchpoint during the 4th larval instar, influencing developmental timing and growth, and that JH degradation is likely regulated in a caste-specific manner. Collectively, these findings suggest that the same ancient insect hormone has facilitated the independent evolution of soldier development in ants.

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## Session 2: Histone Epigenetic and Hormonal Modulation of Temperature and Nutrition During Fire Ant Development

Navid Bahramifarid; Rajendhran Rajakumar

Epigenetics describes heritable alterations in gene activities independent of genetic variation. Environmental variation can influence developmental processes through gene-by-environment (GxE) interactions, mediated by hormonal and epigenetic mechanisms. For example, sex steroid hormones and histone post-translational modifications are mediators of thermal variation by regulating gene activity involved in environmental sex determination. Ants are an emerging model organism to study how hormonal and epigenetic mechanisms mediate GxE interactions. Ant development is plastic; environmental changes generate diverse phenotypic variation ranging from behaviour, lifespan, and morphology. In the context of histone regulation, while ant behaviour and lifespan are regulated via histone modifications, little is known about: (1) how these modifications influence morphology in ants; (2) how they respond to environmental variation; and (3) how hormones influence these histone modifications. Using available ant evolutionary genomic resources and phylogenetics, we identified key histone toolkit genes that are conserved across animals and implicated in ant evolution. Here we show in the

invasive fire ant *Solenopsis invicta*, that the histone code is responsive to both hormonal and environmental (temperature) variation and that this mediates developmental timing and sizing regulation. Currently, we are developing pharmacological methods to perturb histone modifiers. This study will contribute to our understanding of GxE mechanisms that underlie the fire ants' success as an invasive species, facilitating their optimized developmental adaptation to environmental variation. Ultimately, this project will provide a case study for understanding the impact of climate change (rising global temperatures) on development, thereby promoting range expansion of invasive species through developmental epigenetic responses.

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#### Session 2: Regulation of stress granules and P-bodies during hibernation

Carter, R. and Storey, K.B.

Thirteen-lined ground squirrels endure the harsh winter season by resorting to hibernation, a type of dormancy characterized by metabolic rate depression. This season, along with hibernation itself, accompanies various stressors such as low body temperatures, ischemia, food insecurity, and oxidative stress. Post-transcriptional regulation is a recognized facet of hibernation, though it remains unclear how mRNP granules like stress granules and P-bodies are involved. To address this gap in knowledge, we investigated the differential regulation of well characterized stress granule and P-body proteins across five stages of the torpor-arousal cycle in ground squirrel livers through western immunoblotting. Hibernation-responsive differential regulations were observed throughout torpor-arousal cycles: Notably, assemblers of stress granules and P-bodies were upregulated during entrance into torpor and interbout arousal, respectively. The present study is the first to provide preliminary evidences for increased mRNP granule abundance during hibernation.

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#### Session 2: Mitochondrial ATP-dependent K<sup>+</sup> channels downregulate ionotropic glutamate receptors during hypoxia in retinal horizontal cells of goldfish

Mohamed Ramadan, Michael Jonz

Horizontal cells (HCs) are retinal interneurons that are essential in modulating visual contrast and facilitating photoreceptor feedback. Hypoxia, characterized by reduced oxygen availability, can severely disrupt cellular functions, leading to hyperexcitability, elevated cytosolic calcium levels, and subsequent cell death. Remarkably, goldfish exhibit a tolerance to hypoxia through the ability to regulate intracellular calcium under metabolic

stress. This study highlights how goldfish HCs contribute to hypoxic resilience by regulating ionotropic glutamate receptors (iGluRs). Horizontal cells were clamped at -60 mV using perforated-patch electrophysiology. Responses from iGluR were evoked by a 2-minute application of 100  $\mu$ M glutamate every 5 minutes through a superfusion system, while cells were exposed to either normoxic or hypoxic conditions. Under hypoxia, we observed a decrease in iGluR activity which did not recover after 10 minutes of reoxygenation. By contrast, normoxic controls showed no significant changes in current activity over time, confirming that this response was specific to hypoxia and not a baseline cellular response to glutamate. Preliminary work shows that inhibiting mitochondrial ATP-dependent K<sup>+</sup> (mKATP) channels with 100  $\mu$ M glibenclamide in the presence of hypoxia abolishes the decreased current response. Together, these findings suggest that goldfish HCs tolerate hypoxia through the downregulation of iGluR activity, potentially through the activation of mKATP channels. The present thesis introduces a mechanism that enhances the cell's ability to conserve ATP and maintain function under stress, demonstrating a potential neuroprotective mechanism that mitigates hypoxic damage in goldfish retina.

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## Talk Session 3

Session 3: dna-parser: a Python library written in Rust for fast encoding of DNA and RNA sequences

Matthieu Vilain, Stéphane Aris-Brosou

A steep decrease in sequencing prices has led to a rapid rise in genomic sequences available for analysis. As a result, biologists have started using more machine learning (ML) algorithms to process increasingly large datasets, which require preprocessing before being analyzed. One common preprocessing step consists of encoding DNA and RNA sequences into numerical representations, also called descriptors. Unfortunately, current Python tools available for this preprocessing step are not well suited to be integrated into pipelines resulting in slow encoding speeds. We introduce dna- parser, a Python library written in Rust to encode DNA and RNA sequences into numerical features. This library regroups many widely used types of numerical feature schemes coming from bioinformatics and natural language processing into a single library. The benchmarks we conducted indicate that encoding functions written in Rust are up to 23 times faster than equivalent functions from other state-of-the-art Python libraries. Additionally, dna-parser can distribute sequences across multiple CPU cores to encode them at once further reducing preprocessing time for larger datasets. Altogether, this work highlights how Rust

can be used to easily create tools that are very performant and effortlessly accessible to many users.

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### Session 3: Elucidating Global Patterns of Viral Biodiversity across the Latitudinal Gradient

Vaibhav Kulkarni

Viruses permeate every microscopic corner of our biosphere—silently shaping ecosystems, driving evolutionary processes, and outnumbering all other biological entities by orders of magnitude, despite not being considered alive. Their enigmatic nature challenges our understanding of life and leaves much about them shrouded in mystery. This knowledge gap, often referred to as "viral dark matter," mirrors the concept of dark matter in physics. While recent technological advancements have accelerated rates of viral discovery, our understanding remains superficial. Given their host-dependent replication, viruses are expected to follow a latitudinal diversity gradient (LDG)—a well-documented ecological pattern where species richness increases from the poles to the equator. However, current evidence for a viral LDG is sparse and often conflicting. I propose that even the most comprehensive viral databases are biased against the harsher and undersampled polar latitudes. Consequently, I hypothesize that viruses in polar regions exhibit significant genetic divergence from those in tropical regions and those found in existing reference databases due to under-sampling, unique environmental pressures, and geographic isolation. This divergence likely reflects the viral LGD and eco-geographical drivers such as host diversity and environmental adaptation. To test this hypothesis, I am conducting a global comparative analysis of viral components in metagenomes sampled across diverse latitudinal regions. This study aims to provide new insights into viral diversity patterns and their ecological drivers whilst also contributing to global health preparedness and ecosystem resilience amid accelerated anthropogenic climate change.

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Session 3: Human-Candida interactome prediction discovers novel protein virulence markers in *Candida* sp.

Al-gafari, M., Kazmirchuk TDD., Moteshareie, H., Wang, J., Bradbury-Jost, C., Tayabali, A., Golshani, A.

Yeasts play an important role in biotechnology, though some species used in these applications have relatives harmful to human health. *Candida albicans* is the most frequent agent of Candidiasis, a fungal infection that predominantly affects immunocompromised hosts. Emergent species/strains such as *Candida auris* are of

concern as they are multiple drug resistant and challenging to treat, with mortality rates reaching more than 50% among vulnerable populations. In collaboration with Health Canada, we employed an in-silico approach for protein-protein interaction predictions between different *Candida* species and the human host cells. By comparing the interaction profiles of biotechnology-related and pathogenic *Candida* species, we were able to find key differences that relate to human pathogenicity potential. We noticed that proteins of pathogenic *Candida* species had a higher proportion of interactions associated with the human immune response, while biotechnology-related species were less involved in such interactions. A novel candidate virulence protein identified by this computational approach was knocked out and the resulting strain had reduced virulence in various human macrophage assays. Compared to the wild type, the deletion strain induced increased macrophage survival and reduced hyphae growth. Host immune responses were also observed to be different in exposures to wild-type *Candida albicans* compared to the deletion strain. These findings illustrate the potential of in silico tools for predicting putative virulence factors and assessing the public health risk of microorganisms, especially for otherwise difficult-to-characterize organisms due to biosafety concerns.

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Session 3: WGCNA and multiWGCNA identifies environmentally-influenced gene modules from soybean grown across eastern and western Canada

Julia C. Hooker, Elroy R. Cober, Steve J. Molnar, Ashkan Golshani, Bahram Samanfar

Soybean is a globally significant agronomic crop valued primarily for its high seed protein and oil content. Seed protein concentration is one of the critical determinants of soybean quality and, as such, is a key trait prioritized by breeders and farmers. Observations that soybeans cultivated in western Canada (Manitoba, Saskatchewan) exhibit lower seed protein content compared to those from eastern regions (Ontario, Québec) have been made for decades. To investigate the environmental effects on seed protein accumulation, ten soybean genotypes with varying seed protein content were grown at four experimental field sites (one eastern, three western) during the 2018–2021 growing seasons. A transcriptomic approach using Weighted Gene Co-Expression Network Analysis (WGCNA) identified gene modules exhibiting differential co-expression patterns between regions, and multiWGCNA was used to identify modules differentially co-expressed between low-medium- and high-protein seed trait groups between regions. Three region-associated modules were evaluated based on their intramodular connectivity and functional roles. Region-associated gene modules were found to be primarily linked to photosynthetic response, light response, and circadian rhythm regulation. Consistent patterns of differential co-expression across all three years revealed three PSI-LHCI proteins are

central components of environmental adaptation to light spectrum variation. This study highlights the utility of WGCNA and multiWGCNA in disentangling complex gene expression patterns and trait associations, providing valuable insights into the genetic regulation of soybean seed protein content in response to environmental factors.

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Session 3: Platelet GPIIb/IIIa harbouring PT-VWD mutations binds the VWF-C4 domain and competes with  $\alpha$ IIb $\beta$ 3 integrin

Calvin Bradbury-Jost, Thomas DD Kazmirchuk, Jiashu Wang, Anastasiia Koziar, Janice Corbette, Maha Othman, and Ashkan Golshani

We previously identified G14, a peptide inhibitor with therapeutic potential in platelet-type von Willebrand disease (PT-VWD) - a rare bleeding disorder caused by gain-of-function mutations in platelet glycoprotein IIb/IIIa (GPIIb/IIIaGOF: Gly233Val, Met239Val). These mutations enhance the glycoprotein's interaction with von Willebrand factor (VWF). We found that G14 disrupted full-length VWF binding to GPIIb/IIIaGOF yet did not affect binding to VWF-A1 - the canonical GPIIb/IIIa site. This suggests that an alternative binding site for GPIIb/IIIaGOF exists within VWF. To elucidate this putative site, HIS-tagged VWF domains (C3-C5, C4) were expressed and purified from BL21 E. coli for protein pull-down assays with GPIIb/IIIaGOF, using G14 as a competitive inhibitor. Eluates were probed via western blotting. PIPE-Site software was used to predict the site of interaction between GPIIb/IIIaGOF and VWF. Binding was predicted via molecular docking using Molecular Operating Environment software and AlphaFold3. G14 was originally identified using a GPIIb/IIIaGOF-mediated aggregation assay, where GPIIb/IIIaGOF-coated latex beads aggregate with VWF. G14 inhibits this aggregation. Under the same conditions, VWF adopts a globular conformation. Our PIPE-Site software identified interaction sites for GPIIb/IIIaGOF at the VWF-A1 and C4 domains. Supporting this, GPIIb/IIIaGOF interacts with C3-C5 and C4 domains, with G14 subsequently disrupting these interactions. As C4 also mediates  $\alpha$ IIb $\beta$ 3 integrin binding, we introduced  $\alpha$ IIb $\beta$ 3 after incubating GPIIb/IIIaGOF with VWF.  $\alpha$ IIb $\beta$ 3 competes with and partially displaces GPIIb/IIIaGOF. Thus, GPIIb/IIIaGOF binds to VWF-C4 domain and competes with  $\alpha$ IIb $\beta$ 3 for this site. This work supports new insights into platelet-VWF interactions, and the pathologies of platelet disorders including PT-VWD.

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## Talk Session 4

Session 4: A role for purinergic signaling in the transmission of the hypoxic response in the gills of the adult zebrafish (*Danio rerio*)

Anthea Mavridis, Dr. Michael Jonz

The ability to sense and respond to low oxygen, or hypoxia, is essential for vertebrate homeostasis. In aquatic environments, where the amount of available oxygen fluctuates, fish maintain homeostasis through sensing hypoxia via gill neuroepithelial cells (NECs) and the subsequent initiation of compensatory physiological responses such as hyperventilation. Several neurotransmitters have been implicated in the transmission of the hypoxic hyperventilatory response including adenosine triphosphate (ATP). However, physiological evidence for ATP in hypoxia signaling at the level of the NEC is lacking. The goal of this study was to determine purinergic signaling involved in the transmission of the hypoxic response in the adult zebrafish gill. This was done by imaging of intracellular  $\text{Ca}^{2+}$  concentration ( $[\text{Ca}^{2+}]_i$ ) of a transgenic zebrafish line having a genetically encoded  $\text{Ca}^{2+}$  indicator driven by the expression of a pan-neuronal marker  $\text{Tg}(\text{elavl3}:\text{GCaMP6s})$ . Changes in  $[\text{Ca}^{2+}]_i$  were recorded in post-synaptic neurons as a proxy for cell excitation. Neurons were exposed to the broad-spectrum purinergic antagonist and agonist, suramin and ATP $\gamma$ S, respectively. Suramin attenuated hypoxia-induced  $[\text{Ca}^{2+}]_i$  response suggesting endogenous ATP release acts on post-synaptic neurons during hypoxia. ATP $\gamma$ S, increased  $[\text{Ca}^{2+}]_i$  suggesting an excitatory post-synaptic effect of exogenous ATP in the absence of hypoxia. These results indicate ATP acts post-synaptically to facilitate hypoxia signalling towards the CNS. Studying this mechanism of purinergic signalling may provide a more complete picture of the initiation and control of the hypoxic ventilatory response in the zebrafish and allow further understanding of the evolution of such an essential physiological response.

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Session 4: A human's trash is an insect's treasure; sustainable feed products for farmed crickets to further a circular bioeconomy

S.Y.Kasdorf\*, J.E.Mills, M.J.Muzzatti, F.Haider, S.M.Bertram & H.A.MacMillan

Farmed insects are an attractive source of sustainable protein to feed the growing global population. The unsustainability of traditional feed ingredients used for commercial insect farming like fishmeal and soy has led to interest in environmentally-friendly alternatives. High-volume organic waste products, among other sustainable options, can contain balanced nutritional profiles, and are often cost-effective to obtain. Therefore, these

products are promising feedstock for insects that may fit within the framework of a circular bioeconomy. However, there is limited knowledge on the short- and long-term impacts of alternative feed inclusion in insect diets. We investigated high-protein by-products of the brewing industry (brewer's spent grain and brewer's spent yeast) as feed ingredients for farmed crickets (*Gryllobates sigillatus*). While brewery waste inclusion at higher rates leads to reductions in adult mass, survival is unaffected. We found that crickets can be raised for multiple generations on spent grain-based diets without observable declines in performance, and that lower inclusion rates (15-30%) have a beneficial effect on the mass of crickets harvested. We also investigated microalgae as a feed ingredient. Inclusion of microalgae up to 40% in feed does not have negative impacts on cricket growth and survival. As microalgae has the potential to be grown using insect frass as a source of organic carbon, this is promising for the development of circular microalgae-based feed systems. Overall, waste and other sustainable products are valuable resources for cricket feed, highlighting the potential of insect farming to help build a more sustainable agricultural sector.

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Session 4: Enhanced scavenging of reactive oxygen species as a neuroprotective mechanism in cortex of hypoxia-tolerant naked mole-rat

EATON, L. and PAMENTER, M. E.

Reactive oxygen species (ROS) are important cellular messengers, but overproduction can induce oxidative damage to lipids, proteins, and DNA. ROS are primarily generated as a by-product of oxidative phosphorylation; therefore, mitochondria are considered the primary contributors to basal ROS generation in brain. Hypoxia may further promote excess ROS production, as electron flow for oxidative phosphorylation is staggered. As such, oxidative damage typically occurs during hypoxia and subsequent reoxygenation in most mammalian brains. However, hypoxia-tolerant species may attenuate or avoid this damage through enhanced ROS-scavenging. Of particular interest are hypoxia-tolerant naked mole-rats (NMRs, *Heterocephalus glaber*), which putatively experience recurrent hypoxia/reoxygenation cycles in their burrows. Notably, NMRs have enhanced mitochondrial ROS scavenging capacity in skeletal and cardiac muscle, which led us to hypothesize that, relative to mice, NMR cortex also has enhanced scavenging capacity. Such a neuroprotective adaptation to life in intermittent hypoxia would support ROS homeostasis; avoiding oxidative damage. To test this, I designed a high-throughput assay using an amplex ultrared detection system to measure ROS scavenging capacities in NMR and mouse cortex homogenates. I also evaluated the role of glutathione- and thioredoxin-dependent scavenging pathways using specific antagonists (1-chloro-2,4-dinitrobenzene

(CDNB) and auranofin, respectively). We found that, as in other tissues, NMR cortex has significantly greater scavenging capacity than mouse across all treatments. Notably, this includes mitochondria respirating through complexes-I and/or II, and when ROS scavengers were inhibited. Together, our results suggest NMR cortex employs enhanced ROS scavenging capabilities to help mitigate redox damage during natural hypoxia/reoxygenation cycles in their intermittently-hypoxic burrows.

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Session 4: Investigating the role of serotonin receptors in the hypoxic response in the gills of *Danio rerio*

Louise C. Walker, Michael G. Jonz

When environmental oxygen levels are low (hypoxia), animals regulate arterial oxygen through physiological and cellular changes, known as the hypoxic response. Fish gills contain chemoreceptive neuroepithelial cells (NECs) that sense changes in oxygen. NECs contain serotonin (5-HT), a key neurotransmitter in the hypoxic response, and 5-HT receptors are expressed in the gills. A more complete understanding of the role of 5-HT is possible by localizing receptors, such as 5-HT<sub>2A</sub> and 5-HT<sub>3</sub>, potentially involved in neurochemical communication. Using adult zebrafish, immunohistochemistry and fluorescence microscopy were employed to locate 5-HT<sub>2A</sub> and 5-HT<sub>3</sub> receptors in the gills. 5-HT<sub>2A</sub> receptor immunoreactivity was detected in cells along the afferent epithelium, in the interlamellar regions of the gill filaments, and on gill rakers. 5-HT<sub>3</sub> immunoreactivity occurred as punctate labelling on the efferent aspect of gill filaments near serotonergic NECs and sensory nerve fibres. To test whether 5-HT receptors may be involved in the hypoxic response, zebrafish were acclimated to hypoxia for two weeks and changes in immunoreactivity were quantified. Preliminary evidence indicates that the number of cells with 5-HT<sub>2A</sub> receptors did not change following acclimation. These studies will help to further characterize the potential role of 5-HT receptors in the hypoxic response of zebrafish.

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Session 4: Is thermal plasticity in *Aedes aegypti* sensitive to photoperiod?

De Nicola, E.H.M., Ritchie, M.W., Biggar, K.K, MacMillan, H.A

Thermal plasticity allows insects to adjust physiological traits in response to changing environmental temperatures. In temperate winter climates, low temperatures often coincide with shorter daylight periods. Photoperiod, the duration of darkness and daylight in a 24-hour cycle, affects many aspects of insect physiology, including seasonal plasticity

and circadian rhythms. The yellow fever mosquito, *Aedes aegypti*, historically confined to tropical regions, is expanding its geographic range into poleward, temperate climates where it would experience varied temperature and photoperiod conditions. *Ae. aegypti* is capable of cold acclimation under a standard tropical photoperiod (12h:12h). Cold acclimation reduces injury and enables survival at otherwise lethal low temperatures. To test whether the ability to acclimate was tied to photoperiod, and when during the lifecycle photoperiod is important to *Ae. aegypti* thermal tolerance, we used an extreme photoperiod outside of their typical range (20h:4h), introduced at three different life stages; during egg development, during adult acclimation and at in the parental generation. A chill coma onset (CCO) assay was used to confirm the capacity for cold acclimation. Here, we present the first evidence of a photosensitive acclimation phenotype in this species. Extreme photoperiod significantly influenced CCO temperature, however, the magnitude of plasticity depends on when during development a light-cycle was introduced. To investigate the possible molecular mechanisms underlying this photosensitive acclimation phenotype, we are using qPCR to measure expression of known clock genes. This approach will help us gain a deeper understanding of the complex relationship between photoperiod cues and cold acclimation in *Ae. aegypti*.

