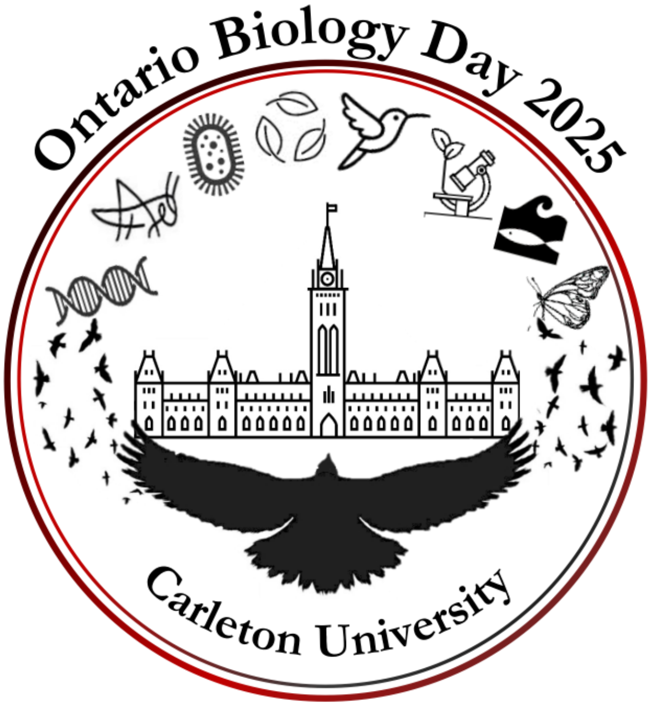
Ontario Biology Day

37th Annual Conference

Poster Presentation Abstracts



Carleton University

March 22-23, 2025

Carleton
University

Posters – By Poster Presenter Surname

#	First	Last	University
30	Celeste	Abraham	McMaster University
57	Hanin	Al-Ezzi	McMaster University
11	Sophia	Anazia	Toronto Metropolitan University
1	Emily	Archambeault	University of Windsor
68	Washma	Arshad	Algoma University
6	Daniel	Bekele	Toronto Metropolitan University
65	Roxanne	Bergeron	Algoma University
46	Saniya	Bhalla	Wilfrid Laurier University
49	Morgane	Brading	Wilfrid Laurier University
62	Alicia	Bruni	Algoma University
59	Emily	Cacchione	McMaster University
45	Qing Gui Queenie	Chung	Toronto Metropolitan University
43	Anastasia	Chuprakova	McMaster University
19	Anastasia	Cornea	McMaster University
4	Eric	Deaconu	Western University
44	Connie	Di Raimo	Toronto Metropolitan University
51	Alyssa	Dupuis	University of Windsor
55	Zahava	Dworkin	McMaster University
40	Abby	Eaton	McMaster University
47	Shahmeen	Farooqi	Wilfrid Laurier University
23	Raina	Fatima	Toronto Metropolitan University
61	Kendra	Favaro	Algoma University
37	Chilyn	Fenton-Stickle	University of Toronto - Mississauga
8	Alizée	Fieffé-Bédard	McMaster University
41	Nicolas	Fragoso Wandurraga	University of Toronto - Mississauga
66	Haiely	Frasier	Algoma University
28	Priscilla	Fung	University of Ottawa
24	Simer	Gill	McMaster University
14	Ben	Harrison	University of Ottawa
63	Kristin	Hillier	Algoma University
39	Anya	Hu	University of Toronto
36	Kristen	Huang	University of Ottawa
52	Tiffany	Huang	University of Windsor
34	Laiba	Jamal	University of Toronto - Mississauga
2	Hania	Kusznirewicz	Wilfrid Laurier University
7	Veronica	Langdon	Carleton University
21	Sharifa	Lomiyev	Toronto Metropolitan University
32	Danielle	MacNeil	McMaster University
10	Amasha	Malawiya Arachchige	Toronto Metropolitan University
15	Shruti	Manna	Toronto Metropolitan University
12	Christina	Meier	Queen's University
53	Laura	Middleton	University of Windsor

22	Shikha	Narula	Toronto Metropolitan University
54	Linda	Nguyen	University of Windsor
5	Alexandria	Ojha	Western University
56	Sofiyyah	Oladipupo	McMaster University
60	Vaidehi	Patel	Algoma University
50	Katrina	Pegg	Wilfrid Laurier University
69	Anton	Peter	Algoma University
29	Pakin	Pongpaiboon	Trent University
58	Olivia	Robillard	McMaster University
17	Pooja	Samaraweera	Toronto Metropolitan University
25	Tayin	Seeton	McMaster University
9	Ornella	Shaikovsky	Toronto Metropolitan University
26	Nojan	Shishechiha	Toronto Metropolitan University
42	Niha	Sohail	University of Toronto - Mississauga
27	Arianna	Stanley-Harrison	Carleton University
35	Ayesha Siddiqua	Syeda	University of Toronto
13	Brianna	Tapia	University of Toronto
70	Lucy	van Haaften	Trent University
3	Vanessa	Vashishth	Wilfrid Laurier University
67	Audrey	Verra	Algoma University
31	Sydney	Williams	Carleton University
33	Benjamin	Winchester	McMaster University
16	Jessica	Yemen	McMaster University
18	Alacea	Yerxa	Toronto Metropolitan University
38	Mutsuko	Yoshida	Carleton University
64	Bryanna	Zimbaro	Algoma University

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69	Anton	Peter	Algoma University
70	Lucy	van Haaften	Trent University

001

USING NOVEL PHYSIOLOGICAL INDICATORS TO DETECT INVESTMENT IN AND TIMING OF BREEDING IN AN ARCTIC-BREEDING SEADUCK.

Emily A. Archambeault*[1], Holly L. Hennin[1,2] Chris M. Harris[1], Christina A.D. Semeniuk[1], H. Grant Gilchrist[2], Oliver P. Love[1]
[1]University of Windsor, Windsor, ON, Canada, N9B 3P4
[2]Environment and Climate Change Canada, Ottawa, ON, Canada, K1H 1E1

Life-history investment theory predicts that some individuals may be better at using physiological and behavioural mechanisms to meet the energetic demands from environmental challenges to maximize breeding success. However, field-testing these predictions is complicated by the challenge of quantifying environmentally induced flexibility in mechanisms before breeding investment. Nonetheless, these questions are vital to answer in places such as the Arctic, which is experiencing climate change 3-4 times the global average. Here we use a 16-year dataset from Canada's largest colony of Arctic-breeding common eiders (Somateria mollissima), located at East Bay Island, Nunavut, to field-test these investment predictions. Specifically, from 2006-2023, we captured and blood-sampled almost 3000 pre-laying females following arrival on the breeding grounds as birds began fattening and investing in follicle (yolk) recruitment. We then followed individuals to assess two reproductive decisions that impact breeding success: whether birds bred, and if so, when they initiated laying. To answer these questions, I am quantifying levels of vitellogenin (VTG) and plasma estradiol (E2) prior to laying as biomarkers of breeding investment. To quantify the length and timing of this investment period I will explore patterns of VTG, E2, plasma triglycerides, and body mass in relation to lay date. These results will also shed light on whether temporal overlap between fattening and follicle recruitment is possible in this species. Filling in these challenging life history gaps is vital for predicting whether individuals and the populations they make up can persist and succeed in the face of rapidly increasing change in the north.

002

SILK NANOPARTICLE DRUG DELIVERY OF DOUBLE-STRANDED RNA AS AN EPITHELIAN OVARIAN CANCER TREATMENT

Hanna Kusznirewicz*, Samuel Peters, Nirosha Murugan
Department of Health Science Wilfrid Laurier University, Waterloo, Ontario, Canada N2L 3C5

In epithelial ovarian cancer, late detection and limited treatment options contribute to high mortality rates. Common applications of platinum-based chemotherapy are ineffective due to chemo-resistance and cumulative toxic effects from the platinum. This research project investigates the use of silk nanoparticles (sNPs) as a potentially safer drug delivery system for double-stranded RNA (dsRNA) in ovarian cancer cells in order to observe the treatment's potential cytotoxic effects. dsRNA has shown promise in triggering a caspase-dependent apoptotic response, while sNPs are noted for their biocompatibility and low toxicity. Given that sNPs naturally exhibit a negative charge, they will be modified to carry a positive charge to facilitate binding with dsRNA. The methodology of this project entails that the liquid silk, derived from Bombyx mori silk cocoons, is processed via nanoprecipitation. The size and size distribution of the sNPs is analyzed using a dynamic light scattering technique. Cytotoxicity will be assessed by comparing cell viability following treatments with free dsRNA, unloaded sNPs (negative control), modified sNPs (control), and dsRNA-coated sNPs, using an Alamar Blue assay. This project is expected to provide further insight into dsRNA-based therapies and understanding the efficacy of silk nanoparticles as a drug delivery system. These findings could inform future cancer-related clinical strategies, offering a novel approach to ovarian cancer treatments and potentially other cancer types as well.

003

MELANIN'S IMPACT ON CHEMOTHERAPY EFFICACY IN LUMINAL A BREAST CANCER

Vanessa Vashishth*[1], and Nirosha J.Murugan[1]
[1]Wilfrid Laurier University, Waterloo, Ontario, Canada, N2L 3C5

Luminal A breast cancer is the most common subtype of breast cancer, known for its favorable prognosis due to its lower expression of genes associated with cell proliferation. However, its resistance to chemotherapy, particularly doxorubicin, poses a challenge in treatment. This study investigates the potential of melanin, specifically synthetic eumelanin, to enhance the efficacy of doxorubicin in treating Luminal A breast cancer. Melanin is known for its antioxidant properties and ability to protect against oxidative stress, and recent advancements have shown promise in using melanin in drug delivery and cancer therapy.

