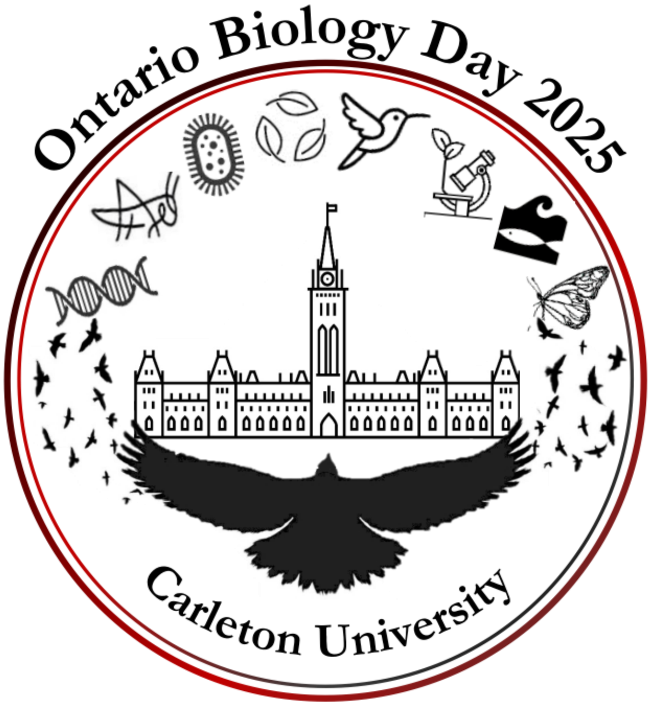
Ontario Biology Day

37th Annual Conference

Oral Presentation Abstracts



Carleton University

March 22-23, 2025

Carleton
University

Talks – By Presenter Surname

#	First	Last	University
27	Rosa	Adams	Brock University
21	Dorcas	Adewumi	Brock University
35	Sally	Adil	University of Ottawa
86	Ellis	Albrecht	Laurentian University
97	Yamamah	Al-Jumaili	Laurentian University
89	Owen	Allard	Laurentian University
101	Amna	Arif	Algoma University
37	Amber	Austin	McMaster University
57	Kyle	Banwell	University of Windsor
79	Hazel	Barr	Laurentian University
40	Christina	Bethune	Western University
26	Ishaan	Bhathal	McMaster University
107	Jaskarn	Bola	McMaster University
25	Grant	Booth	Brock University
93	Decklyn	Brodersen	Laurentian University
98	Lorriana	Broglio	Laurentian University
28	Robin	Brown	McMaster University
58	Madison	Bygrove	University of Windsor
15	Ummuhan	Canatan	Toronto Metropolitan University
2	Maira	Chaudhry	University of windsor
107	Taha	Cheema	McMaster University
59	Callia	Collard	University of Windsor
80	Shannon	Crockford	Laurentian University
48	Logan	Dammer	Wilfrid Laurier University
47	Kiersten	Deviller	Carleton University
34	Deandra	Dixon	Brock University
60	Michael	Douaihy	University of Windsor
61	Rana	Elkafarneh	University of Windsor
24	Nour	Elshobary	McMaster University
62	Natalie	Emerick	University of Windsor
8	Erlin	Espina	McMaster University
76	Akudo	Eze-Onuorah	McMaster University
63	Lama	Farah	University of Windsor
11	Andrea	Fernandes	Brock University
81	Joshua	Freimanis	Laurentian University
19	Harnoor	Gahir	Toronto Metropolitan University
103	Kristian	Gapp	Algoma University
96	Mackenzie	Hobbs	Laurentian University
108	Ricky	Hongri	McMaster University
7	Maha	Jahangir	University of Toronto
18	Kennedy	Jamieson	Western University
49	Avneet	Kahlon	Wilfrid Laurier University

64	Kristine	Kamensky	University of Windsor
16	Kevin	Kattathara	Toronto Metropolitan University
50	Ravleen	Kaur	Wilfrid Laurier University
51	Mustajab	Khalid	Wilfrid Laurier University
41	Ahmed	Khalil	McMaster University
65	Zain	Khan	University of Windsor
77	Kyle	Kim	McMaster University
14	Margaret	Kitney	Brock University
1	Gabby	Kohut	Western University
66	Renil	Kooplicat	University of Windsor
5	Basak	Korkmaz	Toronto Metropolitan University
13	Angel	Lainscek	Brock University
22	Emily	Laver-Shareski	Western University
78	Cameron	Lefebvre	Laurentian University
83	Sabrina	Lepage	Laurentian University
109	Sharifa	Lomiyev	Toronto Metropolitan University
104	Joel	Lucenay	Algoma University
43	Willamina	MacDonald	University of Ottawa
94	Emma	Mageau	Laurentian University
84	Josée	McDavid	Laurentian University
105	Austin	McGonegal	Algoma University
3	Alyssa	McInally	Brock University
92	Claire	McInroy	Laurentian University
67	Reese	Miller	University of Windsor
23	Kaylyn	Montoya	McMaster University
4	Niamh	Moreton	Western University
52	Spenser	Morouney	Wilfrid Laurier University
53	Maryem	Naimee	Wilfrid Laurier University
87	Naomi	Naokwegijig	Laurentian University
68	Tamjeed	Nawaz	University of Windsor
69	Genie	Nehruji	University of Windsor
29	Iman	Nemar	McMaster University
91	Olivia	Norman	Laurentian University
100	Ruth	Ogiri	Algoma University
85	Kate	Pappin	Laurentian University
17	Britt	Petersen	Trent University
30	Madelaine	Picard	Western University
102	Kumar	Pokharel	Algoma University
99	Diya	Prajapati	Algoma University
39	Maria	Proskurina	University of Toronto
31	Shahrzad	Rahmani	York University
46	Erin	Ricaloglu	McMaster University
10	Sofya	Rudovskaya	Toronto metropolitan university
70	Chris	Sankarlal	University of Windsor
44	Anneliese	Schall	McMaster University
20	Intesar	Shah	Toronto Metropolitan University

54	Najiba	Soudi	Wilfrid Laurier University
75	Holly	Stibbe	McMaster University
106	David	Storms	Algoma University
42	Guoria	Sun	University of Toronto - Mississauga
55	Shakiraa	Suntharalingam	Wilfrid Laurier University
9	Adam	Sutoski	McMaster University
33	Amiel	Terrenal	York University
6	George	Thomas	University of Toronto - Mississauga
45	Alyssa	Tinella	University of Guelph
90	Sirui	Tong	Laurentian University
95	Kayla	Twilley	Laurentian University
36	Lucy	van Haaften	Trent University
12	Isabelle	Venzon	Brock University
82	Matteo	Vocaturo	Laurentian University
74	Olivia	Wahby	University of Windsor
32	Alexandra	Weber	Carleton University
71	Amesh	Wickramasinghe	University of Windsor
88	Miah	Wildschut	Laurentian University
56	Eryn	Wolfe	Wilfrid Laurier University
38	Ruby Tsz Ying	Yip	University of Toronto

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001

PERCEIVED HUMAN PRESENCE ALTERS COYOTE BEHAVIOUR, REDUCING ACTIVITY AND FORAGING

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Western University

Coyotes are highly adaptable to urban environments and now inhabit most North American cities, highlighting the need to understand their behavioural responses to human interactions. Humans play a dual role in shaping coyote behaviour, posing risks through direct and indirect predation while simultaneously providing abundant, easily accessible food sources. This creates complex risk-reward trade-offs that coyotes must balance when navigating environments where humans are present. My research investigates these trade-offs by examining how coyotes alter their activity patterns and foraging behaviour in response to perceived human presence. We conducted a manipulative field experiment by broadcasting localized, long-term, predator (human) and control (native frog) vocalizations at 13 independent study sites across the Buffer Nature Preserve in Northern Florida, USA, where we recorded animal behaviours at bait stations using motion-triggered camera traps. Under human vocalization treatments, coyotes were significantly less likely to approach bait stations and spent less time foraging than when under the control treatment. Additionally, we observed differences in coyote behaviour between the vocalization treatments. Our findings demonstrate that coyotes exhibit significant behavioural shifts in response to human presence, providing crucial insights for wildlife management and conservation. As coyote management becomes increasingly necessary, these insights can inform strategies to manipulate their spatial and temporal activity patterns, mitigate human-wildlife conflicts and guide conservation efforts where coyote predation on vulnerable prey requires intervention.

002

ASSESSMENT OF FRAILTY INDEX IN 5XFAD MICE DURING DISEASE PROGRESSION: A NEUROLOGICAL PERSPECTIVE

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Alzheimer's disease (AD) is a major cause of neurodegenerative morbidity and death globally, affecting cognitive and functional capacities, especially in the elderly. Given its profound effects on memory and cognitive abilities, Alzheimer's disease (AD) is a serious public health concern. Gaining a deeper knowledge of AD is crucial as the population ages. The 5xFAD mouse model, which is well-known for its severe Alzheimer's pathology and quick development, offers a great foundation for researching both cognitive decline and related frailty, a multifactorial disease that many elderly people experience. Research on early-onset AD benefits greatly from the use of the 5xFAD mouse model, a genetic mimic of familial Alzheimer's disease that shows increased amyloid deposition from an early age (Smith & Jones, 2020). Frailty is a medical condition often seen in older adults, characterized by a decline in multiple physiological systems, which results in an increased vulnerability to stressors and a diminished ability to maintain or regain health after an illness or injury.The primary objective of this study is to contribute to the development of a validated frailty index for 5xFAD mice, enhancing the tool's accuracy and applicability in modeling Alzheimer's disease progression. This will involve adapting the comprehensive frailty assessment techniques established by Dalhousie University, which have been widely recognized for their effectiveness in quantifying frailty across various health and aging studies (Rockwood et al., 2005; Pulok et al., 2020).

003

THE IMPACT OF CLIMATE CHANGE ON TEMPERATE BROADLEAF FORESTS IN THE NIAGARA REGION, CANADA.

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Climate change is altering forest ecosystems by shifting temperature and precipitation patterns, increasing competition among tree species, and intensifying disturbances such as wildfires and pest outbreaks. This study investigates how managed (burned) and unmanaged temperate broadleaf forests in the Niagara Region respond to these changes. Fieldwork was conducted in forests under the jurisdiction of the Niagara Parks Commission and Parks Canada, where three 20 × 20 m plots were established in each forest type. Within each plot, all trees were identified to species and cored using an increment borer, yielding a total of 165 samples. Dendrochronological techniques were used to assess tree growth patterns and determine how management practices influence resilience to climate change. It is hypothesized that trees in the managed forests will show greater resilience, benefiting from prescribed burns that reduce competition and improve resource availability. The results of this study will contribute to understanding the role of forest management in mitigating climate change impacts and supporting long-term forest health.

004

TEMPORAL DYNAMICS OF MOUNTAIN PINE BEETLE (*DENDROCTONUS PONDEROSAE*) POPULATION STRUCTURE OVER AN OUTBREAK

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Climate change has the potential to drastically change the distributions of species, which can lead to changes in population structure, which is the partitioning of genetic differentiation, of expanding populations. A case study for this is the mountain pine beetle (MPB), which is a small insect native to British Columbia. Populations of MPB oscillate in size over time in four phases: endemic, incipient-epidemic, epidemic, and post-epidemic. Spatial population structure is often examined during range changes, whereas temporal dynamics of the same change are rarely studied, and differences between outbreak phases remain a large gap in the vast knowledge of the MPB system. The purpose of this project was to investigate the change in population structure and genetic distance between the epidemic and post-epidemic phases using whole genome sequence (WGS) data. Population structure was analyzed by examining genetic clustering of individuals and by an analysis of molecular variance (AMOVA), and genetic distances among sampling sites were used to characterize isolation by distance. Populations were moderately spatially structured, with an F_{ST} value from the epidemic phase samples of 0.03 and an F_{ST} value from the post-epidemic phase samples of 0.08. Along with this, populations showed clear isolation by distance patterns in both the epidemic and post-epidemic outbreak phases. From this, we found that genetic differentiation between sites was driven by space and weakly differentiated by time. This provides insight into the temporal dynamics of MPB outbreaks, and thus the recent MPB expansion, supporting further research into spatial dynamics.

005

STUDYING THE ROLE OF UBIQUITINATION IN CLATHRIN-MEDIATED ENDOCYTOSIS DURING REPLICATIVE AGING

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Toronto Metropolitan University

Clathrin-mediated endocytosis (CME) is an essential and highly conserved cellular process where external materials and plasma membrane (PM) components get internalized into the cell. Internalized cargo is recycled back to the PM, sorted to other organelles, or degraded in vacuoles/lysosomes. CME involves the sequential recruitment of proteins from several functional modules, including early proteins, coat proteins, WASp/myosin, actin and amphiphysin. Ubiquitination plays a role in CME by marking cargo for internalization, with α-arrestin family proteins acting as adaptors for the ubiquitin ligase Rsp5. Deubiquitinases counteract this by removing ubiquitin, thus recycling the CME machinery. We have shown that CME progressively declines during replicative aging, and this depends on vacuolar pH and the TORC1-Npr1 signalling pathway. In this project, we aim to determine the effect loss of ubiquitination/deubiquitination has on CME in replicatively aging budding yeast cells. We constructed single and double mutants of ubiquitination and deubiquitination genes, and fluorescently tagged the Sla1 coat protein to monitor CME dynamics. We used wheat germ-agglutinin, a lectin that binds to chitin-rich bud scars, to determine the replicative age of individual cells. We then prepared imaging samples of our strains grown in control condition, in lifespan-expanding caloric restriction condition, and treatment in the V-ATPase inhibitor concanamycin-A. We acquired real-time movies using spinning disk confocal microscopy, extracted quantitative data on endocytic patch formation, and evaluated differences in CME dynamics between young and old cells. With this project we aim to understand how ubiquitination/deubiquitination defects affect endocytosis during replicative aging in budding yeast.

006

HOST-VIRUS-VIROPHAGE DYNAMICS: VIROPHAGE-MEDIATED PROTECTION OF FRESHWATER HAPTOPHYTE ALGAE

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Several giant dsDNA viruses and their putative virophages that co-infect their host cells are known to parasitize the globally distributed, freshwater haptophyte alga *Chrysochromulina parva*. This study examined the influence of the virophage CpVV-Moe on the growth of *C. parva* and CpV-BQ3 replication. Triplicate experimental infections were set up with variable ratios of Moe:BQ3 (10:1, 900:1, 1000:1) at a constant multiplicity of infection for BQ3 (~0.01 viruses per cell). Each infection was monitored over 20 days using bright-field microscopy and quantitative PCR to estimate cell and virus/virophage abundances, respectively. Our results demonstrated that Moe protected *C. parva's* growth in the presence of BQ3, but the effect depended on the ratio of Moe to BQ3. At higher Moe-to-BQ3 ratios (e.g. 1000:1), BQ3 replication was suppressed and its final abundance did not exceed the initial ~5.5 x 10^4 units/mL inoculum. In the same treatment, *C. parva's* abundance after 20 days (~2.07 x 10^6 cells/mL) was comparable to that in the no-infection control (~2.27 x 10^6 cells/mL). Conversely, when infected with BQ3 alone, *C. parva's* abundance was observed at 2.8 x 10^5 cells/mL while BQ3's abundance increased 3,000-fold reaching ~1.55 x 10^6 units/mL. At lower Moe-to-BQ3 ratios, the protective effect of Moe was negligible, and infections with Moe alone demonstrated that it did not replicate without BQ3, confirming its obligate dependence on BQ3 for its replication. These findings define the role of CpVV-Moe in this tripartite infection system, highlighting the influence of virophages on algal virus dynamics and primary production in aquatic ecosystems.

007

MODIFYING ANTITHETIC INTEGRAL FEEDBACK (AIF) BASED ON THEORETICAL PREDICTIONS FOR ENHANCED REGULATION AND NOISE SUPPRESSION IN GENE EXPRESSION

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Precise regulation of gene expression is crucial for creating stable and reliable biological systems, fundamental to synthetic biology advancements. Controlling gene expression finely tunes cellular functions, leading to predictable and efficient outcomes. Antithetic Integral Feedback (AIF) is a biochemical feedback mechanism that regulates intracellular molecular species in *Escherichia coli* (*E. coli*). However, traditional AIF implementations often increase noise, complicating precise regulation. Recent theories suggest robust regulation and minimal noise can be achieved under specific conditions. This research aims to experimentally validate these predictions by replicating and modifying the AIF system to enhance performance. Modifications involve altering the feedback network to reduce the target species' production, thereby decreasing noise levels. The study includes designing and assembling DNA constructs using molecular cloning techniques, and integrating these constructs into *E. coli* strains, and verifying functionality through PCR. Fluorescence microscopy will measure protein expression levels, followed by data analysis to assess gene expression fluctuations. The objective is to demonstrate that the modified AIF system can achieve near-perfect regulation with reduced noise, enhancing gene expression systems' stability. This research will contribute to developing reliable engineered biological circuits, offering insights into designing efficient gene regulation mechanisms in synthetic biology.

008

PHARMACOLOGICAL AMPK ACTIVATION INFLUENCES SKELETAL MUSCLE CATABOLISM IN CANCER CACHEXIA

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[1]Department of Kinesiology, McMaster University, Hamilton ON, Canada
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Cancer cachexia is a muscle wasting syndrome affecting more than half of people with cancer and characterized by the loss of skeletal muscle mass, adipose tissue mass, anemia, anorexia, and loss of strength. These energetic and functional deficits impact treatment efficacy, thereby worsening patient prognosis. AMP-activated protein kinase (AMPK) plays a key role in cellular energy homeostasis and muscle preservation and has been implicated in cancer cachexia. We investigated the impact of direct pharmacological AMPK activation via MK-8722 (MK) in mice inoculated subcutaneously with Lewis Lung Carcinoma (LLC) cells. LLC mice received oral administration of MK ($\mathrm{LLC}^{\mathrm{MK}}$) or PBS ($\mathrm{LLC}^{\mathrm{PBS}}$) starting 7-days post-LLC inoculation and tissues were collected 21-days thereafter. Skeletal muscle protein quantification with western blotting identified increases in LC3I and LC3II in $\mathrm{LLC}^{\mathrm{MK}}$ compared to $\mathrm{LLC}^{\mathrm{Veh}}$ and $\mathrm{PBS}^{\mathrm{Veh}}$ respectively, while p62 accumulated in $\mathrm{LLC}^{\mathrm{Veh}}$ but decreased in $\mathrm{LLC}^{\mathrm{MK}}$. In response to cancer cachexia, immunofluorescent staining of the extensor digitorum longus muscle (EDL) demonstrated a significant increase in p-ATG16L puncti in $\mathrm{LLC}^{\mathrm{Veh}}$ and $\mathrm{LLC}^{\mathrm{MK}}$ compared to $\mathrm{PBS}^{\mathrm{Veh}}$ ($p=0.0027$ and $p<0.0001$, respectively), indicating phosphorylation of ATG16L by ULK1, a kinase activated by AMPK. MK treatment in LLC mice did not restore p-ATG16L levels to baseline and remained elevated. Although, cancer-related increases in MURF1 and Atrogin1 mRNA content improved with MK treatment. Collectively, the data suggests that MK treatment influences catabolic processes during cancer cachexia, as indicated by improvements in markers of autophagy and atrophy. Future aims include assessing mitochondrial morphology and mitophagy to better understand muscular adaptations in cancer cachexia.