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## Talk Session 5

Session 5: Temperature-diet interactions impact the ability of farmed crickets *Acheta domesticus* to turn feed into body mass

Émile Vadboncoeur\*, Susan M. Bertram and Heath A. MacMillan

The high environmental cost of traditional livestock production restricts the capacity of the agricultural industry to support growing global protein demand. Farmed insects are touted as a more sustainable alternative that require minimal resources and can efficiently turn feed into body mass. Many aspects of those claims need to be further researched.

Optimization of rearing parameters (e.g. temperature and diet) is ongoing to maximize total biomass. Optimizing production requires balancing feed efficiency with survival rates to maximize biomass yield, while minimizing the amount of feed used. However, the ability of insects to turn feed into biomass, a key aspect of agricultural sustainability, is rarely included in optimization studies. We reared farmed crickets (*Acheta domesticus*) in individual containers at four temperatures (24, 30, 36 and 38 °C) and three diet compositions (high carbohydrate, balanced and high protein) in a fully factorial design. Crickets were reared from hatch, and their mass was recorded weekly until they reached a

mass plateau in adulthood. A second batch of crickets was reared individually under identical conditions. We measured mass gain, feed consumed and frass produced weekly from the time at which crickets were 25% of their final mass to just before adult ecdysis. Increasing temperature and protein content led to increased efficiency at converting feed into biomass, but also concurrent reductions in cricket survival that offset these gains. These data provide a broad view of how temperature and diet composition can interact to affect the sustainability of insect farming.

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Session 5: Cisplatin disrupts long-term blood glucose control in high-fat diet-fed male mice, but not females

Lahari Basu, Jana Palaniyandi, Ma. Enrica Angela Ching, Erin van Zyl, Myriam P Hoyeck, Ineli Perera, Jennifer E Bruin

Pancreatic islets are critical for regulating blood glucose through the secretion of hormones such as insulin. Dysfunction in islets can cause abnormal regulation of glucose homeostasis, leading to Type 2 diabetes. Previous research suggests chemotherapy may contribute to increased risk of Type 2 diabetes in cancer survivors. The Bruin lab has previously shown that cisplatin, a commonly used chemotherapeutic agent, has acute adverse effects on both mouse and human islet function. The goal of our current study is to characterize how cisplatin impacts long-term islet function in the presence of metabolic stress in mice. Male and female mice were fed a standard chow or 45% high-fat diet (HFD) for 3 weeks before being injected with 2 mg/kg/day cisplatin or saline (vehicle) every other day for 2 weeks. Mice were then tracked for 4 months following this exposure period while being maintained on either chow or HFD. At 1-week post-exposure, male cisplatin-chow mice had increased blood glucose and lowered plasma insulin compared to vehicle-chow males, but recovered within 1 month. Both cisplatin-HFD and vehicle-HFD male mice had increased blood glucose levels compared to chow-fed mice throughout the study. However, cisplatin-HFD males did not elevate their plasma insulin to adapt to HFD like vehicle-HFD males at any timepoint. Cisplatin exposure did not affect blood glucose, insulin sensitivity, or plasma insulin levels in female mice, but there was a significant effect of diet on all measures of metabolic function. Our data suggests cisplatin exposure significantly disrupts long-term mouse islet function under metabolic stress, especially in males.

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Session 5: Keep an ion it! Prevention of cold-induced ionoregulatory collapse in the freeze-tolerant Asian longhorn beetle (*Anoplophora glabripennis*)

Fraser, S.M.\*, Roe A.D., Easson, M.L.A.E., Dean R.A., Ritchie M.W., Andersen, M.K., Bohlmann, J., Cullingham, C.I., MacMillan, H.A

Temperature is a key environmental constraint on insect population size and distribution, and a crucial factor limiting establishment and spread of invasive species. For most insects, cold exposure results in progressive loss of ion balance dependent on both exposure duration and intensity. This ionoregulatory collapse, characterized by extracellular hyperkalemia, causes cell death, tissue damage and eventually death. However, unlike these chill-susceptible species, recent work shows that truly cold hardy insects (e.g. freeze-avoidant mountain pine beetle larvae) only partially lose ion balance during severe cold exposure and maintain extracellular  $[K^+]$  just below lethal cellular limits. Whether this is a common capacity amongst cold-hardy species is unknown, as are the mechanisms behind this phenomenon. Asian longhorn beetle larvae (*Anoplophora glabripennis*; ALB) are a destructive invasive forest pest that accumulates cryoprotectants and becomes partially freeze-tolerant in winter. We tested whether cryoprotectants can increase cold tolerance by acting as osmoprotectants that mitigate cold-induced ionoregulatory collapse. Specifically, we explored the ability of this species to maintain ion balance in the cold by measuring hemolymph ion concentrations (e.g.  $Na^+/K^+$ ) and cryoprotectants during a prolonged cold stress. ALB larvae lab-reared on artificial diet were sampled at multiple time points during cold exposure at temperatures approaching and beyond their freezing point to measure hemolymph osmolality and ion and cryoprotectant concentrations. Results from this study suggest that ALB have an ability to prevent ionoregulatory collapse in the cold, and by extension that such an ability may be a prerequisite to evolving freeze tolerance or freeze avoidance in insects.

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Session 5: Molecular consequences of mild and severe short-term hypoxia exposure in rainbow trout (*Oncorhynchus mykiss*)

Liam Johnston, Jan Mennigen

In aquatic environments, environmental hypoxia can lead to stress, injury, or death for many animals. While there is a wide variation in the ability of aquatic animals like fish to tolerate hypoxic conditions, all animals have some physiological and molecular responses to hypoxia. Rainbow trout are an economically important species with a global spread, making them a good model to understand how cold-adapted freshwater fish will be affected by near-future changes in their habitats. This research project investigated the metabolic consequences of short-term mild hypoxia exposure relevant to climate change in rainbow trout and compared it to short-term severe hypoxia exposure by examining the

molecular markers of hypoxia-sensing, lactate, and energy metabolism pathways across several tissues. Initial increases in gene expression were mostly found in tissues from trout exposed to severe hypoxia, with the highest increases in gene expression being for pck1 in liver from rainbow trout exposed to severe hypoxia and for gcka in liver from rainbow trout exposed to both mild and severe hypoxia. This project will increase our knowledge of the hypoxia response in rainbow trout, a widespread and economically important fish. As anthropogenic activity continues to increase the amount and severity of hypoxic events in freshwater bodies around the world, a precise and detailed knowledge of hypoxia responses in fish will be necessary to understand how well they will adapt to this new world.

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Session 5: Dam it, I'm stranded: evaluating fish stranding downstream of a hydropeaking facility.

Raegan Davis, Dr. Steven Cooke, Dr. Karen Smokorowski

Hydropower is a renewable energy source that offers the capacity to produce low carbon energy and the flexibility to meet daily fluctuating energy demands. Hydropower facilities that use hydropeaking regimes operate at different flow discharges to supply energy to the grid as required to accommodate changes in energy demand throughout the day. Large changes in wetted areas occur downstream of the dam when they dam discharge changes from minimum flow to maximum flow and then back to minimum flow known as a peaking event. The change in wetted area may potentially result in fish becoming stranded on dry substrate or pools disconnected from the main channel. To investigate the factors that drive fish stranding on rivers that operate with hydropeaking regimes, we deployed cameras on the Michipicoten River below the Scott Falls Generating Station from June to October in 2023 and 2024 ( $n_{2023} = 11$ ,  $n_{2024} = 33$ ) to remotely capture occurrences of fish stranding. Scott Falls GS has a 22.5 MW generation capacity, a maximum turbine flow of 100 m<sup>3</sup>/s and a minimum flow of 17 m<sup>3</sup>/s. Cameras captured 47 (2023) and 76 (2024) stranded fish. To understand what factors drove fish to strand at these locations a predictive model was created, initially using calendar day, substrate (mm), wetted history (minutes), and horizontal ramping rate (cm/h) as factors known to influence stranding rates. This model will allow for comparison between other hydropeaking rivers to better understand if factors driving stranding are common among rivers.

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## Talk Session 6

Session 6: Evaluating the ecological trade-offs of formal versus informal campsite management

Sara Steel, Dalal Hanna

Recreational spaces vary in their management schemes, each with their own set of advantages and challenges. Here, we investigate the trade-offs between formally managed campsites within a pay per use park and freely accessible unmanaged campsites on adjacent public land. Using 13 indicators of ecological integrity and human impact, we assessed 20 managed and unmanaged campsites to evaluate how management influences ecological integrity and human impact. Our results revealed few significant differences between management schemes. However, unmanaged campsites did exhibit larger campsite sizes, more fire pits per site, accumulation of garbage, and wider trails. Conversely, park-managed campsites showed significantly higher soil compaction on trails, suggesting that while formal management can help reduce several elements of human impact, it may also concentrate use and increase environmental damage in more confined areas. Our findings showcase differences in outcomes of ecological integrity and human impacts when campsites are formally managed versus informally managed and provide park managers with information that can be used to help refine conservation strategies, balancing ecological integrity with visitor use.

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Session 6: Measuring the chemical contaminant burdens of Arctic nesting geese in Arviat Nunavut – a community-based monitoring project.

Emily Wong, Jennifer Provencher, Christina Davy, Shirley Tagalik, Kukik Baker

Arctic-nesting geese are a vital country food for Inuit and protected migratory birds in North America. Our research investigates the chemical contaminant burdens of geese through an Inuit-led project with Aqqiumavvik Society, a community research organization in Arviat, Nunavut. This is one part of a larger goose health project exploring whether increasing goose harvest is sustainable, healthy, and could improve Inuit food sovereignty. The co-developed goals guiding this project are: (1) To identify and quantify target contaminants in geese across species; (2) To characterize the effect of cooking on metal concentrations in meat and; (3) To test whether eggs gathered near local sources of pollution are more contaminated than eggs picked from remote areas. Inuit youth in Aqqiumavvik Society's Young Hunters Program participated in geese hunting, dissection, and egg picking between 2022 and 2024 with the research team. We sampled snow geese (*Anser caerulescens*),



Ross's geese (*Anser rossii*), and cackling geese (*Branta hutchinsii*) for trace metals, legacy contaminants (pesticides), and contaminants of emerging Arctic concern (UV stabilizers, flame retardants). Guided by Elders, we prepared and sampled matched raw, boiled, and roasted breast meat. All samples are currently being processed at the National Wildlife Research Centre (NWRC) to quantify contaminant levels. In this presentation, we will present preliminary results from egg sampling. We will also share our successes and lessons learned from our efforts to draw together the expertise of Inuit hunters, elders, youth, and non-Inuit researchers to generate knowledge that is meaningful at both local and national levels.

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Session 6: Using passive monitoring to determine the outcomes of temporary road closures on bird and mammal diversity at an urban-wildland interface

Millicent V. Gaston, Joe R. Bennett, Rachel T. Buxton

Roads and traffic threaten the viability of bird and mammal populations by reducing landscape connectivity, increasing mortality, and reducing habitat quality. However, when the threat of traffic is removed, responses vary across species and context. To evaluate how temporary road closures affect bird and mammal communities across Gatineau Park, Québec, we deployed 30 autonomous recording units and camera traps at varying distances to roads across three treatment areas: (1) permanently closed roads (reserved for active use); (2) temporarily closed roads (periodically reserved for active use); and (3) permanently open roads (always accessible to vehicles). Using acoustic and image data, we built generalized linear mixed models and used AIC c model selection to weigh evidence for the competing hypotheses that bird and mammal diversity metrics are best explained by treatment area, distance to road, day of the week when roads are opened or closed, and habitat features. We found no significant effects of roads or traffic on bird and mammal community diversity metrics. However, species-specific responses differed across multiple species, including a species at risk, the eastern wood-pewee (*Contopus virens*), which had a higher daily detection rate at sites further from roads, and a traffic-sensitive species, the black bear (*Ursus americanus*), which had a higher probability of daily occurrence at sites with less traffic. Our findings highlight the potential conservation value of temporary road closures to protect sensitive species at urban-wildland interfaces, along with the importance of evaluating conservation interventions to ensure effective management outcomes.

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## Session 6: Examining the long-term effects of upstream timber harvesting on freshwater biodiversity in Quebec

Felix Chan, Dalal E. Hanna

Numerous studies have documented detrimental effects timber harvesting on freshwater ecosystems. However, much of this research does not take place across large temporal and spatial scales. To address this gap, we investigate the relationship between timber harvesting and benthic invertebrate biodiversity throughout southern Québec using a benthic invertebrate dataset collected from 652 streams between 2002 and 2022. Using a geographic information system-based analysis we examine the relationship between the proportion of upland timber harvesting, land use and freshwater invertebrate diversity. Preliminary findings suggest that the proportion, timing and spatial arrangement of timber harvesting across these streams' watersheds (up to 52% cumulatively in 15 years) does not have detrimental effects on benthic invertebrate diversity. These findings highlight that it may be possible to harvest small proportions of a watershed without negative consequences on the invertebrate diversity of hydrologically connected fresh waters. Further research is needed to understand if the relationship we documented changes as proportions, timing and the spatial arrangement of timber harvesting in a watershed changes.

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## Session 6: Evaluating the Efficacy of Treated Windows to Reduce Bird-Window Collisions in Ottawa

Stasha Lysyk, Barbara Frei, Rachel Buxton

Collisions with windows is a leading anthropogenic cause of avian mortality in Canada, resulting in ~16-42 million deaths each year. Window treatments can be highly effective at reducing collisions when applied to best guidelines, but treating windows is uncommon. If present, they are often applied against best practices (e.g., exceed maximum spacing or on interiors) and less is known about the efficacy of varied treatment application. We aim to evaluate the efficacy of window treatments to reduce bird-window collisions in Ottawa by conducting collision surveys at treated and untreated windows during 2024 spring and fall migration. We documented 142 total collisions of 45 species, with 124 collisions at untreated windows and 18 at treated windows. To investigate the effect of window treatments in reduced collision numbers, we modeled the rate of collisions with environmental and building factors as predictor variables. We found that presence of window treatment has a significant relationship in reduced collision rates. Further, this relationship is stronger with window treatments that are applied to best guidelines than

those applied against best guidelines. To further evaluate the efficacy of window treatments, we will build a predictive model of collisions using environmental factors at untreated windows. This will be used to predict an expected “before” rate of collisions at treated windows if they were not currently treated. This predicted-if-untreated rate will be compared to the observed treated rate to evaluate efficacy. This study contributes to understandings of window treatment efficacy by describing effectiveness across a range of conditions.

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## Talk Session 7

Session 7: Chromosome-level Genome Sequencing and 3D-genome Analysis of *Gigaspora margarita*

Ken Mugambi, Jordana IN Oliveira, Nicolas Corradi

Arbuscular mycorrhizal fungi (AMF) are widespread root symbionts that improve nutrient acquisition for most plants. Recent advances in long-read sequencing and chromatin conformation capture (Hi-C) technologies have enabled chromosome-level assemblies and 3D-genome analysis in the model species *Rhizophagus irregularis*. However, whether the findings such as A/B compartments, associated with active and repressed chromatin, respectively, are conserved across AMF species is unclear. There also exists an open question on whether the chromosome 3D-genome conformation of these fungi changes depending on surrounding conditions. Here, we combine HiFi PacBio sequencing with Hi-C to produce a chromosome-scale assembly of *Gigaspora margarita*. The complete assembly reveals 43 chromosome-level scaffolds with 20 divergent rDNA copies distributed across five scaffolds. Hi-C analysis confirms the presence of A/B compartments in *G. margarita*, an indication that this genome organization is universal to AMF. Remarkably, these compartments are dynamic, switching in response to the endosymbiotic bacterium *Candidatus Glomeribacter gigasporarum* (CaGg), and we present evidence for the physical interaction of rDNA copies in AMF, presumably within the nucleolus. Overall, our findings provide a deeper understanding of the AMF nuclear genome biology, highlighting the plasticity and molecular function of their 3D genome.

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Session 7: EDNA biomonitoring: how does metabarcoding compare to sampling stream macroinvertebrates?

Bresolin, Andrea R. & Hanna, Dalal E.L.

Macroinvertebrates are popular bioindicators used to infer ecosystem health, but conventional sampling methods can be labour-intensive and require technical expertise. In the past decade environmental DNA (eDNA) has been explored as an innovative way to sample stream communities, but its potential to replace conventional sampling is unclear, given limitations with metabarcoding. To better understand implications of eDNA in biomonitoring, this research compares biodiversity captured by conventional macroinvertebrate sampling and eDNA metabarcoding. We sampled 8 streams across northern Québec for eDNA and macroinvertebrates, and compared resulting communities, biodiversity and ecosystem health metrics. Metabarcoding captured 86% of families detected in conventional sampling, as well as 31 additional taxa. Significant differences were observed for family richness ( $p=0.0082$ ) and Hilsenhoff Biotic Score (HBI;  $p=0.0048$ ), but not Ephemeroptera, Trichoptera and Plecoptera (EPT) richness ( $p=0.18$ ) or Indice de Santé Benthique (ISB;  $p=0.3600$ ). This work further explores community composition between methods, revealing that eDNA captures biodiversity differently than conventional methods with important implications for biomonitoring. These findings suggest that eDNA metabarcoding may be able to supplement – but not replace – conventional macroinvertebrate sampling.

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## Session 7: Omicsflow, a robust and reproducible bioinformatic platform

Mohamad Elian, Ashkan Golshani, Bahram Samanfar

Next-generation sequencing has resulted in an exponential increase in multi-omic data. This calls for the development of efficient and user-friendly bioinformatic packages to analyze and interpret the vast amount of information. Over time, bioinformatics pipelines have increased in complexity which raises concerns about the reproducibility of the data. Workflow managers have been developed not only to help with reproducing pipelines, but also with automation and parallelization of pipeline tasks allowing for greater efficiency in execution. Additionally, due to the varying biological histories of various species, a one-size fits all pipeline typically does not produce the best results; pipeline customizability is therefore a priority in pipeline design. Computing resources also present a potential bottleneck for computational analysis of biological data. As such, high performance computing environments have become key factors in completing analysis projects. Here, we present Omicsflow, a nextflow based bioinformatics platform offering reproducible and customizable multi-omic analysis of sequencing data. Omicsflow contains reproducible pipelines for RNAseq, and DNAseq analysis with planned implementation of future pipelines such as de-novo genome assembly and protein-protein interaction prediction.

This presentation will focus on explaining the architecture behind such a platform, its integration in high performance computing environments as well as its usage.

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#### Session 7: Diversity and evolution of transposable elements in arbuscular mycorrhizal fungi

Catrina Lane, Jordana Inácio Nascimento-Oliveira, Nicolas Corradi

Arbuscular mycorrhizal fungi (AMF) are symbionts associated with the roots of most land plants. Mycorrhizal symbiosis helps plants gather more soil nutrients. The fungi receive carbohydrates and lipids in exchange. Despite their low morphological diversity, gene content and genome structure vary substantially among AMF species. A significant correlation between genome size variation and the abundance of transposable elements (TEs) has been observed; however, the exact origin of these TEs is unknown. Considering that TEs are repetitive DNA fundamental to building genetic diversity and regulating genes, I aimed to annotate these elements in 31 AMF species with available genome sequence data. A second annotation, following a personalized curation of TEs, showed improved classification of TE sequences. Specifically, the average percentage of known sequences improved from 20.8% in the first annotation to 34.3% in the second. I observed large expansions of LINEs in the order Diversisporales and of DNA/TIRS in Glomerales. As expected, the small genomes of the order Paraglomerales displayed the lowest portions of TE; these sequences compose under 10% of the genomes. Additional, lineage-specific TE expansions have been detected, further highlighting the large genome diversity existing in these plant symbionts. These species-specific expansions may represent AMF diversification through TE insertions.