This study examines whether combining doxorubicin with melanin can reduce the necessary chemotherapy dosage while improving cancer cell death and minimizing side effects brought upon by treatment. The study will utilize MCF7 cells, a well-established Luminal A breast cancer cell line, and assess the effects of a combination treatment on cell proliferation and viability. The hypothesis driving this research is that melanin will enhance doxorubicin's ability to induce cancer cell death while reducing proliferation rates, compared to chemotherapy alone. This study aims to provide insight into whether melanin could serve as an adjunct to conventional chemotherapy, potentially improving treatment outcomes and offering a strategy to overcome chemotherapy resistance in Luminal A breast cancer. By investigating melanin's interaction with chemotherapy, this research has the potential to lead to more effective, targeted therapies, improving survival rates, reducing relapse, and enhancing the quality of life, thus contributing to the advancement of precision medicine in oncology

004

SPATIAL GENE EXPRESSION PATTERNS OF DIGESTIVE CYSTEINE PROTEASES IN *TETRANYCHUS URTICAE*

Eric Deaconu*[1], Zoran Culo[1], Vinayak Singh[1], Vojislava Grbic[1]
[1]Department of Biology, University of Western Ontario, 1151 Richmond St., London, Ontario, Canada N6A 3K7

The two-spotted spider mite, *Tetranychus urticae*, is a highly polyphagous agricultural pest capable of feeding on over 1,100 plant species. Central to its adaptability and extreme generalism is a robust digestive system, in which cysteine proteases are proposed to facilitate intracellular digestion. This study investigates the spatial gene expression patterns of selected cathepsin L and B family digestive cysteine proteases in the *T. urticae* midgut, focusing on their role in the proposed intracellular digestive processes taking place within free-floating digestive cells, and their potential preloading in midgut generative epithelial cells, in advance of digestive cell budding. Using *in situ* hybridization, we mapped the localization of the selected cathepsin L, *TuPap-41*, and selected cathepsin B, *TuPap-9*, across the *T.urticae* midgut cells. Our findings reveal that the selected cathepsin L is expressed in generative cells with an apparent patterning in expression over the midgut generative epithelia, perhaps indicative of preloading in advance of digestive cell budding, supporting the hypothesis that digestive cells are preloaded with digestive enzymes before entering the gut lumen. In contrast, the selected cathepsin B appears to be predominantly expressed in generative cells, though without the distinct organization observed with the selected cathepsin L. Additionally, we observed potential expression of the selected cathepsin B within other midgut cell types, suggesting further non-digestive roles. These findings demonstrate functional differentiation among digestive cysteine proteases in *T. urticae*, and improve the understanding of the proposed *T. urticae* intracellular digestive mechanism.

005

EVALUATING DIMETHOATE RESISTANCE OF SPIDER MITE POPULATIONS FROM SOUTHWESTERN ONTARIO SOYBEAN CROPS.

Alexandria Ojha*[1], Joseane Moreira do Nascimento[1], Reagan Michiels[1], Mikaelison da Silva Lima[1], Kristie Adriana Bruinsma[1], Tracey Baute[3], Ian Scott[2], Vojislava Grbic[1]
[1]Department of Biology, University of Western Ontario, 1151 Richmond St, London, Ontario, Canada N6A 3K7
[2]London Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 1391 Sandford St, London, Ontario, Canada N5V 4T3
[3]Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA), 120 Main Street East, Ridgetown, Ontario, Canada N0P 2C0

Tetranychus urticae (Koch) (Acari: Tetranychidae) is an extreme generalist spider mite that is highly resistant to acaricides and severely threatens economically important crops. Due to its ability to rapidly adapt to chemical controls, it is crucial to evaluate the effectiveness of currently available products, such as dimethoate—the only registered acaricide for spider mite control in Ontario soybean fields. Dimethoate is an organophosphate (OP) which is an acetylcholinesterase (AChE) inhibitor that functions by preventing the hydrolysis of acetylcholine. This leads to its accumulation in the synaptic cleft, disrupting neural transmission, and ultimately causing paralysis and death in mites. This project aims to evaluate dimethoate resistance in eight spider mite populations from Southwestern Ontario soybean fields and to develop a streamlined molecular approach for resistance detection in comparison to conducting laborious toxicity bioassays. The molecular analysis focused on the AChE gene. All populations were screened for known target-site mutations (G119S, A201S, T280A, G328A and F331W/C/Y) using Sanger sequencing, AChE expression levels were quantified using RT-qPCR, and copy number variation was assessed using q-PCR. For the toxicity bioassays, mites were placed on leaf discs treated with dimethoate (50 ppm) or water (control), to assess adult mortality. The data from the bioassays demonstrated that four of the eight populations are resistant to dimethoate, and the molecular analysis is still in progress. These results highlight the importance of assessing dimethoate's effectiveness against spider mite populations and developing efficient, reliable methods to detect resistance.

006

INVESTIGATING THE ROLE OF UGD IN *SHIGELLA FLEXNERI* POLYMYXIN B RESISTANCE THROUGH PMRAB-DEPENDENT REGULATORY SYSTEM

Daniel Bekele*[1], Joseph McPhee[1]
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

Shigella flexneri has undergone genetic inactivation of key regulatory genes, including PmrD and PmrAB, which are responsible for lipopolysaccharide (LPS) modifications crucial for resistance to cationic antimicrobial peptides. In *Eschericia coli*, PmrD links the PhoPQ and pmrAB systems and mediates LPS modifications in response to magnesium and iron levels. In *S. flexneri*, under conditions of high magnesium, which inactivates PhoPQ, and high iron, activating PmrAB, we have observed partial resistance to polymyxin B, suggesting residual PmrAB activity still mediates some protective modifications. However, the loss of ugd, a downstream gene regulated by PmrAB that is required to make the 4-aminoarabinose modification, may limit the extent of resistance. We plan to investigate this by restoring ugd function in *S. flexneri* and assessing its role in PmrAB-dependent polymxyin B resistance. This will be explored using minimum inhibitory concentration (MIC) assays to quantify resistance levels and killing assays to evaluate bacteria survival under antimicrobial stress. These findings will further elucidate the genetic determinants of antibiotic resistance in *Shigella* and their broader implications for bacterial pathogenesis.

007

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

Veronica Langdon[1], Nick Westcott[2], Jeff Dawson[1], Iain McKinnell[1]
[1]Department of Biology, Carleton University, Ottawa, Ontario, Canada K1S 5B6
[2]Recreation and Athletics, Carleton University, Ottawa, Ontario, Canada K1S 5B6

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

008

THE EFFECT OF TNF ON DENSITY AND MORPHOLOGY OF MICROGLIA IN THE CA1 REGION OF THE BRAIN

Alizée Fieffé-Bédard[*,1,2], Braeden Cowbrough[1,2], Sofya Ermolina[1,2], Erica DeJong[1,2], Dr. Dawn Bowdish[1,2]
[1] McMaster Immunology Research Center, Hamilton, Ontario, Canada, L8N 3Z5. [2] Firestone Institute of Respiratory Health, St. Joseph’s Healthcare, Hamilton, Ontario,Canada, L8N 1Y2.

Microglia play an active role in the central nervous system, they are involved in synaptic pruning, neurogenesis, crosstalk with other glial and modulating the immune response. With age, microglia show both an altered morphology and inflammatory profile leading to an overactive microglia population that has been linked with cognitive decline. Within the CA1 region of the brain, linked to memory consolidation and spatial reasoning, microglia are known to increase in density with age. One pro-inflammatory cytokine shown to activate microglia is TNF which serves as a major regulator of many immune processes. TNF stimulation increases microglia proliferation, induces increased phagocytosis and increases neuron pruning. We hypothesize that microglia from TNF-deficient mice (TNFKO) will have lower microglia density as well as reduced somas and larger arborization compared to wild-type (WT) mice. We compared images taken from the CA1 region of TNF KO and WT mice brains that were stained with Iba1 and TMEM119 to examine the difference in microglia morphology and density. We found that TNF KO mice had a lower microglia density but no significant differences in morphology. The next steps of the project will be to isolate microglia from whole brains using a mojosort kit. The success of the Mojosort kit was measured by Flow Cytometry. The microglia will be stimulated with TNF and cytokine levels (IL-6, IL-1β and IL-10) will be measured with ELISA assays. We hope that these results will help elucidate the long term effects of exposure to TNF on microglia.

009

THE ROLE OF A FLUORESCENT WBOX2 PEPTIDE IN CLATHRIN MEDIATED ENDOCYTOSIS: ASSESING SPECIFICITY WITH IKARUGAMYCIN

Ornella M. Shaikovsky, BSc Student [1], Natalie Uzynski, MSc Student[1], Costin Antonescu, PhD[1], Eden Fussner-Dupas PhD[2]
[1]Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, M5B 2K3
[2] Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, British Columbia, V6T 1Z3

Clathrin-mediated endocytosis (CME) is a critical pathway for cellular uptake, enabling the internalization of surface proteins through clathrin-coated pits (CCPs). This study explores the specificity of Ikarugamycin (IKA) as an inhibitor of CME by evaluating its potential to displace the Wbox2 peptide, a clathrin-binding marker that facilitates the study of clathrin recruitment dynamics, from CCPs. The Wbox2 peptide was engineered with a TAT sequence to facilitate cellular entry and an HA detection tag for visualization, allowing for precise tracking within ARPE-19 cells.The methodology involves incubating cells with the TAT-Wbox2 peptide, confirming recruitment to CCPs using Total Internal Reflection Fluorescence (TIRF) microscopy. Following localization verification, IKA is introduced to determine its ability to displace the peptide from CCPs. Quantification of fluorescence signals will provide a measure of peptide displacement, enabling an assessment of IKA's specificity as a CME inhibitor.It is anticipated that IKA significantly reduces peptide localization within CCPs, indicating that it effectively disrupts clathrin recruitment. This would support IKA's potential as a selective inhibitor of clathrin-mediated endocytosis, offering valuable insights into its feasibility for therapeutic applications targeting endocytic pathways.