009

EVALUATING THE THERAPEUTIC POTENTIAL OF MK-8722 IN ENHANCING SKELETAL MUSCLE REGENERATION IN DUCHENNE MUSCULAR DYSTROPHY

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McMaster University

Introduction: Duchenne muscular dystrophy (DMD) is the most common form of muscular dystrophy, characterized by chronic muscle damage due to mutations in the dystrophin gene. The loss of functional dystrophin protein causes muscles to experience continuous injury and impaired regeneration, leading to the replacement of muscle by fibrous and fatty connective tissue. Pharmacological stimulation of adenosine monophosphate-activated protein kinase (AMPK) has shown promise in mitigating DMD pathology. In an acute investigation, treatment with the AMPK agonist MK-8722 (MK) promoted a slow, oxidative muscle phenotype with heightened disease resistance. Considering this finding, this study aimed to determine the therapeutic potential of MK on skeletal muscle regeneration in DMD. Methods: Five-week-old male D2.mdx and DBA/2J control mice ($n = 8$) were administered MK (5 mg/kg) or a vehicle solution daily for seven weeks via oral gavage. Following treatment, the triceps muscles were harvested for analysis of muscle regeneration. Immunofluorescence was used to investigate the presence of muscle fibres expressing embryonic myosin heavy chain (eMHC) and centrally located nuclei. Results: We found that MK treatment reduced the number of eMHC-positive fibres ($p < 0.05$) but did not significantly alter the amount of centrally nucleated fibres in the triceps muscles compared to genotype-matched, vehicle-treated mice. Conclusion: These results indicate that pharmacological AMPK activation via MK administration attenuates dystrophic muscle damage, demonstrating its potential as a therapeutic intervention for DMD. Future directions for this study will assess the role of MK on muscle quality by measuring inflammatory cell infiltration and collagen deposition.

010

CHARACTERIZATION OF QUEE-DEPENDENT FILAMENTATION IN *ESCHERICHIA COLI* AND *YERSINIA PSEUDOTUBERCULOSIS*

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Bacterial pathogens like *Escherichia coli (E. coli)*, Salmonella, and *Yersinia pseudotuberculosis (Y. pseudotuberculosis)* are all *Enterobacteriaceae* that can cause foodborne illnesses. The immune system protects against these infections through antimicrobial peptides (AMPs) like LL-37, which disrupt bacterial membranes. However, bacteria have evolved countermeasures like filamentation, a process where cells elongate without dividing. Our lab has shown that filamentation helps bacteria survive LL-37 attacks. QueE, an enzyme involved in queuosine biosynthesis and cell division control, regulates filamentation. The PhoQ/PhoP system controls *queE*, and while the gene is conserved, its function varies by species. In *E. coli*, *queE* orthologs from *Salmonella* and *Klebsiella pneumoniae,* induce filamentation, but those from more distant species like *Yersinia pestis* and *Pseudomonas aeruginosa* do not. Here, we investigated the role of $queE_{Ec}$ and $queE_{Yp}$ in cell division control in both *E. coli* and *Y. pseudotuberculosis*. In *E. coli*, overexpression of *queE* orthologs from closely related species induces filamentation. However, overexpression of $queE_{Ec}$ and $queE_{Yp}$ in *Y. pseudotuberculosis* did not induce filamentation. A positive control using *sulA* from *E. coli*, a component of the SOS system, induced pronounced filamentation in *Y. pseudotuberculosis.* As an enterobacter, *Y. pseudotuberculosis* provides a valuable model for comparing filamentation regulation with *E. coli* and related species, helping to identify differences in cell division control. These results highlight species-specific regulation of filamentation and offer insights into bacterial adaptation under host stress.

011

HORIZONTAL TRANSMISSION OF MODIFIED NEGEVIRUS VIA ORAL INGESTION OF SPIKED SUGAR MEAL.

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Vector-borne diseases (VBDs) pose significant public health challenges, with mosquitoes acting as primary vectors for arboviruses such as dengue, Zika, and chikungunya viruses. *Aedes aegypti*, in particular, is a key transmitter due to its close association with human populations. While traditional vector control strategies have focused on reducing mosquito populations, insect-specific viruses (ISVs) have emerged as a promising alternative for disrupting arbovirus transmission. Negeviruses, a newly identified group of ISVs, can potentially interfere with arboviral replication, providing a novel biocontrol approach. This study aims to assess the horizontal transmission efficiency of a modified Negevirus in *A. aegypti* mosquitoes via oral ingestion of a sugar meal. Using a Negevirus construct containing a green fluorescent protein (GFP) marker and a 2A self-cleaving sequence, we seek to establish its ability to infect and persist in mosquito populations. *A. aegypti* mosquitoes were reared under controlled laboratory conditions and exposed to a sucrose solution containing the modified Negevirus at the adult stage. The infection rates were quantified using two-step quantitative PCR (qPCR) after 14 days post-infection, confirming viral genome presence within the mosquitoes. This study will enhance our understanding of mosquito-virus interactions and pathways of transmission and assess Negevirus as a potential biocontrol agent. By evaluating its ability to infect *A. aegypti*, our findings would support the development of ISV-based vector control strategies, paving the way for environmentally sustainable and targeted approaches to mitigating arbovirus transmission.

012

IMPACT OF ECOWOOL ON CROP QUALITY

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In order to reduce environmental impact, sustainable agriculture is reliant on organic amendments to improve soil fertility and promote plant growth. Sheep wool as an amendment is slowly being researched more, but further research is needed to determine its effects on nutrient levels and plant growth within a greenhouse setting. This project explores the impact of sheep wool pellets from EcoWool Canada on the growth and uptake of nutrients in various crops including perpetual spinach, roquette arugula, and White Icicle radish. Each of these crops were grown in a greenhouse at Brock University and treated with five different treatments including 3% EcoWool (T1), 5% EcoWool (T2), 10% EcoWool (T3), synthetic fertilizer (T4), and water as the control (T5). The plant tissues were analyzed for chlorophyll and various nutrients, and results showed that in many cases nutrient uptake was affected by EcoWool additions, but this was also often crop dependant due to different plant needs and compositions. In arugula crops there was an increasing linear relationship between chlorophyll levels and EcoWool percentage which could be due to increasing nitrogen levels with EcoWool additions. Copper concentration in all crops also increased as percent EcoWool increased likely because copper is present in sheep wool and is essential for production and development of plants. The use of EcoWool as an amendment could enhance soil health and plant productivity, reduce synthetic fertilizer use, and promote a more sustainable option for agricultural practices.

013

THE INFLUENCE OF POSITION AND COLOURS OF STICKY TRAPS ON LEAFHOPPER DETECTION IN ORGANIC VINEYARDS

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Leafhoppers are sap-sucking insects that have become prominent pests in Canadian vineyards. They damage crops, and some species can spread plant diseases through their feeding habits. As a result, effective monitoring of leafhopper presence is crucial for vineyard management. They damage crops, with some species spreading plant diseases through their feeding habits, making effective monitoring crucial for vineyard management.
This study used sticky traps to monitor leafhopper populations in three organic vineyards in the Niagara Region. Three coloured sticky traps (yellow, red, and green) were placed at three different height levels within the same panels of grapevine rows, positioned at the edge or in the middle of the rows. Rows were classified as internal (surrounded by other grapevine rows) or external (next to open land on one side). The traps were set up for three days in August and three days in September, and the collected invertebrates were identified in lab.
The results suggest that trap colour, trap height, and the row's position (internal vs. external) has a tendency of influencing leafhopper presence. However, the trap's position within the row (edge vs. middle) and the cover crop treatments showed more inconclusive effects on leafhopper abundance.

014

THE EFFECT OF SEX ON THE THERMOREGULATORY BEHAVIOUR OF THE GUPPY (*POECILIA RETICULATA*)

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Animals thermoregulate to maintain a core body temperature that is within their optimal physiological range. As ectotherms, fish must rely on external conditions to regulate their body temperature and primarily do this by changing their behaviour. Studies have found that the temperatures that fish select and tolerate change based on the animal's health, sex, and reproductive state. However, few studies have focused solely on the effect of sex on thermal preference. The current study assesses the thermoregulatory behaviour of guppies (*Poecilia reticulata*) in a dual-chambered shuttle box system to determine whether male and female fish have different thermal preferences. We found that there was no significant difference between the temperatures that male and female guppies selected in the shuttle box. These results differ from previous work that suggested that male and female guppies do have different thermal preferences. This study provides background for further work on whether gravid female guppies select different temperatures than non-gravid females and males, which would add to the growing research on how gravidity affects thermoregulation in a diverse range of species.

015

MOTHER-DAUGHTER PROTEIN ASYMMETRY DURING BUDDING YEAST REPLICATIVE AGING

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Budding yeast *Saccharomyces cerevisiae* undergo asymmetric cell division, where an aging mother cell produces a rejuvenated daughter. During this process, damaged cellular components are usually retained in the mother, while rejuvenating factors are enriched in the daughter. As yeast progress through their replicative lifespan (number of cell divisions before senescence), they lose the ability to produce rejuvenated daughters. One of the consequences of asymmetric inheritance is the uneven distribution of proteins during cell division. However, there is limited information on how protein asymmetry changes as the cells age. Using high-throughput microscopy, we aim to observe the effects of replicative aging on asymmetrical localization and abundance of individual proteins. First, we have compiled a list of 174 proteins with reported asymmetry between mother and daughter cells. This includes proteins enriched in mother or daughter cells, asymmetry generating genes (AGGs) and long-lived asymmetrically retained proteins (LARPs). Next, we used the synthetic genetic array (SGA) method to introduce cytosolic and nuclei fluorescent markers into strains expressing GFP fusion constructs of our asymmetric proteins of interest. We then acquired fluorescence micrographs of the constructed strains with an automated high-content imaging system. Quantitative analysis of cell features will allow us to assess changes in protein abundance and localization between aging mothers and their daughters. This data will provide insights into the role of protein asymmetry in cellular aging and help identify new aging and rejuvenation factors.

016

STUDYING THE EFFECTS OF CELLULAR AGING ON CLATHRIN-MEDIATED ENDOCYTOSIS IN HUMAN CELLS

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Aging is a complex process that leads to cellular senescence, a state of irreversible growth arrest accompanied by extensive cellular changes. Senescence is characterized by alterations in trafficking pathways, affecting various cellular functions. Clathrin-mediated endocytosis (CME) is critical in maintaining cellular homeostasis by regulating nutrient uptake, receptor recycling, and signal transduction. However, its dynamics in aging and senescent cells remain largely unexplored. This study aims to investigate CME in aging and senescent cells by examining the morphology and dynamics of clathrin-coated pits (CCPs) using live-cell total internal reflection fluorescence (TIRF) microscopy. To investigate the effects of senescence on CME, we used ARPE-19 cells stably expressing GFP-tagged clathrin. Senescence was induced by activating the DNA damage pathway with the drug doxorubicin, or by inducing oxidative stress with hydrogen peroxide. We observed that senescent cells exhibit unevenly distributed CCP clusters, a striking contrast to the non-senescent controls. To determine if these structures correspond to bona fide CME sites, we performed immunofluorescence staining for Adaptor Protein 2 (AP2), a key component of CME. Image analysis confirmed signal overlap between clathrin and AP2 in these clustered structures. Next, we are serially passaging cells to determine when CME alterations first appear during aging, and which mechanistic steps in forming clathrin-coated pits (CCPs) are affected. By elucidating how CME is altered during cellular aging, this study seeks to provide insights into the molecular mechanisms underlying senescence and identify potential early markers of age-related cellular decline.

017

SHINING A LIGHT ON THE SHADOWS: EXAMINING THE CASCADING EFFECTS IN NATIVE GARDENS ON NOCTURNAL POLLINATORS AND THEIR PREDATORS

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Native gardens are planted in urban areas to attract and support pollinators such as moths, but limited research has examined the cascading effects native gardens have on moth predators. Using non-invasive acoustic technology, I recorded the presence of bat species at 90 native gardens and 90 control sites in Peterborough, ON between May – October 2024. These recordings were taken within two hours of sunset during the optimal foraging time for bats. I then analyzed the data using a general linear mixed model to account for potential variables such as Julian date, light intensity, and time after sunset. Results showed the presence of tri-colored bats (*Perimyotis subflavus*), silver-haired bats (*Lasionycteris noctivagans*), little brown myotis (*Myotis lucifugus*), and big brown bats (*Eptesicus fuscus*) increased at native garden sites compared to control sites located 100m away. In contrast, eastern red bats (*Lasiurus borealis*) had an increased presence at control sites compared to native garden sites. Hoary bat (*Lasiurus cinereus*) results were inconclusive, and neither northern long-eared myotis (*M. septentrionalis*) nor eastern small-footed myotis (*M. leibii*) were detected during the study. These results suggest that native gardens attract several endangered species of insectivorous bats found in urban environments. Conversely, there may be unknown factors attracting eastern red bats to other landscape covers.

018

DO ELEPHANTS IN PROTECTED AREAS KNOW THAT THEY ARE PROTECTED? AN EXPERIMENTAL TEST OF ANTIPREDATOR BEHAVIOURS IN AFRICAN ELEPHANTS, *LOXODONTA AFRICANA*.

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African elephants, *Loxodonta africana,* are of major interest to the South African National Parks Service due to their endangered status and the disruptive activities of their increasing local populations. Previous experimental evidence has demonstrated that elephants utilize ecological knowledge to adjust their antipredator behaviour according to the level of perceived predation threat. Using 1,421 videos collected via Automated Behavioural Response systems, we analyzed eight different elephant behavioural responses after exposure to auditory playbacks of human vocalizations, lion vocalizations, tourist sounds (engine noise or engine noise mixed with human vocalizations), and control noise (bird calls). The playbacks were broadcast across two regions with contrasting ecotourism levels within Greater Kruger National Park (GKNP), South Africa. The results demonstrate that the strength of elephant antipredator behaviours differed significantly across playback treatments, whereas ambient ecotourism level did not have a significant effect on behaviour. Specifically, elephants were more likely to respond aggressively to lion vocalizations and evasively in response to human vocalizations regardless of ecotourism activity. This suggests that social trauma from past culling in GKNP has a long-lasting influence on elephant antipredator responses, making them more fearful of humans than lions, even when vocalizations are associated with benign tourism. This provides experimental support for utilizing human playbacks as a non-lethal elephant management tool in African protected areas.

019

THE ROLE OF UROPATHOGENIC *ESCHERICHIA COLI* FILAMENTATION ON RESISTANCE TO CLINICALLY RELEVANT ANTIBIOTICS USED TO TREAT URINARY TRACT INFECTIONS

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Uropathogenic *Escherichia coli* (UPEC) is the primary cause of urinary tract infections (UTIs), affecting 150 million people worldwide annually. In severe cases, UPEC infections can progress to pyelonephritis and urosepsis, causing death in 10-30% of the infected population. Upon entering the bladder epithelium, UPEC cells can undergo filamentation — a morphological change that enables growth without the occurrence of cellular division. Previous research in the McPhee lab has shown that filamentous cells exhibit enhanced resistance to elements of the host innate immune system. Given the high failure rates of current treatments, and that certain antibiotics induce filamentation, we wanted to investigate whether genetically induced filamentous UPEC cells would result in altered susceptibility to drugs commonly prescribed for these infections. In this study, filamentation was induced in wild-type *Escherichia coli (E. coli)* through the overexpression of QueE and SulA, both of which use different mechanisms to interact with FtsZ polymers at the mid-cell site to inhibit cellular division. The susceptibility of each strain to antibiotics was assessed through minimum inhibitory concentration assays. Although no statistically significant alteration in susceptibility was observed for ciprofloxacin or trimethoprim-sulfamethoxazole, *E. coli* expressing QueE showed a statistically significant increase in susceptibility to nitrofurantoin when compared to control strains. Nitrofurantoin is a commonly prescribed antibiotic with an unusual multi-target mechanism of action. This work suggests that the induction of filamentation can alter susceptibility to a routinely administered antibiotic and provides key evidence for studying this further.

020

THE IMPACT OF HEAT AND HYDROXYUREA ON REACTIVE OXYGEN SPECIES LEVEL IN SCHIZOSACCHAROMYCES POMBE.

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Cells constantly encounter environmental stresses that can disrupt homeostasis and threaten viability. Environmental stress including heat can influence cellular metabolites, including reactive oxygen species (ROS). ROS play a variety of functions in the cell, but can cause damage to proteins and nucleic acids when produced in excess. The fission yeast *Schizosaccharomyces pombe* (*S. pombe*) is an effective model organism for studying eukaryotic cell cycle mechanisms. Cds1 and Rad3 are cell cycle checkpoint proteins that are involved in the regulation of the *S. pombe* cell cycle.

Work in the Sabatinos lab demonstrated that environmental stress signaling may be similar to oxidative stress responses in *S. pombe.* In this study, we investigate the effects of heat stress and hydroxyurea (HU) treatment on ROS level in *S. pombe* checkpoint deletion mutants. Using an ROS-sensitive fluorescent dye called CellROX Green, we stained cells and assessed ROS level using flow cytometry. We tested the impact of DNA replication checkpoint function by comparing ROS levels in wild type and *rad3*Δ or *cds1*Δ mutant cells. The absence of Rad3 (*rad3*Δ*)* or Cds1 (*cds1*Δ*)* makes cells unable to stabilize DNA replication forks in HU causing death. We hypothesized that loss of replication checkpoint would increase ROS level. We compared the effect of HU on ROS with heat treatment. We have previously shown that heat decreases HU effects. We found that ROS increases in heat, but decreases in HU. This research provides insights into how eukaryotic cells modulate redox homeostasis when checkpoint pathways are compromised, contributing to a deeper understanding of oxidative stress biology.

021

DEVELOPMENT OF AN INEXPENSIVE METHOD FOR MEASURING OXYGEN CONSUMPTION RATE IN CULTURED CELLS IN SITU.

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Oxygen consumption rate (OCR) is a key indicator of cellular metabolism, providing insights into mitochondrial function and metabolic adaptation. Traditional OCR measurement methods for cells in culture have some limitations: the Clark electrode is typically used with stirred cell suspensions, requiring their trypsinization from culture plates; the Seahorse Extracellular Flux Analyzer is used with adherent cells, but it is relatively costly, invasive, and labor-intensive. There is a need for inexpensive and non-invasive methods for measuring OCR in cultured cells in situ. Here I describe the use of the PreSens OxoDish system to continuously monitor OCR in cell culture. The OxoDishes have oxygen-sensitive optodes adhered to the bottom of each well that report local oxygen levels. Fick's First Law was used to calculate cellular OCR in an open system at steady state from this pericellular oxygen level. MCF7 human breast cancer cells were used to validate the method since a number of OCR per cell values have been published and could be used for comparison. For MCF7 cells growing in standard conditions (DMEM with 10% FBS) my method yielded OCR values of 14-32 amol/cell/s, compared to 32.5-39.9 amol/cell/s reported using other methods. This suggests that my method can be applied to OCR measurements of cultured adherent cells, which will be a valuable tool in the field.

022

THE EFFECTS OF WARMING ON PREDATOR-PREY INTERACTIONS USING MICROARTHROPODS AS A MODEL.

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Climate change is estimated to increase global temperatures between 2°C-6°C within the next century. Warming of this degree will have several effects on how species interact, such as predator-prey relationships. For instance, if predators and their prey differ in their ideal temperature range (T_{opt}), then warming may benefit one while having adverse effects on the other. Using microarthropod models in a lab-based mesocosm warming experiment, the objective of this study was to examine predator-prey interactions under different temperature scenarios. Specifically, this mesocosm warming experiment aimed to understand how warming of +6°C influences predator-prey ratios in samples collected from two systems that differ in their growing season temperatures (cool-temperature = 12°C vs. warm-temperature = 18°C). I found that in the cool-temperature system, warming of +6°C had no effect on predator abundances but increased prey abundances, resulting in a lower predator-prey ratio than in the control temperature. In the warm-temperature system, warming of +6°C had no effect on either predators or prey, resulting in no significant difference in the predator-prey ratio between the two temperature treatments. This experiment demonstrates that warming may lead to thermal mismatches in predator-prey dynamics, particularly in cool-temperature systems.