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#### Session 7: Conservation genomics to inform seed provenance for translocation of spotted wintergreen in Canada

F. Alice Cang, Jenny L. McCune, and Julie A. Lee-Yaw

Genetically-informed population translocation can be a powerful tool for species conservation, and vascular plants are particularly suitable candidates. Existing paradigms that prioritise seed sourcing from the closest geographic populations rely on presumed local adaptation, but risk ignoring substantial genetic variation. Admixture between genetically heterogeneous founders can be beneficial for preventing inbreeding depression and structuring populations able to respond to environmental change. However, a majority of plant species-at-risk lack genetic data, without which we cannot estimate fundamental

metrics of genetic diversity or differentiation critical to long-term success of translocation programs. Here, we propose a case study for integrating genetic diversity and structure into a translocation program for spotted wintergreen (*Chimaphila maculata*). Spotted wintergreen is a perennial evergreen herb inhabiting the understories of boreal forests, ranging from its northern limit in Canada to the US and disjunct populations in Mexico. Currently, we have silica-dried leaf tissue samples from eight of the twenty-two censused populations in Ontario. We intend to use ddRAD-seq data to: (1) assess the distribution of genetic variation and (2) identify genetic clusters delineating potential seed sources. DNA extractions of Canadian populations are underway, but tissue collection of US samples is ongoing. Although the Canada-US border does not reflect a biological reality, it induces chilling effects on translocation programs as regulators hesitate to move plants across without a detailed understanding of the underlying genetic structure. Collectively, this highlights the need for population genetic surveys as essential components of plant conservation translocations.

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## Talk Session 8

Session 8: Movement of Brook trout in a small river in Southern Quebec with implications for the conservation of imperiled molluscs

Kara M. Scott, Lauren J. Stoot, Brittany Bard, Peter Holder, Liane Nowell, Katriina Ilves, André L. Martel, Graham D. Raby, and Steven J. Cooke

A population of the at-risk Eastern Pearlshell mussel (*Margaritifera margaritifera*) has recently been found within the Kinonge West River system in Southern Quebec, a river system where lives its presumed host fish, the native Brook trout (*Salvelinus fontinalis*). Protecting this host relationship requires understanding and proper management of the trout population and its habitat selection and use. The aim of this project was to understand potential thermal and physical barriers that could threaten stream connectivity for the Kinonge West River Brook trout. We found that neither water temperature nor waterfalls acted as barriers for trout movement. Furthermore, we found that the Brook trout population displayed high site fidelity throughout much up the year with increased movement during the late fall/winter. This provides assurance that glochidia of the Eastern Pearlshell can be freely transferred throughout the system by their Brook trout host. The preservation of future stream connectivity within this river system must be prioritized to ensure the perennity of this salmonid-mussel relationship.

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## Session 8: Legwork and Brainwork: Neural Control of Amphibious Locomotion

Kennis Ross

There are three main components to the neural control of vertebrate locomotion: The brain, the spinal cord, and sensory feedback. The brain provides top-down control of the body, the spinal cord can produce rhythmic outputs without constant rhythmic inputs, and sensory feedback is the information received about the environment that can influence changes in top-down and local rhythmic outputs that cause gait changes. What makes amphibians exciting is that they must live both on land and in water, which are two very different physical environments that require two different ways of moving. While in water, amphibians hold their limbs against their body and swim by passing a travelling wave from head to tail, much like elongate fishes. While on land, amphibians step with their limbs and their body displays a standing wave, where their pectoral and pelvic girdles act as nodes and the body oscillates with a fixed amplitude between them. In the literature, these individual gaits are well characterized, but there is little research on how amphibians can transition between them. Land and water provide different sets of sensory feedback, so the transition between walking and swimming will be kinematically different depending on if the animal is entering or leaving water. Using video recordings of salamanders walking down or swimming up a small incline, the kinematic output of the transition period can be analyzed. In both conditions, the transition period featured a hybrid gait between walking and swimming, but how the gait was hybridized varies between the two conditions.

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## Session 8: Interspecific male aggression in *Mnais* and its consequences for character displacement and male-limited polymorphisms

Isaac Finkelstein, Tom Sherratt, Karl Loeffler-Henry

Japanese damselflies, *Mnais costalis* and *M. pruinosa*, are closely related and very similar in appearance (to human observers). In some regions, both species express a male-limited polymorphism: males are either orange-winged or clear-winged. However, in other regions, *M. costalis* is monomorphically orange-winged and *M. pruinosa* is monomorphically clear-winged. To test if male-male agonistic interactions are driving the divergence in morph phenotypes when sympatric, we conducted an experiment in which we sequentially presented the same orange-winged *M. costalis* male with a tethered clear-winged *M. pruinosa* male and a tethered orange-winged *M. costalis* male. The results indicate that, as expected, in the monomorphic region *M. costalis* males were far less aggressive towards clear-winged heterospecifics than orange-winged conspecifics, where wing colour can be used to indicate species identity. However, in the polymorphic region where wing colour is

not an indicator of species identity, *M. costalis* males were only moderately less aggressive towards clear-winged heterospecifics than orange-winged conspecifics. The results support our hypothesis that heterospecific male-male aggressive encounters drive selection for character displacement in *Mnais* and suggest that the sympatric polymorphic region represents recent secondary contact between the two species compared to the more distant secondary contact of the monomorphic region. The results have implications for our understanding of how male-male aggressive interactions can affect phenotypic expression and speciation between closely related species.

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#### Session 8: Foraging behavior predicts the evolution of humeral shape in hummingbirds

Juan Camilo Ríos-Orjuela, Illias Berberi, Lauren Miner, Daniel Cadena, Alejandro Rico-Guevara & Roslyn Dakin

Understanding how behavioral ecology shapes skeletal morphology provides critical insights into the evolutionary diversification of locomotor systems. In hummingbirds, distinct foraging strategies—territorial defense, traplining, and opportunistic feeding—are associated with different flight behaviors and energy demands. Given the biomechanical constraints of hovering and maneuverability, we hypothesized that humeral shape would reflect these foraging modes. To test this, we performed a geometric morphometric analysis of the humerus in cranial view across 80 hummingbird species, each representing one of the three major foraging strategies. Using 25 landmarks per specimen, we applied a canonical variation analysis (CVA) to assess shape differences among foraging groups. Our preliminary results reveal a clear morphological separation among the three foraging categories, with CVA showing distinct clustering and statistically significant group differences under permutation tests. Classification accuracy exceeded 60%, confirming that variation in humeral shape is not random but aligns with ecological behavior. Phylogenetic structure suggests a strong functional signal in shape data. These findings support the idea that selective pressures linked to foraging behavior may drive morphological divergence in the hummingbird humerus. Moreover, this study highlights the value of linking ecology and form to understand the evolution of vertebrate musculoskeletal systems.

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## Talk Session 9

Session 9: Nesting resource limitation: Determinants of upper-elevation range limits in cavity-nesting bees?

Lydia Wong, Jessica Forrest

Range shifts are among the most common biological responses to climate change. We examined the potential for upslope range-shifts in cavity-nesting bees and ask whether future shifts may be limited by the lack of nesting cavities at high elevations in the Colorado Rockies. We tracked cavity-nesting bee occupancy in artificial wooden nests placed at increasing elevations from treeline and conducted surveys at these sites to characterize the relative abundance of cavity- versus ground-nesting bees. Nest occupancy decreased with increasing distance from treeline; however, the average number of offspring per nest remained constant. Declines in bee abundance with increasing distance from treeline were more pronounced for cavity-nesting bees relative to ground-nesting bees. Predicting whether and how species will respond adaptively to climate change remains a pressing challenge. Species ranges may be limited not only by their climatic niches as is often assumed, but also by habitat requirements which may respond differently to climate change. This study provides field-based insights into the role habitat requirements as determinants of range limits in an ecologically-significant group of insects.

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Session 9: Pronounced genetic structure associated with differences in a reproductive trait and climatic barriers in Canadian populations of western toads (*Anaxyrus boreas*)

Jayna Bergman, Juan Enciso, Roseanna Gamlen-Greene, Melissa Todd, and Julie Lee-Yaw

The geographic ranges of widespread species often contain physical barriers and diverse environments, leading to distinct genetic subgroups. Understanding this structure informs our knowledge of the history of species' distributions, early divergence processes, and aids in identifying conservation units. Western toads (*Anaxyrus boreas*) are a widespread species in western North America, but their genetic structure in Canada remains poorly understood. However, they are legally assigned as two Designatable Units (DUs): a Calling population in Alberta, characterized by a vocal sac and pronounced breeding calls, and a Non-calling population in BC, which lacks these traits. To assess genome-wide structure, we analyzed tissue samples from 34 sites across BC and Alberta using a double digest restriction site-associated DNA sequencing dataset of 11,950 SNPs, alongside phenotypic and ecological data. Multivariate statistical analyses identified three distinct genetic groups: the Calling and Non-calling populations, and a third group in southeastern BC and

southwestern Alberta. A phylogenetic tree supported these findings, with high genetic differentiation among groups ( $F_{ST}=0.32-0.52$ ). Isolation-by-distance alone could not explain the observed genetic structure. Additionally, phenotypic call differences had high concordance with genetic boundaries, and ecological analyses revealed overlapping environmental niches but geographic separation by climatic barriers. These results support the continued recognition of the Calling and Non-calling populations as DUs and reveal an additional genetic group, suggesting cryptic genetic structure within this species in Canada. This highlights the need for range-wide genetic assessments and the integration of multiple lines of evidence to uncover cryptic diversity and inform conservation strategies.

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Session 9: Mosquito-borne arboviruses in eastern Ontario: Vectors, ecology, and seasonality (2017–2021)

\*Marc Avramov, Vanessa Gallo, Emilia Craiovan, Heidi Wood, Heather Coatsworth, Mahmood Iranpour, David R. Lapen, Catherine I. Cullingham, Antoinette Ludwig

In Canada, California serogroup viruses (CSGv), West Nile virus (WNV), Cache Valley virus, and eastern equine encephalitis virus, are the main mosquito-borne arboviruses of public/animal health concern. Lists of mosquito vectors and animal host species remain incomplete. We report findings from a 2017–2021 sampling campaign in eastern Ontario, Canada. A total of 12,413 species pools were tested, revealing the presence of CSGv in 922 pools from 17 species (including 14 first Canadian records), WNV in 22 pools (primarily *Cx. pipiens-restuans* gr.), one Cache Valley pool, and one eastern equine encephalitis virus pool. Maximum infection likelihood estimates (x 1000 mosquitoes) for CSGv were higher in natural biotopes (up to 13.15 [95% CI: 11.64-14.81]) vs. agricultural biotopes (up to 6.37 [95% CI: 5.66-7.14]). Conversely, WNV infections were higher in agricultural biotopes, but the effect size difference was not significant. CSGv peaked in late spring and early summer, while WNV infections peaked starting mid-summer. Findings emphasize the need for 1) targeted vector competency assays, and 2) genomic sequencing to characterize and validate circulating arboviruses.

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## Talk Session 10

Session 10: Proteomic mapping of the stress responsive MYB41 regulatory network in *Arabidopsis*

Kassandra Fugard, Chris Rampitsch, Rajagopal Subramaniam, and Owen Rowland

Plants have evolved a broad range of strategies to adapt to changes in environmental conditions. The formation of specialized cell wall-associated barriers, such as suberin (cork), is important for protecting plants by controlling water and mineral movement through the root. Suberin is an aliphatic and phenolic heteropolymer deposited throughout normal development and in response to environmental pressures. As a stress-responsive barrier, suberin can allow plants to adapt to challenges such as drought, salinity, and pathogens. A complex network of transcription factors (TFs) regulates the biosynthesis and deposition of suberin. MYB41 is activated in response to abiotic stress and is required for suberin synthesis in *Arabidopsis thaliana*. MYB TFs frequently interact with other proteins in transcription-activating complexes; however, the precise regulatory mechanisms remain to be uncovered. Here, we report the use of a proteomics-based approach called proximity labelling to identify the protein-protein interactions of the positive suberin regulator MYB41. To perform proximity labelling, a biotin ligase (TurboID) was translationally fused to MYB41 to endogenously tag adjacent proteins, which were then purified and analyzed via mass spectrometry. Using TurboID, we identified several potential protein interactors, some which may be directly involved in suberin synthesis, while others may participate in alternative stress response pathways. Uncovering the regulatory factors involved in suberin development will provide insight into the molecular mechanisms that plants use to adapt to changing environments.

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#### Session 10: Using AI to generate peptide theranostics for rare bleeding disorders

Thomas D.D. Kazmirchuk, Jiashu Wang, Loredana Bury, Anastasiia Koziar, Calvin Bradbury-Jost, Mustafa Al-gafari, Sarah Takallou, William G. Willmore, Frank Dehne, Paolo Gresele, Maha Othman, and Ashkan Golshani

Platelet glycoprotein-1b alpha (GPIb $\alpha$ ) is a surface glycoprotein that is functionally defective in platelet-type von Willebrand disease (PT-VWD). Gain-of-function mutations (GOF) within the  $\beta$ -sheet of the glycoprotein convert GPIb $\alpha$  to an open conformation, resulting in the excessive association of GPIb $\alpha$ GOF with its receptor von Willebrand factor (VWF), and counterintuitively a bleeding phenotype. The  $\beta$ -sheet mutations (clustered within the Trp230 - Met239 window) represent an attractive site to develop therapeutics. We recently developed the In-Silico Protein Synthesizer (InSiPS) – an artificial intelligence that designs small peptides which interfere with important protein-protein interactions (PPIs). We used InSiPS to generate peptides specific to GPIb $\alpha$ GOF, with the resulting peptides validated in-silico via AlphaFold3. Peptide specificity towards GPIb $\alpha$ GOF was assessed in-vitro using aggregation assays, protein pulldown assays, circular dichroism (CD) spectroscopy, enzyme linked immunosorbent assays (ELISA), and ex-vivo patient

platelet assays. One peptide (G14) was found to disrupt the interaction between GPIb $\alpha$ GOF and VWF via an aggregation assay in a dose-dependent manner. These results are supported by a pulldown assay, which indicate that G14 disrupts and outcompetes the PPI. ELISAs reveal that G14 displays specificity towards GPIb $\alpha$ GOF whilst avoiding off-target interactions. G14 also displays a 6.6 pM dissociation constant towards GPIb $\alpha$ GOF. When assessed for ex-vivo efficacy, G14 was found to restore healthy function to PT-VWD patient-derived platelets, restoring normal interactions. This work therefore demonstrates that the AI-generated G14 peptide effectively disrupts the interaction between GPIb $\alpha$ GOF and VWF, while avoiding off-target interactions in-vitro and ex-vivo. Thus, we now introduce G14 as a theranostic candidate for PT-VWD.

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Session 10:  $\beta$ -cell specific AhR expression is critical to high-fat diet induced hyperinsulinemia in mice

Ma. Enrica Angela Ching, Myriam P. Hoyeck, Renee Tejani, Lili Grieco-St-Pierre, Jennifer E. Bruin

Type 2 diabetes is characterized by chronically elevated blood sugar levels due to insufficient insulin production or insulin resistance. The aryl hydrocarbon receptor (AhR) is a ligand-activated transcription factor involved in diverse biological processes, ranging from xenobiotic metabolism to energy homeostasis. Rodent studies suggest that whole-body Ahr deletion protects against high fat diet (HFD)-induced metabolic dysfunction, but little is known about the role of AhR in insulin-producing  $\beta$ -cells (located in the endocrine pancreas, i.e., “islets”). We used a  $\beta$ -cell-specific Ahr knockout mouse model ( $\beta$ AhRKO) to investigate the role of  $\beta$ -cell AhR in the early adaptation to HFD feeding. We fed male and female  $\beta$ AhRKO mice and Ins1-Cre genotype controls ( $\beta$ AhRWT) with 60% HFD or a matched 10% low-fat diet (LFD) for 7 days. HFD-fed mice developed glucose intolerance irrespective of genotype, but only  $\beta$ AhRWT mice exhibited HFD-induced hyperinsulinemia. There were no genotype-based differences in body weight, % fat mass, fasting blood glucose levels, or islet morphology. When we assessed islet function ex vivo, HFD-fed  $\beta$ AhRWT females oversecreted insulin in response to high glucose, while HFD-fed  $\beta$ AhRWT males exhibited impaired glucose-induced insulin secretion compared to their LFD-fed  $\beta$ AhRWT counterparts; these phenotypes were abolished in islets from HFD-fed  $\beta$ AhRKO mice. On LFD,  $\beta$ AhRKO male islets were less glucose-responsive than  $\beta$ AhRWT male islets, despite having slightly elevated expression of insulin processing (Pcsk1) and glucose sensing (Glut2) genes. Collectively, we provide novel evidence suggesting  $\beta$ -cell AhR plays a basal role in insulin secretion and is essential for adaptation to HFD-induced stress.

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## Poster Session

### 1: Involvement of dl3 neurons in spinal motor learning

Emam Khan, Sarah Chiasson, Sarah Goltash, Lauren Couvrette, Shahriar Nasiri, Alex Laliberte, Tuan Bui

The nervous system integrates sensory input from the environment with motor output to muscles. This enables adaptive muscle activity based on external stimuli—for example, adjusting leg movements when running on uneven terrain. This adaptation of motor output in response to sensory information is referred to as ‘motor learning’. Motor learning is a complex process governed by the nervous system, and its mechanisms in advanced motor behaviors such as locomotion remain poorly understood. Moreover, the extent to which the spinal cord itself contributes to motor learning is only beginning to be explored.

Investigating spinal motor learning will deepen our understanding of the spinal circuits responsible for integrating sensory input and motor output. Our aim was to develop a simplified model of spinal motor learning. Using stationary, spinalized mice, we assessed their ability to modify hindlimb vertical position in response to electrical stimulation of a hindlimb nerve. Specifically, we recorded video and electromyographic activity of the hindlimb and stimulated the nerve if the toe dropped below a defined vertical threshold. We then examined the spinal circuits involved in this learning process, focusing on a specific class of excitatory spinal interneurons—the dl3 neurons—which are known to receive sensory input and project to motor neurons. We therefore hypothesized that dl3 neurons are necessary for motor learning to occur without connections from the brain, which we tested by inhibiting dl3 neural activity. Our results will serve as a foundation to study motor learning in more complex behaviors, such as locomotion.

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### 2: Pharmacological manipulation of vasotocin and oxytocin receptors reduces reproduction performances in female zebrafish (*Danio rerio*)

Dinusha Rajapaksha<sup>1</sup>, Vance L. Trudeau<sup>1</sup>, Jan A. Mennigen<sup>1</sup>

Vasopressin (Avp) and oxytocin (Oxt), also known as vasotocin and isotocin in teleosts, are nonapeptides with pivotal roles in regulating various physiological processes, including stress response, reproduction, and behavior. They exert their effects through G-protein-coupled receptors which mediate cellular signaling pathways. In zebrafish, multiple Avp (Avp1a1, Avp1a2, Av1b, and Avp2) and two Oxt receptor paralogues (Oxtra and Oxtrb) are

present, with distinct and/or overlapping expression patterns in hypothalamus pituitary gonadal (HPG) axis tissues, though their roles in reproduction remain largely unexplored. To investigate the functional significance of Avp and Oxt receptors in reproduction, wild-type female zebrafish were pharmacologically manipulated with Avpr1a antagonist (Manning's compound; MC) and Oxtr antagonist (L-368,899). Injections of MC (5, 50 and 500 ng/g body weight) resulted in a significant, concentration-dependent reduction in successful breeding events, viable egg production, and clutch sizes. In contrast, L-368,899 injections (2500 and 5000 ng/g body weight) significantly reduced breeding success, viable egg production, and clutch sizes only at the 5000 ng/g body weight dose. However, neither antagonist affected hatching success or survival rates compared to control and saline-treated groups. These findings highlight the critical role of Avpr1a in females, revealing nonapeptide receptor specificity in the regulation of zebrafish reproduction.

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3: Networking in the cold: connecting renal transcriptional plasticity to chill injury prevention through gene network analysis.

Dean, R. A.<sup>1\*</sup>, DeNicola, E. H. M.<sup>1</sup>, Ritchie, M. W.<sup>1</sup>, MacMillan, H. A.<sup>1</sup>

Most insects, including *Drosophila melanogaster*, suffer from a progressive loss of ion and water balance that causes cell, and ultimately organismal, death. This ionoregulatory collapse has been linked to temperature-induced reductions in membrane-bound transporter activity (e.g. Na<sup>+</sup>/K<sup>+</sup>-ATPase, H<sup>+</sup>-ATPase) in the renal system. Cold acclimation can improve low temperature tolerance and is associated with an increase in water and ion transport rates in the Malpighian tubules (analogous to kidneys) of cold acclimated flies, but a paradoxical reduction in the activity of ATPases in the same tissues. These findings raise questions about whether the current models of ion transport apply to cold-acclimated insects, or if modulation by other mechanisms, such as membrane structural reorganization allow for improved renal function in the cold. Here, we report the results of transcriptomic sequencing of the anterior Malpighian tubules of warm and cold-acclimated flies before, during, and after a cold stress. We used these results to construct gene networks, using a weighted gene correlation network analysis method. These results link networks of genes to specific traits and suggest that physiological state of the tubules before a cold stress is more important to preventing downstream injury than a short-term response to chilling. They further suggest that cold acclimation elicits a tissue repair response in the tubules during recovery, as opposed to an immune response seen in warm acclimated flies. Together, these findings allow us to generate new hypotheses on how cold acclimation allows insects to adjust their cold tolerance, and hint at novel renal mechanisms that may serve to mitigate chilling injury.