010

DOES MICROBIAL FUNCTION VARY WITH STREAM HEALTH? COMPARISON OF DON RIVER AND EAST HUMBER TRIBUTARIES WITH POOR TO GOOD QUALITY CONDITIONS.

Amasha Malawiya Arachchige*
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

The Don River, located in Toronto, Ontario, is situated in a highly urbanized area, contributing to its 96% urbanization. Combined sewer overflows (CSOs) and effluent from wastewater treatment plants (WWTPs) contribute to approximately 51% of the Don River's flow, significantly impacting its pollution levels. Biofilm serves as an important bioindicator of pollution in aquatic ecosystems; its community structure adapts to increased pollution by favoring more tolerant species, thereby altering its metabolic functional diversity. This study aimed to assess the water quality of various Don River tributaries, including the heavily polluted Taylor-Massey Creek and the relatively healthy East Humber River. Two of the sampling sites were located upstream and downstream of the North Toronto Treatment Plant (NTTP), an area known for frequent CSO events. These sites were evaluated to determine whether pollution from CSOs or improperly treated effluent is affecting water quality. A microbial metabolic fingerprint of each site was generated using Biolog EcoPlates™, providing insight into the metabolic rate and community structure of the biofilm. Additional water quality parameters, such as nitrate and chloride concentrations, were also measured to further assess stream health. Initial results suggest that the metabolic rates across most sites are similar, potentially indicating consistent pollution levels and metabolic functional diversity among the tributaries. Furthermore, the sites upstream and downstream of the NTTP exhibited comparable metabolic functional diversity, which may suggest that CSOs or WWTP effluent are not contributing significant additional pollution to these areas.

011

REGULATION OF GSK3β IN NUTRIENT STARVATION AND CELLULAR DIFFERENTIATION VIA CLATHRIN-MEDIATED LYSOSOMAL PATHWAYS

Sophia Anazia*[1], Rebecca Cabral-Dias[1,2], Laura A Orofiamma[1,2], Ayshin Mehrabi[1], Diana S Forkel[1,2], Costin N Antonescu[1,2,3]
[1]Department of Chemistry and Biology, [2]Graduate Program in Molecular Science, Toronto Metropolitan University, Toronto Ontario, Canada, M5B 2K3, [3]Keenan Research Centre for Biomedical Science of St. Michael's Hospital, Toronto, Ontario, Canada, M5B 1W8

Cells continuously adapt to nutrient availability, relying on tightly regulated signalling pathways to control survival and differentiation. Glycogen Synthase Kinase 3β (GSK3β) plays a key role in these processes, with its nuclear-cytoplasmic localization influencing transcriptional regulation. However, the mechanisms governing its trafficking remain unclear. This study investigates how clathrin-mediated endocytosis (CME) regulates lysosomal function and, in turn, GSK3β localization. Lysosomes are critical for controlling GSK3β's nuclear export, and clathrin is essential for maintaining lysosomal integrity. Disrupting clathrin function alters lysosomal morphology, leading to enlarged lysosomes fragmenting into smaller vesicles, ultimately affecting GSK3β localization. Using Ikarugamycin, a clathrin inhibitor, we examine its impact on lysosome dynamics and the subsequent mislocalization of GSK3β. Methanol fixation enables precise imaging of these interactions under nutrient-rich and nutrient-deprived (EBSS media) conditions. By comparing GSK3β localization across different nutrient environments and clathrin inhibition conditions, this study aims to clarify how lysosomes regulate nuclear-cytoplasmic shuttling. These findings will provide insights into the role of clathrin in lysosomal homeostasis and its broader implications for nutrient sensing and cellular differentiation.

012

TIME-OF-DAY DIFFERENCES IN CELL COMPOSITION IN CHRONIC PAIN

Christina Meier*[1], Amanda Zacharias[2], Courtney A. Bannerman[2], Jaqueline Raymondi Silva[2], Robert Colautti[1], Qingling Duan[2,3], and Nader Ghasemlou[2,4].
[1]Department of Biology, [2]Department of Biomedical and Molecular Sciences, [3]Queens School of Computing, [4]Department of Anesthesiology, Queen's University, Kingston, Ontario, Canada

Chronic pain is caused by damage to the nervous system. Although highly prevalent, it lacks effective treatment options. Circadian rhythms are roughly 24-hour cycles in biological processes that have been observed in the pain sensitivity of both mice and humans. Understanding why pain follows these rhythms could provide new insights into the development and persistence of chronic pain. The dorsal root ganglia (DRG) and spinal cord (SC) are key structures in the nervous system that contribute to the initiation and maintenance of this pain. Throughout the pain signaling pathway, neurons constantly communicate with immune cells, including microglia, macrophages, and astrocytes, to mediate pain sensitivity. A computational approach called cell deconvolution was used to estimate the proportions of different cell types in heterogeneous samples of DRG and SC tissue in a model of chronic pain (spared nerve injury (SNI)). This study aims to 1) compare cell type compositions in naive and SNI conditions in the DRG and SC, and 2) explore how cell type compositions in the DRG and SC vary across the day-night cycle. Cell type compositions in the DRG and SC differed significantly between naive and SNI conditions ($p < 0.05$). Notable differences were also observed in LDA axes between day and night sample groups. These findings show that further characterization of rhythmicity in the DRG and SC is needed, which may lead to novel therapeutic options for treating chronic pain.

013

IDENTIFYING AND EXPRESSING PIP-BOXES AND HRP-BOXES UPSTREAM OF T3SEs IN XANTHOMONAS AND PSEUDOMONAS GENOMES

Brianna Tapia*[2], Viplav Agarwal[2], and Marcus M. Dillon[1,2]
[1]Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Ontario, Canada M5S 3B2
[2]Department of Biology, University of Toronto Mississauga, Mississauga, Ontario, Canada L5L 1C6

Bacterial plant pathogens such as Xanthomonas and Pseudomonas utilize the Type III Secretion System (T3SS) to inject effector proteins (T3SEs) into host cells, manipulating plant immunity and promoting infection. The expression of these effectors is regulated by conserved promoter elements, including Pip-Boxes in Xanthomonas and Hrp-Boxes in Pseudomonas. However, the ability of these regulatory elements to control horizontally transferred effectors across genera remains poorly understood. This study aims to determine whether Pseudomonas T3SEs can be expressed in Xanthomonas and vice versa, and whether these effectors retain the ability to trigger Effector-Triggered Immunity (ETI) in host plants.

To address these questions, bioinformatics analysis using R was performed to identify Pip-Boxes and Hrp-Boxes upstream of T3SE genes across multiple Xanthomonas and Pseudomonas genomes. Motif searches and Position Weight Matrices (PWMs) were used to detect conserved sequences, followed by sequence alignment and phylogenetic analysis to evaluate evolutionary conservation. Cloning experiments involved inserting effector genes into the broad-host-range plasmid pBBR1-MCS-2, which was subsequently introduced into recipient strains via triparental mating (TPM). Successful transconjugants were selected using antibiotic resistance markers.

Effector expression will be confirmed in future experiments through spray assays conducted on Arabidopsis thaliana and followed up with Western blot analysis. This study enhances our understanding of regulatory mechanisms governing T3SE expression and their potential for functional conservation across bacterial genera, contributing insights into pathogen evolution and plant disease management.

014

IMPACT OF SERT KNOCKOUT ON SURFACING BEHAVIOUR IN *DANIO RERIO*

Ben Harrison*, Michael Tea and Kathleen Gilmour
University of Ottawa, 75 Laurier Ave E, Ottawa, ON K1N 6N5

Serotonin transporters (*sert*) reuptake serotonin from the synapse within the brain. Zebrafish (*Danio rerio)* express two *sert* paralogues (*serta* and *sertb*) which are not co-expressed in the brain. Zebrafish lacking functional expression of *serta*, *sertb*, and both paralogues were generated using CRISPR-Cas9 technology. The *sertb*-knockout (KO) zebrafish exhibited surfacing behaviour in which they remain near the surface of the water without any environmental stimulus. The pathways underlying surfacing behaviour are unknown. Previous studies have linked higher tank region preference to an anxiolytic phenotype. Similarly, we show through the novel tank dive test that larval *sertb*-KOs and *sert*-KOs exhibited increased surface preference relative to wild-types. We asked whether surfacing behaviour is a result of visual differences because serotonin accumulation is known to lead to changes in the visual system and the zebrafish retina expresses only Sertb. To assess both responses to light, as well as anxiety, locomotion was measured in an open field test under light and dark conditions, and a scototaxis test was performed to determine whether time spent under light versus dark conditions differed across genotypes. Differences in activity between genotypes may provide insight into the role of serotonin signalling in surfacing behaviour.