023

THE EFFECTS OF SKELETAL MUSCLE-SPECIFIC AMPK ON EXERCISE-INDUCED MITOCHONDIRAL REMODELLING

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AMP-activated protein kinase (AMPK) mediates mitochondrial functions like biogenesis, dynamics and mitophagy in response to energetic stress. Its importance in mitochondrial adaptation following chronic exercise remains to be fully elucidated. Previous literature has utilized transgenic mice with germline deletion of skeletal muscle AMPK, which exhibit exercise intolerance interfering with normal muscle development. The purpose of this study is to investigate exercise-induced mitochondrial adaptations in a novel muscle-specific AMPK $\beta1\beta2$ inducible knockout (imKO) model. Male and female 16 weeks old wild-type (WT) and imKO mice were treated with tamoxifen daily for five consecutive days. Twelve weeks after the last tamoxifen dose, WT and imKO mice were randomly assigned to sedentary and exercise groups. The exercise protocol consisted of progressive treadmill training 5 days/week over 6 weeks. Subsequently, quadriceps muscles were collected for high resolution respirometry, immunoblotting and transmission electron microscopy (TEM). The basal mitochondrial leak from complex I (CI) showed no significant differences between WT and imKO groups. We observed a significant increase in ADP-stimulated CI-specific and CI+II specific oxygen consumption rates in exercised WT animals. However, no differences were observed in mitochondrial respiration with training in imKO mice. We next quantified IMF mitochondria using TEM. Sedentary WT and imKO mice had similar amounts of IMF mitochondria. Exercise elicited a significant increase in IMF mitochondria in exercised WT animals only relative to sedentary counterparts. Data suggest that AMPK plays a role in exercise-induced mitochondrial upregulation. Future work aims to elucidate the impact of AMPK on mitochondrial morphology and its role in exercise adaptation.

024

INVESTIGATING AND DISRUPTING ANTIBIOTIC REPRESSION BY THE GLOBAL REGULATOR WBLA IN *STREPTOMYCES VENEZUELAE*

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Regulating antibiotic production by *Streptomyces* bacteria involves the integration of a myriad of environmental and developmental signals. Recently, the transcription factor WblA has been identified as a global repressor of antibiotic synthesis in multiple *Streptomyces* spp., where disruption of *wblA* results in increased antibiotic production. Due to the increasing incidence of antibiotic resistance, *wblA* is an interesting target to exploit for the discovery of novel antibiotics with unique mechanisms of action. Nevertheless, how WblA controls antibiotic production remains unknown. To determine how WblA exerts its regulatory activity, Chromatin Immunoprecipitation Sequencing (ChIP-seq) in the model *Streptomyces venezuelae* will be conducted. This involved generating a tagged variant of *wblA* and introducing it into a Δ*wblA* background. Following this, the tagged WblA can be cross-linked to DNA, the chromosomal DNA sheared, WblA-DNA complexes are purified using tag-specific antibodies, the stabilizing cross-links are reversed, and the associated DNA fragments are purified and sequenced. In parallel, we are designing constructs that will allow us to manipulate *wblA* expression and promote new antibiotic production. We have developed a CRISPR-based interference construct that is intended to disrupt transcription of *wblA* in any *Streptomyces* species, as the *wblA* sequence is highly conserved across this bacterial genus. As *Streptomyces* encode a diverse array of specialized metabolites, introducing the *wblA* CRISPR interference construct has the capacity to relieve repression of novel antibiotics. Collectively, these studies are providing insight into the mechanistic control of antibiotic repression by WblA and generating genetic tools to manipulate it for the purpose of antibiotic discovery.

025

GENERATION OF A 5-CHANNEL FLUORESCENT IMAGING TECHNIQUE THROUGH THE INSERTION OF A LONG STOKES SHIFT FLUORESCENT PROTEIN ALLOWING FOR THE COMPLETE IMAGING OF THE NOTCH TRANSCRIPTIONAL ACTIVATION COMPLEX

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In the field of biology, molecular pathways have been discovered, developed, and studied for over 100 years. The principles and foundations developed by molecular biology and biotechnology are utilized to obtain a better understating of these pathways, which allow for the production of pharmaceuticals, biological products, and medical discoveries worldwide. The localization, activity, and dynamics of these pathways were originally hypothesized, but modern technology, such as fluorescent microscopy and genetic engineering, have allowed for the visualization and quantification of these pathways. The information obtained from these visual models elucidate the mechanisms behind these pathways and the affects that they have on the cells in which they occur. Techniques such as multi-channel image analysis can be used to gain a greater understating of how these signalling pathways function, and how the individual proteins which comprise these pathways and complexes localize and interact with each other. Unfortunately, many large complexes such as the Notch transcriptional activation complex, simply contain too many elements to be imaged in their entirety by current 4-channel fluorescent image acquisition techniques. This negatively impacts the ability for these techniques to accurately measure and illustrate the dynamics and interplay of the individual proteins of which these complexes are comprised. The insertion of an additional channel using a fluorescent protein, LSSmOrange, should expand this technique to allow for visualization of the entire complex of Notch, while increasing the ability of this technique to obtain accurate data on molecular dynamics and localization.

026

EXAMINING CHANGES IN TREE SWALLOW (*TACHYCINETA BICOLOR*) GUT MICROBIOME AS A RESULT OF POLLUTION ACROSS SOUTHERN ONTARIO

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Pollution affects diverse ecosystems and species including gut microbiomes. This complex community which evolves throughout an organism's life is essential for processes such as growth, nutrition and ultimately survival. This study aimed to assess the impact of pollution on the gut microbiome makeup of tree swallows across wastewater treatment plants (WWTPs) and non polluted reference sites in southern Ontario. Sampling sites across southern Ontario included polluted locations such as Brantford, Woodard and Dundas WWTPs as well as unpolluted reference sites at McMaster Forest Nature Preserve and Mountsberg Conservation Area. Fecal samples were collected directly from 10 day old nestlings. Microbial diversity was assessed through 16S rRNA gene sequencing. Data was mapped against morphometric measurements, including mass, tarsus length and wing chord to explore potential correlations between nestling condition and gut microbial diversity. While morphometric and phylum-level analyses revealed high variation, the phylum *Chlamydiota* was detected at only one site (Dundas Wastewater Treatment) where it exhibited a higher relative abundance than other phyla. As *Chlamydiota* has been linked to bacterial diseases, its presence in a highly polluted site suggests that pollution may influence gut microbiome composition in a potentially harmful manner

027

CUTICULAR CUES INVOLVED IN LOCUST INFECTION BY THE INSECT SPECIALIST *METARHIZIUM*.

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Fungal pathogens have evolved sophisticated ways to infect their hosts, but what makes some fungi capable of attacking a broad range of insects, while others are highly selective? *Metarhizium*, known as an insect-pathogenic fungus, exhibits varying degrees of host specificity. Specialists such as *M. acridum* primarily infect orthopteran hosts like locusts (*Locusta migratoria*), while generalists such as *M. anisopliae* can infect a broad range of insect hosts.

This study investigates the role of locust cuticular lipids in fungal infection, examining how these surface components influence *Metarhizium* specialists' ability to recognize and penetrate host cuticles. Specifically, we ask: What chemical cues in *L. migratoria* cuticular lipids enable selective fungal infections, and can they influence infection in non-host insects? Our results confirm that specialists do not naturally infect non-specialist targets, *Tenebrio molitor* or *Galleria mellonella* larvae, unless injected, reinforcing the importance of the cuticle as a barrier. However, exposure to polar cuticular lipid extracts from *L. migratoria* potentially influenced the ability of specialists to infect non-host insects. In contrast, non-polar lipids did not appear to enhance infection, but further research is needed to clarify their specific contributions.

Understanding these mechanisms could have broader implications for biological pest control and microbial interactions and highlights the need for further exploration of cuticular components in fungal pathogenesis.

028

MUSCLE ADAPTATION TO HIGH ALTITUDE IN THE WORLD'S HIGHEST DWELLING MAMMAL, *PHYLLOTIS VACCARUM.*

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Surviving at extreme altitudes requires physiological adaptions to combat severe hypoxia (low oxygen) and cold stress. Skeletal muscles, which are essential for both shivering and non-shivering thermogenesis, face significant challenges in these conditions due to their high metabolic cost and reliance on oxygen for energy production. We investigated muscle adaptations in the gastrocnemius, a large hind limb muscle involved in locomotion and shivering, in the Andean leaf-eared mouse (*Pyllotis vaccarum*), which has been documented as the highest-dwelling mammal at ~6,739m above sea level. Specifically, we analyzed capillarity and fiber compositions by sectioning 10 µm slices of preserved gastrocnemius tissue using a cryostat. This was followed by histochemical staining to visualize individual capillaries and oxidative capacity of muscle fibers. These analyses allow us to assess structural modification that may enhance oxygen delivery and utilization in high-altitude populations. Preliminary results indicate no significant differences in capillary density or capillary to fiber ratio between high-altitude populations of *P. vaccarum*, its low-altitude conspecific, and a closely related lowland species *P. darwini*. However, differences in fiber-type composition may still play a role in enhancing physiological performance at high altitudes. Ongoing analyses will further examine fiber compositions (oxidative vs. glycolytic fibers) to determine whether structural muscle adaptations support high-altitude survival. These finding will provide valuable insight into the muscle plasticity and metabolic strategies that support survival in high-altitude environments. Understanding these mechanisms could reveal broader principles of physiological evolution in extreme environments. Supported by NSERC.

029

UPTAKE AND EFFECTS OF MICROPLASTIC FIBER ON FRESHWATER SNAILS

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Microplastics are among the most prevalent contaminants in aquatic water systems. While previous studies have shown that microplastics can cause a decrease in nutrient intake, reproductive output, and survival in some macroinvertebrates, the impacts of mixed microfibers on snails are not fully understood. This study explored how a mixture of polyethylene terephthalate and nylon microfibers affects freshwater snail reproduction and mortality. Accumulation of microplastics in snails was also analyzed to determine if ingested microplastics remained in snails post-exposure. 96 specimens of *Planorbella pilsbryi,* a species of freshwater snail, were exposed over 28 days at control, low (100 parts/L), medium (10,000 parts/L), and high (1,000,000 parts/L) concentrations. Snails were then chemically digested using 10% potassium hydroxide to quantify ingestion of microplastics. A Shapiro-Wilk test assessed for normality and a Kruskal-Wallis test and Dunn's post hoc test were used to find significant differences between treatment groups. Results showed that egg cluster production decreased by 18.4% at medium concentrations, and accumulation of microfibers significantly increased at low and high concentrations by 2.1 and 5.6 times compared to controls. Microplastics exposures did not affect mortality in exposed snails. These findings suggest that freshwater gastropods ingest a significant amount of microplastics, and exposure significantly impacted reproductive success. Ingested microplastics also remained after exposure, suggesting that microplastic retention may have long-term impacts on organisms. This experiment contributes to an improved understanding of the risks microplastics pose to benthic macroinvertebrates like snails, which play a key role in nutrient cycling in aquatic environments.

030

NATIVE INTERTIDAL BIODIVERSITY PLAYS A ROLE IN RESISTING THE ESTABLISHMENT OF THE INVASIVE EUROPEAN GREEN CRAB, *CARCINUS MAENAS*

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Invasive species are among the leading causes of global biodiversity loss. Given the ongoing biodiversity crisis, there has never been such necessity for advancements in our understanding of invasion ecology. Such advancements should emphasize prevention and predicting spread, as it is exceptionally difficult to eradicate invaders once they are established. This challenge is heightened in marine ecosystems. One hypothesis that attempts to explain the factors contributing to an invader's success is the biotic resistance hypothesis which proposes that areas with higher biodiversity are more resistant to invasion. The European Green Crab (*Carcinus maenas*: EGC) has previously established populations worldwide and has done considerable damage to local communities. The EGC has recently invaded northern British Columbia (BC) and poses a threat to many native species of cultural and economic importance. This new population offers a unique opportunity to test the biotic resistance hypothesis because the region is still in the early stages of EGC invasion. I surveyed sites across northern BC and documented the presence of EGC and the native intertidal species richness at those sites. I found that sites with EGC tend to have lower native species richness than sites without EGC. Co-occurrence patterns revealed no species-specific relationships that might impact the EGC's ability to establish. These results provide insight into the ecological mechanisms behind the biotic resistance of invasions. The results can also be used to identify sites most vulnerable to EGC invasion, thereby aiding in their management and protecting native biodiversity.

031

THE EFFECT OF AUTOPHAGY ON CIRCADIAN RHYTHMICITY VIA TARGET OF RAPAMYCIN (TOR) PATHWAY IN *NEUROSPORA CRASSA*

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Circadian rhythms regulate essential biological processes, traditionally understood through transcription-translation feedback loops (TTFLs), but recent studies suggest that metabolic pathways, such as the Target of Rapamycin (TOR) signaling pathway, may also contribute to circadian regulation. TORC1 integrates nutrient availability and cellular energy status, promoting growth while inhibiting autophagy under nutrient-rich conditions, and activating autophagy under starvation to maintain metabolic balance. This study explored the interaction between autophagy and TOR activity in *Neurospora crassa*, hypothesizing that autophagy sustains TOR activation by recycling amino acids. Using the autophagy inhibitors Bafilomycin A1 and MRT68921, we measured TORC1 activity through S6 phosphorylation levels under starvation conditions. Additionally, VTA and GTR2 knockout mutants, key regulators of TOR signaling, were analyzed for their role in this feedback mechanism. Our results indicate that inhibiting autophagy reduces TOR activity, as shown by decreased S6 phosphorylation, supporting the idea that autophagy plays a crucial role in sustaining TOR activation. Furthermore, the effects were dependent on VTA and GTR2, suggesting their involvement in the autophagy-TOR regulatory axis. These findings provide new insights into the role of metabolic oscillators in circadian regulation and highlight a potential conserved mechanism across eukaryotes.

032

A FUNCTIONALLY JAWLESS MUTANT OF THE ZEBRAFISH *DANIO RERIO*

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Zebrafish (*Danio rerio*) are a widely used model organism in molecular genetics and developmental biology. However, both normal and abnormal zebrafish anatomy have been poorly documented, and most phenotypes are only followed to the larval phase. We describe normal and abnormal skull anatomy of zebrafish at the adult phase to: a) provide a resource for late development phenotype analysis; and b) understand the morphological changes that occur in a mutant line with a drastic adult phenotype. We compare wildtype and *nkx3.2*-/- mutant zebrafish, which are functionally jawless (upper and lower jaw fused together). To do this, we developed µCT-based 3D anatomical atlases for both lines. This allowed for direct visual comparison of the two skulls in each individual element. The most striking changes occur in the mandibular arch, particularly in the palatoquadrate. These changes include the fusion of the dentary, the functional separation of the maxilla and premaxilla from the dentary, and the hyperossified jaw joint. These phenotypes arise through plastic remodeling and facilitate bizarre skull morphology that mimics some extinct jawless vertebrates. Using these models, we will next reconstruct skull kinematics in the *nkx3.2*-/- mutant zebrafish in 3D.

033

CYCLOHEXIMIDE MODULATES TARGET OF RAPAMYCIN PATHWAY ACTIVATION IN *NEUROSPORA CRASSA*

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We are studying circadian rhythms, the 24-hour clocks that are present in most eukaryotes and some prokaryotes. The clock protein frequency (FRQ) is important in maintaining circadian rhythms in the fungus *Neurospora crassa*. However, rhythmicity persists in FRQ-less strains. Existing evidence in our laboratory suggests that the Target of Rapamycin (TOR) pathway may function as a circadian oscillator in FRQ-less strains. The protein synthesis inhibitor cycloheximide (CHX), affects the phase of the circadian rhythms in *Neurospora*. Interestingly, the TOR pathway can be activated by CHX, although, the mechanism is not fully understood. Therefore, this work aims to test the hypothesis that CHX-mediated TOR activation occurs through regulation by amino acids. Mutant strains that block amino acid signalling to TOR will be used. The phosphorylation states of S6, a protein in the TOR pathway, will be determined using Western blot analysis to assay for TOR activation. Feedback regulation of TOR by protein synthesis and amino acid pools might contribute to the mechanism of a TOR-based oscillator. This work will help us understand TOR regulation and its role in circadian rhythms.

034

DEVELOPMENT OF SEX-SPECIFIC PLASMA-LIKE CELL CULTURE MEDIA

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Cell culture is widely used to study cells under conditions in which cellular activities can be visualized and measured. Cell culturists have historically aimed to provide their cells with an excess of nutrients to ensure their continued viability and growth. However, this is now understood to affect most cellular functions, including gene expression, metabolism, and growth rates. Recently, Physiological media like Plasmax have been developed and cells cultured in these media have been shown to react differently than in traditional media. Physiological media have been formulated with a population average in mind and do not consider sex, which is not consistent with the Tri-agencies policies to consider sex as a biological variable. My thesis aimed to address this deficiency by developing masculinized and feminized cell culture media, that could be used with cells from male and female donors, respectively. I collected male and female data for 47 human plasma metabolites, from 19 papers and the Human Metabolome Database. The data were from healthy human subjects between the ages of 20-50 years old. I found that concentrations of 21 plasma metabolites were significantly different between males and females ($P<0.05$). I then formulated a male plasma-like medium (MPLM) and a female plasma-like medium (FPLM). Cells will be cultured in these media and supplemented with male or female human serum to create a full cell culture environment. RNA will be extracted and subjected to RNAseq and gene set enrichment analysis to evaluate the effects of the same cells growing in these different media.

035

ACUTE OXYGEN-DEPENDENT EPIGENETIC REGULATION IN RAINBOW TROUT LIVER: IS H3K4ME3 LINKED TO INDUCED METABOLIC GENES?

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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_2 saturation) in the trout liver. Contrary to prediction, results show 25% O_2 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_2 dependent (epigenetic) molecular mechanisms are involved in the induction of these enzymes. Additional studies looking at different hypoxia regimes and O_2 sensitive epigenetic markers are warranted to further address the role of epigenetic regulation on metabolic pathways in hypoxia response in fish.

036

EXAMINING THE CAUSE AND PATTERNS OF ULTRAVIOLET-INDUCED FLUORESCENCE IN NORTHERN (*GLAUCOMYS SABRINUS*) AND SOUTHERN FLYING SQUIRRELS (*G. VOLANS*) IN ONTARIO, CANADA

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Many animals across several taxa exhibit ultraviolet-induced fluorescence. The pelage of all New World flying squirrels (*Glaucomys* spp.) fluoresces under ultraviolet light, with some variability among individuals. The hypothesized fluorophores responsible are porphyrins – photodegradable compounds produced during the heme production pathway. To further test the porphyrin hypothesis and assess and characterize the variation in flying squirrel fluorescence, I photographed northern flying squirrels (*G. sabrinus*) and southern flying squirrels (*G. volans*) under ultraviolet light at an established field site in Central Ontario. To determine what intrinsic and extrinsic variables might be related to inter- and intraindividual differences in fluorescence, I categorized each set of photos (n = 265) based on whether they showed any of the standard fluorescence patterns I defined. I then performed general linear mixed effects models to determine which variables (species, sex, age, date) predict the presence of each pattern. If porphyrins are responsible, I would expect fluorescence to change around moulting time and be different in juveniles vs. adults due to differing amounts of light exposure to the pelage. I found that nearly all fluorescence patterns were predicted by date, and some were additionally predicted by sex or age. These temporal and age- and sex-based differences could suggest some ecological importance of fluorescence or could simply reflect the photodegradable nature of porphyrins. Future work is needed to assess whether these fluorescence patterns hold ecological importance for species in this genus.