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#### 4: Hypoxia-responsive lysine demethylase expression in two tissues of anoxic red-eared slider turtles

Tighe Bloskie, Kenneth B. Storey

Lysine demethylases (KDMs) have garnered significant interest in recent years alongside the emergence of lysine methylation as a ubiquitous post-translational modification, particularly on histone proteins. Interestingly, the promoters of various KDM enzymes contain hypoxia-response elements (HREs), leading to their activated expression as part of many hypoxic transcriptional programs. Adult red-eared slider turtles (*Trachemys scripta elegans*) are champion hypoxia-resistant vertebrates that spend their winter months in ice-locked oxygen-free water, where they exhibit substantial (>90%) global gene silencing in support of hypometabolic anoxia tolerance. The involvement of KDMs, and their role in transcriptional regulation of *T.s. elegans* anoxic responses is poorly understood. In the current study, we use quantitative polymerase chain reaction (qPCR) to investigate the relative expression of nine notable demethylase genes (*kdm1a*, *kdm1b*, *kdm2b*, *kdm3a*, *kdm4b*, *kdm4c*, *kdm5b*, *kdm6b*, *kdm7c*) between normoxic and 5-hour anoxic red-eared slider liver and red skeletal muscle. Prior, we use determine optimal reference genes for each tissue from a list of seven prominent candidates (*actb*, *gapdh*, *b2m*, *rpl13a*, *sdha*, *ywhaz*, *tbp*) using NormFinder software. This work adds an additional layer to the growing epigenetic landscape of animal extreme stress adaptation.

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#### 5: Role of the Novel Hormone Secretoneurin in Zebrafish Ovarian Function

Paola Figueroa, Udeesha Erandani, Majd Sabbagh, Vance Trudeau

In vertebrates, reproduction is controlled by hormones within the brain-pituitary-gonadal axis. For decades, gonadotropin-releasing hormone (Gnrh) was considered the key regulator. However, recent evidence suggests that secretoneurin (SN), a neuropeptide derived from secretogranin-2 (Scg2), also stimulates gonadotropin release, possibly independent of Gnrh. Teleost fish express two Scg2 paralogs, Scg2a and Scg2b, which produce SNa and SNb, respectively. In zebrafish, frameshift mutations in the *scg2a* and *scg2b* genes disrupt the expression of key neuroendocrine genes and impair ovulation, which is partially restored by SNa injection. Both SNa and SNb stimulate germinal vesicle breakdown in isolated late-stage ovarian follicles, highlighting their direct involvement in oocyte maturation and ovulation. Mass spectroscopy analysis indicates that the gonads contain both SN peptides, yet their localization and role at the ovarian level remain

unexplored. Immunohistochemistry was performed using a rabbit-anti-goldfish polyclonal SNa and a novel mouse-anti-zebrafish monoclonal SNb primary antibody, which have been previously validated for specificity in pituitary tissue. Intrinsic autofluorescence in ovarian tissue posed a challenge by concealing target signals. The most effective method to resolve this issue was the use of the Vector® TrueVIEW® Autofluorescence Quenching Kit, which significantly reduced yolk and erythrocyte autofluorescence. Results suggest that SNa is localized in the thecal and follicle cell layers of late-stage follicles, while SNb is present in the zona radiata of late-stage oocytes. These findings offer novel insights into the potential ovary-specific production and release of the SN peptides in teleost fish, ultimately enhancing our understanding of their role in vertebrate reproduction.

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6: Does FKBP5 contribute to chronic cortisol elevation in subordinate rainbow trout?

Donna St-Amant and Kathleen M Gilmour

In fishes, as in other vertebrates, environmental challenges activate the hypothalamic-pituitary-interrenal (HPI) axis, increasing synthesis of the glucocorticoid stress hormone cortisol. Cortisol binds to the glucocorticoid receptor (GR), activating negative feedback regulation of HPI axis activity. In mammals, expression of the gene *fkbp5* is cortisol-responsive. FK506-binding protein 51 (FKBP5) is a co-chaperone of GR that inhibits GR activity, resulting in an ultra-short negative feedback loop that impairs regulation of HP-adrenal axis activity. We hypothesize that FKBP5 and GR interactions similarly contribute to prolonged elevation of cortisol during chronic stress in rainbow trout (*Oncorhynchus mykiss*). In the dominant-subordinate social hierarchy model, we predicted that subordinate trout would show elevated cortisol concentrations, mediated by increased transcript abundance of *fkbp5*, but transcript abundance of *klf9* (Krüppel-like factor 9), a GR-responsive gene, would not be elevated owing to inhibition of GR activity. Pairs of rainbow trout were assessed after 6 h or 4 d of interaction, or 4 d followed by 1 day of recovery. Plasma cortisol was significantly elevated in subordinates after 4 d but not 6 h of interaction. Subordinates showed significant elevation of *fkbp5* mRNA abundance in the preoptic area (POA) and head kidney at 6 h and 4 d of interaction. Unexpectedly, *klf9* mRNA abundance was also increased in 6-h and 4-d subordinates. These findings support the presence of FKBP5-GR interactions in rainbow trout, contributing to prolonged cortisol elevation in subordinate fish.

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## 7: Mitigation of chilling injuries in *Drosophila melanogaster* through antioxidant supplementation

El-Saadi, M. I., MacMillan, H. A.

Chill-susceptible insects suffer negative effects of chilling at low temperatures above the freezing point of their body fluids. At the organismal level, chilling injuries commonly manifest as a loss of neuromuscular function that affects an insect's ability to stand, walk, or fly. These injury phenotypes can be evident quickly, or with some delay, following removal of the insect from the cold. We have characterized how and when "latent" chilling injuries appear in female *Drosophila melanogaster* in the hours and days following a cold stress, but their underlying mechanisms remain unclear. Oxidative stress during rewarming, commonly characterized by increased antioxidant enzyme production, may contribute to latent chilling injuries. We therefore hypothesized that Reactive Oxygen Species-induced damage is a secondary consequence of cold stress that drives latent chilling injury. We supplemented female *D. melanogaster* with the antioxidant ascorbic acid (AA) before a cold stress ( $-2^{\circ}\text{C}$  for 2, 3, or 4 h), and found that latent injuries were significantly mitigated in flies that were fed the AA, regardless of how long they were exposed to  $-2^{\circ}\text{C}$ . Additionally, benefits of AA supplementation were observed regardless of whether it was administered before, after, or both before and after a cold stress, indicating that timing was not critical. To confirm that AA mitigates latent injury by preventing oxidative damage, we then examined whether AA supplementation reduced macromolecular damage by carrying out Western blots on 4-hydroxynonenal, a common marker for lipid peroxidation. This work allows us to better elucidate the connection between oxidative stress and cold tolerance in insects.

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## 8: Degrees of survival: Testing the fitness effects of incubation temperature in at-risk turtles

Hossam Ehab, Brandon Lee, Christina Davy

Incubation temperature influences the growth, development, and phenotype of embryos in oviparous animals, including hatching rates and juvenile fitness. Ex-situ incubation is often used as a conservation tool for freshwater turtles, but it is unclear what temperature regimes best support hatchling health and their chances of surviving to the next age-class in the wild. Here, we tested hatching outcomes in two at-risk turtles, the eastern spiny softshell (*Apalone spinifera*) and the Blanding's turtle (*Emydoidea blandingii*). We collected 36 clutches from *A. spinifera* ( $n = 839$  eggs) and 7 clutches from *E. blandingii* ( $n = 68$  eggs) during 2024 field season. We tested the effects of five viable incubation temperatures (26-30C) on hatchling incubation duration, hatching success, mass, incidence of

developmental abnormalities, corticosteroid production, and performance (righting time). Incubation duration was highest for clutches incubated at 26C and lowest at 30C, but hatchlings incubated at warmer temperatures were, on average, smaller and took longer to right themselves than those incubated at cooler temperatures. This is the second year of a three-year study. Full, final results and recommendations for ex-situ incubation will be shared after the 2025 field season. Alongside the direct applications of this research to turtle incubation and headstarting projects, understanding how hatchlings fitness may be impacted by rising ambient temperatures associated with climate change will also help inform future recovery planning for these and other freshwater turtle species.

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#### 9: Determining the Efficacy of Novel Peptides on Increasing Bacterial Susceptibility to Ampicillin through Inhibition of the TEM-1 beta - lactamase

Johanna Enright, Ali Shukri, Julia Desbiens, Isabella G Miron, Alex Wong, Kyle Biggar

$\beta$ -lactamases are one of the main defense mechanisms against  $\beta$ -lactams, a widely used class of antibiotics, in gram-negative bacteria. Due to increased selective pressure from improper antibiotic use,  $\beta$ -lactamases have collectively evolved resistance to all  $\beta$ -lactam antibiotics. Inhibitors of  $\beta$ -lactamases, such as clavulanic acid have been implemented to restore the efficacy of  $\beta$ -lactams, although resistance to certain inhibitors has evolved as well. Previously, we had designed a 14-mer novel peptide which was shown to effectively inhibit TEM-1, a common serine  $\beta$ -lactamase, in-vitro. Using checkerboard assays, we have tested if the peptide can act synergistically with ampicillin to inhibit bacterial growth. Synergistic action was observed for three tested strains of TEM-1 containing *Escherichia coli*, suggesting effective TEM-1 inhibition in-vivo. Further replicate testing is needed to confirm these results. Successful inhibition of TEM-1 would provide a foundation for further peptide optimization and therapeutic development. Ultimately, this would offer another approach to the design of  $\beta$ -lactamase inhibitors in the battle against antimicrobial resistance.

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#### 10: Small RNA and Freeze Survival: The Cryoprotective Functions of MicroRNA in the Frozen Muscle Tissue of The Grey Tree Frog

Saif Rehman and Kenneth B. Storey

The grey tree frog, *Dryophytes versicolor*, survives whole-body freezing for weeks during cold winter months. Survival in a state devoid of available food, water, or oxygen forces a reliance on metabolic rate depression (MRD) and the reprioritization of bodily functions.

This study utilizes next-generation sequencing (NGS) and bioinformatic analyses to characterize changes in the microRNAome of *D. versicolor*. When comparing control to frozen groups, five microRNAs (miRNA) were found to be differentially regulated (miR-143-3p, miR-30e-3p, miR-10a-5p, miR-140-3p, and miR-148a-3p), suggesting that they play key roles in freeze survival. The KEGG and GO analyses of these changes predicted a significant negative enrichment of terms associated with cell proliferation and active metabolism while simultaneously predicting the upregulation of cell signalling terms. These results suggest a fast-acting regulatory role for miRNA in contributing to the reorganization of gene expression and the limitation of energy-expensive processes during MRD in the hind leg skeletal muscle of the frog.

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## 11: The Evolutionary Dynamics of GBM and Intra-tumor Heterogeneity as a Potential Predictor of Tumoral Fitness

Hussein Omran, Andrew Simons, Bruce McKay

Glioblastoma multiforme (GBM) is a highly aggressive primary brain tumour that primarily affects adults. The prognosis is very poor, with a median survival time of 14–15 months after diagnosis. The specific cell of origin responsible for initiating GBM pathogenesis reflects its diverse molecular and phenotypic profiles. As a result, GBM tumours are highly heterogeneous, posing a significant barrier to targeted therapeutic efforts. In this experimental evolutionary study, the therapeutic resistance of two GBM cell lines was evaluated in response to two selective pressures: the targeted therapeutic drugs Taxol and Affinitor. The two cell lines used were an isogenic pair of U-87MG wild-type and U-87MG mutant cells. The mutant line was engineered to express the R132H mutation, which is associated with increased production of the oncometabolite 2-HG. A cumulative value representing intratumoral heterogeneity (ITH) was derived mathematically using morphometric measurements obtained from fluorescent micrographs analyzed in Fiji. The relationship between ITH and therapeutic resistance was examined to determine whether a statistically significant correlation exists between the two variables. Preliminary studies conducted on the isogenic pair have revealed insights into growth dynamics and therapeutic response.

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## 12: Phylogenetic evolution of the actinodin (and) and augurin (ecrg4) genes

ATHO JEREMY, STEPHANE ARIS-BROUSO, MARIE ANDREE AKIMENKO

Actinodin genes encode proteins involved in the formation of fin fibers called actinotrichia. Like fins, these actinodin genes have not been found to date in tetrapods. We believe that the loss of these genes during evolution allowed the transition from aquatic life to terrestrial life. On the other hand, in tetrapods, there is the augurin gene ECRG4, a putative tumor suppressor gene whose N terminal part is partly similar to that of the actinodin genes. How does the phylogenetic analysis of actinodin genes elucidate their evolutionary trajectory, from origin to loss in certain lineages? This is the main question of our research. In summary, I can say that my research has three short term goals: The first is to perform a phylogenetic analysis of the actinodin and ecr4 genes by considering only the N-terminal part of and which has some similarities with ecr4 to date and estimate the appearance and disappearance of actinodin genes during evolution. The second objective is to do the synteny of the actinodin genes in different species of vertebrates in order to confirm the loss of the gene in tetrapod but also to confirm the results of my phylogenetic analysis. I will also do an analysis of the synteny between different species of teleost in order to observe the divergences that could exist in acantomorphs due to the presence of spinous rays. The third objective will be to make a prediction of the three-dimensional structure of proteins allowing the formation of ceratotrichia in chondrychians to compare them with those of actinotrichia in osteichthyes such as zebrafish and acantomorphs. This prediction will allow to understand the morphological difference at the level of the fin rays of different species of fish. The long-term goals of this study are to understand the evolution of actinodin genes and their role in the formation of fish fin rays, by exploring the morphological differences between soft and spiny rays."

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### 13: Functional Diversity of Microbes in Metal Detoxification within High Arctic Lake Sediments

Franck Ouedraogo

The High Arctic is experiencing accelerated environmental change due to climate warming, with increased glacial runoff modifying sediment chemistry and microbial community dynamics in aquatic ecosystems. Lake Hazen (Nunavut, Canada) displays pronounced spatial variability in sediment geochemistry, driven by differential glacial runoff inputs, which may select for distinct microbial functional adaptations, particularly in metal detoxification pathways. Here, we investigate the diversity and abundance of metal resistance genes in sediment microbial communities across high-runoff, low-runoff, and control transects in Lake Hazen. We hypothesize that high-runoff sediments will exhibit reduced diversity and abundance of metal detoxification genes compared to low-runoff and control areas, reflecting microbial adaptive constraints under elevated sedimentation

and geochemical stress. We evaluate how environmental gradients shape microbial functional potential using metagenomic sequencing, offering insights into microbiome resilience to climate-induced disturbances. Our results will enhance predictions of how Arctic warming alters microbial-driven biogeochemical cycling and ecosystem stability in rapidly changing freshwater environments.

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#### 14: Development of Adverse Outcome Pathways to Describe Declines in Male Fertility

Reyna Tao<sup>1</sup>, Vicky Wang<sup>1</sup>, Paloma Medeiros<sup>2</sup>, Daniel Cyr<sup>2</sup>, Francesco Marchetti<sup>3,4</sup>, Carole Yauk<sup>1</sup>.

Sperm quantity and quality have declined over recent decades, with environmental contaminants being a major contributing factor. We are developing Adverse Outcome Pathways (AOPs) to improve understanding of male reproductive toxicity and inform toxicity testing strategies. AOPs describe a series of key events (KEs) that progress from molecular changes to organism- or population-level effects. Key event relationships (KERs) link two KEs and are developed through systematic evidence collection and evaluation.

Quantitative understanding of KERs enables predictions of adverse outcomes based on measurements of early KEs. We developed a preliminary AOP network beginning with “increased NADPH oxidase activation” and/or “decreased antioxidant enzyme activity” and ending with “impaired fertility”. Many KERs in the AOP network up to “oxidative stress leads to increased cell death” were already in the AOP Wiki. Thus, we began by developing subsequent KERs. We used Ovid MEDLINE and AOP-helpFinder 2.0 to retrieve articles, and Covidence to screen for relevant articles for relationships between cell death, testicular histopathological changes, sperm quantity, and impaired fertility, as well as testosterone levels, epididymal histopathological changes, sperm quality, and impaired fertility. The evidence supports the causal associations of these KEs with moderate to high confidence. However, quantitative understanding was minimal. This AOP network will enhance understanding of which KEs are connected to impaired male fertility and highlight KERs with data gaps. The new KE(R)s will be available in the AOP Wiki. The developed AOPs will be used as a framework to assess if nano/microplastics exposure contributes to impaired male fertility through similar mechanisms.

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#### 15: AI-designed peptides in detection of HPV 18 L1 protein

Jiashu Wang, Ashkan Golshani

Human papillomavirus (HPV) represents a group of over 200 types of non-enveloped DNA viruses that increase the risk of cancers development. They can be categorized into high-risk, such as HPV 16 and 18 which cause most cervical cancers and low-risk types, such as HPV 6 and 11 which cause genital warts. The detection of HPV infections, especially by high-risk strains like HPV 18, face significant challenges due to its asymptomatic nature, slow progression to disease and strain diversity. To address this issue, we utilized the In-Silico Protein Synthesizer (InSiPS), an artificial intelligence that designs peptides which deactivate or detect critical proteins of interest. We applied InSiPS to develop detection peptides against the L1 capsid protein of HPV 18. Using the primary sequence of the L1 protein, InSiPS uses advanced protein-protein interaction (PPI) analytics in predict interaction hotspots on L1 facilitating the development of highly specific peptides. We used enzyme-linked immunosorbent assays (ELISAs) to validate the designed peptides. We found that some of the designed peptides were effective at detecting the L1 protein under various conditions, including extended storage at room temperature and exposure to high temperatures. Our peptides have successfully detected L1 protein in 30 ng/mL with designed peptides. The findings suggest a potential for these peptides to enhance HPV detection, offering a scalable and cost-effective alternative to traditional methods. Future work will focus on comparing with other screening methodologies, validating their application in human samples as well as the cross-reactivity against other HPV strains.

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#### 16: MicroRNA expression in the heart of estivated *Scaphiopus couchii*

Mairelys Naranjo, Sarah A. Breedon, and Kenneth B. Storey

Couch's spadefoot toad faces prolonged exposure to extremely dry conditions in the deserts of the Southern USA and Mexico. In order to survive these arid climates, they spend most of the year underground in a hypometabolic state known as estivation, whereby they are severely dehydrated and lack food access. The ability to survive many months of estivation is achieved through the use of various regulatory mechanisms, including microRNA-mediated mRNA silencing. Next-generation sequencing was used to determine microRNA expression, finding that 15 microRNAs were differentially expressed in the heart of estivated *S. couchii* compared to control. KEGG and GO gene set analyses predicted that terms associated with ribosome and cardiac muscle contraction were upregulated, whereas cell signaling and fatty acid metabolism terms were downregulated. Overall, these results suggest that miRNAs contribute to the regulation of gene expression related to cardiac muscle physiology and energy metabolism during estivation.

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## 17: Sequence Analysis of Stx2i-Producing Escherichia coli Strains Isolated from Lamb

Noor Shubair, Mathu Malar, and Catherine Carrillo

Shiga toxin-producing Escherichia coli (STEC) cause a range of illnesses, and their pathogenicity is highly dependent on the production of Shiga toxins (Stx). These toxins are categorised as Stx1 or Stx2, and variants within these groups are further divided into subtypes (Stx1a, 1c – 1e, Stx2a – 2o). Differences among subtypes have been associated with severity of disease and host specificity of Shiga toxins. STEC encoding the Stx2i variant have rarely been recovered, and have thus far only been identified in sheep, shrimp, and raw milk. Here, we describe a collection of seven STEC strains recovered from six samples of raw lamb products encoding the Stx2i Shiga toxin variant. Genomic analysis of draft and closed genomes revealed high genetic diversity among these strains, including strains with four different serotypes (OUNT:H21, O8:H19, O8:H25, O9:H30). Two unique strains encoding Stx2i were isolated from the same sample, indicating active prophage mobility within this food commodity. Comparative alignment of the Stx2i-encoding prophage regions indicated a high degree of similarity among the isolates, supporting the idea of a conserved phage backbone. Recent isolates of STEC encoding the Stx2i toxin have been identified in sheep and clinical samples, highlighting a potential host association of this variant with sheep, and raising concerns regarding food safety and zoonotic transmission.