015

INVESTIGATING THE IMPACTS OF REPLICATION STRESS UPON WILD-TYPE AND GSK3Δ MDA-MB-231 CELLS IN PRESENCE AND ABSENCE OF PYRUVATE

Shruti Manna*, Cindy Ong and Sarah A. Sabatinos
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada, M5B 2K3

Breast cancer is the most diagnosed cancer among women. Glycogen synthase kinase 3 (GSK3) is a serine/threonine kinase that regulates cell metabolism and growth. GSK3**β** plays a role in breast cancer development and is studied for its role in the β-catenin/Wnt signalling pathway. Our lab's recent work found that GSK3 loss in TNBC cells may alter drug sensitivity and that these values are sensitive to the pyruvate present in the medium. Pyruvate is produced via glycolysis and feeds into the Krebs Cycle for energy production. This study examines how DNA replication instability drugs impact GSK3**β**+ and GSK3**β**-knockout TNBC cells in the presence and absence of pyruvate. We tested chemotherapeutic drug doses required to inhibit TNBC cell line MDA-MB-231 growth. This includes the drug gemcitabine, which causes an S phase arrest in cells by acting as a nucleoside analogue to halt DNA replication. We used the cell counting kit reagent CCK8 to monitor proliferation in GSK3**β** + or knockout cells in the presence/absence of pyruvate and under DNA replication stress drugs. The half-maximal inhibitory concentrations (IC50) for replication stress drugs differed in the absence of pyruvate. Further, the nuclear area of MDA-MB-231 cells changes when exposed to gemcitabine in various conditions (GSK3**β** knockout; without pyruvate). Our data shows that TNBC cells' sensitivity to chemotherapeutic agents depends on external metabolites and the metabolic regulation of energy by GSK3**β**. This reinforces work showing that tumour starvation alters the response to drugs and that DNA replication stress is sensitive to metabolic signalling.

016

EVOLVED CHANGES IN PULMONARY VASCULAR FUNCTION IN HIGH-ALTITUDE DEER MICE

Jessica C. Yemen*[1], Kayla M. Garvey[1], Graham R. Scott[1]
[1]*Department of Biology, McMaster University, Hamilton Ontario, Canada*

High-altitude environments present extreme challenges for endotherms, including severe cold and low oxygen availability, which impact cardiorespiratory function and aerobic metabolism. Hypoxic pulmonary hypertension (HPH) is a debilitating condition that occurs in low-altitude humans, other mammals, and birds that travel to high altitude. In mammals, HPH results from pulmonary vasoconstriction and arterial remodeling in response to hypoxia, increasing blood pressure and cardiac workload, which can lead to edema and, in severe cases, death. Prior research suggests that high-altitude deer mice (*Peromyscus maniculatus*) exhibit an attenuated HPH response compared to low-altitude conspecifics. Here, we investigated whether evolved changes in pulmonary vascular function mitigate HPH in high-altitude mice. Deer mice from high- and low-altitude populations were born and raised to adulthood in captivity, then acclimated for >6 weeks to either warm normoxia (25°C, 20 kPa O_2) or cold hypobaric hypoxia (5°C, 12 kPa O_2). *Ex vivo* wire myography was used to evaluate vascular sensitivity to low oxygen (1% O_2, 5% CO_2, 94% N_2) and to stimulation of alpha-adrenergic receptors (phenylephrine), beta-adrenergic receptors (isoproterenol), and endothelium-derived nitric oxide (acetylcholine). Among normoxic mice, preliminary results indicate that highlanders exhibit reduced sensitivity to the vasoconstricting effects of phenylephrine and increased sensitivity to the vasodilating effects isoproterenol and acetylcholine as compared to lowlanders. These findings suggest that evolved changes in adrenergic receptor sensitivity may promote vasodilation in pulmonary vessels and avoid maladaptive HPH in high-altitude deer mice. Supported by NSERC.

017

ELEVATED DIRECT BILIRUBIN DOES NOT PREDICT ELEVATED CONJUGATED BILIRUBIN IN NEONATES

Pooja Samaraweera*[1,2], Herbert Brill[2],
[1]Toronto Metropolitan University
[2]William Osler Health System

Neonatal cholestasis, characterized by elevated conjugated bilirubin, is a serious condition requiring prompt identification and treatment. Current guidelines use direct bilirubin, which includes both conjugated and delta bilirubin, as a proxy for conjugated bilirubin. However, this equivalence has not been well established. This study evaluated whether direct bilirubin accurately reflects conjugated bilirubin levels in neonates and assessed its utility as a reliable screening tool for neonatal cholestasis. A retrospective analysis was conducted on data from neonates under three months old at William Osler Health System, from 2015 to 2024, with direct bilirubin levels of 20 µmol/L or higher, where samples were sent for conjugated bilirubin testing. Results demonstrated no significant correlation between direct and conjugated bilirubin levels, especially when direct bilirubin was below 22 µmol/L, and showed no significant differences in the rate of further investigations based on direct versus conjugated bilirubin ($\chi^2 = 0.0719$, $p = 0.7887$). These findings suggest that direct bilirubin is not a reliable proxy for conjugated bilirubin and may lead to unnecessary investigations. Future research should compare these results with historical data to refine neonatal bilirubin testing protocols and improve clinical decision-making in neonatal care.

018

THE ROLE OF ADAPTOR PROTEIN COMPLEXES IN PHAGOCYTOSIS OF OPSONIZED PARTICLES

Alacea Yerxa*[1], Melanie Mansat[2], Muhammad Butt[2], Roberto J. Botelho[1,2]
[1]Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada, M5B 2K3.
[2]Toronto Metropolitan University MaRS Biomedical Research Facility, MaRS Discovery District, Toronto, Ontario, Canada, M5G 1M1.

Immune cells called macrophages play a major role in eliminating dangerous particles like microbes through phagocytosis. Phagocytosis encompasses several stages: recognition and engulfment of target particle into a phagosome, phagosome maturation (particle digestion), and phagosome resolution to recycle phagosomal membrane. Each stage of phagocytosis requires key proteins. Phagosome formation requires clathrin, a protein characterized for its role in endocytosis and recently, phagosome resolution. Clathrin depends on adaptor protein (AP) complexes to select cargo and assemble onto membranes during fission. There are at least four AP complexes, where AP1 and AP2 associate with the Golgi and plasma membrane. However, AP complexes may work at other sites like endosomes and lysosomes. Since clathrin was found to drive phagosome resolution, this raised the hypothesis that AP complexes could be involved in phagocytosis or subsequent stages. To test this hypothesis, I silenced AP1 or AP2 with siRNA-oligonucleotides against the mu subunit in RAW macrophage cell lines, obtaining 50% protein silencing. After challenging macrophages with non-opsonized *E. coli* or antibody-opsonized polystyrene beads, we observed a significant decreased in uptake of *E. coli* in AP1 or AP2-silenced cells through microscopy. However, phagocytosis of IgG-coated beads was not significantly affected by AP1 or AP2-silencing. These findings suggest AP1 and AP2 may modulate phagocytic uptake in a manner dependent on particles and/or receptor. To expand our understanding, we will measure the levels and recruitment of phagocytic receptors to the plasma membrane, during phagocytosis. Additionally, we will examine the role of AP1 and AP2 in phagosome maturation and resolution.

019

CONCENTRATION DEPENDENT EFFECTS OF BENZALKONIUMCHLORIDES ON FRESHWATER BENTHIC INVERTEBRATE COMMUNITIES

Anastasia Cornea[1]*, Claire Estey[1], Jose Luis Rodriguez[2], Lauren Timlick[2], and Karen Kidd[1]
[1]McMaster University, Department of Biology, Hamilton, ON, [2]International Institute for Sustainable Development, Experimental Lakes Area, Winnipeg, MB

The use of antimicrobials has increased considerably in recent years. Benzalkonium chlorides (BACs) are a common ingredient in non-alcohol-based disinfectants worldwide. After their use in products, most BACs go down the drain and enter municipal wastewater systems. During wastewater treatment, they adsorb to organic molecules which prevents their degradation and facilitates their release into aquatic ecosystems. BACs have shown toxicity to a variety of low-trophic organisms, but the literature lacks *in situ* data on benthic organisms. We investigated the effects of environmentally relevant concentrations of benzalkonium chloride on the makeup of benthic invertebrate communities. We expect to see a decrease in abundance and diversity as BAC concentration increases. In 2023, an eleven-week mesocosm study was conducted at the IISD-Experimental Lakes Area where we compared five environmentally relevant concentrations of BACs (nominal 20, 112, 632, 3556, and 20 000 ng/L, plus three controls of 0 ng/L). Hester-Dendy traps were deployed in each mesocosm and sampled for benthic invertebrate community composition six times over the study. Invertebrates were quantified and identified to the lowest possible taxonomic level. The most common taxa found were from orders Amphipoda and Diptera, with the majority of Diptera represented by the family Chironomidae. Results will help quantify the effects of BACs on the invertebrates that live in the sediment where these compounds tend to adsorb. Shifts in the benthic zone can cause cascading changes, so by identifying concentrations at which invertebrates experience adverse effects, we can help inform guidelines that favour the health of the entire ecosystem.

020

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

Ricky K Hong**,** Andrew I Mikhail, Sean Y Ng, Stephanie R Mattina, Magda Lesinski, Vladimir Ljubicic
Department of Kinesiology, McMaster University, Ontario, Canada L8S 4L8

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.

021

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

Lomiyev, Sharifa*, Jenkins, Nicala, Adamji, Zainab, Almasri, Nourhan, Botelho, Roberto J.
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

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 α-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.

022

INVESTIGATING PMK1’S ROLES IN THE FISSION YEAST CELL CYCLE

Shikha Narula*[1], Cindy Ong[1], Sarah A. Sabatinos[1]
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

Mitogen-activated protein kinase (MAPK) pathways play a crucial role in cellular stress responses, metabolism, and cell cycle regulation. Pmk1, a MAPK homolog of ERK in *Schizosaccharomyces pombe*, is known to contribute to cell integrity, metabolism, and cytokinesis. Yet, the precise role of Pmk1 in cell cycle regulation is unclear. We examined the function(s) of Pmk1 in fission yeast cell cycle response. We used single and double mutants of *pmk1*Δ, and checkpoint kinases (*cds1*Δ, *chk1*Δ, *rad3*Δ, *mrc1*Δ). Through mutagenesis assays, we found that *pmk1Δ* strains show lower mutation rates than single checkpoint kinase mutant strains. We conclude that Pmk1 influences cell survival and may allow mutated cells to survive. We are testing the impact of *pmk1*Δ on drug sensitivity using half-maximal inhibitory concentration (IC50) tests. IC50 doses of *pmk1+* and *pmk1*Δ strains will compare the impact of Pmk1 in surviving DNA replication instability caused by hydroxyurea, or DNA damage stress caused by phleomycin, and camptothecin. Since these chemotherapy drugs induce replication stress and DNA damage, our study provides insights into how MAPK signaling influences cellular responses to genotoxic agents. Given the conservation of MAPK pathways across eukaryotes, understanding Pmk1’s role may help uncover mechanisms of drug resistance in cancer cells. This research enhances our understanding of stress adaptation mechanisms in the cell cycle, with broader implications for genomic stability and therapeutic strategies targeting MAPK signaling.