037

AMPK: A Key Player in Combating Skeletal Muscle Fibrosis in Cancer Cachexia

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Introduction: Cancer cachexia affects 50-80% of cancer patients, causing severe muscle loss, systemic inflammation, and metabolic dysregulation, which significantly reduces patient survival and quality of life. AMP-activated protein kinase (AMPK) is an energy sensing enzyme that regulates various signaling pathways that ultimately influence skeletal muscle morphology and function. Disruptions in AMPK signaling have been documented in cachectic patients suggesting a role for this kinase in maintaining skeletal muscle mass. **Methods:** To study the role of AMPK in this atrophic model, cancer cachexia was induced in 11-week old mice with a subcutaneous injection of 1 million Lewis Lung carcinoma (LLC) cells, with healthy controls treated with PBS. 1 week post-tumour inoculation, LLC mice began daily oral administration of the AMPK activator MK-8722 (LLC^{MK}) or a vehicle (LLC^{Veh}). Mice were sacrificed 4 weeks post-tumour inoculation and the extensor digitorum longus (EDL), quadriceps and blood serum were collected. Skeletal muscle fibrosis was analyzed using Picrosirius Red staining. **Results:** The LLC^{Veh} group had a significantly greater percentage of collagen deposition within the EDL, compared to the control ($p<0.05$), while MK treatment decreased fibrosis to healthy levels. Serum from LLC^{MK} mice exhibited a significant increase in C-C motif chemokine ligand 2 (CCL2) concentration ($p<0.05$) compared to the control while skeletal-muscle derived tumor necrosis factor alpha (TNF-α) mRNA was increased in the LLC^{MK} group compared to LLC^{Veh} ($p<0.05$). **Conclusion:** This study provides evidence that pharmacological AMPK activation can mitigate skeletal muscle fibrosis in cachectic mice despite concurrent increases in systemic and local cancer-related inflammatory markers.

038

A PILOT INTRODUCED-PLANT-FOCUSED CITIZEN PROJECT IN CHURCHILL, MANITOBA

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Plant invasions currently are scarce at high latitudes, likely as a result of low temperatures and short growing seasons, but this may change as the climate warms: temperatures are increasing at up to 4 times the global average in arctic regions. For instance, more than 100 introduced plants already have been recorded in Churchill, Manitoba (58.5° N), an exception to the rarity of introductions in tundra and treeline habitats. Most of these plants have not persisted, but an unknown number of species have established long-term populations. I have been investigating the feasibility of launching a citizen science project on plant invasions in Churchill, in order to allow cost-effective, long-term collection of data on species occurrence and persistence. Introduced plant observations from iNaturalist, although low in number, have helped to identify observation and invasion hotspots. A literature review and investigation of established citizen science projects suggest that the feasibility of launching an introduced-plant-focused citizen science project is low to moderate, mostly due to the low number (870) of residents in Churchill. Nevertheless, I have designed a trial introduced-plant-focused citizen science project for Churchill, “Ecology IN You”, including an online training phase and a data collection phase. “Ecology IN You” is expected to be further refined in the summer of 2025, and if successful, could be useful in tracking populations of invasive species. Educational materials on introduced plant are also being developed to help recruit volunteers, and to provide information on non-native species to the local community.

039

EVALUATING THE ACCURACY OF VEGETATIVE INDICES IN TRACKING DROUGHT INDUCED PIGMENT CHANGES IN CONIFERS

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Extreme drought is expected to increase in severity with climate change, posing a serious threat to boreal forest health. Spectral reflectance has streamlined vegetation health assessment by enabling the rapid assessment of plant physiological traits, such as photosynthetic efficiency and water stress. This study aims to evaluate the sensitivity and accuracy of different vegetative indices for detecting drought stress in two abundant Canadian conifer species, *Picea glauca* and *Pinus strobus*. Specifically, we assessed the ability of frequently used indices, including the normalized difference vegetation index (NDVI), the photochemical reflectance index (PRI), and the chlorophyll/carotenoid index (CCI), to detect drought-induced pigment changes. Additionally, we determined the relationship between leaf- and canopy-level measurements, and explored additional indices that may serve as effective drought stress indicators. In response to drought stress, chlorophyll pool sizes were reduced, while photoprotective carotenoid pigments were accumulated. Additionally, the shift towards photoprotection was observed through the increased de-epoxidation of violaxanthin into zeaxanthin through the xanthophyll cycle. The strong correlations between pigment changes and PRI and CCI suggest that these indices are very effective in drought stress detection. Additionally, the strong correlation between leaf- and canopy-level measurements suggests that canopy-level data can effectively represent leaf-level physiological changes. These findings highlight the potential applications of spectral reflectance for forest health monitoring and management in a changing climate.

040

EFFECTS OF TLR4 INDIVIDUAL GENETIC DIVERSITY ON MATE CHOICE AND SURVIVORSHIP IN SONG SPARROWS (*MELOSPIZA MELODIA)*

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The ability of natural populations to defend themselves against infectious diseases depends on immune gene genetic diversity. Toll-like receptors (TLRs) play key roles in recognizing pathogens and initiating innate immune responses. In song sparrows (*Melospiza melodia*), although no strong link has been found between individual genetic diversity at Toll-like receptor 3 (TLR3) and apparent survivorship, mating is non-random with respect to TLR3 genotype, indicating that TLR genotypes may influence mate choice. Toll-like receptor 4 (TLR4) recognises lipopolysaccharides, which are common in major avian pathogens. Despite TLR4's importance, little is known about how genetic diversity at this locus affects fitness or whether individuals mate non-randomly with respect to TLR4 genotype. To explore this, I tested how individual genetic diversity at TLR4 affects apparent annual survivorship and social mate choice in song sparrows. Through PCR amplification and Sanger sequencing of the extracellular domain of TLR4, I characterized individual genetic diversity. Using Program MARK, I assessed whether increased TLR4 genetic diversity leads to increased apparent survivorship (inferred from annual encounter histories), potentially due to a greater ability for pathogen recognition. Then, to assess whether mate choice is non-random with respect to TLR4 genotype, I calculated and compared pairwise TLR4 genetic distance (UniFrac) between socially mated pairs to all possible pairings to determine if song sparrows are mating disassortatively at TLR4. Results will be discussed. This research will shed light on the extent to which natural and sexual selection maintain genetic diversity at this innate immune gene.

041

BACTERIAL TRANSLOCATION AND IMMUNE CELL INTERACTIONS IN A MOUSE RESTRAINT STRESS MODEL

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Bacterial translocation is defined as the migration of bacteria or bacterial fragments from the gut to extraintestinal organs. This process has been implicated in the pathophysiology of gastrointestinal disorders, including irritable bowel syndrome (IBS). Experimental stress models reproduce some features of IBS, showing that gut bacteria can translocate into distal organs. However, the mechanism and impact of bacterial translocation remain unclear. To investigate bacterial translocation in a mouse restraint stress model, focusing on immune interactions in the intestine. SPF C57BL/6 mice were assigned to either the restraint stress group or the non-stress control group. Each group was further divided into two subgroups: one receiving a vehicle and the other inoculated with auxotrophic *Salmonella enterica* serovar *typhimurium HA630* via oral gavage three times per week during the stress period (n=6-14 per group). We collected jejunum, colon, myenteric lymph node, liver, and spleen samples for histology and performed iterative bleaching extends multiplexity (IBEX) staining and fluorescence in situ hybridization (FISH). We also sampled blood, liver, spleen, and brain for bacterial cultures under aseptic conditions. Our culture and histology data showed that transient colonizer *Salmonella typhimurium* enhanced stress-induced bacterial translocation. IBEX and FISH staining demonstrated that intestinal bacteria invaded the intestinal mucosa and co-localized with goblet cells in the intestines. Further, in the stress + *Salmonella* group, some bacteria were found were in close proximity with CD103$^+$ cells and neurons. This study provides mechanistic insight into stress-related disorders and offers new perspectives on the role of the gut microbiota in neuroimmune regulations.

042

INVESTIGATING THE ROLE OF ARPC4 IN HUMAN NEURODEVELOPMENTAL DISORDERS

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Mutations in the ARPC4 gene, which encodes a critical structural scaffold for the Actin-Related Protein 2/3 (ARP2/3) complex, have been implicated in neurodevelopmental disorders characterized by microcephaly and speech impairments. The ARP2/3 complex plays an essential role in creating branched actin networks that facilitate cellular movement, vesicle trafficking, and organelle remodeling. Recent clinical findings have identified a *de novo* p.Arg158Cys mutation in ARPC4 as pathogenic, affecting seven individuals who present with severe motor delays, speech impairments, and primary microcephaly. This study aims to further characterize the functional role of ARPC4 in neuronal development through in vitro analysis of neuronal morphology and electrophysiology. We hypothesize that ARPC4 deletions will disrupt the actin cytoskeleton, resulting in reduced neuron size, impaired dendritic outgrowth, and inappropriate synaptic activity. Our research will employ three main approaches: (1) generation of induced pluripotent stem cell (iPSC) lines with ARPC4 deletions, (2) morphological analysis using 2D assays, and (3) development of organoids from clonal ARPC4 mutant human pluripotent stem cells (hPSCs). By comparing these genetically modified cultures with wild-type controls, we aim to elucidate the significance of ARPC4 in neurodevelopment and identify potential therapeutic targets to rescue abnormalities associated with ARPC4 dysfunction or related pathways.

043

IDENTIFICATION OF MONOAMINERGIC AND CHOLINERGIC PATHWAYS IN CUTANEOUS SENSORY CELLS OF DEVELOPING ZEBRAFISH.

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Many physiological mechanisms are still undescribed in sensory systems of developing vertebrates. Such pathways are essential to our understanding of these species, and the methods by which they sense their environment to maintain homeostasis. One 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), mitochondrion-rich cells (MRCs) and neuromast cells (NMs). NECs are implicated in sensing and responding to hypoxia, MRCs are important in the maintenance of osmotic homeostasis, and NMs 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 catecholaminergic 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, a novel catecholaminergic pathway in MRCs, and characterized, for the first time, a dopaminergic receptor (the D2 receptor) in NMs. The results not only enhance our understanding of physiology in developing zebrafish but further inform existing applications and give insight into novel uses for zebrafish as a model organism.

044

AGE-ASSOCIATED SKELETAL MUSCLE LOSS IS MITIGATED WITH CHRONIC AMPK ACTIVATION

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Background: Age associated skeletal muscle loss predominantly impacting glycolytic muscle fibers, can result in an increased risk of hospitalization, loss of independence and all-cause mortality. Glycolytic muscle fibers enable quick movements, essential for daily activities. Reduced AMP-activated protein kinase (AMPK), an enzyme supporting muscle homeostasis, may contribute to increased deterioration of muscle fibers with aging. Thus, the purpose of this study is to determine whether chronic AMPK activation can mitigate the age-related loss of muscle mass and cross-sectional area (CSA) in aged mice. **Methods:** Old (~18 months) wild-type C57BL/6J mice, were randomly assigned to receive either 10mg/kg of the small molecule AMPK activator MK8722 (Old-MK) or a vehicle (Old-Veh). Both groups received their respective doses every other day via oral gavage for a duration of 6 months. Young 3-month-old mice were used as a control. The gastrocnemius (GAST) was then extracted, weighed and stained to investigate muscle fiber CSA. **Results**: Muscle mass of the GAST was significantly greater in MK8722 treated animals as compared to Old-Veh mice. Furthermore, we demonstrated a significant decrease in CSA and minimum feret diameter in the glycolytic regions of GAST muscle from Old-Veh mice relative to young mice, which was not observed in treated animals. Observations were due to a rightward shift in the fiber size distribution of Old-MK mice relative to Old-Veh. Oxidative fibers showed no significant difference across all groups. **Conclusion**: Direct AMPK activation via MK8722 may play a protective role in age-related muscle deterioration primarily through the preservation of glycolytic fiber size.

045

TAKING THE PERMAFROST’S PULSE: PLANT COMMUNITY RESPONSE TO PERMAFROST THAW.

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With rapid surface warming, permafrost soils are thawing and releasing vast stores of resources previously sequestered in the frozen ground. Permafrost contains twice as much carbon as the atmosphere, and as it thaws, this carbon and associated nitrogen become biologically available, allowing microbial activity to convert them into greenhouse gases. This release amplifies climate change through a conversion from a carbon sink to a carbon source. Past studies have investigated how this newly available nitrogen will impact vegetation of upland systems, but not yet for a lowland system. This study investigates the impacts of a simulated permafrost resource pulse on plant community structure, biomass, plant available nutrients, and foliar C:N in a nitrogen-limited Alaskan lowland system. The study was conducted in a bog near Fairbanks, Alaska, to examine how nutrient additions at two different soil depths and two different times influence plant response in permafrost plateau and active thaw margin areas. The effects of increased nitrogen availability will be assessed using a combination of vegetation surveys, foliar chemistry analysis, and plant root simulator probes. This study is critical for understanding how resource pulses from permafrost thaw influence permafrost peatlands and to provide insights for predicting global climate change processes through permafrost thaw effects.

046

HOW DO SMALL HABITAT PATCHES SUPPORT HIGHER BIODIVERSITY FOR AN EQUIVALENT HABITAT AREA?

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Habitat fragmentation is widely recognized as a threat to biodiversity, yet some studies suggest that small habitat patches can support higher species diversity than larger ones. This study explores the mechanisms behind this phenomenon, focusing on spatial turnover (species replacement between patches) and species sorting with local stability (specialists establishing stable populations in small patches). Using a metacommunity model, we simulated landscapes of 25, 81, and 289 patches, maintaining constant ecological parameters such as species reproduction, movement, and habitat suitability. Each scenario was replicated 30 times over 250 generations, tracking species richness (S), total abundance (N), and turnover rates. Results showed small patches supported nearly twice the species richness of large patches. However, turnover increased over time in large patches, indicating species loss, while small patches maintained stable turnover, suggesting compositional stability. Specialist turnover declined faster than generalists, reinforcing their stability in small patches. Habitat suitability influenced richness differently by patch size: generalist richness increased with suitability in large patches, while specialist richness followed an unimodal pattern. In contrast, small patches showed no clear generalist trend but a unimodal specialist response. These findings indicate that species sorting, rather than high spatial turnover, drives biodiversity in small patches. Small patches act as ecological filters, favoring specialists and stabilizing biodiversity. This challenges the assumption that large, continuous habitats are always superior and highlights the conservation value of small, well-connected patches in fragmented landscapes.

047

CAUGHT IN THE ACT: ASSESSING LURE TYPE EFFECTS ON JAPANESE BEETLE (POPILLIA JAPONICA) TRAP CAPTURE

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Japanese beetle (*Popillia japonica*) is an invasive pest of over 300 host plant species, including ornamental trees and shrubs, nursery plants, and agricultural crops. Recent establishment of Japanese beetle in British Columbia demands an urgent and robust response to prevent its spread. Efficient biosurveillance methods and a thorough understanding of Japanese beetle's biology and behaviour are important for continued management and monitoring of the species. Kairomone and pheromone dual lures are commonly used in Japanese beetle traps and have been shown to result in effective capture, however, little is known about the influence of lure type on the sex distribution and magnitude of trap capture, especially when considering potential phenological patterns. To explore this relationship, we examined catch rate and sex ratio in Japanese beetle traps baited with kairomone, pheromone, and dual lures during the adult activity period (July-August). Our results suggest that lure type influences trap catch rate as well as the sex ratio of the trap capture. Additionally, these effects appear to be connected to phenological patterns in Japanese beetle sex distribution within the population and may provide evidence for early male emergence.

048

REFINING CELL CULTURE TEST METHODS FOR ENVIRONMENTAL PROTECTION

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The 2023 revisions to the Canadian Environmental Protection Act (CEPA) have led to commitments to eliminate vertebrate testing. This will pose challenges for Environment and Climate Change Canada seeing as environmental quality guidelines depend on toxicity tests of vertebrates (e.g fish). Alternative methods are the answer to overcoming these challenges. By observing the responses of cultured cells exposed to copper concentrations we can uncover obstacles and work towards solutions. Cell cultures were used as an alternative method to observe the effects of copper and its free ion forms. Cells from the cell line RTG-2 (rainbow trout gonad) were exposed to high and low ranges of copper on a 96-well plate, to effectively measuring the cell viability. Different geochemical variables will be employed to observe the bioavailability of metal ions and corresponding cellular effects. Using simulation programs and free ion electrodes, the free ion concentrations under different environmental conditions will be measured. The cell viability assays showed the toxicity of copper to not be considerably strong when below 160 mg/L. The simulator showed numerous non-toxic products formed from the complexations of copper with components in the growth media, which reduce cytotoxic effects. Regulations in Europe like registration, evaluation, authorization and restriction of chemicals (REACH) drive the reduction in animal use around the world. This research aims to provide reliable metal toxicity data that can be used as an alternative to vertebrate testing for water quality guidelines in Canada. Research supported by NSERC and Environment and Climate Change Canada.

049

THE ROLE OF MALE BODY SIZE AND EYE COLOUR IN MEDIATING FEMALE REPRODUCTIVE DYNAMICS IN *Drosophila melanogaster*.

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In *Drosophila melanogaster*, like many species, selection on individual fitness often results in conflicting reproductive tactics in males and females. While both sexes benefit from reproductive success, their optimal mating strategies conflict, resulting in intersexual conflict. This conflict arises because males aim to mate as frequently as possible to maximize reproductive output, whereas females benefit from fewer matings to conserve energy for offspring production and feeding. These conflicting reproductive interests drive costly behaviours. One prominent manifestation of sexual conflict in *D. melanogaster* is male harassment, where persistent courtship and repeated mating attempts disrupt female behaviours and negatively affect offspring production. While the effects of sexual conflict are well-known, there is variation in its expression, potentially due to male characteristics. We investigated two male traits important to harassment dynamics: body size (large males may harass more than small males) and eye colour (being able to locate females more easily may increase harassment). In our first assay, we studied the effect of male eye colour on mate tracking, courting, and harassment. The second assay focused on how male body size influenced harassment intensity and female reproductive success. Surprisingly, female flies housed with males visited food patches more frequently and produced more offspring than those kept alone. This increase was not due to remating or the fecundity boost from accessory proteins (Acps) but likely a social signal associated with male presence. These findings suggest male presence influences female reproductive outcomes through social cues and that sexual conflict dynamics have unexpected dimensions.

050

IMPACT OF CHRONIC SUBLETHAL NEODYMIUM EXPOSURE ON FATHEAD MINNOWS AND ARCTIC CHARR.

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The increasing prevalence of Neodymium (Nd), a rare earth element, in aquatic ecosystems due to industrial runoff necessitates an understanding of its chronic effects on freshwater organisms. This study investigates Nd bioaccumulation in Fathead minnows (*Pimephales promelas)* both adults and juveniles, and Arctic char (*Salvelinus alpinus*) alevins under controlled laboratory conditions. Adult minnows were exposed to sublethal Nd concentrations (100, 200, and 400 µg/L) for 96h in a flowthrough system, maintaining water parameters (80–100 µs/cm, 10–40 mg/L hardness, pH 7.2, and 19–21°C) to reflect natural conditions. Tissue samples from gills, liver, kidney and muscle were analyzed for Nd accumulation. Juvenile minnows were exposed to either 50 and 100 µg/L Nd for 72h under similar conditions, with whole-body samples collected for analysis. Arctic char alevins underwent a 3-week exposure of 7 Nd concentrations (10–640 µg/L) in soft water (200–205 µs/cm, 80–95 mg/L hardness, pH 6.9–7.5, and 7°C), and whole-body samples were examined for bioaccumulation. Findings from this study provides crucial insight into the extent of Nd accumulation across different life stages and species, highlighting potential ecological consequences. By identifying Nd bioaccumulation patterns, this research informs environmental risk assessments and supports the need for regulatory measures for environmental protection. This work is funded by NSERC & Environment and Climate Change Canada with contributions from Stantec and Vital Metals.