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## 18: Evaluating Population Genetic Clustering Methods Under Different Migration and Sampling Scenarios

Bianca R. Tassi and Catherine I. Cullingham

Accurately identifying genetic populations is important in evolutionary biology, population genetics, and conservation, as it aids in species identification, understanding disease spread-risk, and resource management. Misidentification of populations can lead to negative consequences like over-harvesting and loss of genetic diversity. The clustering software, Structure, is currently the standard in estimating the most likely number of populations (K). PopCluster, a newer software, has a more efficient algorithm for handling large genomic data, and it is more accurate in handling small or highly unbalanced sampling. It does this by introducing a scaling parameter taking values 0 to 4 (no scaling to very strong scaling). However, there is limited understanding of how/when to use the scaling parameter to ensure an accurate clustering solution. Therefore, our project will test the scaling parameter by simulating three populations under an island model of migration at three different migration scenarios, and four different sampling schemes, that include equal sampling, and strong skews. We will estimate K using best practices in Structure, and

PopCluster, and then compare estimated K to the simulated K to assess the performance and level of agreement between the programs. Empirical data sets will also be used in simulations to compare to the simulated data. This comparative analysis will contribute to refining best-practices in estimating genetic populations based on the software, type of data, and parameters inputted.

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#### 19: Understanding the Genetic Underpinnings of Climate Change Acclimation and Temperature Stress Resilience in an Antarctic Green Algal Extremophile

Danielle Bowman, Pomona Osmers, Mackenzie Poirier, Marina Cvetkovska

*Chlamydomonas priscui* is a green psychrophilic alga adapted to the extreme Antarctic cold. Psychrophiles thrive in the cold but cannot survive even minor temperature increases, which makes them very vulnerable to climate change. *C. priscui* resides in a perennially ice-covered lake and is adapted to high salinity (700mM) and extreme shading (<15  $\mu\text{mol m}^2/\text{s}$ ). Due to trends in global warming, polar regions are undergoing rapid ice loss that increases light availability and decreases salinity in the water column. These changing conditions may constitute stress for an organism adapted to a stable below-ice habitat.

The goal of this study is to understand the adaptation to conditions that accompany climate change (low salinity, increased light) compared to the current conditions in polar under-ice habitats (high salinity, low light). Furthermore, we are examining whether acclimation to such conditions impacts the algal ability to withstand acute heat stress. To determine the effect of acclimation on stress resilience, cultures were grown until mid-exponential growth phase then subjected to 24°C, heat stress temperature in *C. priscui*, followed by a period of recovery at 4°C. RNASeq analysis revealed that native conditions (high salinity, low light) prime cells to withstand heat stress and recover, while cells acclimated to putative climate change scenarios (decreased salinity, increased light) suffer significant damage and are unable to recover at the level of the transcriptome. This study is the first of its kind to examine the ability of this vital primary producer to withstand climate change conditions and recover from acute heat stress.

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#### 20: Understanding the effects of ciliopathy gene LRRC56 mutation on model species *Danio rerio*

M. S. Wredenhagen, J. Ivare, V. Saxena, M. Akimenko



A missense mutation in the leucine-rich repeat (LRR)-containing gene 56 (LRRC56) was discovered in two stillborn fetuses presenting with situs inversus and was linked to the function of motile cilia, which are microtubular organelles that form and project from the epithelial surfaces of the respiratory tract, middle ear, the ventricles of the central nervous system, the node, and the fallopian tubes. To confirm that the observed phenotypes of the human fetuses are the result of a mutated LRRC56 protein, a *Danio rerio* (zebrafish) knockout model was created using CRISPR/Cas9. Homozygous mutant zebrafish present with cilia-related defects in their visceral organ placement, such as the heart, otolith deposition and spinal curvatures. By using Wildtype (WT) siblings instead of WT, a Points Classification System (PCS) based off Padilla et al. (2011) to classify spinal curvatures and observing important timepoints in zebrafish development, we show that zebrafish phenotypes are impacted by the *lrrc56*  $-/-$  mutation. Defects between heart placement, otolith defects and spinal curvature defects often appear together in the same individual. Vertebral spacing is unaffected by the mutation in both mutant individuals with severe spinal defects and those without. After a week, mortality rates of *lrrc56*  $-/-$  individuals are higher than WT sibling individuals depending on the severity of spinal curvature defects. Interestingly, fertility, which is often affected in ciliopathies, is not affected in both male and female homozygous mutants. Ciliary pathways are not well understood; thus, their associated mutations present an opportunity to examine their function and manifestation in the phenotype.

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## 21: The Role of the Hippo-Yorkie Pathway in Caste Development in Ants.

Thalia Molloy Charette, Rajendhran Rajakumar

The Hippo-Yorkie pathway is an ancient cell signalling pathway that is highly conserved across species. This pathway has been extensively studied in the context of cancers, as it plays an important role in tumorigenesis. For example, when the pathway is off, it simultaneously promotes cellular proliferation and inhibits cellular apoptosis, making it a key pathway for studying the growth and sizing of organs during development. Ants have evolved multiple female 'castes' that form a colony of individuals which possess variation in traits including orders of magnitude difference in growth and yet these individuals are of the same genotype. Rather than genetic variation, this variation is due to environmental perturbations during development. While research has been done to investigate the role of the Hippo-Yorkie pathway in the development of organs, there is minimal research examining how environmental sensitivity of this pathway can contribute to growth variation. Therefore, ant castes are an excellent model to study the role the Hippo-Yorkie pathway plays in regulating growth.

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## 22: Comparative analysis of physiology and stress response in closely related Arctic and Antarctic green algae

Allison Szenasi & Marina Cvetkovska

With Polar regions warming at twice the rate of temperate regions due to climate change, psychrophilic microbes that populate these regions are increasingly threatened. Psychrophiles are cold extremophiles that cannot survive even moderate temperature increases (>20°C), but thrive under multiple extreme conditions, including high salinities, extreme photoperiods, and shading. My goal is to compare closely related but geographically distant species to identify if habitat and geographical distances affect their physiology and resilience in the face of climate change. The focus is on the order Chlamydomonadales, as it has over one-third of known algal psychrophiles and well-studied green algal models.

First, I will construct a phylogenetic tree of Chlamydomonadales species using public genomic data and identify closely related species from the Arctic and Antarctic. This will ensure that observed differences reflect habitat-specific adaptations rather than species-level variation. After selecting a model group with members from both Poles, growth and physiology will be characterized under conditions reflecting their natural habitat ranging from stable ice-covered lakes to dynamic marine waters. I hypothesize that despite close evolutionary relationships, algal physiology will differ between species resulting from adaptation to different environments. I will also observe algal responses to climate-change driven stress at the level of viability, physiology and cellular biology. I hypothesize that species from dynamic environments (e.g., marine waters) are more resilient to stress than those from stable habitats (e.g., ice-covered lakes). This study aims to elevate psychrophilic algae, the foundation of all polar food webs, as key biomarkers for assessing ecosystem health amid climate change.

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## 23: The role of fin-specific structural fibers in guiding the development of fin cartilages in the zebrafish and the small-spotted catshark

Paulina Hanzelova, Camille Martinand-Mari, Mélanie Debiais-Thibaud, & Marie-Andrée Akimenko

Actinotrichia are rigid fibers that provide the first skeletal support to the developing fins of bony fishes (Osteichthyes). Osteichthyan fins develop through the elongation of a fin fold (FF) containing two arrays of actinotrichia. Actinotrichia guide migrating mesenchymal

cells into the FF, where they contribute to the developing fin structures, including the rays. Actinotrichia are considered homologous to ceratotrichia, large fibers found in cartilaginous fishes' (Chondrichthyes) fins. However, while the actinotrichia are restricted to the tips of adult osteichthyans' rays, ceratotrichia are much larger, occupying a significant proportion of the fin. We recently showed that the absence of actinotrichia in zebrafish (Osteichthyes) results in FF defects and truncated fins with malformed rays, supporting the importance of actinotrichia in proper fin development. Unexpectedly, we found fusions of the hypural bones in uniquely the caudal fin endoskeleton. The zebrafish hypurals are the only fin endoskeletal elements developing within a FF. We show that the cartilage template of the hypurals normally develops between the actinotrichia arrays, but becomes disorganized in their absence, leading to fusions. This shows that actinotrichia influence the patterning of all skeletal structures forming in the FF, including the rays and the caudal fin endoskeleton. Histological analyses on the small-spotted catshark (Chondrichthyes) show that similarly, the cartilaginous radials of the fins develop close to the ceratotrichia. Therefore, both actinotrichia and ceratotrichia seem to influence the growth of the fin cartilages developing in their presence. This supports a functional homology of actinotrichia and ceratotrichia since the divergence of Osteichthyes and Chondrichthyes.

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#### 24: Anoxic Adaptations: Histone acetylation and deacetylation in the wood frog brain

Imane Rhzali and Dr. Kenneth B. Storey

The wood frog, *Rana sylvatica*, faces numerous challenges due to the climate of the region it inhabits including oxygen deprivation whilst the frog is frozen. To withstand prolonged periods of oxygen deprivation (anoxia), they must employ many mechanisms and pathways which allow for survival of anoxia for an extended period of time. Histone lysine acetylation and deacetylation are one way in which these frogs likely use to protect themselves against anoxia. Immunoblotting was performed to evaluate the relative protein levels of various lysine acetyltransferases (KATs), histone lysine marks, and histone deacetylases (HDACs and SIRT6). The results indicated that these proteins were differentially regulated with KAT1, KAT2A, KAT5, KAT8, H3K14Ac, H3K23Ac, H3K27Ac, H3K56Ac, HDAC3, HDAC4, HDAC6, HDAC7, SIRT4, and SIRT6 all showing significant changes in response to 24 h anoxia compared to normal (control) conditions.

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#### 25: The Ionophore Resistance Genes *narA* and *narB* are Geographically Widespread and Linked to Resistance for Medically important Antibiotics

Asalia Ibrahim, Jason Au, Alex Wong

Ionophores are a class of antibiotics used widely in animal production as anti-coccidials and for growth promotion. Since ionophores are not used in human medicine, it has largely been assumed that they do not contribute to medically important antimicrobial resistance (AMR). Nonetheless, there is increasing concern that ionophore usage could co-select for clinically relevant AMR, since the ionophore resistance genes *narA* and *narB* have been found in linkage with multiple AMR genes. We investigated the global distribution and AMR linkage of *narA* and *narB* using publicly available data. These ionophore resistance genes can be found worldwide, with >2400 *narA/B*-bearing isolates reported from 51 countries. Isolates were derived from a range of host species, including poultry, cattle, and humans. *narAB* was linked with an average of over 10 resistance determinants for antimicrobial resistance, including many medically important antibiotics. These observations indicate that we cannot assume that ionophore use is risk-free, with clear potential for co-selection for clinically relevant AMR.

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## 26: Characterizing the role of candidate maize genes in tar spot resistance

E. MARION 1,2, A. KEBEDE 1, E.K. BRAUER 1,2.

Tar spot is an emerging foliar disease of corn for which no genetic resistance exists in cultivated varieties. Caused by the fungus *Phyllachora maydis* and first detected in Ontario corn fields in 2020, the disease poses a growing threat to maize production. Recent work has identified a resistance-associated genetic locus on chromosome 8, highlighting five candidate genes. Two genes were selected for further investigation based on their potential roles in disease resistance: a putative UDP-xylose transporter and a leucine-rich repeat receptor-like kinase (LRR-RLK). While maize encodes over 248 LRR RLKs, only five UDP-xylose transporters are known to be expressed. Sequencing of both genes in resistant and susceptible maize lines revealed a number of differences in their genomic sequences. Comparative analyses identified 56 SNPs in the LRR-RLK coding region, including three frameshift mutations, as well as eight SNPs in the UDP-xylose transporter, which may impact protein function. Quantitative PCR analysis shows elevated expression of *PR5*, a marker gene for pathogen-related pattern-triggered immunity, along with increased expression of the UDP-xylose transporter in the resistant line CML495. Additionally, reactive oxygen species (ROS) assays indicated a stronger oxidative burst in the resistant line. Future work will focus on microscopic comparisons of cell wall differences between the resistant and susceptible lines, as well as subcellular localization of the proteins during transient expression. Understanding the genetic mechanisms underlying pathogen

resistance will help inform breeding programs and provide deeper insights into plant immune responses against emerging pathogens.

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#### 27: Soil bacterial community selection by conspecific AMF strains

Robert Ferguson, Dr. Nicolas Corradi

Arbuscular mycorrhizal fungi (AMF) are obligate symbionts of most plants that improve plant growth by transferring nutrients into plant roots through networks of soil hyphae. Multiple studies have found AMF species-dependent shifts in soil microbial communities via to the enrichment of specific microbial taxa, yet none have investigated this phenomenon at the level of fungal strain. This study will seek to characterize the effect of conspecific AMF strains on the presence and relative abundance of bacteria in soil grown with two different host plants. *Sorghum x drummondii* and *Medicago trunculata* seeds were inoculated with one of eight strains of *Rhizophagus irregularis* (a model AMF species) and grown in the presence of a field-sampled bacterial community. DNA will be extracted from frozen soil samples for 16S rRNA sequencing to generate bacterial community profiles of each AMF strain treatment. Each profile will be assessed for alpha and beta diversity. PERMANOVA will be performed on beta diversity data to test for significant differences between communities. Additional grouping factors such as plant and fungal biomass will be added as explanatory variables to identify potential drivers of bacterial community composition. The PICRUSt pipeline will be used to compare inferred functional variation among treatments, to predict potential effects on the greater soil ecosystem. The many plant health benefits provided by AMF are the result of synergistic interactions between plants, their fungal symbionts, and soil bacteria. Once completed, this methodology will provide a close examination of AMF strain identity as a driver of soil bacterial community composition.

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#### 28: Investigating differential host sensitivity to the *Fusarium graminearum* virulence factor gramillin in barley

Siddharthan Lakshmanan, Dr. Elizabeth. K. Brauer

*Fusarium graminearum* (Fgr) is the primary causal agent of Fusarium Head Blight (FHB), a devastating fungal disease that impacts the economic value of cereal crops globally. Fgr produces a range of secondary metabolites, some of which act as virulence factors, making infected crops unsuitable for consumption and industrial use. One such newly identified metabolite, gramillin, enhances Fgr virulence in maize and barley by disrupting

membrane potential, triggering host stress responses, and promoting production of other Fgr virulence factors. Notably, wheat is resistant to gramillin, while barley exhibits quantitative resistance. QTL analysis has mapped gramillin sensitivity in barley primarily to chromosome 5H, with phenotypic characterization linking gramillin sensitivity to necrotic lesion formation on barley leaves. A range of gramillin sensitivities observed across barley genotypes has prompted us to investigate the genetic basis for this variation. Comparative transcriptomic analysis reveals that gramillin triggers distinct gene expression patterns in barley, unlike conserved PAMPs such as flg22. Gene ontology (GO) enrichment analysis of gramillin-insensitive barley highlights downregulation of defense-related genes and upregulation of genes associated with catalytic activity and membrane function. To further investigate the link between plant defense and gramillin sensitivity, gramillin-induced lesion assays were performed on barley leaves that were pre-treated with flg22, a known inducer of plant stress response. Preliminary results support the hypothesis that timing and amplitude of induced stress responses may influence gramillin sensitivity. In addition, preliminary biochemical analysis of gramillin degradation in barley apoplastic fluid indicates a potential role of extracellular proteolytic enzymes in conferring resistance. Overall, this research aims to identify molecular markers and traits linked to gramillin resistance and contribute to the development of FHB-resistant barley cultivars. Given that FHB causes an estimated \$1.5 billion in annual losses to the Canadian grains industry, these findings have significant agricultural and economic implications.

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#### 29: Regulation and virulence function of *Fusarium graminearum* secondary metabolites during *Arabidopsis* seedling infection

Marielle Zouein, David Overy, Rajagopal Subramaniam, Elizabeth Brauer

*Fusarium graminearum* is a fungal pathogen of cereals that reduces grain quality due to the deposition of secondary metabolites during infection. Secondary metabolite production is temporally regulated, with specific gene clusters involved in virulence factor production being induced during host colonization in response to unknown plant host factors. Previous research identified the *Arabidopsis* gene *RbohD* as promoting production of the DON mycotoxin and promoting susceptibility to the pathogen, however its effect on secondary metabolite production is unclear. We used transcriptomic profiling to identify 712 fungal genes whose expression is dependent on *RbohD*, including biosynthetic gene clusters associated with the production of butenolide, fusaoctaxin A, FDDP, and DON. To determine if the *RbohD*-dependent mycotoxins contribute to the virulence of *F. graminearum*, we infected *Arabidopsis* with *Fusarium* mutant strains lacking production of butenolide, fusaoctaxin A, FDDP and DON. Preliminary results reveal that mutants lacking fusaoctaxin

A, FDDP, and DON production exhibit significantly reduced virulence compared to the wild-type strain indicating these secondary metabolites could be virulence factors. Together, this suggests that host-derived factors promote virulence of the pathogen by activating secondary metabolite production.

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30: Titanium dioxide and human large intestinal epithelial cells: the effect of particle size and dispersion method on cell proliferation and viability

Sambina Bevilacqua, Grant Frahm, Michael Johnston, Laurie HM Chan, Xiaolei Jin

Food-grade titanium dioxide (TiO<sub>2</sub>-FG) is widely used as a whitening additive but has come under scrutiny as research reveals it can contain a significant proportion of TiO<sub>2</sub> nanoparticles (TiO<sub>2</sub>-NP; <100 nm). Both TiO<sub>2</sub>-FG and TiO<sub>2</sub>-NP have been linked to cytotoxicity, though findings remain inconsistent. TiO<sub>2</sub> is insoluble and prone to agglomeration, thus were often dispersed by probe sonication (PS) for toxicological studies. However, PS can generate reactive oxygen species and/or change the reactivity of TiO<sub>2</sub>, potentially amplifying its cytotoxicity. Additionally, smaller particle sizes can increase cellular uptake and surface reactivity, leading to greater toxicity. This study evaluated the effects of two TiO<sub>2</sub>-FG products (161 ± 75 nm and 109 ± 36 nm) and one TiO<sub>2</sub>-NP (19 ± 6 nm) in human large intestinal epithelial cells. Particles were dispersed in distilled and deionized water containing 0.05% bovine serum albumin using PS or bead-milling (BM) under optimized settings and applied to cells at 0, 1, 5, or 25.6 µg/mL TiO<sub>2</sub> daily for five days. Total, live, and dead cell numbers were measured using the trypan blue exclusion assay. PS and BM generated similar dispersion efficiencies for both TiO<sub>2</sub>-FG products, but BM was less efficient for TiO<sub>2</sub>-NP. Neither TiO<sub>2</sub>-FG products affected cell proliferation or viability, regardless of dispersion method. PS, but not BM, of TiO<sub>2</sub>-NP significantly reduced live and total cell numbers, but had no effect on dead cell numbers, suggesting inhibition of cell proliferation. These findings suggest that small particle size and PS contributed to the cytotoxic effects of TiO<sub>2</sub>-NP.

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31: The Effect of Seed Size on Expression of Maternal Effects

Melissa Labelle, Andrew Simons

Maternal effects are influences from the maternal environment on progeny phenotype and are most often of interest for their fitness effects on offspring. However, more general explanations for the source and strength of maternal effects are lacking. Here, we propose and test the hypothesis that the strength of maternal effects on offspring phenotypes will

be stronger in plant species with larger seeds (diaspores) because maternal tissue and maternal provisioning increases relative to genetic contributions with seed size. To test our hypothesis, we use four accessions of *Arabidopsis thaliana* chosen for their contrasting seed sizes. Maternal effects were first generated by growing a parental generation of all accessions in both “conducive” and “stressful” environments; their offspring were then grown under common garden conditions where maternal effects were observed. The effect of parental seed size on the relative strength of maternal effects was then assessed in the offspring for several traits including final height and number of fruits. This research will contribute to the understanding of mechanisms underlying cross-generational plasticity and the potential for the evolution of adaptive maternal effects.