023

THE ROLE OF SHP-1 IN MACROPHAGE PHAGOCYTIC CAPACITY DURING FcγRIIB MEDIATED INHIBITORY SIGNALLING

Raina Fatima*, Elijah Urdaneta, Roberto Botelho
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada, M5B 2K3

The maximal phagocytic capacity of macrophages is governed by various factors, including enzyme and membrane availability. However, there are many gaps in literature regarding the signaling mechanisms that limit the maximal phagocytic capacity of macrophages. FcγRs are critical surface receptors found on macrophages and other immune cells that signal the process of phagocytosis and trigger subsequent immune responses. We have previously found that SHP-1, a downstream protein of the inhibitory receptor FcγRIIB, exhibits maintained activity and phosphorylation levels as macrophages approach capacity. We sought to further investigate the role of SHP-1 by first determining whether the inhibitory effects of SHP-1 during phagocytosis require a continuous feeding source or can be triggered by a brief uptake event. To explore this, we fed macrophages 2.97µm polystyrene beads for 30 minutes, followed by varying chase times. We show that SHP-1 activation diminishes after a macrophage's food source is removed, suggesting that SHP-1 activity may be crucial for regulating phagocytosis in the presence of a continuous feeding supply. Additionally, we aim to visualize the engulfment of beads before and after SHP-1 inhibition using TPI-1, hypothesizing that macrophages may be able to engulf additional particles upon inhibition. Overall, this study provides new insights into the molecular mechanisms regulating macrophage phagocytic capacity, highlighting the inhibitory role of SHP-1.

024

THE ROLE OF ESTROGEN-RELATED RECEPTOR ON EXERCISE TRAINING IN ZEBRAFISH

Simer Gill*, Riley Mantulak, and Alexander Little.
Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4L8

Zebrafish (*Danio rerio*) are valuable biomedical models for metabolic and cardiovascular disease due to their genetic tractability, scalability, and rapid development. Exercise training has been explored as a therapeutic intervention for metabolic and cardiovascular disease in this species, but mechanisms underlying physiological responses remain poorly characterized. In mammals, the nuclear receptor estrogen-related receptor (ERR) mediates exercise-induced remodelling by enhancing vascularization, oxidative phosphorylation (OXPHOS), and cell proliferation in metabolically active tissues, such as skeletal muscle and brain. In mammals, these effects are primarily driven through ERR's interaction with peroxisome proliferator-activated receptor gamma coactivator 1α (PGC1α). However, sequence analyses suggest that PGC1α of fish lacks the functional domains that promote metabolic regulation (e.g., NRF1 binding and AMPK phosphorylation sites) in mammals. We exercise-trained zebrafish for 6 weeks (forced swimming protocol) to test whether exercise enhances performance via an ERR-mediated pathway. Specifically, we hypothesized that exercise training would enhance swim performance, aerobic scope, and boldness. Although exercise training improved these performance traits, global proteomics (skeletal muscle and brain) suggests that ERR-mediated exercise remodelling is not conserved in fish. These data highlight fundamental differences in the molecular mechanisms underlying exercise-induced plasticity between fish and mammals. Therefore, careful consideration is needed when applying zebrafish as biomedical models of metabolic and cardiovascular diseases, and alternative pathways regulating physical activity responses in vertebrates warrant further investigation.

025

THE EFFECTS OF PATERNAL PRE-FERTILIZATION THC EXPOSURE ON FERTILIZATION SUCCESS AND EARLY EMBRYONIC DEVELOPMENT

Tayin Seeton*[1], Jonathan Stone[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4L8

THC, or *Δ9-tetrahydrocannabinol* usage among the reproductively active (ages 18-44) has increased significantly since its legalization in 2018. THC reduces fertilizing capacity of male gametes by inhibiting the acrosomal reaction while also reducing sperm count and sperm motility. While the impacts of THC-influenced sperm on fertilization is widely studied, the influence of THC on early embryonic development is largely understudied. Given the evolutionary similarities of the endocannabinoid system in sperm, first discovered in sea urchins, we used *Strongylocentrotus droebachiensis* as a model organism to investigate this relationship. Sperm were exposed to different concentrations of THC, attempting to mimic therapeutic (0.032uM), medium (0.32uM) and heavy cannabis use (3.2uM). The sperm were then mixed with healthy eggs to achieve fertilization. It was observed that, consistent with previously observed decreased fertilization, that as the concentrations increased, there was decreased survivorship, coupled with abnormal development. These findings suggest that paternal THC exposure may negatively impact early embryonic development, warranting further research.

026

EFFECT OF ARBUSCULAR MYCORRHIZAL FUNGI ON BACTERIAL METABOLISM IN AN ACTIVE HYDROPONIC GREEN WALL SYSTEM

Nojan Shishechiha*, and Dr. Stephanie Melles.
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada, M5B 2K3.

Arbuscular mycorrhizal fungi (AMF) are symbiotic soil microorganisms that enhance plant nutrient uptake and stress resistance in exchange for carbohydrates. While extensively studied in traditional soil systems, their role in hydroponics remains underexplored. AMF has shown potential in hydroponic systems by improving plant health, reducing chemical input dependence, and modulating microbial interactions. This study investigates the impact of AMF inoculation on bacterial metabolic activity in active wet hydroponic systems, addressing a critical knowledge gap in soilless agriculture. Precisely, we assess how AMF influences bacterial communities by modifying root exudates, potentially suppressing pathogenic bacteria while promoting beneficial ones. Unlike prior studies that focus primarily on plant growth, this research takes a comprehensive approach, evaluating shifts in bacterial metabolism in AMF-inoculated hydroponic systems. Our findings aim to enhance plant health, foster beneficial bacterial activity, mitigate non-beneficial microbial growth, and promote sustainable hydroponic practices. By elucidating the multifaceted interactions between AMF, plants, and microbial communities, this study contributes to the broader understanding of AMF applications beyond soil-based agriculture.

027

SPECIES IN FECES: EXAMINING THE EFFECTS OF PER- AND POLYFLUOROALKYL SUBSTANCES ON THE MICE GUT MICROBIOME

Arianna Stanley-Harrison[1], Amélie Blais[2], Lauren Bradford[2], Matt Meier[2], Euguene Fletcher[1], and Azam Tayabali [1, 2].
[1]Department of Biology, Carleton University, Ottawa, Ontario, Canada K1S 5B6
[2]Environmental Health Science and Research Bureau, Health Canada, Ottawa, Ontario, Canada K1A 0K9

Per- and polyfluoroalkyl substances (PFAS), commonly known as "forever chemicals", are synthetic environmentally persistent contaminants. Historically, PFAS were widely utilized in consumer products such as non-stick cookware, water-repellent textiles, firefighting foams, and cosmetics. However, the PFAS accumulation in environmental matrices and human systems has raised significant health concerns. Previous *in vivo* and epidemiological studies have identified potential adverse health effects, including immune suppression, metabolic dysfunction, and delayed developmental outcomes. Moreover, PFAS may also influence the gut microbial homeostasis. This study investigates the effects of perfluorooctanoic acid (PFOA) and perfluorooctane sulfonate (PFOS) exposure on the gut microbiome of mice exposed to PFOA or PFOS by oral gavage (doses: 0.166, 0.5, 10, or 1.5 mg/kg/day) for 28 or 56 days. Fecal samples were collected, and DNA was extracted using the QIAGEN PowerFecal Pro DNA Kit. DNA quality and concentration were assessed with a Nanodrop spectrophotometer and an Agilent TapeStation system. To analyze changes in the gut, full-length 16S ribosomal ribonucleic acid (rRNA) gene was sequenced on a PacBio Sequel 2 sequencer. The library preparation and sequencing were performed by the Integrated Microbiome Resource (Dalhousie, NS). Sequencing is currently ongoing, and preliminary results are presented here. 16s rRNA sequencing data will provide valuable insights into the mechanisms by which PFAS affect gut microbial communities and host health. These findings will contribute to the understanding of PFAS toxicity, predicting potential human health risks, and informing future public health strategies and regulatory policies.

028

CHARACTERIZING THE FUNCTION OF THE *AKNA* GENE USING DELETION AND KNOCK-IN CRISPR METHODS IN THE ZEBRAFISH

Priscilla Fung*[1], Kevin Ban[2], Sergey V. Prykhozhij[2], Jason N. Berman[2].
[1]Department of Biology, University of Ottawa, Ottawa, Ontario, Canada K1N 6N5
[2]Children's Hospital of Eastern Ontario Research Institute, Ottawa, Canada K1J 8L1

Following the diagnosis of a fatal inflammatory disorder involving profound immune system dysregulation in an Inuit child, whole genome sequencing determined the child to be homozygous for a missense variant in the *AKNA* gene. In humans, AKNA is hypothesized to regulate both neurogenesis and immune cell maturation and function as an AT-hook transcription factor. Due to the limited knowledge of AKNA's roles in development and disease, we used Cas9-directed mutagenesis to create 3 zebrafish models: a deletion (Del) line causing Akna LOF, a knock-in (KI) reporter line employing superfolder green fluorescent protein (sfGFP), and a CRISPR insertional mutagenesis protocol (CRIMP) line involving both Akna LOF and an amplified reporter signal of Akna. Whole-mount in-situ hybridization (WISH) found *akna* mRNA to be expressed in the head region of zebrafish embryos at 2 to 3 days-post-fertilization (dpf), with concentrated expression in the retinal nuclear layers, olfactory bulb, and neuromasts by 5 to 6 dpf. In homozygous Del mutants, DNA and RNA sequencing confirmed the deletion of 13kb from the *akna* gene which prevented mRNA transcription. The consequences of Akna LOF on neurogenesis and immune function will be quantified. Fluorescence microscopy of heterozygous KI mutants determined Akna protein to be expressed in the nervous system until 30 hours-post-fertilization. Homozygous KI embryos will be subsequently studied. The CRIMP line will be used to clarify Akna LOF phenotypes without inducing genetic compensation and enable better visualization of Akna expression patterns using a Gal4/UAS system.