051

THE EFFECTS OF VENLAFAXINE AND HYPOXIA ON RAINBOW TROUT

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Antidepressant prescription rates are increasing, leading to their excretion in a neuroactive form that often bypasses wastewater treatment plants and contaminates surface waters. Within these aquatic environments, multiple stressors exist, including low oxygen levels (hypoxia) resulting from anthropogenic activities like agricultural runoff. They detect changes in oxygen using gill neuroepithelial cells (NECs), which use serotonin to engage coping mechanisms. Fish have developed behavioral adaptations like increased opercular movement and aquatic surface respiration to cope with hypoxia. Considering that venlafaxine, a widely prescribed antidepressant, works by inhibiting the reuptake of serotonin and norepinephrine, how might hypoxia tolerance be affected when exposed to venlafaxine? This study investigated venlafaxine's potential impact on oxygen sensing in juvenile rainbow trout (*Oncorhynchus mykiss*). We exposed fish to control, two environmentally relevant concentrations of venlafaxine (0.1 and 1 µg/L), or a higher concentration of 10 µg/L for 24 hours in 12L tanks. Fish were placed into a flow-through system to gradually reduce oxygen levels to10% dissolved oxygen until loss of equilibrium (LOE) occurred. LOE is often measured to determine hypoxia tolerance. Behavioural metrics such as distance travelled, velocity, acceleration, and time to LOE were quantified using EthoVisionXT video tracking software. Blood glucose levels were collected to measure energy mobilization. Behavioural metrics were not significant among treatments; however, blood glucose levels were significantly lower in the 1 and 10 µg/L treatments compared to the control. This suggests that high concentrations of venlafaxine act as a potential beta-blocker during severe hypoxia and may impair energy mobilization.

052

SEEDS OF CHANGE: IMPACTS OF PERMAFROST DISTURBANCE ON TUNDRA SHRUB REPRODUCTION

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As permafrost thaw in the Canadian tundra accelerates with rapid climate warming, permafrost disturbances are becoming common on the landscape. Thaw slumps and polygonal terrain have both been shown to play a significant role in facilitating vegetation change, especially in the proliferation of tall shrub populations. This shift towards tall shrub tundra landscapes is happening across global arctic environments. Reproduction is a significant driver of change in these systems as it drives dispersal and establishment. Permafrost disturbances provide favorable conditions for shrub establishment with the exposure of open ground, warm conditions, and thicker active layers. This study focuses on the reproductive traits of two common species, green alder (*Alnus alnobetula*) and dwarf birch (*Betula glandulosa*). Their establishment and reproductive success were evaluated at 7 polygonal terrain and 6 thaw slump sites and compared to adjacent undisturbed tundra near Inuvik, NWT. Through in-field surveys of cone presence and juvenile recruitment along with an in-lab viability study on their seeds, their reproductive traits have been quantified. Shrubs within disturbances were more likely to produce cones and their seed exhibited increased germination rates, indicating a positive impact of disturbance on reproductive output. However, the number of juveniles present in control plots was generally higher than within disturbance, indicating growth in disturbance is not positively influencing establishment. As permafrost disturbances become more prevalent on the landscape, the plant communities established within them will shape future arctic ecosystem feedback to global climate systems and ultimately tundra biodiversity as a whole.

053

WAVELENGTHS OF INFLUENCE: BLUE LIGHT AND ITS ROLE IN MEMORY AND MATE-CHOICE IN FRUIT FLIES

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The capacity for learning and memory is crucial for success across species, making it important to study factors that influence these abilities. Recent research suggests blue light negatively impacts physiological and neurological functions, potentially affecting learning and memory. To investigate this, we examined whether blue light had neurodegenerative effects using fruit flies (*Drosophila melanogaster*), a well-established model for studying cognition and aging. In two experiments, virgin female fruit flies were exposed to blue, red, or white light on a 12-hour cycle for three weeks. The first experiment tested their ability to associate an unpleasant taste (quinine) with a visual cue (striped or zig-zag pattern). Learning was generally poor across treatments, but flies associated the negative cue more effectively with the zig-zag pattern than with the striped one. The second experiment examined mate-choice copying by measuring how frequently females selected males with a phenotypic marker (green or pink dust), potentially indicating reproductive quality. A trend toward mate-choice copying emerged in white-light-exposed flies, but no learning was observed in blue- or red-exposed groups. White-exposed flies also behaved differently toward males with cues signaling reproductive success. Overall, these findings suggest that blue light may impair learning in some contexts but have no measurable effect in others, highlighting the complexity of its impact on cognition and pointing to intriguing directions for future research.

054

THE ROLE OF CLAUDIN-14 IN MEDIATING THE PROTECTIVE EFFECTS OF WATER CALCIUM HARDNESS IN FISH EXPOSED TO HIGH PH WATER.

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Many fish struggle to survive in high-pH water because of ion regulation disturbance, increased ion loss and, impaired ammonia excretion which led to physiological stress. Some study has indicated calcium ions mitigate some of these effects however, the exact molecular mechanism remains unclear. This study aims to investigate the role of Claudin-14 in mediating effects of calcium ions on the metabolic stress induced by alkaline condition in *Astyanax mexicanus*. Bothe surface and cave morphs have been exposed to alkaline water with normal and elevated calcium concentration levels. Standard and maximum metabolic rates were measured by respirometry followed by analyzing the ion concentration of plasma and muscle tissue. Claudin-14 expression in the gill will be quantified via western blotting. Results indicate that standard methabolic rate in alkaline water increases for both morphs however, surface morph had a greater increase than cave morph. Moreover, elevated calcium levels significantly reduced standard metabolic rate in both morphs. Moreover, in fish exposed to elevated calcium and alkaline water, it decreased significantly. Maximum metabolic rate was lower in cave morphs than in surface morphs, and alkaline water further decreased it in both groups. Additionally, elevated calcium level led to increase in maximum metabolic rate. These findings suggest that alkaline water stress increases metabolic demand while calcium helps mitigate this stress. Further analysis of Claudin-14 expression will clarify its specific role in this protective response.

055

EXPLORING PHOSPHORUS CONCETRATIONS IN *Tigriopus californicus* SALTWATER HABITATS AND THEIR PROLONGED EFFECTS

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Tigriopus californicus is a saltwater species primarily found along the Pacific Coast of North America. Various environmental stressors can impact species performance, particularly during reproduction, including temperature, salinity, and pH levels. *T. californicus* is a promising model for understanding the mechanisms of environmental stressors on copepods. In assessing these stressors, it is important to evaluate whether *T. californicus* can withstand high concentrations of $NaHPO_4$. To examine phosphorus levels in copepod habitats, two treatment groups were established, each with different phosphorus concentrations. One treatment contained 0.2 ppm $NaHPO_4$, and the other 0.002 ppm, compared to a control with no added phosphorus. Results showed that 0.2 ppm was a high concentration that killed 90% of the population within 30 days, whereas the 0.02 ppm treatment progressed well. By the end of the trial, copepods in the 0.02 ppm habitats matured faster than those in the control. The initial goal was to determine a concentration that supported survival without harm. Unexpectedly, the 0.02 ppm group not only survived and reproduced but also matured significantly faster than copepods in regular habitats during the same period.

056

TESTING THE EFFECTS OF HYPOLIMNETIC AERATION IN A POLLUTED NORTHERN LAKE.

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Over the last several decades, many freshwater lakes exposed to nutrient pollution have been experiencing periodic low oxygen levels as a result of eutrophication. An example is Frame Lake, located in Yellowknife, Northwest Territories. Frame Lake experiences anoxia (the absence of oxygen) in the winter months, resulting in the absence of fish species and a decrease in rotifers, an important group of zooplankton for fish diets. A rehabilitation project is underway on Frame Lake which implements aeration in the hypolimnetic zone (deepest layer in a stratified lake) to increase dissolved oxygen concentrations. This study aims to characterize the effects of hypolimnetic aeration on Frame Lake and identify alterations in water quality and the rotifer community. I will be using survey data for water quality and rotifer samples collected between 2023 and 2024 to provide information on pre-aerator conditions. Rotifer communities will be evaluated for rarefied richness, diversity and total abundance. I have collected new rotifer and water quality data in winter 2024/2025 to characterize post-aerator conditions. This project is important as it will tell us if hypolimnetic aeration is a feasible rehabilitation strategy for northern lakes that have lost biodiversity due to eutrophication.

057

EDNA & SCDNA AS A TOOL FOR CHARACTERIZING PISCIVORE FEEDING ECOLOGY IN LAKE ST. CLAIR

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Freshwater ecosystems are under threat due to a myriad of anthropologic effects and invasive species. Within freshwater habitats, predation is arguably the most influential factor in shaping ecosystem function and serves as the basis of trophic web interactions. This study aims to characterize predator-prey dynamics in Lake St. Clair using mitochondrial DNA analysis of stomach content DNA analysis via HT-qPCR on OpenArray® chips alongside environmental DNA metabarcoding. Stomach content DNA (scDNA) refers to DNA extracted from the digestive tracts of predators to identify consumed prey, while environmental DNA (eDNA) consists of genetic material shed by organisms into their surroundings through skin, mucus, feces, or other biological processes. The data sets analyzed include eDNA sampled from various locations within Lake St. Clair, complemented by scDNA of yellow perch (*Perca flavescens*) and walleye (*Sander vitreus*), collected within 24 hours of the eDNA at the same sites. This dual approach enhances the resolution of predator-prey interactions by linking prey consumption to ambient community eDNA. Data analysis is ongoing; however, preliminary eDNA metabarcoding results have detected the presence of the predator species of interest, as well as multiple prey species. Final results will provide critical insights into trophic linkages within the lake, allowing for better understanding of these predator-prey dynamics. This understanding is essential for ecosystem assessments and can serve as a foundation for evidence-based conservation strategies to preserve biodiversity and ecological integrity in freshwater systems.

058

IMPACTS OF HUMAN-MADE NOISE ON THE PRESENCE AND SONG STRUCTURE OF EURASIAN BLACKCAPS (SYLVIA ATRICAPILLA)

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Human activities have transformed natural environments, introducing noise from traffic, industry, and urbanization. Human-made noise interferes with animal communication, posing a significant challenge for wild animals that rely on vocalizations for territory defense and mate attraction. In some instances, animals are driven out of available habitat by urban noise, while in others, they adapt to urban noise by raising the pitch of their songs to avoid being masked by human-made noise. In this study, our goal was to investigate the impact of urban noise on habitat occupancy and singing behavior of a European songbird, the Eurasian Blackcap (*Sylvia atricapilla*). We used autonomous recorders to collect ambient recordings at 165 sites across urban environments in Paris, France. We evaluated the ambient noise levels within each recording, assessed the presence of Blackcaps, and measured acoustic features of Blackcap songs. We found that Blackcaps were more likely to be present at sites with lower noise levels (49.5 ± 0.9 dB(A)) compared to those with higher noise levels (55.0 ± 0.5 dB(A)), suggesting that Blackcaps preferentially occupy quieter urban areas. We found no correspondence between ambient noise and Blackcap song characteristics, suggesting that Blackcaps do not adjust their song structure in response to high urban noise. We conclude that rather than modifying their songs, Blackcaps adapt to urban noise by avoiding high-noise areas. By understanding how songbirds respond to urban noise, this study can inform urban planning and noise management strategies that support avian populations in increasingly noisy cities.

059

EFFECTS OF ANTHROPOGENIC NOISE IN PARIS ON THE EUROPEAN ROBIN

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Anthropogenic noise levels around the world have been increasing. With this rise in noise levels, we observe changes in animal behavior. The people of Paris, France, have attempted to fight noise pollution in recent years, but are these efforts enough to influence the behaviour of urban birds? In this study, our goal was to investigate European Robins (*Erithacus rubecula*) in an environment with high levels of anthropogenic noise and evaluate whether their presence and song features were influenced by noise levels. We recorded bird song in 166 locations, in parks and urban spaces in downtown Paris. At each location, we determined if robins were present or not. For locations with robins, we isolated one high quality song, measured the number of song syllables, song length and the maximum and minimum song frequency. We observed that European Robins were less likely to be found singing in high levels of anthropogenic noise and our song analyses indicate that there was no correlation between song features and anthropogenic noise. We conclude that European Robins are either not present, or less vocal, in areas with increased anthropogenic noise suggesting a low tolerance to noise. When they are present, they do not show changes in their song structure in relation to noise features. These findings imply that bird species, such as European Robins, are not tolerant of anthropogenic noise and may struggle to communicate in noisy areas or depart from available habitats in an attempt to escape urban noise.

060

WHITE SHARK SCARRING IN AUSTRALIAN WATERS: WOUND CLASSIFICATION, DISTRIBUTION AND ACCUMULATION RATES

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Animal interactions are complex to study underwater due to challenges of the environment and limitations of current direct sampling techniques. Analysis of animal scarring offers an alternative to traditional approaches to assess both intra- and interspecies interactions (i.e. interactions with conspecifics or predators and prey, respectively), while also allowing identification of individual animals, assisting health assessments and monitoring anthropogenic impacts. Here, we quantified injuries observed on white sharks off Southern Australia, identified the origin of these injuries, determined wound acquisition of individual sharks over time and assessed their distribution over 12 distinct body zones on this predator. Assessments were conducted using high quality images of 20 randomly sampled white sharks, 10 females and 10 males, taken during systemic cage diving operations between June 2010 to November 2014. Images were screened for analysis based on pre-defined criteria and provided a time series of wound patterns ranging from weeks to years for each individual. Scarring analysis identified nine distinct injury categories on the body of sampled white sharks: claw marks, tooth rakes, amputation (i.e. part of appendage missing; ex: fin or tail), shark bite, seal puncture wounds, anthropogenic, cookie cutter, invasive science contact and unidentified injuries. These injuries were primarily observed on the dorsal trunk and head regions, with claw marks being the most abundant. Understanding the frequency and extent of white shark predator-prey interactions and anthropogenic threats through non-invasive scarring analysis is necessary to inform on the ecology and impacts to this species for ongoing management and conservation efforts.

061

THE RELATIONSHIP BETWEEN SOCIAL CALLS AND FLIGHT BEHAVIOURS IN BIG BROWN BATS

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The use of echolocation calls for orientation has been well-studied across bat species, but the functions of their social calls have not. Social calls have been documented in many species and appear to have multiple functions, such as food claiming or avoiding collisions. Big brown bats (*Eptesicus fuscus*), which are abundant in North America, have social calls that may be emitted during interactions in flight; however, not all of these social calls have identified functions, or they may have different functions in different contexts. This study documents the interactions between big brown bats to identify the relationship between specific behaviours and specific social calls. Pairs of male bats were released into a large flight enclosure and their calls and behaviour were recorded on microphones and an acoustic camera to determine the relationship between calls and behaviour. The acoustic camera overlays a heatmap of the sound onto video, providing information about which bat produced each call. Preliminary results suggest that one type of call signals avoidance behaviour, but further analysis is required to identify the behaviours pertaining to specific social calls.

062

WHAT'S ALL THE BUZZ ABOUT: HABITAT USE OVERLAP IN BATS AND AERIAL INSECTIVORE BIRDS

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Aerial insectivores are a charismatic group of birds and bats that consume insects during flight. In southern Ontario, aerial insectivore birds have gained attention from the scientific community by being classified as the steepest declining bird population, becoming locally endangered. This is thought to be due to the reduction of insect populations from human disturbances. Essex County has a mix of natural and urbanized areas, which provides an ideal environment for investigating how different habitat types might be used by local species of aerial insectivores. The objective of the current study is to compare the habitat use by aerial insectivores in naturalized and human-modified environments. This study recorded vocal activity of aerial insectivore birds and the echolocation calls of bats across four unique habitat types (forest vs suburban; prairie vs agricultural). The short echolocation buzzes indicative of feeding behaviour were also quantified for bats. Bird and bat vocal activity were analyzed using both automated software and visual inspection of spectrograms. if human habitat modification decreases daytime and nocturnal flying insect abundance, then it is expected that both aerial hawking bird and bat activity will be higher in natural than modified habitats. Results are expected to demonstrate an overlap in aerial hawking bird vocal activity with bat feeding buzzes, particularly in naturalized habitats. Aerial insectivores uniquely benefit ecosystem health by providing natural insect control. Observing the overlap of daytime and nocturnal aerial insectivore habitat use can be used to inform conservation strategies for these species.

063

ASSESSING THE IMPACT OF ENVIRONMENTAL NOISE ON AUDITORY HAIR CELL DENSITY IN BLUEGILL SUNFISH (*LEPOMIS MACROCHIRUS*)

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Rising environmental noise in aquatic ecosystems threatens fish auditory structures, potentially impairing key behaviours such as communication, navigation, and predator avoidance. The current study investigates the impact of environmental noise levels on auditory hair cell density in Bluegill (*Lepomis macrochirus*), a freshwater species that relies on auditory cues for survival. Fish were collected from two distinct environments—one characterized by low noise levels and the other by elevated anthropogenic noise. Fish were euthanized in 2 phenoxyethanol and then preserved in 4% paraformaldehyde (PFA) following collection. Ears were dissected from heads and sensory macula and otoliths were removed for analysis. Hair cells visualization was achieved using Oregon Green Phalloidin staining, which binds to actin filaments within the hair cell microvilli. Hair cell density was then quantified and analyzed to assess the effects of noise exposure. Fish from noisier habitats exhibited reduced hair cell density compared to those from quieter environments, indicating structural damage associated with chronic noise exposure. These apparent differences in hair cell density provide evidence that environmental noise negatively impacts auditory system integrity in fish. Understanding these effects may inform conservation efforts by highlighting the need for noise management strategies in freshwater ecosystems. Additionally, this study lays the groundwork for future research on the broader ecological consequences of auditory impairment in fish, including potential impacts on population dynamics, predator-prey interactions, and species resilience in noise-polluted habitats. This research bridges gaps in sensory biology and aquatic conservation by demonstrating how environmental noise affects fish auditory structures.

064

THE EFFECTS OF ANTHROPOGENIC NOISE ON THE SONG STRUCTURE AND HABITAT OCCUPANCY OF THE EURASIAN WREN (*TROGLODYTES TROGLODYTES*)

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Animals living near humans have to deal with high levels of anthropogenic noise, which can disrupt their acoustic communication. Paris, France, is a particularly interesting city for studying anthropogenic noise because the French government has made significant efforts to reduce anthropogenic noise levels. Eurasian Wrens (*Troglodytes troglodytes*), a common species in urban Paris, sing highly variable songs with a broad frequency range, including lower frequencies typically masked by the urban noise of traffic and industry. In this study, our goal was to determine whether levels of anthropogenic noise influence both habitat occupancy and song structure of Eurasian Wrens. From 2023 springtime field recordings, we analyzed field recordings collected in urban areas, green spaces, and parks at 134 sites in Paris. We evaluated whether wrens were present at each site and compared this to the ambient noise levels. For each site where a wren was recorded, we measured minimum frequency, maximum frequency, song length, and number of notes in their song. Our results reveal that wrens are more likely to be present in areas with lower noise levels. Within the sites where wrens are present, our results suggest that as noise levels increase, wrens raise their minimum frequency and shorten their song length. In contrast, we found no evidence of changes in maximum frequency or number of notes. We conclude that wrens modify their song features in response to increasing noise levels, and the likelihood of their presence is influenced by ambient noise levels.

065

BIOTIC AND ABIOTIC INFLUENCES ON FISH DIVERSITY AND DISTRIBUTION IN THE ST. LAWRENCE RIVER USING ENVIRONMENTAL DNA

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Environmental DNA (eDNA) has emerged as a powerful tool for assessing fish biodiversity and informing conservation efforts in aquatic ecosystems. This study examines how biotic (e.g., phytoplankton, bacterial diversity) and abiotic (e.g., temperature, dissolved oxygen, water flow, contaminants) factors correlate with fish diversity and distribution in the St. Lawrence River, with a focus on endangered and invasive species. As part of the 2020 *Lampsilis* survey mission, eDNA samples were collected from multiple river sites and processed to determine fish species presence. Metabarcoding and quantitative PCR (qPCR) will be used to analyze species composition and compare detection efficiencies of these molecular techniques. Statistical analyses, including correlation tests and multivariate approaches, will be applied to explore relationships between environmental factors and fish community composition. By identifying key ecological drivers of species distribution, this research will contribute to improved conservation strategies for at-risk native species and management interventions for invasive species. Additionally, this study highlights the potential of eDNA as a non-invasive, efficient tool for monitoring biodiversity in large freshwater ecosystems.