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32: Quantifiable measures of eye-tracking and their correlation with the VOMS score in concussed subjects

Katherine Wiebe, Iain McKinnell, Jeff Dawson, Andy Adler

Concussion prevalence has become a concerning issue, compounded by limitations in current assessment tools that rely on subjective, qualitative data with only moderate test-retest reliability. The need for a quantitative assessment tool is apparent. The objective of this study was to determine the extent of the correlation between measures of eye-tracking and the VOMS test score in concussed subjects. Participants completed the VOMS test before a series of saccadic visual tasks, the eye-tracking was then processed in the open-source Tracker software and run through a code that detected the eye transitions. It is predicted that there will be a positive correlation between the eye-tracking metrics and the VOMS test score. As well, that increased measures of tau (ms) and error (%) will be seen shortly after sustaining a concussion and will improve throughout the recovery period.

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33: Avian Influenza H5N1 in Ontario: Landscape Drivers of Wildlife-to-Poultry Transmission

Amélie Boutin, Dr. Dalal Hanna, Dr. Jennifer Provencher

Highly pathogenic avian influenza virus (HPAIV) poses a significant threat to agricultural biosecurity, wild bird conservation, and public health. Since arriving in North America in 2021, HPAIV has caused widespread wildlife mortality and led to the mass depopulation of poultry on infected premises in Canada. Wild birds, especially waterfowl, are key virus carriers due to their high infection rates while often remaining asymptomatic. Using a



landscape epidemiological approach and 2021-2025 Canadian Food Inspection Agency data for Ontario, we tested whether waterfowl stopover, feeding, and wintering sites near commercial poultry farms increase the risk of HPAI outbreaks. We examined land use and land cover around farms and found no significant differences in wetland cover percentages between buffer zones of infected (n=52) and non-infected (n=539) farms in initial univariate analyses. This suggests that wetland presence alone does not drive HPAI outbreaks, which has positive conservation implications by reducing pressure on farmers to modify or drain wetlands near poultry operations. This research aligns with the OneHealth framework by investigating pathogen transmission at the wild bird–domestic poultry interface, informing biosecurity practices, and supporting wildlife conservation through collaboration with industry and government partners.

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34: dl3 neurons form sensorimotor circuits across the cervical and lumbar spinal cord for motor control

Shahriar Nasiri, Alex Laliberte, Tuan Bui

Neural networks in the spinal cord integrate sensory feedback to adapt motor activity and facilitate complex motor behaviours and reflexes, such as locomotion or hand grasp, in response to various stimuli. This important ability of modulating the activity of motor networks in response to changes in the body or external environment is partly mediated by a population of spinal interneurons, called dl3 neurons. These dl3 neurons receive diverse cutaneous and proprioceptive feedback, which convey information regarding fine touch and the positioning of the limbs, and they provide excitatory inputs to motoneurons that directly control muscle activity. Previous work has demonstrated that sensory drive to dl3s is implicated in recruiting spinal networks involved in locomotion, hand grasp, and motor recovery after spinal cord injury; however, it is unclear how dl3 neurons are connected to motor networks across the spinal cord to facilitate these complex functions. Through optogenetic activation of dl3s and electrophysiological recordings, we mapped the functional connectivity of dl3s to different circuits throughout and across the lumbar and cervical spinal cord. We demonstrate that the activation of dl3 subpopulations activates specific pools of motoneurons throughout the lumbar and cervical spinal cord in a bilateral manner. Furthermore, we found that continuous photoactivation of specific dl3s recruited locomotor networks independently from the brain, highlighting their potential as targets for motor recovery after spinal cord injury. Our findings suggest that dl3 subpopulations integrate specific sources of sensory information and fine tune the activity of appropriate groups of muscles.

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### 35: IMPACT OF SERT KNOCKOUT ON SURFACING BEHAVIOUR AND VISUAL FUNCTION IN DANIO RERIO

Benjamin Harrison, Michael Tea and Kathleen Gilmour

Zebrafish (*Danio rerio*) possess two serotonin transporters (*Serta* and *Sertb*) that are responsible for serotonin reuptake into the synapse. Zebrafish that lack functional expression of *serta*, *sertb*, and both paralogues (*sertab*) were generated through knockout lines (KO). The *Sertb*-KO zebrafish exhibited a unique behaviour referred to as 'surfacing', where they spent the majority of their time near the surface of the water without any environmental stimulus. The pathways underlying surfacing behaviour are currently unknown. Previous studies have linked higher tank region preference to an anxiolytic phenotype. To further investigate the cause of *Sert*-KO influenced behaviour, a novel dive test is performed on larval zebrafish to observe if the surfacing behaviour was present in juvenile fish. The findings of this illustrated that *Sertb*-KO as well as the *Sertab*-KO larval zebrafish follow the same pattern of surfacing behaviour as seen in the adults relative to the wild type fish exhibiting an increased surface preference. We then asked if this behavioural phenotype observed could potentially be a result of visual differences induced by the different *Sert*-KO genotypes. Serotonin accumulation is known to lead to changes in the visual system due to the two *Sert* paralogues have complementary tissue distribution. *Sertb* is uniquely expressed in the retina, leading to the investigation on the effect that *Sertb*-KO had on visual acuity in zebrafish. To assess both response to light, as well as anxiety, locomotion was measured in an open field test under light and dark conditions, and a scototaxis test was performed to show if there was an impact between light and dark activity based on the different genotypes. The different activity between genotypes may provide insights into the role of serotonin signalling on zebrafish surfacing behaviour."

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### 36: EFFECTS OF GROUND VIBRATION EXPOSURE DURING INCUBATION ON THE BEHAVIOUR OF HATCHLING SNAPPING TURTLES (*CHELHYDRA SERPENTINA*).

Douglas Strick\*, Charlotte Galloway, and Christina M. Davy

Road mortality is a leading cause of mortality for snapping turtles (*Chelydra serpentina*) in Canada. However, female *C. serpentina* often nest in the gravel shoulders of roads or train tracks, where eggs developing in underground nests are exposed to ground vibration from passing cars or trains. During incubation, *C. serpentina* embryos use physical vibration cues to synchronize development. This study aimed to examine the potential impact of

ground vibration exposure from passing vehicles during incubation on exploratory and vibration avoidance behaviour of hatchling *C. Serpentina*. Eggs were artificially incubated on vibration tables to expose developing *C. serpentina* embryos to intermittent, low-frequency vibration, intermittent, high-frequency vibration, constant high-frequency incubation, or no vibrations (control group) during incubation. After emergence, hatchlings were placed in a choice arena to test whether they would orient towards or away from vibrations mimicking those of road traffic. Hatchlings exposed to intermittent high-frequency vibration during incubation exhibited less vibration avoidance behaviour than those in the other treatments or control group. However, *C. Serpentina* hatchlings in the other 2 treatment groups did not differ significantly in their behaviour from the control group, and none of the 3 treatment groups exhibited more exploratory behaviour than the control group. These results suggest that hatchlings exposed to intermittent, high-frequency vibration during incubation are at a higher risk of road mortality, however those exposed to the low-frequency vibration of rural roads face no increased risk.

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### 37: No Rest for the Rodent: Energy Management Strategies in the Naked Mole-Rat (*Heterocephalus glaber*)

Turchyn, D.1, Chan, P.1, Pamenter, M.E.1, Careau, V.1

Energy is a limited currency in animals, allocated between essential physiological processes and active energy expenditure (AEE). Understanding how energy is distributed between resting metabolic rate (RMR) and AEE, which together form daily energy expenditure (DEE), provides insights into energy management strategies. Whether activity is independent of maintenance costs or requires compensation can be described by the three energy management models: (1) the additive model, where changes in AEE do not alter RMR (DEE-RMR slope  $b = 1$ ); (2) the allocation model, where increases in AEE decrease RMR in a compensatory manner due to energy restraints (DEE-RMR slope  $b < 1$ ); and (3) the performance model, where increases in AEE increase RMR (DEE-RMR slope  $b > 1$ ). Despite their high lifetime energy expenditure and resistance to age-related metabolic decline, energy management is yet to be explored in the African naked mole-rat (NMR, *Heterocephalus glaber*). To investigate metabolic strategies in the NMR, repeated metabolic and activity measurements were taken in 32 individual NMRs using a multiplexed metabolic system and the relationships were partitioned at the among- and individual-levels. At the among-individual level, the slope of RMR and DEE ( $b < 1$ ) suggests that NMRs follow the allocation model. In contrast, at the within-individual level, the slope ( $b > 1$ ) indicates support for the performance model, suggesting that energy expenditure patterns differ between levels of analysis.

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### 38: THE KINEMATICS OF MULTIMODAL LOCOMOTION IN SALAMANDERS

Agape Williams, Dr. Emily Standen

Salamanders are a model for researching the evolution of tetrapod locomotion because of their capacity to move between aquatic and terrestrial environments. Although salamander locomotion in both water and on land has been studied in the past, little is known about the kinematic techniques used when alternating between these environments. The transitional locomotion of *Ambystoma laterale* is the subject of this study, which looks into the variations in kinematic strategies between land-to-water and water-to-land travel. We evaluate the salamander's body movements during these transitions by using high-speed video recordings made with a GoPro HERO8 Black and processed using MATLAB, ImageJ, and DeepLabCut. It is clear that salamanders have both a swimming gait and a walking gait, and we test the hypothesis that sensory feedback plays a role in initiating that transition.

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### 39: Investigating the longevity and healthspan of ants under different social conditions

Sophia Perrakis, Olivia MacMillan, Amin Galuta, Rajendhran Rajakumar

Ant longevity can vary greatly between different individuals, ranging from months to decades depending on diet, environmental conditions, and genetics. However, factors affecting health span, the length of time where an organism maintains adequate quality of life, are not as well-known. Ants are holometabolous insects, meaning they undergo complete metamorphosis through three main developmental stages: embryonic, larval and pupal. They reside in social colonies, where they are divided into groups called castes, based on division of labour. Larger major workers (soldiers) defend the colony, while smaller minor workers forage for food and take care of the brood. Brood-adult relationships vary greatly between species, for example; *Solenopsis invicta* adults depend on larvae to process food as the larvae contain metabolic enzymes lacking in adults. However, *Camponotus floridanus* adults, the species studied in this project, engage in cannibalistic behaviours with larvae if food is scarce. Current literature estimates the lifespan of a *C. floridanus* minor worker at 90-120 days, but, in this project, we will be investigating the effects of altering the social environment on the lifespan, activity and development of minor workers. Interestingly, our results suggest that the presence of larvae may have a pivotal influence on life and health span. Overall, this project seeks to elucidate brood care dynamics in *C. floridanus* and reveals mutual worker-brood lifespan benefits distinct to

certain types of young, refuting previous beliefs that brood care behaviours are prompted by a purely altruistic evolutionary drive.

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#### 40: They'll Grow Out of It: Investigating the effects of moulting on microplastic retention in arthropods

Jennie E. Mills\*, Marshall W. Ritchie & Heath A. MacMillan

Microplastic (MP) pollution is prevalent in terrestrial and marine environments and poses a major ecological concern. Arthropods, particularly those on lower trophic levels, will consume and even breakdown MPs to smaller fragments. We used a cricket, *Grylloides sigillatus*, to investigate the effects of moulting on MP retention and breakdown since they ingest and tolerate MPs throughout development and experience a period of frequent moulting between approximately 2 and 4 weeks of age. We hypothesized that the life-stage of insects would affect the retention and breakdown of MPs in their gut due to differences in moulting frequency throughout development. We exposed 140 adults (6-7 weeks) and 260 juveniles (2-3 and 3-4 weeks) to control or 1% w/w MP feed for 24 hours and tracked moulting in 60 juveniles. We then quantified the number and area ( $\mu\text{m}^2$ ) of retained plastic particles in the gut of each cricket. This approach allowed us to test whether juveniles shed MPs within their gut during moulting, which would substantially reduce plastic retention time relative to adults that no longer moult.

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#### 41: Effects of daily temperature fluctuations on growth and nutrient assimilation in a farmed cricket

Hannah Ross, Jacinta Kong, Sue Bertram, Heath MacMillan

The house cricket, *Acheta domesticus*, is farmed for food production and often used for scientific research. Its growth and metabolic performance are optimized at a constant high temperature. For producers, maintaining high temperatures year-round can come with significant financial costs in cold climates, and night-time cooling may reduce these costs. In their natural habitats, *A. domesticus* experience daily temperature fluctuations. Metabolic theory suggests that such fluctuations increase metabolic rate, impact nutrient assimilation, and slow growth. We reared crickets under constant (32C) and fluctuating thermal conditions to test the hypothesis that crickets develop at different rates under these conditions. Crickets were reared on a thermal gradient plate, with one end

maintaining a constant temperature of 32C, and the other experiencing a 40C peak and 24C low. This produced eight intermediate amplitudes of thermal variation across the plate. Growth rate, nutrient intake and macromolecule content (including lipids, proteins and carbohydrates) were assessed at the end of the rearing period to determine the effect of thermal variability on traits relevant to farming *A. domesticus*. Contrary to our expectation, we found that crickets grew at similar rates and had similar macromolecule concentrations, regardless of the amplitude of daily thermal fluctuations. These findings suggest that *A. domesticus* have sufficient plasticity to tolerate thermal variability without compromising growth or metabolic efficiency. This has potential implications for cost-effective cricket farming, as implementing thermal cycles could reduce energy expenditure without having a negative effect on yield.

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#### 42: Identification of Monoaminergic and Cholinergic Pathways in Cutaneous Sensory Cells of Developing Zebrafish

Willa MacDonald, Michael Jonz

In developing aquatic vertebrates, many sensory cell types are present in the skin. However, these cell types and the mechanisms by which they sense and initiate responses to environmental cues are not well described. One aquatic vertebrate of particular relevance to scientific research is *Danio rerio* (zebrafish) as they are commonly used as a model organism. Three important sensory cell types present in the skin of developing zebrafish are neuroepithelial cells (NECs), ionocytes and neuromasts. NECs are implicated in sensing and responding to hypoxia, ionocytes are important in the maintenance of osmotic homeostasis, and neuromasts are important for sensing the flow of water to detect predators and prey. Each of these cell types is innervated. Therefore, an important first step in understanding the physiological mechanisms that underlie the function of these cells is the identification of neurotransmitters at their afferent or efferent synapses. Using whole-mount immunohistochemistry, monoaminergic and cholinergic pathways were identified in zebrafish between 3- and 7-days post fertilization. Antibodies raised against neurotransmitters and the proteins involved in their synthesis, release, and uptake were assayed. The experiments revealed a novel cholinergic signaling pathway in cutaneous NECs, novel catecholaminergic and serotonergic pathways in ionocytes, and characterized, for the first time, the presence of D2 receptors in neuromasts. These results not only enhance our understanding of sensory cells in developing zebrafish but further inform existing applications and give insight into novel uses for zebrafish as a model organism.

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#### 43: Acute oxygen-dependent epigenetic regulation in rainbow trout liver: Is H3K4me3 linked to induced metabolic genes?

Sally Adil, William Johnston, Dr. Jan Mennigen

Environmental hypoxia in freshwater systems is increasing, even more so with climate change. Among freshwater fishes, some are relatively more tolerant to hypoxia, like the goldfish (*Carassius auratus*); others, such as the rainbow trout (*Oncorhynchus mykiss*), are intolerant. Physiological responses to acute hypoxia exposure vary, among them is metabolic plasticity. At least in part, metabolic plasticity is mediated via transcriptional changes in rate-limiting enzymes of metabolic pathways involved in glucose and lipid metabolism. Transcriptional responses are well-known to be mediated via the Hypoxia-Inducible Factor oxygen sensor system. Recent in vitro evidence revealed that oxygen-dependant epigenetic machinery may also be involved in direct regulation of transcripts. Here, we probe whether the activating histone modification, H3K4me3, enhanced in hypoxic condition in vitro, is linked to metabolic transcript induction by acute 4h hypoxia exposure (50% and 25% O<sub>2</sub> saturation) in the trout liver. Contrary to prediction, results show 25% O<sub>2</sub> saturation induced transcripts involved in gluconeogenesis (*pck1*) and fatty acid synthesis (*fasn*) exhibit a decrease in H3K4me3 modification in the upstream putative promoter region. These observations suggest that under the experimental conditions tested, other O<sub>2</sub> dependent (epigenetic) molecular mechanisms are involved in the induction of these enzymes. Additional studies looking at different hypoxia regimes and O<sub>2</sub> sensitive epigenetic markers are warranted to further address the role of epigenetic regulation on metabolic pathways in hypoxia response in fish.

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#### 44: Differential Tissue-Specific HIF-1 $\alpha$ Expression in Naked Mole-Rats and Mice Exposed to Hypoxia and LPS

Neha Erukulla, Karen Kadamani, Matthew Pamerter

Hypoxia, or reduced oxygen availability, disrupts cellular homeostasis, induces metabolic stress, and activates energy-intensive immune responses in most species. Conversely, hypoxia-tolerant animals such as the naked mole-rat (NMR) instead employ energy-conserving strategies to thrive in hypoxia. These strategies likely involve altered molecular pathways, and particularly the transcription factor hypoxia-inducible factor 1-alpha (HIF-1 $\alpha$ ), which is a key regulator of the cellular hypoxic response. Although well studied in hypoxia-sensitive species, the regulation of HIF-1 $\alpha$  and how hypoxia signalling interacts with immune system activation has received little attention in NMRs. To investigate this, we treated hypoxia-tolerant adult male NMRs and hypoxia-intolerant CD-1 mice with

lipopolysaccharide (LPS; a bacterial immune stimulant) or saline and then exposed to normoxia (21% O<sub>2</sub>) or moderate hypoxia (11% O<sub>2</sub>) for 24 h. Tissues were then collected and HIF-1α expression in liver and lung was measured via Western blotting. We found that liver HIF-1α expression was significantly lower in NMRs than in mice across all treatment groups and didn't vary between conditions. In mice, liver HIF-1α levels decreased in response to LPS and hypoxia individually but was unchanged when both were combined. In the lung, HIF-1α levels were unchanged by any treatment. These findings suggest tissue-specific suppression of HIF-1α expression in NMR liver as a potential energy-conserving strategy. Understanding how NMRs balance hypoxia and immune signaling could inform novel therapeutic strategies for managing ischemic injury, inflammation, and cancer-related hypoxia.

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#### 45: Detection of Secondary Sodium Pump Variant Expression in *Drosophila melanogaster* Anterior Malpighian Tubule Tissue Through Long-Read IsoSeq mRNA Sequencing

Kostyleva, T.1\*, Dean R. A.1, MacMillan, H. A1.

Chill-susceptible insects, like *Drosophila melanogaster*, are susceptible to the effects of low temperatures on physiological systems. During prolonged cold exposure, loss of ion and water homeostasis across cell membranes drives cell depolarization, in turn causing cell and organismal injury and death. Ion and water homeostasis in insects is maintained by the renal system, specifically the Malpighian tubules and hindgut, in part through the action of the sodium pump: Na<sup>+</sup>/K<sup>+</sup>-ATPase. Chilling suppresses activity in these tissues driving a loss of osmotic balance. Cold acclimated *D. melanogaster* retain such balance during cold exposure, protecting against downstream tissue damage. Yet, Na<sup>+</sup>/K<sup>+</sup>-ATPase activity remains unchanged in the tubules and hindgut of cold acclimate flies, suggesting another mechanism helps regulate ion and water fluxes in the organism. The presence of other, ouabain-insensitive variants of Na<sup>+</sup>-ATPase, have been implicated, but quantifying relative expression of highly-similar isoforms is technically challenging using conventional approaches. Here, we present plans for the use of long-read IsoSeq mRNA sequencing exploring relative expression of multiple Na<sup>+</sup>/K<sup>+</sup>-ATPase variants in the anterior Malpighian tubules to support their hypothesized role in maintaining cell volume and sodium regulation in cold acclimated insects.

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46: Implicating the serotonergic system in feeding and grown in zebrafish (*Danio rerio*).



Kristen Huang, Michael Tea, Kathleen Gilmour

Zebrafish (*Danio rerio*) have two paralogues of the serotonin transporter (Sert) uniquely expressed in the brain, *Serta* and *Sertb*, which re-uptake serotonin from the synapse into the presynaptic neuron. Zebrafish lines lacking the expression of either *serta*, *sertb*, or both were generated using CRISPR/Cas9 technology. To investigate the consequences of Sert loss-of-function on feeding behaviour and growth as a function of food intake, feeding behaviour in adults as well as growth indices in larval, juvenile, and adults were measured. Interestingly, all Sert knockout adult zebrafish consumed less food than their wildtype counterparts. Parallely, adult *serta*<sup>-/-</sup> averaged less total body weight than wildtype fish, while both *sertb*<sup>-/-</sup> and *sertab*<sup>-/-</sup> displayed intermediate body masses. Similarly, at 1 day post fertilization, *serta*<sup>-/-</sup> fish exhibit smaller growth indicators (yolk sac area) compared to the other genotypes. These measurements at 1 dpf did not prove to be a major indicator for the body lengths variations in the 4 dpf fish. The results found in this study, particularly relative to food intake and growth rate indicators, provide insight into the complementary and distinct roles of the serotonin transporter paralogues in altering growth by regulating food intake and metabolism in unique areas.