029

ANALYSING SEX-DEPENDENT EFFECTS OF MONOCROTALINE (MCT) THROUGH GLYCOGEN STORAGE

Pakin Pongpaiboon
Department of Biology, Trent University, Peterborough, ON, Canada
Contact Email: pakinpongpaiboon@trentu.ca

The monocrotaline (MCT) model is a pharmaceutical approach to studying cardiac cachexia, a multiorgan syndrome that results in extreme lean body mass and skeletal muscle loss in heart failure patients. Although the MCT model of cardiac cachexia is prevalent, the physiological basis for sex-dependent effects is not well-studied. Previously, our lab has detected results that suggest that male mice are more adversely affected by MCT-induced cachexia as the whole-body weight of male but not female mice was reduced. It was found that the cross-sectional area of skeletal muscle was reduced in male and female samples while fat was reduced in male samples. As skeletal muscles are a site for glycogen storage and many skeletal wasting conditions are associated with reduced glycogen, it was suspected that glycogen could be different in MCT-treated mice, particularly in males with reduced body and adipose mass.

It is hypothesized that males' skeletal muscle glycogen storage will be more adversely affected than females treated with MCT. Greater glycogen storage in females will provide support that skeletal muscle and body weight are lost in a sex-dependent fashion through glycogen changes in the MCT model of cardiac cachexia. Periodic Acid Schiff (PAS) stain was applied to paraffin-embedded skeletal muscle sections of the tibialis anterior and gastrocnemius from the previous study to quantify glycogen. The results and analysis, which are in progress, will verify the potential sex-dependent effects of skeletal muscle loss in MCT-induced cachexia.

030

EXPLORING THE EFFICACY OF PROBIOTIC TREATMENTS IN REDUCING *PSEUDOGYMNOASCUS DESTRUCTANS* CONCENTRATIONS IN BATS AFFECTED BY WHITE-NOSE SYNDROME

Celeste Abraham*[1], Chadabhorn Insuk[1], Heather Yoell[1], Abby Tobin[2], Cori Lausen[3], Jianping Xu[1].
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4L8
[2]Wildlife Ecology, School of Forestry, Northern Arizona University, Flagstaff, Arizona, United States of America 86011
[3]Wildlife Conservation Society Canada, Kaslo, BC, Canada V0G 1M0

White-nose syndrome, caused by *Pseudogymnoascus destructans* (*Pd*), poses a significant threat to bat populations across North America. Previous research suggests that probiotics may mitigate the impact of *Pd*, but evidence of their efficacy remains limited. This study investigates the correlation between probiotic treatments and *Pd* concentrations in Yuma myotis (*Myotis yumanensis*) and little brown bats (*Myotis lucifugus*) from Washington State. This research focuses on a probiotic cocktail consisting of *Pseudomonas lactis* A&B, *Pseudomonas synxantha*, and *Pseudomonas antarctica*. 478 samples from March to August 2024 were analyzed using quantitative PCR to assess *Pd* and probiotic concentrations. We test the hypothesis that the presence of probiotic bacteria on bat wings will be associated with low *Pd* concentrations. Results show that high probiotic concentrations align with lower *Pd* concentrations, supporting probiotics' potential to mitigate WNS in bat populations. Spearman's rank correlation demonstrated a significant negative correlation between total probiotic and *Pd* concentrations. This study provides insights into probiotic effectiveness and lays a foundation for further research.

031

EXPLORING THE IMPACT OF INTERFERENCE COMPETITION ON FOOD ACCESS IN HUMMINGBIRDS

Sydney Williams*, and Roslyn Dakin.
Department of Biology, Carleton University, Ottawa, Ontario, Canada K1S 5B6

An uneven distribution of food is expected to increase competitive interactions, yet the relationship between aggression and food access remains underexplored. One form of such competition is interference competition, where one individual directly interacts with another while competing for the same resource. These interactions can reduce a subordinate individual's access to resources. This study examines whether wild-caught hummingbirds would engage in interference competition during competition trials in captivity, where three individuals had to rely on a single food source. We defined interference as instances where an aggressor displaced a competitor at the feeder, but did not stop to feed itself afterward. Our results show that interference was frequent, occurring in 56% of interactions at the feeder, suggesting that displacements were often driven by a motivation to exclude competitors. Next, we assessed whether individual birds differ in their tendency to interfere with others across repeated trials, and whether this behaviour is also associated with aggression at perches. Individual differences explained approximately 20% of variation in interference frequency, and hummingbirds that performed more interference at the feeder also performed more aggression at the perches. Finally, we investigated whether hummingbirds encountered each other at the feeder more often than expected, based on a null model. We find that some, but not all, of the hummingbirds exhibited significantly higher co-occurrence at the feeder than expected. These findings indicate that interference competition can occur in captive hummingbirds, and highlight individual variation in competitive behaviours within the same species.

032

EXPLORING THE ECOLOGICAL NICHES OF EUROPEAN STARLINGS (*STURNUS VULGARIS*), TREE SWALLOWS (*TACHYCINETA BICOLOR*) AND INSECT COMMUNITIES THROUGH STABLE ISOTOPE ANALYSIS TO IDENTIFY FOOD WEB LINKAGES FOR PFAS-TRANSFER AT CONTAMINATED AND NON-CONTAMINATED SITES IN SOUTHERN ONTARIO

Danielle MacNeil*[1], Julianna Colafranceschi[1], Kim Fernie[2], Emily Choy[1].
[1] Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4E1
[2] Ecotoxicology and Wildlife Health Division, Environment and Climate Change Canada, Burlington, Ontario, Canada L7S 1A1

Per- and polyfluoroalkyl substances (PFAS) are anthropogenic chemicals widely used in consumer and industrial products. Due to their persistence, toxicity, and bioaccumulative properties, PFAS pollution is of growing concern, with increasing evidence of adverse effects on wildlife and human health. While emergent aquatic insects are recognized as vectors for PFAS transfer to terrestrial predators, the role of terrestrial insects in PFAS transfer remains understudied. Additionally, although birds are effective biological indicators of ecological health, little is known about PFAS toxicity in avian species. Therefore, this study aims to identify potential PFAS transfer routes from terrestrial insects to avian predators by examining ecological niches using carbon (δ^{13}C) and nitrogen (δ^{15}N) stable isotope (SI) analysis at PFAS contaminated and non-contaminated sites in southern Ontario. Diet plays a key role in PFAS transfer within food webs, and SI analysis is widely used for characterizing ecological niches, thereby providing insight into PFAS contamination pathways. This study also evaluated the use of bird feather SI analysis as a less invasive alternative to blood SI analysis. Results showed that feather SI values significantly predict blood values ($R^2 = 0.98$ for both δ^{13}C and δ^{15}N, $p < 0.0001$), demonstrating the reliability of feathers for ecological niche characterization. This finding supports the use of feather SI analysis as a viable, less invasive method, particularly useful for studying endangered bird populations. By mapping ecological niches, this study clarifies predator-prey dynamics and potential PFAS transfer pathways, providing a roadmap for future research to directly quantify PFAS contamination and its ecological impact.

033

ANTIBIOTICS AND THEIR EFFECTS ON DEER MICE (*PEROMYSCUS MANICULATUS*) SMALL INTESTINE HISTOMORPHOLOGY

Benjamin Winchester*[1], Caileigh Tomas[1], Graham Scott[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4K1

Gut microbiome research is a diverse and rapidly growing field focusing on the wide array of roles the microorganisms of the digestive tract can have. A common research method to study these roles is through the administration of antibiotics with the goal of disrupting the gut microbiome. Previous studies have shown that antibiotics can have unintended effects on the digestive tract, particularly the small intestine. Moreover, such studies often combine antibiotic treatments with different environmental factors, which may further amplify these effects. We hypothesized that antibiotic treatment would result in a remodeling of both small intestine morphology and digestive function. To test this, two populations (high- and low-altitude natives) of deer mice (*Peromyscus maniculatus*) were acclimated to either warm (25°C) normoxia or cold (5°C) hypoxia (12 kPa O_2) for six weeks. A subset of the deer mice received a broad-spectrum antibiotic in their drinking water for the final four weeks of acclimation. Following treatment, small intestine samples were collected and prepared for histological analysis or stored for enzyme assays. Our results showed that neither antibiotic administration nor environment significantly affected the small intestine histological parameters of both populations. The functional effects of antibiotics on the small intestine are still under investigation. These findings will contribute to our understanding of how antibiotic treatments and environmental factors interact to influence small intestine health.