066

GENE TRANSCRIPTION PROFILE RESPONSE TO HYBRID BREAKDOWN AND TEMPERATURE STRESS IN CHINOOK SALMON FRY (ONCORHYNCHUS TSHAWYTSCHA).

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Hybridization between genetically distinct populations of Chinook salmon (*Oncorhynchus tshawytscha*) can lead to either genetic rescue, where offspring exhibit increased fitness, or hybrid breakdown, where offspring suffer reduced fitness due to genomic incompatibilities. Determining how among-population hybridization interacts with environmental stressors, such as rising water temperatures due to climate change, is critical for conservation efforts that may involve translocation of salmon among watersheds. This study examines the gene transcription profile response of 56 stress-related genes in Chinook salmon fry derived from pure and hybrid crosses across four populations in British Columbia (Nitinat, Chilliwack, Big Qualicum, and Lower Shuswap). Gametes were collected and crossed in all possible combinations to produce 16 family groups, which were then subjected to control or heat stress conditions. Whole-body RNA was extracted, converted to cDNA, and analyzed using OpenArray qPCR technology to assess gene expression differences. We hypothesize that heat stress will induce gene transcription changes in all fish but that hybrids will exhibit more dysregulated transcriptional patterns compared to purebred individuals, indicative of hybrid breakdown. Gene transcription data will be analyzed to assess differences among cross types and treatment conditions. Preliminary findings will provide insight into whether hybridization disrupts regulated gene expression under environmental stress, as well as if potential maternal/paternal effects play a role. These results are essential for evaluating the potential risks and benefits of mixing populations in salmon enhancement thus informing management strategies in the face of climate change.

067

EXPLORING THE BIASES OF BAITED REMOTE UNDERWATER VIDEOS FOR AQUATIC ECOLOGY

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Baited Remote Underwater Video (BRUV) is a popular method for both marine and freshwater research, especially for investigations on species abundance and behaviour. Variations in design, including camera position and bait type, have evolved from increased use of BRUVs so questions remain on whether the BRUV itself selects for certain behaviours or interactions between fish. The purpose of the current study is to see if BRUVs are biased by conditions, soundscapes, or presence of bait, all independent of additional sound. The following can then be hypothesized: if different combinations of habitat noise level and bait show different results and behaviours, then the BRUV is biased towards certain conditions. It is predicted that the BRUV will be biased to quiet environments with bait. Trials were conducted at two different locations with different noise levels. At each location, 10 trials were conducted with bait, and 10 without. The effects of the above variables will be analyzed for time of first appearance, residence times, number of fish, and feeding attempts. Early results indicate the highest number of feeding attempts in the noisy environment with bait. BRUV is a very useful tool in marine and freshwater research, but its usefulness could improve with further knowledge of its biases. The current study will improve our knowledge of how to test this method not only locally, but also globally places to test biases more specific to a certain location with certain species.

068

CONTINUOUS OR BIMODAL: INVESTIGATING VARIABILITY IN MOTH EVASIVE RESPONSES TO BAT PREDATOR CUES

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Prey animals often exhibit bimodal responses to predator cues. If they are outside the predator's range or detection distance, they often engage in simple behaviours such as freezing or moving away from the predator. However, once predators are close, prey typically exhibit more complex and unpredictable escape behaviours. Many moth species can hear the echolocation calls of bats and appear to exhibit similarly categorical responses: fly away from a distant bat or perform erratic evasive flight in response to a close bat. Yet there has not been much research into variability in this supposedly rigid behaviour. To test whether moth evasive response is truly bimodal or exhibits a range of variability within each response type. Noctuid and Erebid moths were exposed in flight to the echolocation calls of *Eptesicus fuscus*, a sympatric bat species, and their behavioural responses were recorded with two video cameras. The 3D flight path of the moth was then mapped using the Pro-analyst software, and key values such as their acceleration, velocity, and angular velocity were recorded. The moths were exposed to different amplitude calls depending on their location in flight when they detected the calls. Preliminary analysis showed that moths perform a variety of responses to bat echolocation calls in flight. Further analyses will reveal whether this variation exists as a bimodal response, or a more graded response to sound amplitude at the moth.

069

EFFECT OF QACA/B EFFLUX PUMPS ON POVIDONE-IODINE RESISTANCE IN STAPHYLOCOCCUS EPIDERMIDIS

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Hospital-acquired infections pose a significant danger to patients—especially those being fitted with implantable medical devices, where opportunistic bacterial colonization can lead to chronic infection. Treatment-resistant chronic infection arises due to a combination of biofilm formation and antiseptic resistance in aggressive pathogens such as *Staphylococcus epidermidis*. This resistance is partly due to the expression of QacA/B efflux pumps that extrude antiseptics such as povidone-iodine (PVP-I) from the cytoplasm, preventing accumulation and decreasing their bactericidal activity. We investigated the role of efflux pumps in PVP-I resistance and explored the potential of efflux pump inhibitors (EPIs), which stop efflux pump functioning, to enhance antiseptic efficacy synergistically. We tested two strains of *S. epidermidis*: ATCC 35984 (qacA/B positive) and ATCC 12228 (qacA/B negative). PVP-I resistance was evaluated through both minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assays. We considered both the antiseptic alone, and its combination with qacA/B EPIs, Reserpine (20 µg/mL), sodium orthovanadate (100 µM), and carbonyl cyanide m-chlorophenyl hydrazone (10 µM). By targeting the efflux pumps directly, we aim to determine the underlying cause of resistance to PVP-I. To further investigate efflux activity, we performed an ethidium bromide accumulation assay in which bacterial cells were incubated with ethidium bromide and the fluorescence intensity measured. Quantitative real-time PCR was performed to determine changes in gene expression in response to the pressure. The findings will provide insight into the role that qacA/B efflux pumps play in mediating PVP-I resistance and could suggest methods to improve antiseptic protocols in clinical settings.

070

EFFECTS OF HANDLING STRESS ON POST-SWIM STRESS PHYSIOLOGY IN JUVENILE LAKE STURGEON (*ACIPENSER* FULVESCENS)

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Lake sturgeon (*Acipenser fulvescens*) populations have declined due to habitat loss, overfishing, and dam construction, leading to ongoing conservation and restoration efforts for the species. Hatchery-reared juveniles are commonly reintroduced into the wild using management practices that involve brief air exposure and handling prior to release. While necessary, these practices may induce physiological stress, potentially impacting post-release survival. This study examines the effects of handling stress on sturgeon stress physiology by analyzing concentrations of physiological stress indicators, such as blood glucose, lactate, and plasma osmolality. Juvenile sturgeon were exposed to standardized handling stress after a swim trial to assess whether standardized handling stress prior to swimming has any effect on stress physiology compared to control fish. Understanding this management practice is crucial for refining and ensuring that current reintroduction methods support sturgeon survival in the wild. If loading practices significantly impact stress physiology, modifications to handling procedures may be necessary to improve the reintroduction process. These findings contribute to the field of restoration physiology and help determine the best practices for managing juvenile lake sturgeon before their release, overall contributing to conservation efforts to restore wild populations.

071

THE HEARTBEAT OF RIVER ECOSYSTEMS: EXPLORING INDICATORS OF ECOLOGICAL HEALTH IN URBAN WINDSOR-ESSEX RIVERS

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The health of headwaters have significant impacts on the broader ecological health of freshwater systems. Anthropogenic inputs from agriculture and urban developments can significantly influence the water quality and ecological health throughout a freshwater system. This study focuses on examining the ecological health of four river systems in largely agricultural or urbanized areas in the Windsor-Essex region (WER) with the focus being on the Little River system. This research aims to answer two primary questions; (1) What suite of metrics best captures the ecological health of rivers in the Windsor-Essex region? (2) What is the ecological health status across Windsor-Essex rivers? Water samples were taken from Little River and three analogous river systems in the WER and were analyzed for water quality, nutrient composition, and carbon characterization. The expected results for the analysis are that areas along the river systems in closer proximity to urbanized or agricultural land will exhibit relatively poor ecological health. Overall, this study aims to create a baseline of measurements for the ecological health of Little River to determine the health status of the river as well as inform future decisions in restoration and management practices in the WER.

075

POTENTIAL REGULATION OF THE RAC EXCHANGE FACTOR PREX1 BY THE TRANSCRIPTION FACTOR KAISO

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Vertebrate development is the process whereby a fertilized egg transforms into an adult form of the organism. In addition to playing a role in several human cancers, the POZ-ZF transcription factor Kaiso has been implicated in vertebrate development, with its highest expression occurring in the brain. Unpublished data from our lab and others suggest that Kaiso malfunction or loss contributes to human developmental disorders. Individuals with Autism Spectrum Disorder (ASD) are believed to have atypical development, sometimes starting prior to birth. Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 (PREX1) is a guanine nucleotide exchange factor associated with normal vertebrate development, but is also implicated in the pathogenesis of ASD and several human cancers. Kaiso binds to Kaiso Binding Sites (KBS) or methylated CpG dinucleotides to regulate gene expression. The *PREX1* promoter contains methylated CpG sites in colon tumours, which may be potential binding sites for Kaiso. A young adult male with developmental delays and behavioural issues was recently found to have point mutations in the Kaiso (*ZBTB33*) and *PREX1* genes. We hypothesize that Kaiso regulates the expression of *PREX1*, and that the *PREX1* mutation affects its function. Kaiso knockout in a human breast cancer cell line resulted in decreased PREX1 expression, as assessed by immunoblot and quantitative reverse transcription polymerase chain reaction (RT-qPCR), but Kaiso knockdown in a human brain cancer cell line had no effect on PREX1 expression. Understanding this molecular mechanism is crucial for identifying biomarkers for developmental disorders.

076

INVESTIGATING THE INVOLVEMENT OF KAISO IN CHEMOTHERAPY DRUG SENSITIVITY OF TRIPLE-NEGATIVE BREAST CANCER CELL LINES USING KNOCKOUT CELLS

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Triple-negative breast cancer (TNBC) is a very aggressive breast cancer subtype that is characterized by a lack of Estrogen Receptor, Progesterone Receptor, and Human Epidermal Growth Factor Receptor 2 (HER2) expression. TNBC disproportionately affects Women of African Ancestry (WAA), who have been found to have high nuclear expression of the transcription factor Kaiso and which correlates with TNBC's poorer prognosis and survival. Previous research in our lab has implicated Kaiso in tumourigenesis, cancer cell survival, inflammation in many human cancers, and regulating epithelial-mesenchymal transition (EMT). Through EMT, tumor cells inducing drug resistance, which lends current TNBC treatment strategies ineffective. Recent studies suggest that Kaiso plays a key role in drug resistance in TNBC by promoting EMT. This study investigates how Kaiso influences TNBC cells' response to chemotherapy using two TNBC parental cell lines and their Kaiso knockout (KO) derivatives. Cell viability and apoptosis was evaluated after treatment with the chemotherapeutic drugs Cisplatin and Doxorubicin. Preliminary results revealed that cells Kaiso KO cells were more sensitive to the drugs, suggesting that Kaiso plays a critical role in TNBC drug resistance. Interestingly, EMT markers like SNAI2 are absent from Kaiso KO derivatives after treatment with Doxorubicin, reinforcing the link between Kaiso and EMT. Our findings highlight Kaiso as a possible regulator of TNBC drug resistance and suggest that targeting Kaiso or its downstream pathways may improve therapeutic outcomes in patients.

077

KAISO REGULATES ANDROGEN RECEPTOR TARGET GENES ASSOCIATED WITH INCREASED CELL PROLIFERATION IN TRIPLE-NEGATIVE BREAST CANCER (TNBC)

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Breast cancer (BCa) is a heterogeneous disease and is the leading cause of female deaths worldwide. Triple-negative breast cancer (TNBC) is an aggressive BCa subtype characterized by the absence of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). This results in limited treatment options and poor prognoses, particularly among women of African ancestry (WAA). Quadruple-negative breast cancer (QNBC) is a TNBC subtype that lacks the androgen receptor (AR), is more aggressive and thus has increased mortality rates. Interestingly, the transcription factor Kaiso is highly expressed in TNBC and is implicated in cancer progression due to its key role regulating genes associated with proliferation and metastasis. Recently, AR has emerged as a potential therapeutic target for TNBC. *In silico* analysis identified a strong correlation between Kaiso, AR, and ACSL4, a gene involved in lipid metabolism and tumour growth. Unpublished data from our lab has confirmed that Kaiso knockout increases AR expression, and thus we hypothesized that Kaiso influences AR downstream target genes. Immunoblot analyses revealed decreased ACSL4 expression in Kaiso knockout TNBC cell lines compared to parental cell lines. This suggests that Kaiso is a key transcriptional regulator of AR-mediated gene expression. Ongoing research aims to further elucidate the correlation between Kaiso and AR's downstream target genes in QNBC and TNBC. Understanding these molecular mechanisms is crucial for identifying targetable biomarkers for drug development to improve the prognosis of TNBC and QNBC patients.

078

GASTROINTESTINAL PARASITE INFLUENCE ON GLUCOCORTICOIDS IN WILD DEER MICE (PEROMYSCUS MANICULATUS)

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Parasite-host interactions are crucial factors influencing population dynamics of animals. Glucocorticoids (GCs) play a significant role in modulating immune function with corticosterone being one of the primary GCs found in many rodents. Elevated levels of corticosterone increase the likelihood of parasitic infection because of its role in suppression of the immune response. This can lead to a positive feedback loop once infected, with the parasite presence further increasing GC levels. We expect to find helminth parasite eggs within our fecal samples. The primary objectives are to assess the gastrointestinal helminth parasite load and determine fecal corticosterone concentrations in wild populations. We predict that individuals with parasitic infections will exhibit higher fecal corticosterone levels compared to their uninfected counterparts. Additionally, we aim to explore whether parasite intensity and diversity influence corticosterone levels, predicting that different parasite species may exert varying degrees of physiological stress on their hosts. Fecal glucocorticoid analysis allows for analysis of GC levels over a roughly 24-hour period, offering advantages over short-term (30-60 seconds) blood or long-term (several months) hair sample GC analysis. We collected fecal samples from adult Deer Mice (*Peromyscus maniculatus*) populations in Algonquin Park and preserved them in 80% methanol. Parasite presence and load was evaluated using the McMaster egg counting technique, a widely used method for quantifying helminth infections. Fecal corticosterone levels were measured using an enzyme immunoassay. Preliminary results found *Capillaria* sp., *Hymenolepis* sp., and *Strongyloides* sp. in most of the fecal samples.

079

CORRIDOR ECOLOGY: ANIMAL ACTIVITY NEAR SHORELINES IN THE LAKE LAURENTIAN CONSERVATION AREA, SUDBURY, ONTARIO

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Fragmentation creates natural corridors used by animals to reach different habitat patches. Land animals avoid clearings and water, and riparian corridors may be used by semi-aquatic animals. Six trail cameras were deployed in six pre-selected sites in the Lake Laurentian Conservation Area (LLCA) between May and October 2024, with three cameras near water bodies and three in the forest. Each micro-site was photographed, trees were measured to document forest cover and the distance to water was also measured. A tree on the site was marked using a few drops of commercial animal lure, refreshed every 2 weeks. At each visit, the camera was checked, and the SD card was swapped with an empty card. The SD card with data was downloaded on a laptop for further analysis and positive wildlife captures were extracted. The average % herbaceous layer was similar between the two types of sites, but the average % shrub layer was slightly higher in forest sites. The average diameter of trees was higher in Riparian sites. The tree species that were found were Jack pine, White pine, Red pine, Trembling aspen, White birch, Red oak and Red maple. During this study, cameras captured three species of large predators, three small predators, one ungulate, three rodents and four species of birds. The forest sites have more visits than riparian sites, but both types of sites had similar richness and diversity index (H’). Most animals were seen during the day and they left after a short while.

080

FOREST SUCCESSION 2003-2024 AND ANIMAL ACTIVITY IN LAKE LAURENTIAN CONSERVATION AREA IN SUDBURY, ONTARIO, CANADA

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The Sudbury area underwent catastrophic environmental degradation after the introduction of the mining industry in 1883, which drove the city to take action in 1978, implementing the Sudbury Land Reclamation project. There has been immense recovery since the beginning of the project, and forest succession has been used to track this progress. In 2003, a study was conducted at LLCA to observe where the forest area lies in succession by measuring tree diameters and recording the surroundings. This study is a follow-up of the original study, sampling comparable sites at LLCA. In addition to this, wildlife cameras were monitored to observe wildlife activity in plantation and natural regeneration sites. Forest composition has shifted and it has been found that DBH and CWD has increased over the last 21 years, with herbaceous and shrub coverage decreasing. A wider variety of animal species were observed in plantation sites. Initial data indicates that LLCA has indeed progressed in forest succession, showing success in growth, even after such intense deterioration to the forest community.

081

REACTIVE OXYGEN SPECIES IN CHEMOTHERAPY-DEPENDENT RNA DISRUPTION AND DEATH IN OVARIAN TUMOUR CELLS

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RNA disruption is a phenomenon characterized by chemotherapy-induced degradation of ribosomal RNA and is currently being assessed in clinical trials as a biomarker of complete tumour destruction in patients. While the cellular mechanisms which drive RNA disruption are poorly understood, many chemotherapeutics strongly induce the production of reactive oxygen species (ROS) in cancer cells. In this study, we examined a potential mechanistic link between chemotherapy-dependent ROS generation, RNA disruption, and cell death. To do so, we investigated the ability of the antioxidant N-acetyl cysteine (NAC) to mute ROS production, RNA disruption, and cell death in A2780 ovarian tumour cells treated with the chemotherapeutic doxorubicin (DOX). Preliminary experiments using 2',7'-dichlorodihydrofluorescein diacetate (H2DCFDA) to detect ROS by fluorimetry suggest that while DOX treatments were able to increase cellular ROS levels, NAC appeared unable to significantly mute these increases. Consistent with these results, capillary gel electrophoresis of cellular RNA revealed that NAC did not significantly prevent RNA disruption caused by DOX. DNA content analyses showed that NAC also failed to prevent DOX-induced cell death. While an association between DOX-induced ROS production, RNA disruption, and cell death was established, it is unclear why NAC did not inhibit ROS production by DOX. Overall, this study will provide guidance for future investigations which can benefit from larger sample sizes to further elucidate the role of ROS, if any, in the ability of chemotherapy agents to promote RNA disruption and cell death.

082

MORE ON BITE FORCE AND ENCEPHALIZATION IN THE FAMILY CANIDAE AND IN WOLVERINES (*GULO GULO*).

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Cranial morphology can explain many aspects of an animal's life. Features such as bite force and brain volume can inform us about ecological niches and evolutionary adaptations. Bite force is influenced by factors like prey type, and brain volume may be influenced by an animal's cognitive abilities. This study aims to review different estimators for bite force and brain volume, and to compare these traits between two groups of animals, social canids including eastern wolves (*Canis lupus lycaon*) and coyotes (*Canis latrans*) and solitary mustelids, specifically wolverines (*Gulo gulo*). We will contrast ecological roles and behaviors with relative bite force and brain volume. Twenty-four skulls were analyzed including twelve canids and twelve wolverines. Each fresh head underwent a defleshing process which involved manual removal of soft tissue and boiling. Using ImageJ software, measurements were taken including length, width, height to estimate cross sectional areas of the masseter and temporal muscles and thereby, bite force based on existing models. Brain volume was estimated by filling the endocranium with copper pellets with a diameter of 4.5mm through the foramen magnum, thus assessing cranial capacity. I further calculated bite force and brain volume quotients (BFQ and BVQ) to compare observed values with those expected from calculations using skull length as an index for body size. Differences in bite forces, brain volumes, BFQ and BVQ between canids and wolverines will be discussed in relation to their respective behavioral ecologies.