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#### 47: Ca<sup>2+</sup> Mitochondrial Buffering and Impact on Mitochondrial Respiration in Goldfish Brain

Khaled Mkarem, Liam Eaton, Matthew Pamerter

Hypoxia disrupts mitochondrial Ca<sup>2+</sup> regulation, often leading to neuronal injury and cell death. However, some vertebrates, such as the goldfish (*Carassius auratus*), have evolved exceptional tolerance to low-oxygen conditions. This study characterized two mitochondrial parameters in the goldfish brain: Ca<sup>2+</sup> buffering capacity and the effects of Ca<sup>2+</sup> exposure on mitochondrial respiration. Mitochondrial Ca<sup>2+</sup> uptake was measured using fluorometric assays, revealing a mean buffering capacity of 40.2 ± 3.2 μM/mg/mL at 13°C. Mitochondrial respiration was assessed using a substrate-uncoupler-inhibitor titration (SUIT) protocol across four CaCl<sub>2</sub> concentrations (0–200 μM). Respiration remained stable or mildly increased during early Complex I-linked phases but declined significantly at later stages, particularly after ADP and succinate additions, indicating Ca<sup>2+</sup>-dependent impairment of oxidative phosphorylation. Complex IV respiration remained unaffected, and membrane integrity was preserved throughout. These results suggest goldfish mitochondria maintain structural integrity under Ca<sup>2+</sup> load, though functional suppression occurs at higher concentrations. Rather than drawing conclusions about Ca<sup>2+</sup> tolerance, this study establishes a physiological baseline for comparison to trout, a

hypoxia-sensitive species. Future comparative work will determine whether mitochondrial  $\text{Ca}^{2+}$  handling is a conserved feature of hypoxia tolerance or reflects species-specific adaptation in goldfish.

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#### 48: Directed Evolution in Action: Mutagenesis Strategy for Enhanced Plastic-Eating Enzymes

Said Abubakar and Eugene Fletcher

Our dependence on synthetic plastics has resulted in a buildup of plastic waste in our environment, which eventually fragments into micro- and nano-plastics. These particles eventually end up in our food and water, posing potential health risks, highlighting the urgent need to develop efficient processes to effectively hydrolyze plastic waste. The intrinsic chemical bonds in plastic polymers make biodegradation of plastics challenging. Interestingly, some microbial enzymes, particularly cutinases, have been reported to hydrolyze certain plastics, including polyethylene terephthalate (PET) and polyurethane, into their basic building blocks. However, these enzymes exhibit a low catalytic efficiency in plastic hydrolysis, and most of the studies have only focused on bacterial cutinases, emphasizing the need to develop and optimize new cutinases. In this study, we expressed and tested the activity of a novel fungal cutinase in a bacterial host. Using two rounds of error-prone PCR mutagenesis, we screened >200 mutant cutinases using the tributyrin and p-nitrophenyl butyrate (pNPB) assays and identified three mutants with enhanced activity compared to the original cutinase ( $p < 0.05$ ). Additionally, we selected three mutants with reduced enzymatic activity and three mutants that lost all activity due to mutagenesis. Sequencing these variants allowed us to identify key amino acid residues crucial for enhancing cutinase activity. This research highlights the importance of specific amino acid mutations in enhancing enzymatic activity. Understanding which residues drive activity brings us closer to bioengineering efficient enzymes as sustainable solutions to plastic pollution.

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#### 49: New Tricks for an Old Kit: Engineering the Metabolism of the Yeast *Torulaspora delbrueckii*

Angtai Shi, Eugene Fletcher

Non-conventional yeasts have received considerable attention in recent years as microbial platforms for industrial applications, as metabolic differences from *Saccharomyces cerevisiae* may be leveraged to improve the production of industrially relevant

biochemicals and bioproducts such as organic acids. *Torulaspora delbrueckii* is a non-conventional yeast notable for its biotechnology applications in wine-, bread-, and beer-making, where, for instance, its resistance to freeze-thaw cycles and osmotic stress are valuable in producing frozen dough, while its secondary metabolite profile improves the aroma of wines. However, while *S. cerevisiae* is exceptionally well-studied, *T. delbrueckii* has not been well-characterized, and molecular tools for manipulating *T. delbrueckii* are underdeveloped.

This work therefore aimed to characterize the growth of a wild *T. delbrueckii* isolate and develop a CRISPR toolkit to facilitate engineering this non-conventional yeast. To do this, the strain's tolerance to an organic acid and its growth on fermentable and non-fermentable carbon was assayed in liquid cultures. Compared to the model yeast *S. cerevisiae*, the *T. delbrueckii* isolate was less tolerant to propionic acid. *T. delbrueckii* grew on glucose and fructose, but not on galactose, with an optimal temperature of 30°C. To develop the *T. delbrueckii* CRISPR toolkit, genomic integration sites for DNA insertion were carefully chosen and validated. A corresponding guide RNA for each integration site was assembled into a Cas9-containing plasmid. By assessing its growth performance and increasing the ease of manipulating its genome, this work facilitates further investigation into the metabolism and fermentation of *T. delbrueckii* and its suitability for industrial biotechnology applications.

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## 50: Milking the Potential of Yeast: Engineering Yeast to Combat the Dairy Waste Problem

Yusuf Moussa, Dr. Eugene Fletcher

For every litre of milk processed, ten litres of waste is produced. If left untreated, dairy waste can have significant impacts on the environment because of its high concentration of organic matter. It mainly consists of high levels of lactose, nitrogen and other ions. The treatment of dairy waste produced from industries can be costly, requiring innovative approaches to valorize the waste by yeast fermentation. However, the industrial yeast strain, *Saccharomyces cerevisiae*, is unable to consume lactose in dairy waste due to the absence of the permease and beta-galactosidase genes. In this study, *S. cerevisiae* was engineered to efficiently consume lactose. Using the CRISPR/Cas9 technology, we inserted a non-native lactose permease gene into three genomic loci to enable the yeast to take up lactose. Next, we used Error-prone PCR mutagenesis to obtain a mutant library of beta-galactosidase variants which we screened for enhanced enzyme activity and lactose consumption in yeast. These results will inform new strategies required to develop an

industrial yeast strain for the conversion of dairy waste into biofuels and valuable bioproducts.

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## 51: CAN YEAST SURVIVE A TOXIC DIET OF PLASTIC COMPOUNDS?

Hannah Doyle\*, Sarah Takallou, and Eugene Fletcher

Our world faces a plastic crisis, with plastics polluting every corner of the planet. Current recycling methods involve hydrolyzing plastics into their basic building block then repolymerizing them into new plastics. In the long term, this is not a sustainable method to remove all plastic waste found across our environment. Therefore, the need to upcycle plastic waste by converting compounds obtained from plastic hydrolysis, including terephthalic acid (from PET plastics) and benzoic acid (from polystyrene plastics), into valuable chemicals by microbial fermentation offers a plausible approach. Yeast, particularly *S. cerevisiae*, remains an industrial workhorse used to ferment non-conventional feedstocks into ethanol, making it an important microorganism that could potentially be engineered to convert terephthalic acid and benzoic acid into bioethanol used as a biofuel. However, these plastic compounds are toxic to yeast and inhibit growth and fermentation. Thus, in this thesis project, we performed a chemogenomic screen of three yeast mutant libraries, previously generated from long-term laboratory evolution experiments, for later growth on solid media containing toxic amounts of terephthalic acid, benzoic acid, a mixture of both, and on NaCl (obtained from alkaline hydrolysis of PET plastics). The objective of this mid-throughput screening was to identify yeast mutants that show cross-resistance to the compounds tested which will be followed by whole genome sequencing to identify any key driver mutations responsible for enhanced tolerance to the toxic compounds. Ultimately, the project will steer microbial engineering strategies to develop industrial yeast strains to successfully upcycle homogenous plastics and mixed plastics.

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## 52: Long Noncoding RNA Diversity in AMF Heterokaryons and Homokaryons

Fiona Hutchinson, Jordana Inácio Nascimento Oliveira, Ken Murithi Mugambi, Nicolas Corradi

Arbuscular Mycorrhizal Fungi (AMF) form symbiotic relationships with most plant species, facilitating nutrient exchange. In *Rhizophagus irregularis*, the model AMF species, chromosome-level assembly has revealed significant variation in protein-coding genes, suggesting similar diversity in long non-coding RNAs (lncRNAs). This study aimed to

identify and classify lncRNAs across nine *R. irregularis* strains to improve understanding of AMF genomic regulation. Using CPAT, trained on *Candida* transcripts and refined for *R. irregularis*, we predicted coding potential of transcripts acquired through PacBio sequencing. BLASTn was used to confirm similarities with other fungi and to assess sequence similarities between other species using the RNA families database RNACentral. On average we found 870 lncRNA genes for each strain, with an average of 1335 transcript isoforms. Additionally, we found that around 72% of lncRNA were shared across all strains, whereas 1.2% are strain specific. Around 64% of lncRNA across the 9 strains showed some similarity with known lncRNA from fungi and other organisms. Our findings suggest that lncRNAs may play a role in strain-specific symbiotic interactions, providing insight into AMF gene regulation. This research enhances our understanding of lncRNAs in AMF and their potential role in gene expression, with implications for agriculture and ecosystem management.

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### 53: Evolution of the lac operon in the Enterobacteriaceae Family in Response to Lactose and Glucose

Nusrat Tazkia and Dr. Xuhua Xia

The lac operon in *Escherichia coli* has been extensively studied for its role in lactose metabolism, yet the function of lacA, encoding  $\beta$ -galactosidase transacetylase, remains less understood. This study investigates the evolutionary significance of lacA deletion in the Enterobacteriaceae family and its potential role in pathogenicity. We analyzed genomic sequences from 92 species of this family using DAMBE software and reconstructed their phylogenetic relationships. Bacterial species were categorized based on their environmental exposure to glucose and lactose to assess correlations with lacA conservation. Our results suggest that lacA deletion is more frequent in bacterial lineages with limited lactose exposure, supporting the hypothesis that lacA plays a role in lactose metabolism. Phylogenetic analysis indicates that the loss of lacA is often associated with bacteria that are intracellular pathogens, implying different evolutionary pressures on lacA compared to other lac operon genes. Additionally, we propose that lacA gene deletion may be influenced by the environmental conditions the bacteria are exposed to, such as the availability of glucose or lactose, which could shape the evolutionary trajectory of these species. These results offer new insights into the adaptive significance of lacA loss and its potential contribution to bacterial evolution, particularly regarding pathogenicity and environmental adaptation.

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54: Comparaison des effets des délétions and1 (1214pdb et 669pdb) sur le développement des nageoires du poisson zèbre.

Fella Gueridi, Paulina Hanzelova, Marie-Andrée Akimenko

Chez les poissons téléostéens, les actinotriches sont des fibres rigides essentielles à l'organisation du repli épidermique au cours du développement des nageoires, jouant un rôle structural et guidant la migration des cellules mésenchymateuses, dont certaines se différencient en ostéoblastes. Codées par les gènes actinodin (and1 à and4), ces fibres se restreignent aux extrémités distales des rayons osseux chez l'adulte. Des études antérieures ont démontré que les doubles mutants pour and1 (669 pdb) et and2 (269 pdb) perdent complètement leurs actinotriches, entraînant de graves malformations des nageoires. Dans ce projet, nous avons étudié des poissons mutants pour and1 seulement portant une délétion étendue de 1214 pdb, recouvrant celle des mutants and 1 (669 pdb), mais incluant une plus grande portion du second intron. Contrairement aux mutants simples and 1 (669 pdb), qui présentent un phénotype de type sauvage, les mutants and 1 (1214 pdb) montrent des défauts marqués au niveau des rayons des nageoires caudales (bifurcations anormales, rayons osseux atteignant l'extrémité du tissu). Ces défauts ne sont pas uniformes parmi les individus, certains présentant des nageoires très altérées, d'autres avec une morphologie normale. Les actinotriches sont visibles tant dans les nageoires intactes que dans les régénérats, même si leur densité reste à quantifier. Ces observations soulèvent la possibilité que la région intronique supprimée soit impliquée dans la formation ou la structure des actinotriches, ou qu'elle influence le mécanisme de compensation entre gènes paralogues. Des analyses complémentaires seront nécessaires pour mieux cerner ces effets potentiels.

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55: The Influence of Ecdysone Signalling on Caste Development in *Camponotus floridanus*

Julia Singer, Olivia MacMillan, Rajendhran Rajakumar

Ants exhibit much phenotypic plasticity, dividing their colonies into reproductive queen castes and non-reproductive worker castes, including smaller workers and larger soldiers (Chittka et al., 2012). Steroid hormones including ecdysone have been known to regulate castes in insects by regulating the timing of molting and metamorphosis (Kapali et al., 2022). The addition of ecdysone treatments during development of the ant species *Myrmica rubra* has caused premature metamorphosis resulting in abnormal phenotypes not belonging to a naturally observed caste (Brian, 1974). However, the effects of ecdysone on caste development have not been thoroughly investigated yet in *Camponotus floridanus*. The goal of our project is to investigate the role of ecdysone on larval

development and ant sizes for caste development in *Camponotus floridanus*. We hypothesize that ecdysone treatments will cause premature pupation, faster eclosion rates and smaller worker ant measurements in *Camponotus floridanus*. 100ng/uL of 20-hydroxyecdysone (20E) as well as ethanol and PBS control groups were microinjected into bipotent larva. Developmental progress was recorded daily until the ant emerged, where it was placed in ethanol for preservation once emerged. The ants were dissected and measurements of the left hind tibia, left scape and head were taken. Initial results indicate no significant differences between 20E pupation and eclosion rates compared to our control groups, however additional trials and ant measurements are currently in progress. From our results, we intend to further our understanding of hormonal developmental timing, pest control and disease management.

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56: Histone modifiers at the crossroads between environmental variation and hormones during fire ant development

Kami Fabien, Navid Bahramfarid, Dr. Rajendhran Rajakumar

Epigenetics is an emerging field that explores heritable changes in gene expression without altering the initial DNA sequence. Epigenetic mechanisms, namely histone (de)methylation, have been shown to influence growth in the fruit fly model organism *Drosophila melanogaster*. Specifically, histone demethylase UTX/Y is important for both embryonic and adult-stage development. In general, arthropod development is facilitated with the metamorphosis-related hormone 20-hydroxyecdysone (20E). Environmental factors, namely nutrition, have been shown to affect 20E with starvation reducing and delaying 20E production. Similarly, in *Solenopsis invicta*, an emerging ant model species sensitive to environmental and hormonal variations, 20E regulates growth and metamorphosis. However, the role of 20E and starvation on histone (de)methylation in *S. invicta* remains unknown. Using larval starvation, 20E treatment and qPCR techniques, we analyze the relationship between 20E, induced starvation, and their effects on UTX expression in *S. invicta*. Contrary to predictions, neither starvation nor 20E demonstrate any significant effects on UTX expression in *S. invicta*. Notably, 20E injections led to larger pupal sizing, as compared to ethanol controls. Our results highlight the complex interactions of environmental factors and epigenetic modifications. This research opens opportunities for further investigation into the relationship between the environment and epigenetic modifications in *S. invicta* development.

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## 57: Investigating the Activation of XBP1 by Splicing Inhibitors: A Study Using Reporter Cell Lines and Chemical Inhibitors.

Bruce McKay, Farha Gooma

Numerous cellular processes, including protein synthesis, folding, and quality control, depend on the endoplasmic reticulum (ER). Unfolded proteins build up when ER homeostasis is disturbed, resulting in the Unfolded Protein Response (UPR). Three primary pathways mediate this response: ATF6, PERK-ATF4, and IRE1 $\alpha$ -XBP1. Protein folding and degradation genes are regulated by the highly conserved IRE1 $\alpha$ -XBP1 pathway. Although the underlying mechanisms are still unknown, unpublished work in our laboratory has indicated that splicing inhibitors like Isoginkgetin (IGG) and Pladienolide B (PB) can activate XBP1. The purpose of this work is to examine how these inhibitors activate XBP1. We sought to evaluate the impact of splicing inhibitors using flow cytometry on XBP-1 regulation using genetically modified HCT116 colon cancer cell lines that express fluorescent (GFP) reporters that model XBP1 regulation. We found that the IRE1 $\alpha$  inhibitor prevented the IGG induced expression of the heterologous XBP1-GFP reporter clearly implicating the UPR in this response. Ongoing efforts are focused on determining if the IRE1 $\alpha$  inhibitor also inhibits the induction of endogenous XBP1 mRNA and protein. This work will provide critical insight into the effects of splicing stress on human cells and may inform the possible therapeutic applications in conditions like cancer and neurological disorders.

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## 58: Investigating the spatiotemporal and functional role of Sex-lethal in ants

Malvina Isaak, Erica Vong, Sarah Heffernan, Dr. Rajendhran Rajakumar

Sexual dimorphism in ants extends beyond reproduction, shaping morphology, behavior, and caste differentiation. Despite its significance, the genetic mechanisms underlying early sex determination in ants remain poorly understood. In *Drosophila melanogaster*, the RNA-binding protein Sex-lethal (sxl) is a key regulator of female development, initiating sex-specific splicing during embryogenesis. While sxl has been well studied in flies, its expression dynamics in ants have not been explored. Here, we investigate sxl expression in *Camponotus floridanus* embryos using in situ hybridization. We observed strong, uniform expression of sxl in females, with little to no detection in males, closely resembling the expression pattern described in *D. melanogaster*. These findings suggest that sxl plays a conserved role in early sexual differentiation in ants. To further examine its function, we are currently conducting RNA interference (RNAi) experiments to assess its developmental



impact. Together, these approaches will provide both spatial and functional insight into how conserved sex-determination genes shape early ant development.

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#### 59: Investigation of TRIM9 as a novel mGluR5 interacting protein

Darius Aliahmad

Metabotropic glutamate receptor 5 (mGluR5) has previously been shown to play a role in pathological amyloid beta (A $\beta$ ) signalling in Alzheimer's disease. Previous experiments revealed that mGluR5 can scaffold A $\beta$  and PrPc in male but not female mouse cortex. The mechanisms underlying this sex-specific A $\beta$ -mGluR5 interaction are largely unknown. Our lab has recently identified tripartite motif containing 9 (TRIM9), an E3 ubiquitin ligase, as a novel mGluR5 interacting protein. Preliminary data has shown enriched TRIM9 co-immunoprecipitation with mGluR5 in male mice, and this interaction has also been highly reproducible in HEK293T cells following treatment with the proteasomal inhibitor MG-132. The purpose of this thesis was to examine the interaction between TRIM9 and mGluR5 as well as TRIM9-dependent ubiquitination of mGluR5. Immunoprecipitation and western blot were used to examine the interaction of mGluR5 with TRIM9 deletion constructs to identify key domains. Furthermore, *in vitro* ubiquitination assays will be conducted to quantify mGluR5 ubiquitination in the presence and absence of wild-type and mutant TRIM9. Understanding TRIM9's function in regulating mGluR5 could provide valuable insights into the pathogenesis of neurodegeneration associated with AD.

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#### 60: An optimized protocol for the Agrobacterium-mediated transformation of *Chlamydomonas priscui*

Ella McBoyle, Marina Cvetkovska

Psychrophilic green algae are foundational species that form the base of all cold-water food chains, but their polar habitats are rapidly warming. *Chlamydomonas priscui* is a green alga obligately adapted to life in extreme cold, in other words, a psychrophile. Although it is an emerging model for psychrophily, and a relative of the model *Chlamydomonas reinhardtii*, *C. priscui* has not been genetically transformed by any method. Agrobacterium-mediated transformation is proposed, rather than electroporation or bead beating, to penetrate the thick cell wall *C. priscui* requires to survive extreme cold. Agrobacteria are bacterial pathogens that insert a portion of DNA from a tumor-inducing plasmid into target plant cells. Non-pathogenic strains of Agrobacterium are used in *Chlamydomonas* transformation. Before attempting transformation, Agrobacterium was

subjected to temperature and salinity stress to reconcile algal and bacterial growth conditions. Primers were designed and tested. Selection antibiotic paromomycin was confirmed to kill untransformed *C. priscui*, and Agrobacterial removal antibiotics cefotaxime and carbenicillin were confirmed to have no effect on *C. priscui*. Plasmid pPTN1133 was successfully electroporated into *Agrobacterium*. An optimized protocol for *C. priscui* transformation expands research into functional genomics, making this alga an excellent model for cold adaptations and for primary production at Earth's poles.