034

IMPACT OF FLEXIBLE GRADING SCHEME ON LEARNING ENVIRONMENT AND CLASSROOM DYNAMICS IN BIOLOGY COURSES AT UNIVERSITY OF TORONTO MISSISSAUGA (UTM)

Laiba Jamal*, Ilyas Wilson, Khaled Fawal, Sharleen Bains, and Sanja Hinic-Frlog
Department of Biology, University of Toronto Mississauga, Mississauga, ON, L5L 1C6

Traditional grading schemes may not always accurately reflect student performance, leading to the increasing adoption of flexible grading in university courses. These alternative grading structures allow students to tailor assessments to their strengths, fostering a more personalized and equitable learning experience. Research suggests that flexible grading enhances student autonomy, motivation, and engagement while reducing stress and anxiety. Additionally, instructors report improved student understanding and higher-quality work. However, there is limited empirical research on how flexible grading influences student perceptions of learning and classroom dynamics, particularly in STEM disciplines. This study aims to assess the impact of flexible grading schemes on student experiences in university biology courses. Surveys will be conducted in Winter 2025 across five biology courses at the University of Toronto Mississauga. A two-part anonymous survey, administered via Quercus, will evaluate key factors such as learning retention, perceived fairness, stress levels, motivation, and overall autonomy in coursework. Data will be analyzed using R, incorporating both descriptive statistics and thematic analysis to provide a comprehensive assessment of the effectiveness of flexible grading. The findings will contribute to ongoing discussions on assessment strategies in higher education, offering valuable insights into the potential benefits and challenges of flexible grading in STEM courses. Understanding these impacts can help educators design grading policies that better support diverse student needs and promote a more inclusive learning environment.

035

THE EFFECT OF *DE NOVO* MUTATION ON PHOTOTACTIC RATE IN *CHLAMYDOMONAS REINHARDTII*

Ayesha S Syeda*[1], Eniolaye J Balogun[1,2], Rob W Ness[1,2,3]
[1] Department of Biology, University of Toronto, Mississauga L5L-1C6, Canada
[2] Department of Ecology and Evolutionary Biology, University of Toronto, Toronto M5S-3B2, Canada
[3] Department of Cell & Systems Biology, University of Toronto, Toronto, ON M5S-3G5, Canada

Chlamydomonas reinhardtii, a unicellular green alga, is a model organism commonly used in evolutionary studies due to its culturing simplicity and flexible genetics. The species demonstrates phototaxis, or directed movement toward light, facilitated by eyespot and ciliary organelles. Previous studies have not thoroughly experimentally validated motility genes specific to *C. reinhardtii*. The motility phenotype additionally allows the exploration of mutational variance (V_m). The V_m metric quantifies the increase of variance in a trait per generation due to mutation. It is a part of genetic variance (V_g), the absolute variance in a trait due to genetic differences among individuals. Comparison of V_g and V_m can be used to measure the strength of selection acting on a trait, as it involves comparing the amount of variance introduced by mutation to what is remaining after selection in a natural population. By utilizing faster and slower motility phenotypes and their underlying genetics, it is therefore possible to quantify V_g and V_m, to determine the effect of *de novo* mutation on phototactic rate. This study thus aimed to develop a protocol quantifying phototactic rate across natural and mutation accumulation (MA) strains of *C. reinhardtii*, validate candidate genes for motility in a post-assay variant mapping experiment, and calculate V_g and V_m. Preliminary results suggest that differentiation in phototactic rate across MA strains is comparable to that seen in natural strains and that there is not a notable difference in the variance of the phototactic rate in both strain types.

036

IMPLICATING THE SEROTONERGIC SYSTEM IN FEEDING AND GROWTH IN ZEBRAFISH (*DANIO RERIO*)

Kristen Huang*, Michael Tea, Kathleen Gilmour.
Department of Biology, University of Ottawa, 30 Marie Curie Pvt, Ottawa, ON, K1N 6N5, Canada

Zebrafish (*Danio rerio*) have two paralogues of the serotonin transporter (Sert) uniquely expressed in the brain, Serta and Sertb, which re-uptake serotonin from the synapse into the presynaptic neuron. Zebrafish lines lacking the expression of either *serta*, *sertb*, or both were generated using CRISPR/Cas9 technology. To investigate the consequences of Sert knockouts on feeding behaviour and growth as a function of food intake, feeding behaviour in adults as well as growth indices in larval, juvenile, and adults were measured. The *serta*$^{-/-}$ and *sertab*$^{-/-}$ adult zebrafish consumed less food than their *sertb*$^{-/-}$ and *sertab*$^{+/+}$ counterparts. This feeding result corresponds to adult *serta*$^{-/-}$ averaging less total body weight than *sertab*$^{+/+}$ fish. However, both *sertb*$^{-/-}$ and *sertab*$^{-/-}$ displayed intermediate body masses. Similarly, at 1 day post fertilization, *serta*$^{-/-}$ fish exhibit smaller growth indicators (yolk sac area) compared to the other genotypes. These differences in food intake and growth rate indicators between genotypes provides insight into the complementary and distinct roles of the serotonin transporter paralogues in altering growth by regulating food intake and metabolism in unique areas.

037

TWO-EYED SEEING CASE STUDY: INUIT AND MARINE ECOLOGY

Chilyn Fenton-Stickle*, Helene Wagner
Department of Biology, University of Toronto Mississauga, Mississauga, Ontario, Canada
L5L 1C6

This case study aims to apply the Mi’kmaw Two-Eyed Seeing concept to explore how the Inuit Way of Knowing (Qaujimajatuqangit) and Western Science can come together to improve our understanding on climate change impacts on the Arctic marine ecosystem. As a teaching material for university-level ecology courses, the study focuses on providing scholars and learners with perspectives on how one could look at ecosystem functions. By referring to interactive maps, the case study asks users to explore and discuss key questions: When does the ice-free season open? How does the ice coverage shift over seasons and years? How has the interspecific interaction shifted between the sub-Arctic species Orca whale (*Orcinus orca*) and the Arctic species narwhal (*Monodon monoceros*) as a result of ice coverage changes? How can the Inuit Way of Knowing inform ecological monitoring? This study provides the opportunity to reflect on how Indigenous methods and approaches can contribute to conservation strategies, as well as moving towards reconciliation in higher education. It emphasizes the importance of Indigenous Knowledge in climate change research and ecosystem monitoring, that can inform strategies to mitigate the impacts of Arctic warming on the ecosystem.

038

ELECTRICAL IMPEDANCE TOMOGRAPHY (EIT) AS A TOOL TO ANALYZE AQUATIC VENTILATION IN DIVING

Paige Mutsuko Yoshida*[1], Jeff W. Dawson[1], Andy Adler[2]
[1]Department of Biology, Carleton University, Ottawa, Ontario, Canada, K1S 5B7
[2]Department of Systems and Computer Engineering, Carleton University, Ottawa, Ontario, Canada, K1S 5B7

Electrical Impedance Tomography (EIT) is a non-invasive imagine technique that is used to monitor lung function. While it has proved itself beneficial in clinical settings, it’s application and reliability underwater are unknown. To test this, participants were assessed under different water depths and body positions. Our findings indicate that ventilation and air distribution patterns are correlated to both varying water depth and body positioning. This research represents the first study of underwater ventilation using EIT and can provide a foundation for future studies. The findings have implications for individuals working in aquatic environments and those who partake recreationally, contributing to a better understanding of respiratory physiology in these conditions.

039

UNDERSTANDING THE CRYPTIC REGULATION OF GLYCOLYSIS IN CHLOROPLASTS OF *ARABIDOPSIS THALIANA*

Anya Hu*[1], Sonia E. Evans[2], Anya E. Franks[2], and Michael A. Phillips[1,2]
[1]Department of Biology, University of Toronto - Mississauga, Mississauga, ON L5L 1C6, Canada
[2]Department of Cell and Systems Biology, University of Toronto, Toronto, ON M5S 3G5, Canada

Phosphoenolpyruvate (PEP) and pyruvate constitute key precursors for the synthesis of terpenoids, phenolics, and fatty acids in plants. Mature chloroplasts cannot synthesize PEP due to the downregulation of two key enzymes of glycolysis, enolase (ENO) and phosphoglycerate mutase (PGM). Instead, PEP is synthesized in the cytosol and transported into chloroplasts through the PPT1 transporter, where it is used in the biosynthesis of aromatic amino acids. The physiological factors that necessitate this arrangement are unknown. The Arabidopsis cue1 mutant is a powerful tool to understand the regulation of glycolysis in plants. It has a defective PPT1 transporter and is therefore unable to supply chloroplasts with PEP. Its distinctive reticulated phenotype was exploited in this study to visually track the effects of restoring the glycolytic pathway in chloroplasts. Stably transformed lines of Arabidopsis thaliana were created that overexpress plastidial forms of both ENO and PGM in the wild type and cue1 mutant background. Partial complementation of the mutant phenotype in ENO/PGM transformed plant lines suggest that downregulation of glycolysis in the chloroplast is an adaptation that permits otherwise competing biosynthetic processes to function together seamlessly in the same compartment.

040

THE EFFECTS OF FEEDING ON HEART RATE AND BODY TEMPERATURE IN BLACK-LEGGED KITTIWAKES (*RISSA TRIDACTYLA*)

Abby Eaton*[1], Flynn O'Dacre[1], Shannon Leone Fowler[2], Shannon Whelan[3], Scott Hatch[3], Kyle Elliott[4], Emily Choy[1].
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada
[2]School of Life and Health Sciences, University of Roehampton, London, United Kingdom
[3]Institute for Seabird Research and Conservation, Anchorage, Alaska, USA
[4]Department of Natural Resources Sciences, McGill University, Ste-Anne-de-Bellevue, Québec, Canada

Accelerating climate change is causing a shift in prey availability for many species of seabirds, which could affect their daily energy expenditure. Several seabird species have shown an increase in metabolic rate, heart rate, and body temperature with digestion. Known as the heat increment of feeding, this effect contributes to the energy budget of seabirds. The pelagic seabird, the black-legged kittiwake (*Rissa tridactyla*), is widespread throughout the northern Atlantic and Pacific oceans. The objectives of our study were to investigate the physiological response to feeding in kittiwakes by comparing heart rate and body temperature between groups of supplementary fed and unfed kittiwakes. We deployed heart rate biologgers in 60 kittiwakes from May 2024 to July 2024 on Middleton Island, Alaska. We supplementally fed 30 kittiwakes for ten days, providing unlimited capelin (3x per day). Heart rate and body temperature were determined before and after individual feeding events. The difference in these values determined the change in heart rate and body temperature associated with feeding. The difference in heart rate and body temperature associated with the feeding period significantly differed between the 'fed' and 'unfed' conditions. Additionally, the physiological response increased in magnitude with the amount of fish consumed.