083

PATTERNS OF PARASITISM IN URBAN RODENTS AND EFFECTS OF ECTOPARASITE DIVERSITY ON BODY CONDITION.

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Parasites impose an energetic cost on their hosts due to allocation of energy to the immune system, thus reducing the energy available for other functions such as growth and reproduction. We examined ectoparasites on urban deer mice (Peromyscus *spp.*) and assessed patterns of parasite diversity related to age, sex, capture location, seasonality and body condition. We predicted that male mice would have a higher parasite index compared to females. We also predicted that adult mice would have higher parasite diversity than immatures. As part of a larger project, we trapped mice within multiple "wildland" sites adjacent to buildings in the Greater Toronto Area. Parasites were collected and identified, and the number and taxa found in each sample (tick, mite, lice, fleas, and botflies) was used to calculate Simpson's Diversity index. A total of 132 individuals (57%) were infested with ectoparasites. Adults had significantly higher mean diversity compared to immatures. A general linear model also showed significant effects of session, sex, and age on increased parasite diversity, but not location or body weight residual (BWR), despite the decrease in parasite diversity concordant with increased BWR. We concluded that adult deer mice, males and those caught later in the summer (i.e. August vs July) were more likely to have an increased diversity of ectoparasites, but that this diversity had no significant effect on body condition, nor did diversity vary between sites. These findings help better our understanding of ectoparasite patterns of infestation and emergence and can help inform studies of diseases ecology.

084

EXAMINING THE IMPACT OF COLITIS ON INTESTINAL INFLAMMATION AND L-CELL PHYSIOLOGY IN MICE

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Ulcerative colitis (UC) is a type of inflammatory bowel disease that is characterized as a chronic inflammation of the large intestine. With the unknown pathogenesis and increasing prevalence rates worldwide, it is becoming more apparent the need to understand the pathogenesis of this disease to improve treatment options for patients suffering with UC. Within the colon, the enteroendocrine L-cells secrete important peptide hormones such as glucagon-like peptide 1 (GLP-1). GLP-1 has various physiological roles with most recent findings showing an interplay between GLP-1 and inflammation. This study thus aimed to evaluate changes in L-cell physiology and characterize inflammation during colitis. An *in-vivo* model using dextran sulfate sodium (DSS) to induce colitis in mice along with a control group was completed to perform this analysis. Immunoassays on GLP-1 and cluster of differentiation 3 (CD3) (a T-lymphocyte marker), from colonic tissue lysate were completed along with histological staining for goblet cells within the colonic epithelium. Preliminary data indicates L-cell physiology impairments occurring in DSS treated mice with decrease in colonic tissue GLP-1 levels and lower levels of CD3 in the DSS treated group compared to that of the control group. These findings suggest an impairment of immune function in the colitis intestine and an altered L-cell physiology. Further research is required in order to fully understand the involvement of L-cells and GLP-1 in colitis and whether GLP-1 based therapies will have a role to play in colitis.

085

RECOVERY TRAJECTORIES OF BOREAL LAKE ZOOPLANKTON COMMUNITIES IN THE FACE OF MULTIPLE STRESSORS

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The Ontario Ministry of Environment, Conservation and Parks (MECP) has been monitoring Sudbury area lakes for over 40 years. As part of these surveys, zooplankton and chemistry have been recorded to track recovery from acidification, and more recently, effects of emerging stressors. My thesis assessed these parameters to highlight changes in diversity and abundance of zooplankton in the study lakes, their shifting water chemistry, and the complex interactions affecting zooplankton species in Boreal shield lakes, in an attempt to find why some zooplankton are recovering slower than others. Preliminary results show great recovery in many chemical parameters related to acidification. Additionally, many of the lakes showed increases in Simpsons diversity index. Contrastingly, the lakes also showed clear signs of emerging concerns, such as declining calcium levels in 10 of the 11 lakes, or high chloride levels in the more urban lakes. A constrained correspondence analysis (CCA) showed strong impacts of legacy-related stressors (pH, calcium, and nickel concentrations) on relative abundance of zooplankton. The CCA also showed strong relationships between certain zooplankton species and the parameters listed, allowing for the exploration of potential indicator zooplankton that could be used in other lakes to identify health of a lake– both past and present. This exploratory study paves the way for other studies focusing on other influences on zooplankton; either physical, chemical, or biological, and eventually determine the driving forces behind zooplankton recovery and proliferation.

086

CHLORIDE POLLUTION IMPACTS IN BOREAL LAKES: AN INVESTIGATION OF PHYSICOCHEMICAL INTERACTIONS AND BIOLOGICAL RESPONSES USING ZOOPLANKTON COMMUNITIES AS BIOINDICATORS

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The use of road salts is driving freshwater chloride (Cl^-) pollution across the Northern Hemisphere. Cl^- interacts with physicochemical lake processes, altering stratification, mixing regimes, and releasing ions from surrounding soils and sediments. In turn, these environmental changes shift the composition of aquatic communities. The oligotrophic, softwater lakes of Greater Sudbury, Ontario have been particularly sensitive to anthropogenic stressors in the past, namely acidification and metal deposition from mining activities. With this study, we aimed to characterise the interactive effects of freshwater Cl^- pollution in Greater Sudbury and identify candidate indicator zooplankton taxa for future studies of Cl^- polluted lakes across the Boreal Shield. We selected a mix of 18 urban and remote lakes along a gradient of chloride pollution and surveyed their physical characteristics, water chemistry in the surface (epilimnion) and bottom (hypolimnion) water layers, sediment chemistry, and zooplankton communities. Analysis revealed that Cl^- is concentrated in the hypolimnion of the two most polluted lakes and is potentially interacting with the underlying sediments to release sequestered metals (nickel, copper, and zinc) back into the water column. Further, we found that zooplankton communities differed between urban and remote lakes. Urban lakes exhibited significantly lower species richness which may highlight the absence of certain indicator taxa with low Cl^- thresholds. With this study, we began to explore how Cl^- pollution impacts Boreal waterbodies that have a complex history of anthropogenic stressors. Future research should expand on interactive Cl^- effects to establish a comprehensive understanding of how basal taxa will be affected.

087

MESO-CARNIVORES: INVESTIGATING THE DIETS OF THE BOBCAT (FELIS RUFUS) AND EASTERN WOLF (CANIS LUPUS LYCAON)

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The bobcat (Felis rufus) and eastern wolf (Canis lupus lycaon) are two meso-carnivores that share patterns of wide geographic ranges, setting the stage for adaptability when it comes to their diets. The goal of this study is to investigate the diets of eastern wolves from Northern Ontario (collected 2023-2024) and bobcats from Wisconsin (collected 2022-2023). Using fresh stomachs donated from carcasses to the laboratory, the contents were manually sorted, identified and quantified into prey frequencies and volumes comparatively between two species. It was found that bobcats (H’ = 1.12) consumed more food than the more diverse eastern wolves (H’= 1.31). Frequency has shown that sciurids and ungulates were the dominant prey item for bobcats, and ungulates were the dominant prey item for eastern wolves. Volume shows that 66.1% and 61.04% of total volume in bobcats and eastern wolves respectively, can be attributed to ungulates. Results show that bobcats had a less rich and less diverse diet while consuming sciurids and ungulates more out of the 4 prey categories. It also shows that wolves consumed ungulates more out of the 6 prey categories. The chi-square tests show significant differences in sciurid, small mammal, and plant frequencies and significant differences in sciurid and other mammal volumes. This study provides new data for diet studies and together, quantifying volumes and frequencies will help determine the level of similarities between the two species and their feeding niches in terms of richness, diversity and overlap.

088

THE EFFECTS OF URBANIZATION ON THE MORPHOLOGY OF AMERICAN TOADS (*ANAXYRUS AMERICANUS*).

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Urbanization exerts profound impacts on wildlife, often leading to adaptations in morphology. However, the species-specific effects of urbanization on amphibian populations and their responses to urbanization continue to be explored. American toads (*Anaxyrus americanus*) are the most widely distributed toad species in Ontario, and like many amphibian species, they are known as good indicators of environmental health due to the permeability of their skin and dual life strategy, making them vulnerable to environmental changes. Urban American toad populations were predicted to undergo morphological changes such as decreased parotoid gland size, increased limb size, increased tympanum diameter, reduced melanistic patterning, and increased body condition, due to selective pressures imposed by urbanization, driving natural selection. Adult toads were sampled in Lambton County, Ontario, from seven sites categorized into urban and rural areas using the proportion of impervious surface area. Mass, snout-vent length, limb size, tympanum diameter, parotoid area, melanistic patterning, and body condition were measured for each toad. These features were then analyzed in relation to continuous measures of impervious area in linear mixed effects model analyses. Male toads in urbanized sites were found to be in better body condition than those in less urbanized areas. Furthermore, dorsal melanism was found to decrease as urbanization increased; however, females were more affected than males. The results demonstrate that urbanization may drive morphological differences between urban and rural American toad populations, emphasizing the need for further research on the evolutionary and ecological consequences of urban environments on amphibian morphology.

089

MATERNAL GENETIC BACKGROUND INFLUENCE ON PHENOTYPIC VARIATION IN *DROSOPHILA MELANOGASTER*

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Phenotypic variation is the observable differences in traits within a population, which are influenced by a combination of environmental and genetic factors. Environmental factors can be controlled for, so it is of interest to focus on the role of genetic background in shaping phenotypic expression. Commonly, genetic backgrounds are often accounted for by using isogenic, genetically identical, lines. While isogenic lines are valuable for investigating phenotypic variation, they do not reflect the complex biology of a typical population that more genetically diverse models can offer. Crossing isogenic lines to create heterozygous crosses introduces a controlled degree of genetic diversity, enhancing biological relevance. However, in doing so, confounding maternal genetic background effects may be introduced. The role that the maternal genetic background plays in the phenotypic variation seen in heterozygous crosses is not well characterized. We used reciprocal heterozygous crosses of *Drosophila melanogaster* to investigate the impact of maternal genetic background on offspring traits, particularly under metabolic stress induced by nickel exposure. We examined how different maternal genetic backgrounds influence five phenotypic traits, including the activity of three cytosolic enzymes (malic enzyme, isocitrate dehydrogenase, glucose-6-phosphate dehydrogenase), as well as whole body lipid and dietary triglyceride quantification. Using a broad suite of phenotypic traits provides an in-depth organism-wide analysis of the influence of maternal genetic background. Exploring the influence of maternal genetic background provides insight into considerations in future research using heterozygous crosses and deepens our understanding of how maternal genetics shape the diversity within their offspring.

090

RHIZOSPHERE EFFECTS ON ENZYME ACTIVITIES IN RED PINE (*PINUS RESINOSA*) STANDS

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The rhizosphere is a vital component of plant life directly under the plant roots. It is a complex community of microbes, minerals, and enzymatic activity. These components allow for nutrient cycling within the soil and plant roots, making it necessary for plant survival. Several studies have focused on the biogeochemical cycling of elements in this microenvironment. This study aims to better understand the rhizosphere effect on the microbial activity in the soil. Soil samples were collected from three different sites at Laurentian University site. At each site, soil samples were collected from the rhizospheres of the tree red pine (*Pinus resinosa*) trees. Surrounding non-rhizospheric soils were used as controls in three separate areas. Nine different enzymes were analyzed due to their importance in their roles in the ecological processes. They included β-glucosidase (BG), cellobiohydrolase (CBH), β-N-acetylglucosaminidase Nagasee), aryl sulfatase (AS), acid phosphatase (AP), alkaline phosphatase (ALP), glycine aminopeptidase (GAP), leucine aminopeptidase (LAP), and peroxidase (PER). Preliminary results indicate there is a notable increase in certain enzyme activities, within soils collected from rhizospheres compared to control samples. Detailed analyses will provide insights and information on differences between rhizosphere and non – rhizosphere areas at microbial function levels.

091

INVESTIGATING THE ROLE OF CHRFAM7A IN THE IMMUNE RESPONSE OF HUMAN MACROPHAGES

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Macrophages play a key role in initiating the inflammatory response through cytokine production, thus acting on the immune system's first line of defense. THP-1 is a human monocytic cell line that can be used to study monocytes and macrophages in vitro. THP-1 macrophages express the human-specific gene *CHRFAM7A* that encodes a truncated form of a nicotinic acetylcholine receptor (nAChR) with unknown function. To elucidate the role of *CHRFAM7A* in the immune system, CRISPR-dCas9-mediated *CHRFAM7A* overexpression (*CHRFAM7A*$^+$) cell lines were created in human THP-1 macrophages using a lentiviral delivery system. Transcriptional overexpression of *CHRFAM7A* mRNA was validated with RT-qPCR. Following verification, *CHRFAM7A*$^+$ THP-1 monocytic cells were differentiated into naive M0 macrophages using Phorbol-12-Myristate-13- Acetate (PMA). The differentiated M0 macrophages were exposed to the immunogen lipopolysaccharide (LPS) with and without the nAChR agonist nicotine. The nature of the resulting immune response was characterized by ELISA assays to detect and quantify the secreted cytokines Tumor Necrosis Factor alpha (TNF-α), Interleukin-6 (IL-6), and Interleukin-10 (IL-10). In this way, the impact of the gene CHRFAM7A on the immune response in THP-1 macrophages was measured. This study hopes to contribute to an understanding of the implications of *CHRFAM7A* expression in the immune system and generate unique immortal cell lines for future research.

092

INFLAMMATION AS A DRIVER OF AGE-RELATED DNA METHYLATION

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DNA methylation is an important epigenetic regulatory mechanism that is known to influence biological processes such as gene expression. Studies have shown that DNA methylation exhibits systematic changes with age, subsequently impacting gene expression by inhibiting the binding of transcription factors, causing gene repression. However, *how* aging drives changes in DNA methylation is unclear. We hypothesize that chronic inflammation, which also changes with age, reduces DNA methylation. To evaluate this, we have created a laboratory protocol to estimate site-specific DNA methylation status using a sodium bisulfite treatment to convert unmethylated cytosine to thymine, routine PCR using specific primer sets to distinguish between converted and unconverted DNA, and agarose gel electrophoresis for visualization. From there we can determine the influence of chronic inflammation on DNA methylation using our protocol on DNA extracted from monocytes after application of various amounts of pro-inflammatory cytokines, TNF-α and IL-6. Preliminary data has been valuable in the creation of the protocol by showing important trends in DNA concentration, where low DNA yields are occurring throughout the experiment. This indicates that there is likely damage caused to the DNA by the bisulfite treatment, as well as some loss occurring post DNA precipitation. This data and experimentation has been crucial in determining how we assess DNA methylation status and how/why it changes. Understanding the influence of chronic inflammation on DNA methylation in monocytes will allow scientists to better estimate other age-related outcomes such as frailty, mortality, and how inflammation affects immune cell function as we age.

093

TARDIGRADE DIVERSITY AND COMMUNITY COMPOSITION OF AN ONTARIAN FOREST

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Tardigrades are some of the smallest animals on Earth. They can be found in various environments such as ocean bottoms, mountain tops, and Antarctic glaciers, although they are mainly associated with lichens and mosses. The microenvironmental factors that determine their communities show no consistent patterns across the literature. Tardigrade species and community composition were analyzed in moss and lichen samples within the Macnamara Nature Trail in Arnprior, Ontario, and were analyzed to determine what microenvironmental factors predict tardigrade communities. Morphological features were used to identify the tardigrade species. Tardigrade species richness was found to be negatively associated with the horizontal growth of the substrate. Tardigrade individual abundance was found to be significantly greater on lichens than mosses, with significantly higher individual abundance found on foliose lichens than on crustose and fruticose lichens. This study documents the first recorded observations of *Crenubiotus crenulatus; Isohypsibius prosostomus; Guidettion prorsirostre; Paramacrobiotus richtersi*; and *Paramacrobiotus tonollii;* within Ontario, the first recorded observations of *Echiniscus arctomys* and *Echiniscus virginicus* in Canada, and the first recorded observations of *Diphascon greveni* and *Macrobiotus ariekammensis* in North America. This study enhances the understanding of tardigrade biodiversity in Ontario, contributing insight into how ecological variables influence species distribution and community composition.

094

INVESTIGATING THE ROLE OF PROSTAGLANDINS AND ISOPROSTANES MEDIATED BY DYSREGULATION OF INFLAMMATORY ENZYME PTGS2 IN RADIATION RESISTANCE OF TRIPLE NEGATIVE BREAST CANCER CELLS

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Radiation resistance (RR) significantly challenges the treatment of triple negative breast cancer (TNBC). Prostaglandins, a group of bioactive lipid compounds, are involved in various physiological processes. Their dysregulation has been linked to breast cancer progression. Isoprostanes are structurally like prostaglandins, and form through lipid oxidation by reactive oxygen species (ROS). Prostaglandins and isoprostanes may play critical roles in cancer biology, but their involvement in RR is not well understood. Our previous whole-transcriptome analysis revealed significant upregulation of Prostaglandin Synthase 2 (PTGS2) in a RR variant of the MDA-MB-231 TNBC cell line. We hypothesize that PTGS2-mediated dysregulation of prostaglandins and isoprostanes contributes to RR in TNBC cells. We performed RT-qPCR to investigate the relationship between PTGS2 expression and genes involved in cell survival and DNA damage repair. Additionally, since radiation therapy generates ROS, we hypothesize that radiation may increase the production of isoprostanes typically associated with cancer progression. Isoprostane and prostaglandin profiling was done using liquid chromatography tandem mass spectrometry (LC-MS/MS) on PTGS2 overexpressing MDA-MB-231 cells. Results are currently under analysis. Preliminary data indicates that PTGS2 may play a role in RR, specifically at the 6Gy dose. This study will provide insights into the role of prostaglandins and isoprostanes in RR, potentially identifying novel therapeutic targets to enhance sensitivity of TNBC cells to radiation therapy.

095

INFLUENCE OF NUTRIENT AVAILABILITY ON SENESCENCE IN WETLAND MONOCOT SPECIES WITH DIFFERING NUTRIENT ECONOMIES.

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A proper timing of senescence is essential to optimize plant production. A delay of the process to elongate growing season must balance the need to senesce in time for nutrient conservation and redistribution before frost. The timing of senescence is influenced both by abiotic and biotic factors, with abiotic factors such as drought, nutrient limitation, and extreme temperatures being the most prominent. This study aimed to investigate the role of nutrient availability in senescence among plants with differing nutrient economies. *Juncus nodosus* is known to acquire and use nutrients rapidly, whereas *Juncus filiformis*, which acquires nutrients at a slower rate, utilizes them more conservatively. To investigate this, all plants were placed in low-nutrient peat moss and divided into two groups: one received ongoing nutrient treatment, while the other had the nutrient treatment terminated at the onset of autumn. A senescence index was calculated. The ANOVA on the index values revealed that neither nutrient treatment, nor the species had a significant effect on the average index values. This is potentially due to inadequate nutrient limitation in the treatment with the terminated nutrient addition. Further research is needed to clarify the impact of nutrient availability on senescence.