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61: Analysis of hyphal biovolume across strains of *Rhizophagus irregularis* grown with *Sorghum x drummondii*

Whitehead, Dean. Ferguson, Robbie. Corradi, Nicolas.

Arbuscular Mycorrhizal Fungi (AMF) are a group of obligate plant root symbionts. Extraradical hyphae and spores enable nutrient uptake for trade with its host plant, and dispersal/reproduction respectively. The nuclear identity of *Rhizophagus irregularis* strains (homokaryotic or heterokaryotic) has been shown to affect hyphal growth rates in vitro. This study seeks to determine the effect of AMF genotype on hyphal biovolume in vivo. Soil samples from pots of *Sorghum x drummondii* (a plant hosting one of four homokaryotic or four heterokaryotic strains) were collected for hyphal and spore extraction, followed by biovolume and spore count estimation under microscope. I hypothesized that hyphal biovolume will differ between homokaryotic and heterokaryotic strains, as reported in previous in vitro studies. Established methods of extracting and estimating soil hyphal biovolume were collected from the literature and assessed for precision and efficiency. Data collection is still underway due to time requirements of plant maturation and extraction procedure assessment. This research expands on previous work by assessing strain identity as a driver of hyphal growth among AMF strains in a realistic soil environment. Next steps could include biomass estimation, or quantitative comparisons of hyphal extraction methods across soil types.

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62: COLLISION COURSE: HOW WELL CAN WE PREDICT BUILDING COLLISION RISK FOR BIRDS?

Joshua S. Cadieux, Stasha Lysyk, Krista L. De Groot, Barbara Frei, Rachel T. Buxton & Roslyn Dakin

Bird populations in North America are experiencing rapid declines across a wide range of species. Collisions with buildings remain one of the leading causes of mortality. Effective

mitigation requires a clear understanding of which buildings pose the greatest risk, yet it remains uncertain how well this can be predicted based on known risk factors. In this study, we aimed to assess whether collision risk is consistent and predictable across a diverse set of urban building facades, varying in key risk factors such as glass coverage, the presence of collision-preventative treatments, and the extent of surrounding vegetation. To quantify collision risk, we conducted over 8,700 standardized surveys at 216 building facades during spring and fall migration in 2024 and collected data on facade-level features at each of the surveyed buildings. We found that certain facades are consistently associated with higher casualties than others, and that more than 50% of the casualties were concentrated at a small number of facades (8%). Additionally, using generalized linear regression models, we found that simple facade level features could explain some of the variation in collision risk but could not effectively identify the facades responsible for the most collisions in the Ottawa-based sample. Our results suggest that while simple facade-level features are statistically significant predictors of collision risk, they may be insufficient for pinpointing the highest-risk buildings. Accordingly, in the absence of more predictive feature-based models, collision data may be needed to identify the locations that pose the greatest building collision risks to migrating birds.

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63: Examining the impact of wildfire on amphibian microhabitat composition around breeding ponds in Waterton Lakes National Park

Ashley Smith, Tristan Skretting, Julie Lee-Yaw

Wildfires have the potential to dramatically alter microhabitats. Amphibians are sensitive to microhabitat conditions, and minor modifications to microhabitats may have large impacts on amphibian populations. In 2017, the Kenow Wildfire burned roughly half of the amphibian populations in Waterton Lakes National Park (WLNP). In this study, we assessed changes in microhabitat structure around breeding ponds using data collected before and after the wildfire at 21 sites spanning burnt and unburnt parts of the park. At each site, we collected data on 14 microhabitat features at three different distances (0 m, 3 m, 10 m) away from pond edges. Non-metric multidimensional scaling (NMDS), permutational multivariate analysis of variance (PERMANOVA), and indicator analyses were used to visualize and statistically test for an effect of the wildfire on microhabitat composition at each distance class. We found no significant effect at 0 m and 3 m away from the pond edge. However, there was a significant effect of the wildfire at the 10 m distance class, driven by changes from greater moss and lichen cover before the fire to more bare soil after the fire in the burn zone. These results inform conservation efforts for amphibian

populations further from ponds that may be more at-risk of changing microhabitat conditions following a wildfire.

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#### 64: Evaluating the Impact of Academic Integrity Modules on Student Perceptions and Misconduct at the University of Ottawa

Ayai Ofor, Matthieu Delcourt, Elaine Beaulieu

The COVID-19 pandemic affected academic institutions globally by causing them to rapidly transition to remote learning to prioritize the safety of students and staff. The main challenge that instructors and university officials have faced is maintaining good academic integrity practice from online learning and through in-person learning that followed. To address academic misconduct, the University of Ottawa implemented academic integrity modules, yet their effectiveness seems to remain uncertain. This study examines how self-reported misconduct and perceptions of integrity differ among students from 2021 (fully online learning) and 2023 (in-person learning). Survey data from University of Ottawa Students in 2021 and 2023 were analyzed to compare rates of self-reported misconduct and perceptions of integrity. The 2023 group was further divided into students who completed the academic integrity modules and those who did not. Our findings showed that self-reported academic misconduct decreased from 2021 to 2023, although the differences between module-completing and non-completing students were minimal. These findings highlight the need to re-evaluate the effectiveness of the academic integrity modules and explore alternative approaches to promote academic integrity in the student population.

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#### 65: THE EXPLORATION OF METHANOTROPHIC BACTERIA: USING PHOSPHOLIPID FATTY ACID BIOMARKERS FROM CANADIAN OIL SANDS FACILITIES

N. Sandhu<sup>1\*</sup>, G. Josan<sup>2</sup>, G. Slater<sup>2</sup>, A.L. Brady<sup>1</sup>, P. Dunfield<sup>3</sup>

The Athabasca Oil Sands Region (AOSR) is a crucial source of Canadian oil reserves. During the oil extraction process, oil sands facilities produce tailings, which are comprised of water, sand, fine silts, clay, residual bitumen, lighter hydrocarbons, and inorganic matter. The organic matter present in tailings may be converted to methane and further released into the atmosphere. Microorganisms can cycle methane within natural and engineered environments – with methane release reflecting the balance between methanogenesis (microbial methane production) and methanotrophy (microbial methane consumption). However, the balance of these processes in tailings facilities, including the abundance and

distribution of methanotrophic bacteria, is not well-characterized. This study investigated microbial biomass and the presence of bacteria capable of methane oxidation (methanotrophy) using microbial phospholipid fatty acids (PLFA). Ester-linked bacterial PLFA provides a snapshot of the amount of biomass and the diversity of the active community. Water and tailings samples representing a depth profile were collected from an oil tailings facility in Alberta. The frozen samples were thawed and filtered, and PLFA were extracted using organic solvents followed by identification and quantification using gas chromatography-mass spectrometry. PLFA were dominated by mono-unsaturated fatty acids (> 50% of total PLFA); in particular, 16:1 $\Delta$ 9 and 18:1 $\Delta$ 9 were present in the highest abundance and have historically been associated with methanotrophic bacteria. Multi-proxy characterization of the distribution of methanotrophic bacteria within tailings facilities will improve our understanding of methane cycling within these environments. Ultimately, understanding methane cycling could prove useful when mitigating emissions within these environments.

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## 66: IDENTIFICATION OF CORRELATED SOYBEAN GENES WITH LIPID COMPOSITION IN DIFFERENT ENVIRONMENTS THROUGH DIFFERENTIAL GENE EXPRESSION ANALYSIS

Deniz Pourazar, Bahram Samanfar, Ashkan Golshani

Soybean (*Glycine max*) is a widely grown legume species and is considered an affordable source of protein and vegetable oil for human consumption. Variations have been observed in the seed composition in western and eastern regions, including a higher rate of lipid content in western regions. In this study, ten soybean lines were grown in three western locations, Brandon, Morden, and Saskatoon, alongside with an eastern location in Ottawa as control during four consecutive years from 2018 to 2021. This study is using RNA sequencing and differentially expressed genes (DGE) to identify genes in soybean that are influenced by environmental factors and have effects on oil content. Two representative pathways were chosen for further analysis (consistent over-expression of genes within multiple years and locations). Primarily, the first reaction in fatty acid elongation in the endoplasmic reticulum pathway, involving 3-ketoacyl-CoA synthase, was upregulated in western regions. A number of genes on chromosomes 5, 8, 10, 12, 13, 15, 17, and 20, contributed to upregulation of 3-ketoacyl-CoA synthase 6, 11, 12, and 20 enzymes. Secondly, upregulation of genes from Chromosomes 7, 8, 13, and 15 contributed to linoleic acid metabolism increasing LOX1-5, and LOX2S lipoxygenase enzyme activity. Identifying genes involved in oil biosynthesis, will shed light into this complicated and important pathway; alternatively, diagnostic marker (i.e. allele-specific markers) will

be developed assisting breeding programs (marker assisted selection) of oil quality and quantity

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#### 67: Using Specific Primers in PCR to Discern White Footed Mice (*Peromyscus leucopus*) From Deer Mice (*Peromyscus maniculatus*)

Celine Larose, Mehra Balsara, Luigi Richardson, Dr. Albrecht Schulte-Hostedde, Dr. Catherine Cullingham

Deer and white-footed mice have been known to carry illnesses hazardous to human health and other wildlife. Lyme disease and hantavirus pulmonary syndrome pose a threat to human health and have a direct relationship with *Peromyscus* mice. Warfarin is a common rodenticide used to control these species and reduce disease risk, however genetic resistance to warfarin can occur. The purpose of the study is to use PCR to discriminate white-footed mice (*Peromyscus leucopus*) from deer mice (*Peromyscus maniculatus*) for future assessment of mice that have warfarin-resistance. We successfully extracted DNA and tested universal primers on our samples observing white-footed mice at ~159bp and deer mice at ~220bp. 52OC was the optimal temperature for primer annealing in this study. Our next step will be to discriminate between the two species for future warfarin-resistance analysis. Through the identification of deer mice and white-footed mice, researchers can optimize current rodent control strategies to ensure proper disease control in the future.

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#### 68: BIOMECHANICAL ANALYSIS OF FORCE PRODUCTION AND SKATING EFFICIENCY IN FEMALE VARSITY HOCKEY PLAYERS

Veronica Langdon, Nick Westcott, Jeff Dawson, Iain McKinnell

In high-demand sports like ice hockey, optimizing biomechanics and physical performance is crucial for on-ice success. Female athletes have unique anatomical, biomechanical, and physiological differences compared to males, however, the majority of research in this field has focused on male athletes, leaving a gap in understanding the specific needs of female hockey players. This study investigates the relationship between anthropometric factors, force production capabilities, and skating performance in female varsity hockey players. Using countermovement jump (CMJ) performance as a key indicator of lower-body power, we examine its relationship with on-ice speed and efficiency. Given the structural and neuromuscular differences between male and female athletes, this research aims to provide gender-specific insights for improving training strategies. By integrating

biomechanical assessments with anthropometric data, our findings will contribute to developing tailored conditioning programs that enhance performance for female hockey players.

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#### 69: Depressive Symptom Heterogeneity and Inflammation: The Moderating Role of Early-Life Trauma

Aurora Tracy (1), Frances Sherratt (1), Ayeila Daneshmend (1), Ally Villeneuve (1), Dana Jarkas (1), May Crober (1), Noah Bennell (1), Kate Lui (1), Mkeila Sowa (1), Bessan Amer (1), Chelsea Montgomery (1), Robyn McQuaid (1,2)

Despite the high prevalence rates of depression, particularly among young adults, current treatments remain suboptimal, partly owing to the complex and heterogeneous nature of the disorder. While some individuals with depression display elevated inflammation, this is not consistently reported and may depend on the specific symptoms expressed. Moreover, individuals exposed to traumatic events may be more vulnerable to inflammation and mood disorders. In the current study young adults (N=210) completed baseline questionnaires assessing adverse early life experiences and depressive symptoms, provided blood samples to measure C-reactive protein (CRP) levels, and were assigned to either a control (n=106) or a stressor (n=104) task. CRP levels were positively correlated with both typical ( $p=0.02$ ) and atypical depression ( $p=0.03$ ), as well as total trauma ( $p=0.02$ ), general trauma ( $p=0.012$ ), and physical abuse ( $p=0.02$ ) within the stress group. Notably, upon assessing specific symptoms of depression, somatic features including sleep and fatigue correlated with higher CRP levels. Additionally, the relationship between CRP levels and depressive symptoms was moderated by experiences of sexual abuse ( $p=0.033$ ). These findings suggest that the CRP-depression link may be driven by somatic features of depression, and that exposure to early life trauma may play an important role in modulating this relation. Understanding the relationship between adverse early life experiences, inflammation, and specific depressive symptoms can help inform an integrated approach that combines biological, psychological, and social factors to improve both prevention and treatment outcomes for depression.

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#### 70: Assessing myelin integrity and axonal conduction through compound action potentials.

Lina Dulgher, J r mie Lefebvre, Juliet K. Knowles.

Maladaptive myelination, which occurs from aberrant neuronal activity, contributes to epilepsy progression and increased seizure burden in the corpus callosum (CC). The

presence of a relationship between conduction delays and myelination has been asserted and has shown to underlie epilepsy progression. Therefore, this study aims to elucidate the mechanism by which aberrant myelination promotes seizure progression. By leveraging the relationship between conduction velocities and conduction delays, a computational model of a compound action potential (CAP) was developed to simulate and compare normal and hypersynchronous activity, the latter being characteristic in hypermyelinated conditions. The model was validated by comparing its CAP waveforms parameters to experimental data. The findings indicate that reduced conduction delays result in an earlier and more synchronized response, which suggests that increased conduction velocities enhance hypersynchronous activity and contribute to seizure progression. This highlights the contribution of conduction velocity in maladaptive myelination, and parallelly demonstrates the potential of this computational model for investigating network behaviour in epilepsy and other neurological diseases.

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71: Investigating the effects of silencing spinal dI3 interneurons on mouse locomotor behaviour

Christina Tziata, Tuan Bui

Locomotion, crucial for survival, is driven by complex interactions between neuronal circuits, including the central pattern generators (CPGs) in the spinal cord, as well as cutaneous afferents, and motoneurons. While CPGs generate basic rhythmic movements, sensory feedback from the environment plays a crucial role in modulating and adapting motor patterns. dI3 interneurons (INs), part of the spinal circuit, are implicated in integrating sensory inputs from proprioception and cutaneous afferents, and in mediating reflex pathways. This study investigates the role of dI3 INs in modulating locomotor behaviour in mice. Chemogenetic silencing is employed through intraspinal injections of an adeno-associated virus, resulting in the expression of the inhibitory DREADD hM4Di receptor in dI3 INs. hM4Di is activated by injection of the inert ligand JHU37160. The mice are trained to run on a treadmill with or without JHU37160 application; their movements are analysed by DeepLabCut, a machine-learning software. Preliminary data suggests that dI3 INs influence hindlimb movement coordination, but do not alter fundamental locomotor rhythms generated by CPGs. This research provides insights into the sensory-motor integration mechanisms of spinal circuits and their influence on locomotor performance, offering a deeper understanding of how spinal interneurons modulate adaptive motor behaviour.



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## 72: Neural Stem Cell-Mediated Therapy for Glioblastoma

Rekha Govindasamy Ravichandran, Margarita Liu, Ian Lorimer

Despite decades of research, glioblastoma remains incurable with patients being left with an average life expectancy of just 15 months post-diagnosis. It has proven challenging to develop therapies due to the heterogeneity of this cancer and current limitations in the effective delivery of therapeutics within the brain. Engineered neural stem cells (NSCs) offer a promising therapeutic avenue as they are naturally present in the brain and exhibit high motility. Previous studies have demonstrated that NSCs can migrate toward glioblastoma tumours and be engineered to effectively exhibit anti-cancer properties. This study investigated the differentiation of peripheral blood-derived neural stem cells (PBiNSCs) transduced with either GFP alone (WT/NSCs) or GFP and the therapeutic protein lclPTENL (lclPTENL/NSCs). These two cell lines were co-injected with glioblastoma cells (PriGO8A) into the left striata of Fox Chase SCID Beige female mice. One month post-injection, immunohistochemistry staining, immunofluorescence microscopy and colocalization quantitation analysis were performed to reveal greater differentiation in the WT/NSCs compared to lclPTENL/NSCs. These results suggest possible crosstalk between PriGO8A cells and NSCs when PTEN is added or locally restored. Understanding the differential pathways activated in WT/NSCs and lclPTENL/NSCs could inform the development of future NSC-mediated therapeutics for glioblastoma."

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## 73: Investigating the Influences of Green Spaces on Outdoor Learning Implementation Across Canada

Kira Tromp, Tanya Halsall

Outdoor learning (OL) supports children's overall development by promoting mental health, well-being, and enriching their learning experiences with outdoor green spaces. The goal of this paper was to explore barriers and facilitators related to policy designed to support the integration of outdoor learning into Canadian schools, emphasizing its adaptability to both physical outdoor settings and green spaces. We conducted 19 virtual interviews with policy makers, vice principals, and principals, across seven provinces and one territory (Nunavut). A thematic analysis was conducted using NVivo software to code interviews into main themes. This resulted in the identification of four themes related to green space in schools: 1) Current green space availability and accessibility; 2) Strategies to maximize the utility of existing green spaces; 3) Partnerships to facilitate access to green

space; and 4) Building community. The factors shaping these themes were influenced in part by prior levels of OL implementation as well as social contexts related to green space usage. These contextual elements played a key role in how participants engaged with and perceived OL in outdoor environments. These findings highlight effective policy examples that have been applied to enhance outdoor learning as well as future directions to expand policy.

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#### 74: Effects of potassium M-current modulators on swimming behaviour of larval zebrafish Pengdwende

Larissa Carole Ouedraogo, Stephanie Gaudreau, Tuan Bui

Spinal circuits rely on ion channels to generate and regulate rhythmic locomotor activity by shaping neuronal excitability. In zebrafish motoneurons, the M-current (IM) a subthreshold potassium current has been proposed to stabilize firing and influence early motor behavior. IM is also subject to modulation by neuromodulators such as serotonin, dopamine, and acetylcholine, but the functional impact of this modulation during development remains unclear. This study examined how pharmacological and neuromodulatory manipulation of IM affects spontaneous swimming in zebrafish larvae at 3, 4, and 5 days post-fertilization (dpf). Larvae were exposed to M-current modulators (XE-991, ICA-069673) and neuromodulators (serotonin, dopamine, muscarine, etc.), and their swim behavior was tracked using an automated video analysis system (ZebraBox). Swim duration and distance were analyzed separately for slow and fast swim components. Contrary to initial predictions, most behavioral effects were observed at 4 and 5 dpf. Enhancing IM with ICA-069673 increased swim behavior at 3 dpf but reduced fast-swim activity at 5 dpf. Inhibiting IM with XE-991 selectively increased fast-swim behavior at 5 dpf. Neuromodulators showed stage-specific effects: serotonin and TCB-2 (5-HT<sub>2A</sub> receptor agonist) decreased fast swim duration and distance at 4 dpf, while muscarine increased fast-swim duration at 5 dpf. 8-OH-DPAT (5-HT<sub>1A</sub> receptor agonist), dopamine and SKF-38393 (dopamine D1 receptor agonist) produced no consistent behavioral changes. These findings suggest that the developing locomotor system becomes increasingly sensitive to both intrinsic and extrinsic modulation over time and highlight a functional window in which IM and neuromodulators interact to tune motor behavior.

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## 75: Native Grassland Restoration in Southern Ontario: Assessing Vegetation Composition and Changes Post-Seeding

Tessa Wynn, Heather Kharouba

Grasslands in Ontario are critical for biodiversity but are highly threatened by agricultural expansion and urban development. This study investigates vegetation composition and diversity in restored grasslands, focusing on site and plant factors influencing differences between seeded and established plants. Vegetation surveys were conducted at 14 Nature Conservancy of Canada (NCC) sites restored from agricultural land. Presence/absence data and stem density counts from quadrats were assessed and compared to initial seeding records to evaluate establishment success and spontaneous vegetation establishment. Preliminary results indicate that biodiversity generally decreased post-seeding. Higher seeding densities were positively correlated with observed plant density, while increased tree planting density were negatively correlated with plant density. Models suggest that greater seeded species richness led to higher persistence, as measured by the Jaccard Index. Introduced species and genera showed higher appearance rates than non-seeded native plants. These preliminary findings highlight how specific restoration strategies influence biodiversity outcomes in grassland restoration and provide insights into vegetation establishment patterns in Ontario's grasslands. Understanding these dynamics can inform future restoration efforts to enhance long-term grassland biodiversity and stability

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