096

ELEMENTAL COMPOSITION OF OSTRICH FERN (*MATTEUCCIA STRUTHIOPTERIS*) FIDDLEHEADS IN SUDBURY-MANITOULIN DISTRICTS, ONTARIO

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Foraging, driven by the perceived nutritional benefits of wild foods, ever increasing grocery prices, and tradition, is a common practice among locals in Northern Ontario. One of the most commonly foraged foods are ostrich fern fiddleheads (*Matteuccia struthiopteris*), harvested in spring prior to unfurling into fern fronds. A series of 14 sites across the Sudbury-Manitoulin Districts were selected for the collection of soil and ostrich fern fiddleheads, for detailed characterization, and analysis. The soil samples were analyzed for pH, electrical conductivity, and bulk density, with both total and bioavailable estimates for key nutrient elements in the soils being obtained by ICP-MS analysis of strong acid digests and 0.01 M lithium nitrate ($LiNO_3$) extraction solutions. The fiddlehead samples were dried, ground, and digested using strong acids in a programmable digestion block, with the analysis of digest solutions being performed using ICP-MS. The key nutrients found in fiddleheads were calcium (397 ± 84 mg/kg), chromium (0.2 ± 0.03 mg/kg), copper (3.5 ± 0.7 mg/kg), iron (10.8 ± 4.6 mg/kg), magnesium (376 ± 48 mg/kg), manganese (3.9 ± 1.1 mg/kg), phosphorus (961 ± 128 mg/kg), potassium (3707 ± 353 mg/kg), selenium (0.1 ± 0.01 mg/kg), and zinc (8.8 ± 1.5 mg/kg). Commercial and wild sourced fiddleheads showed highly variable concentrations of potentially toxic elements (PTEs), such as lead (0.04 – 0.39 mg/kg) and cadmium (0.02 – 0.56 mg/kg). This study will allow local foragers to review the risks and benefits of fiddlehead consumption from the study area.

097

INVESTIGATING GENE DYSREGULATIONS ASSOCIATED WITH ANTIFUNGAL RESISTANCE IN *C. ALBICANS* STRAINS FROM NORTHERN ONTARIO

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Oral candidiasis is one of the most common fungal infections in the oral cavity of humans. It is caused by the overgrowth of naturally occurring *Candida* fungal species in the oropharynx and debilitates a wide range of the population, most commonly the immunocompromised and elderly. A recurring issue in treating these infections is that many species of interest have varying levels of resistance to antifungal treatments. We hypothesize that genes related to the ergosterol biosynthesis pathway, a target for the antifungals, are upregulated in resistant *Candida* strains. Therefore, the objective of this study is to identify gene dysregulations associated with antifungal resistance in *C. albicans* strains from Northern Ontario. Cultures obtained from oral samples of patients were grown in lab with and without common antifungals such as fluconazole and clotrimazole. Samples were collected at mid-log growth phase. RNA extraction was performed, followed by cDNA synthesis and RT-qPCR (real-time polymerase chain reaction) in order to determine expression levels of genes involved in the ergosterol biosynthesis pathway. This approach will allow measurements of gene expression changes related to antifungal resistance. Preliminary data show that common strains isolated from candidiasis patients in Northern Ontario are resistant to azole treatment. This study will strengthen our understanding of the molecular mechanisms underlying antifungal resistance.

098

FORENSICALLY IMPORTANT INSECTS IN FORESTS OF GREATER SUDBURY: INVESTIGATING IMPLICATIONS FOR FORENSIC ENTOMOLOGY

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Forensic Pathology, the analysis and investigation of a non-natural or suspicious death, requires the identification of the PMI (Post-Mortem Interval) of a deceased person. The PMI determines the amount of time that has passed since an individual's death. Forensic Entomology has been a leading method of analysis in determining PMI, via studying the development and success of entomological activity upon the deceased. In Greater Sudbury, the regreening program aims to restore biodiversity to lands degraded by historical mining and smelting activities. This research seeks to assess the prevalence and success of forensically relevant insect species in various forest fragments across Greater Sudbury, exploring how mining activities and regreening efforts have influenced entomological biodiversity in these areas. Insects have been collected using homemade traps baited with liver to attract forensically relevant species. These traps were placed near three mining areas: Coniston Hydro Road (near the previous site of the Mond Nickel Company), Falconbridge (near Glencore Canada), and Ruisseau Nolin Creek (near the Vale Copper Cliff Complex), as well as a site far from mining, near Laurentian University. The traps have remained in the field for three weeks, with samples collected every four days. Collected insects have then been sorted, pinned, and identified to the familial level. Data on species diversity and abundance have been compiled into tables, and diversity indices sourced from such have been calculated. Statistical analyses will explore patterns across the sampling sites. Such will display the variations in communities among the sampled areas, providing insights into the impact of mining and regreening efforts on forensically important insects.

099

ISOLATION AND QUANTIFICATION OF LIPID POLYESTERS IN THE WET STIGMAS OF NICOTIANA TABACCUM

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The wet stigma possesses a sticky secretion, known as stigmatic exudate, on its outermost surface that traps pollen. These exudates act as a water reservoir and may contain essential macromolecules including lipids. Previous studies have shown that the exudate of *Nicotiana tabaccum* stigma contains 7.4% lipids, which aids in pollen tube development. Tobacco exudate contains lipid estolides (polyesters) that are end-capped with unsubstituted fatty acids (nFA); the estolide bond is an ester between a fatty acid and the hydroxyl group (ω–HFA) of another fatty acid (nFA). These estolides are esterified to glycerol forming triacylglycerides (TAG_n) and diacylglycerides (DAG_n); free fatty acid estolides (FFA_n) and membrane polar lipids (PL_n) are also present (n=number of estolide bonds). This thesis focused on quantifying total lipid polyesters and isolating their four components: TAG_n , DAG_n , FFA_n , and PL_n and further quantifying these components across the seven tobacco flower developmental stages. After lipid extraction from stigmas, thin layer chromatography was performed to isolate the components; depolymerization and transmethylation was then performed to quantify lipids through gas chromatography. The results were consistent with the previous studies that showed that total lipid polyesters quantity increased across the developmental stages, and the ω–HFA increased across the stages indicating an increase in the length of lipid polyesters as stigma develops. The quantification of the four lipid components is underway. This thesis provides an accurate quantification of lipid polyesters in developing tobacco stigmas, a foundational knowledge required to interpret radioisotope labeling experiments that are being conducted in our laboratory.

100

HOW DOES WHITE-THROATED SPARROW SONG LENGTH VARY ACROSS SINGING CONTEXTS

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Song length is one feature of bird song that may vary and may contain important information about individual quality. Birds may also vary their song length depending on the intended receiver or social context. For example, longer songs may be used in long-range advertisement but shorter songs in close territorial contests. In this study, we examined the daily and seasonal song length patterns of the White-Throated Sparrow (*Zonotrochia albicollis*) in Ontario, Canada over two breeding seasons. We used autonomous recorders to record from dusk through 4h after sunrise a day from May to June. We visualized songs in Raven Pro and selected clear songs without overlap and measured song length. Song length peaked earlier in the breeding season and declined with increasing calendar day, suggesting that longer songs may function in mate attraction. Song lengths were significantly shorter at dawn and in the morning than at dusk and night while songs at night were significantly longer than at dusk. Longer songs later in the day may be shaped by predation pressure if it is safer to sing longer at dusk/night when predators are not active. Alternatively, there may be improved sound transmission at dusk and night when fewer species are singing. Overall, this study provides the first quantitative description of the effects of time of day, time of year, and social context on song length in this species.

101

DOES SPRING LEAF OUT TIMING AND VINCA MINOR INVASION REDUCE ARBUSCULAR MYCORRHIZAL FUNGAL ABUNDANCE?

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Vinca minor is an invasive plant species introduced to Canada as an ornamental, now threatening biodiversity by forming dense ground cover in forest understories. This species establishes mutualistic relationships with arbuscular mycorrhizal (AM) fungi, which are essential for soil nutrient cycling and plant health. Climate change has altered the timing of spring leaf-out in deciduous forests, potentially influencing competitive interactions among plants by modifying light availability. However, its impact on AM fungal associations in understory plant communities remains poorly understood. We investigated the effects of altered leaf-out timing and *V. minor* invasion on AM fungal abundance in an understory deciduous plant community using a controlled mesocosm experiment. Specifically, AM fungal abundance was assessed by measuring extra-radical soil hyphal length, an indicator of fungal colonization and nutrient exchange potential. The results showed no significant effect of either shade timing or *V. minor* presence on fungal abundance. These findings suggest that AM fungal associations are tolerant to shifts in canopy phenology and invasive plant encroachment, at least in the short-term and under controlled conditions. However, further research is needed to explore potential long-term ecosystem impacts, including on belowground microbial communities, nutrient cycling, and forest regeneration processes.

102

LIPID POLYESTER PROFILING IN STIGMAS OF TOBACCO (*NICOTIANA TABACUM*) MUTANTS

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Plants produce extracellular lipid polyesters that modify cell walls and contribute to structural integrity and protection. While cutin, the lipid polyester of the plant cuticle, is an insoluble polymer of glycerol and hydroxy fatty acids, *Nicotiana tabacum* stigmas secrete an exudate rich in soluble lipid polyesters that are structurally similar to cutin. Although cutin biosynthesis has been extensively studied, stigma lipid polyester synthesis remains poorly understood. Our lab has analyzed the transcriptomes of developing tobacco stigmas and identified candidate genes for the biosynthesis of these lipids; many of these are genes known to be important for cutin biosynthesis. Here, we investigate the role of candidate genes of stigma lipid biosynthesis using a mutant approach in tobacco. Transgenic tobacco plants carrying constructs to produce either down- or up-regulation of specific genes were genotyped by PCR, and stigma lipid composition was analyzed by gas chromatography-flame ionization detection (GC-FID) after chemical depolymerization of stigmas. This study aims to elucidate the biosynthetic pathways of stigma polyesters, which has potential applications in biomaterial development, and may provide insights into still unknown steps of cutin biosynthesis.

103

INDIVIDUAL DISTINCTION AND MICROGEOGRAPHIC VARIATION OF BLACK-THROATED GREEN WARBLER (SETOPHAGA VIRENS) SONG

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Bird song may exhibit microgeographic patterns of variation where songs may be more similar or dissimilar among neighbours than more distant birds. In addition, songs of most birds have been shown to be individually distinctive, even when similar to others. Wood warblers belonging to the *Setophaga* genus have a song system in which songs can be placed into two categories. Type A song is associated with intrasexual functions, being used to signal between males for functions like territory defense. Type B songs in contrast are used for intersexual functions, such as mate attraction from a male. The black-throated green warbler (*S. virerns*) is a wood warbler with a repertoire size of two, with one of each type A and B categories. To examine individual distinction and microgeographic patterns of type B song automated recording units were placed in a grid in Sault Ste Marie, Ontario to record black-throated green warbler songs. Recordings were analyzed using Raven Pro to ID individual type B songs and clip the best ten from each individual bird (n=61) to use for measurements. Spectrogram cross correlation was used to examine variation within individuals and between neighbour and non-neighbour groups. Cross correlation scores were significantly different between self, neighbour and non-neighbour groups, with neighbours having slightly but significantly higher cross correlation scores than non-neighbours. This indicates that there may be some sharing of type B song among neighbours in black-throated green warblers at levels greater than chance, in contrast with studies on other wood warbler species that find no microgeographic pattern in type B song.

104

IS PLANT SPECIES DIVERSITY IFNLUENCED BY MYCORRHIZAL TYPE AND CLIMATE WARMING IN POST-BURN UNDERSTORIES IN THE ONTARIO BOREAL?

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In the Canadian Boreal Forest, understory plant communities contribute significantly to overall biodiversity. However, increasing wildfire frequency and rising temperatures are expected to impact these ecosystems. The dominant tree species in a stand can shape understory composition, influencing plant-mycorrhizal associations, which are essential for nutrient exchange between plants and soil. Despite this, the effects of anthropogenic disturbances on these relationships remain poorly understood. This study examined how dominant tree species and temperature changes influence plant community composition and mycorrhizal associations after wildfire. We hypothesized that both factors would drive community structure and fungal associations. Using percent cover data, we assessed understory vegetation in recently burned areas and again one year later. Eight sites were selected within jack pine (*Pinus banksiana*)- and white birch (*Betula papyrifera*)-dominated stands, where plots were subjected to contrasting temperature treatments. Our results showed that plant communities varied by dominant stand type, with white birch forests supporting greater diversity than jack pine stands. In addition, an overwhelming presence of arbuscular mycorrhizae-associating plants were in nearly every plot. However, temperature treatments had no significant effect on plant composition. These findings provide insight into the role of mycorrhizal fungi and climate in post-disturbance forest recovery, offering valuable guidance for forest management in the face of climate change.

105

DO NEIGHBOUR TRAITS PREDICT FLOWERING TIME SHIFTS FOR FOCAL PLANTS WHEN COMPETITORS ARE REMOVED?

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Fertilizing plants generally leads to them flowering later, and recent research indicates that neighour removal has a similar effect. This body of research strongly suggests that competition among plants has the potential to significantly alter a plant's flowering time. In other recent research, we identified that competition intensity was not related to abiotic nutrient availability, suggesting a role for the relative traits of competitors. Here, we identified pairs of target plants of the same species growing close together, for seven target species (15 replicate pairs species). We identified all neighbours for the control target plants, and removed the neighbours of the other nearby target plant by regular clipping. We then recorded flowering time for all target plants throughout the growing season. We also determined species-level functional traits for all plant species (mean of 25 measures per species for maximum height, specific leaf areas). We tested whether the mean difference between the traits of neighbours and those of the target plant predicted the degree to which a target plant shifted in flowering time for neighbour-removal target plants. Plants whose neighbours were removed varied in the degree to which their flowering time shifted; however, shifts were not as pronounced as observed in previous growing seasons. Importantly, the degree to which target plants differed from neighbours in maximum species height and SLA did not predict observed shifts in flowering time.

106

THE EFFECTS OF TREE COMMUNITY AND WATER LEGACY ON SOIL MACROFUNGI FRUITING

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Macrofungi play important and contrasting roles in forest ecosystems depending on their strategy. Ectomycorrhizal (ECM) fungi associate with trees, providing soil nutrients in exchange for photosynthetic sugars, while saprobic fungi act as decomposers. These strategies have contrasting implications for soil carbon sequestration in temperate forests: ECM fungi can contribute to increased soil carbon storage by slowing decomposition, whereas saprotrophic fungi accelerate carbon cycling by decomposing organic matter. These guilds compete for soil resources; however, their reproductive responses to factors such as tree functional diversity and water availability are poorly understood. In this study, we sampled sporocarps weekly during a growing season at an International Diversity Experiment Network with Trees (IDENT) site, which contains plots representing a gradient of tree functional diversity, either subjected to a drought treatment or not. Sporocarps were identified morphologically, dried, and weighed. We found that tree species assemblage and water legacy both had significant effects on sporocarp biomass. In addition, ECM and saprobic fungi produced relatively more biomass in plots that were subjected to long-term drought in previous years. These findings indicate that exposure to drought affects fungal fruiting, possibly leading to community shifts consistent with increased stress tolerance.

107

COMPUTATIONAL ASSESSMENT COMPARING THE STANDARD GENETIC CODE'S ABILITY TO MINIMIZE ERROR ACROSS 54 AMINO ACID PROPERTIES WITH AN OPTIMIZED GENETIC CODE

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Various theories have emerged regarding the evolution of the standard genetic code (SGC). The adaptive theory states that the code evolved to minimize the effect of error. This idea is supported by the observation that codons differing by just one nucleotide often encode amino acids with similar biochemical properties—or, in some cases, the same amino acid (Koonin & Novozhilov, 2008). Freeland and Hurst (1998) built on these principles when testing the efficiency of the SGC in minimizing error, using polar requirement as the amino acid property. When comparing with 999999 alternative genetic codes, only one performed better, leading to their famous conclusion that the SGC is "one in a million". Expanding the scope of their study, here a similar analysis was performed on 54 amino acid properties. Wolfram Mathematica was used as the integrated development environment (IDE) to simulate 9999 alternative genetic codes 10 times for each of the 54 properties, to determine an average ranking of the SGC in comparison to all alternative codes. The SGC ranked the highest among the polar requirement, long-range non-bonding energy (E_l), and unfolding entropy change of chain ($-T\Delta S_c$) amino acid properties. The genetic code that performed most optimally in the original 1998 study was then tested against the 10 properties where the SGC ranked the highest, aiming to explore potential relationships among the most conserved properties.

108

NEUROMUSCULAR JUNCTION MORPHOLOGY IS MODESTLY INFLUENCED THROUGH AMPK ACTIVATION IN AGED MICE

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Introduction: The neuromuscular junction (NMJ) facilitates the electrochemical communication between an α-motor neuron and myofiber that is crucial for the induction of a muscle contraction. Accompanying the age-related loss of muscle mass, i.e., sarcopenia, are deleterious alterations to NMJ morphology. Interventions such as exercise and caloric restriction can ameliorate age-associated deficits at the NMJ due, in part, to the stimulation of upstream proteins that are directly or indirectly regulated by AMP-activated Protein Kinase (AMPK). Hence, the purpose of this study is to investigate the effects of chronic AMPK activation on NMJ morphology and health within aged mice. **Methods**: Old C57BL/6 mice ($n = 16$) were randomized at 18-months of age to receive either a vehicle (Old-Veh) or 10 mg/kg of body weight of a small molecule AMPK agonist MK8722 (old-MK) every other day for a total of 6-months. The epitrochleoancoenus muscle was collected, stained and further analyzed. Young 3-month-old mice served as a healthy control **Results**: Our preliminary data (n=2-4 per group) demonstrate a significantly greater nerve terminal perimeter ($p<0.05$) in Old-Veh relative to young mice, which tended to decrease ($p=0.09$) with MK treatment. Furthermore, we observed a greater number of polyinnervated NMJs, and pre-synaptic branch length in Old-Veh mice only. Age also exacerbated post-synaptic fragmentation ($p<0.05$) which was partially decreased in old-MK mice. **Conclusion**: This study provides evidence implicating AMPK's role as an influential molecular regulator at the level of the NMJ. Further work is aimed to achieve a full data set to grasp the extent of this relationship.

109

EFFECTS OF PIKFYVE LIPID KINASE INHIBITION ON ENDOPLASMIC RETICULUM IN THE CONTEXT OF ER-REMODELING

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Lysosomes are important for molecular degradation and regulation of other organelles through membrane contact sites (MCS), including the endoplasmic reticulum (ER), the largest organelle in the cells responsible for protein and lipid synthesis, and calcium signaling. The ER is highly dynamic, constantly changing shape, partly through ER-hitchhiking, a process of ER-remodeling driven by ER-anchoring to motile lysosomes. A key effector of lysosomal dynamics is the kinase PIKfyve, responsible for synthesizing phosphatidylinositol 3,5-bisphosphate. Inhibition of PIKfyve disrupts lysosome shape and dynamics by lysosomal coalescence, reduced motility, and diminished endocytic trafficking and autophagic flux. However, the specific effects of PIKfyve inhibition on lysosomal cross-talk with the ER are unclear. We discovered that PIKfyve inhibition causes a collapsed ER morphology with reduced dynamics and reduced ER hitchhiking. My work aimed to understand these observations by asking if PIKfyve inhibition altered microtubules and contact sites between ER-lysosomes, both needed for ER hitchhiking.

Utilizing high-resolution microscopy of EB1 (a microtubule plus-end marker) and ɑ-tubulin (a standard microtubule marker), we noted that upon PIKfyve inhibition, there are no significant differences in microtubule morphology or dynamics. This suggests that alteration of ER-remodeling via ER-hitchhiking is not influenced by microtubule instability upon PIKfyve inhibition. Given what we discovered, we are utilizing high-resolution microscopy using GCEP1A-ER (an ER-calcium biosensor) to explore the functional consequences of PIKfyve-inhibition on ER-lysosome MCS. Investigating this aims to link lysosomal dysfunction to altered organelle cross-talk and impaired ER functions, offering potential insights for therapeutic intervention in diseases driven by organelle disruption.