041

CHARACTERIZING THE DEVELOPMENTAL BIRTH ORIGINS OF PM NEURONS IN THE DROSOPHILA OPTIC LOBE

Nicolas Andres Fragoso Wandurraga[1], Ted Erclik[1]
Department of Biology, University of Toronto Mississauga, Mississauga, ON[1].

In the *Drosophila* optic lobe, neural progenitors, termed neuroblasts are patterned by independent temporal and spatial inputs to generate >200 neuron types, making it an excellent model for understanding how neuronal diversity is generated. In the temporal axis, transcription factors (TFs) (Hth, Ey, Slp, D) are sequentially expressed in medulla neuroblasts as they age. Additionally, a set of TFs (Vsx1, Optix, Rx) compartmentalize the outer proliferation center, the stem cell pool from which neuroblasts are generated. As a result, neuroblasts generate different neurons based on their spatial-temporal identity. To date, several proximal medulla (Pm) neuron types have been found to possess similar spatial (Vsx1 or Rx) and temporal (Hth or Ey) birth origins. This study aims to map the spatial-temporal birth address of additional Pm neurons (Pm5, Pm6 and Pm11) to determine if they too share developmental similarities. To do this, I used the transgenic split-Gal4 system to independently label each Pm neuron with GFP. Using immunohistochemistry techniques and confocal microscopy, I visualized the expression of different patterning TFs in the Pm neurons to uncover their spatial-temporal origins. Pm5, Pm6 and Pm11 all express Tfap2, a TF only expressed in neurons born in the Hth window. However, these neurons do not express Vsx1, indicating that they are not born from the Vsx1 region. Based on these results, the Pm neurons of this study are born from the early Hth temporal window and are likely to originate from the Rx spatial region, suggesting that all Pm-class neurons possess similar developmental origins.

042

SYNERGISTIC EFFECTS OF SPZ^{2} AND GDI^{N7-3} MUTATIONS ON DEVELOPMENT OF THE NEUROMUSCULAR JUNCTION IN *DROSOPHILA MELANOGASTER*

Niha Sohail*[1], Kathryn Harris-Howard[2], Bryan Stewart[1]
[1] Department of Cell & Systems Biology, University of Toronto Mississauga, Mississauga, Ontario, Canada L5L 1C6
[2] Office of the Vice-Principal Research, University of Toronto Mississauga, Mississauga, Ontario, Canada L5L 1C6

The neuromuscular junction (NMJ) is a site of information transfer between motor neurons and muscle fibers, where various proteins regulate synaptic development and plasticity. This study investigates the effects of knocking down GDI, a Rab regulator protein, using RNA interference (RNAi) at the NMJs of *Drosophila melanogaster*. Additionally, the study examines the impact of spz^{2} and GDI^{N7-3} mutations on NMJ morphology. NMJs from muscles 6 and 7 of third instar larvae were analyzed for changes in NMJ length, bouton number, and synaptic debris accumulation. By creating three heterozygous genotypes—spz^{2}/+, GDI^{N7-3}/+, and a double-heterozygote carrying both mutations—alongside the GDI knockdown by RNAi, the aim is to uncover any potential combined effects on the NMJ, suggesting that these genes interact to regulate NMJ morphology. Results show that the double heterozygote had a significantly increased bouton count, and all experimental genotypes had decreased amounts of synaptic debris compared to the control genotype (w-). These results indicate a novel genetic interaction, implying that Spätzle and GDI have similar and synergistic effects on the NMJ. Further studies may determine the underlying molecular mechanisms by which Spätzle and GDI interact to regulate synaptic development and maintenance at the NMJ.

044

INVESTIGATING THE ROLE OF PIKFYVE INHIBITION ON LYSOSOME-MITOCHONDRIA CO-MIGRATION

Connie Di Raimo*[1], Maria Narciso[1], Roberto J. Botelho[1]
[1]Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

Lysosomes and mitochondria are essential organelles that maintain cellular homeostasis. Lysosomes function as signalling hubs and are the terminal site of the endolysosomal pathway for cargo degradation, while mitochondria drive cellular energy metabolism and production. These organelles can communicate through membrane contact sites, which are key for bidirectional regulation to maintain cellular function and survival. Membrane contact sites hold these organelles together, which allows for their co-migration. However, the mechanisms underlying lysosome-mitochondria co-migration remain poorly understood. PIKfyve is a lipid kinase complex that regulates lysosomal morphology and motility by phosphorylating phosphatidylinositol-3-phosphate into phosphatidylinositol-3,5-bisphosphate. PIKfyve inhibition leads to enlarged vacuoles due to lysosome coalescence. New research from our lab has discovered that PIKfyve inhibition decreases lysosome-mitochondria proximity, impairs organelle motility and increases mitochondrial fragmentation. We hypothesized that PIKfyve inhibition will decrease lysosome-mitochondria co-migration. To test this, we used live cell fluorescence imaging in COS-7 cells and quantified co-migration events by assessing lysosomal influence of mitochondrial displacement. Our results suggest that PIKfyve inhibition using apilimod significantly reduces the amount of lysosome-mitochondria co-migration events, supporting previous unpublished findings. Since mitochondria appear fragmented in PIKfyve-inhibited cells, we are now assessing whether PIKfyve inhibition with apilimod and APY0201 impairs mitochondrial fusion using two HeLa cell lines, each expressing a TOMM20-mCherry or COX8A-emiRFP mitochondrial marker. These two cell populations will then be co-cultured and fused together with polyethylene glycol to measure intermixing of mitochondrial markers to determine fusion rates of mitochondria. Overall, our findings suggest that while PIKfyve controls lysosomes directly, its activity is also critical for mitochondria dynamics.

045

INVESTIGATING A DUAL-FLUORESCENT mCHERRY-GFP SYSTEM FOR TRACKING *SALMONELLA* VIABILITY DURING PHAGOSOMAL MATURATION

Qing Gui Queenie Chung*, Subothan Inpanathan, Maria Narciso, and Roberto J. Botelho.
Department of Chemistry and Biology, Toronto Metropolitan University, Toronto, Ontario, Canada M5B 2K3

Phagocytes play a critical role in host defense by engulfing and degrading pathogens within phagosomes, which undergo acidification and maturation into microbicidal compartments. *Salmonella enterica* sv. Typhimurium (*S.* Typhimurium), a facultative intracellular pathogen, has evolved mechanisms to survive this process, complicating efforts to determine bacterial viability within phagosomes. Conventional methods, such as colony counting and gentamicin protection assays, provide endpoint measurements but lack the capability to monitor bacterial death dynamically. To address this, we are investigating a dual-fluorescent mCherry-GFP reporter system to monitor bacterial viability in real time. GFP is pH-sensitive and loses fluorescence in acidic environments, whereas mCherry remains stable providing a reliable reference across different viability states. Our findings indicate that the GFP-to-mCherry ratio declines at pH 5 in both live and dead bacteria, with a more pronounced drop in Sytox-masked, dead *S. Typhimurium*, confirming its ability to distinguish viable from non-viable cells. Live bacteria retain a higher GFP/mCherry ratio at pH 5, though the observed reduction may result from direct exposure to pH 5 PBS, a relatively infinite system with sustained acidity. In contrast, the phagosomal lumen is a more confined and dynamic environment, where bacteria may better regulate their response to acidification. These results suggest the mCherry-GFP system has the potential to track bacterial viability during phagosomal maturation. Ongoing work aims to validate this system in macrophage infections and assess its reliability in studying intracellular *S*. Typhimurium survival. If successful, this method could provide a powerful tool for investigating host-pathogen interactions and antimicrobial strategies.

046

IDENTIFYING EQUIVALENT GENES ACROSS THE E. COLI PANGENOME

Saniya Bhalla*[1] and Gabriel Moreno-Hagelsieb[2]
[1]Department of Biology, Wilfrid Laurier University, Waterloo, Ontario, Canada N2L 3C5

Understanding what makes *Escherichia coli* strains harmless or harmful starts with decoding their genetic blueprint. The *E. coli* pangenome consists of core genes shared across all strains and accessory genes that influence traits like antibiotic resistance and virulence. Identifying orthologous, or equivalent, genes across strains is the first step for studying genetic conservation and functional differences. This study compares sequence clustering methods to determine the most effective one for identifying equivalent genes across multiple *E. coli* strains. To this end, we tested implementations under MMseqs2 and Diamond of two clustering algorithms: (i) standard clustering, which uses strict similarity thresholds, and (ii) linear-time clustering, a heuristic method optimized for speed and scalability. The tests included speed to obtain results, as well as the similarity of the protein clusters obtained. The study determined that Linclust significantly reduced computational time while maintaining clustering accuracy, making it a viable option for large-scale genomic analyses. Though less than 60% of all complete protein groups were found by all four procedures, deeper comparisons revealed that close to 80% of all protein pairs were kept together. This study advances bioinformatics methods for comparative genomics, providing insights into *E. coli* gene organization and evolutionary conservation. Efficient clustering approaches will facilitate large-scale microbial genome analyses, improving our understanding of bacterial evolution, adaptation, and pathogenicity.

047

INVESTIGATING THE ROLE OF THE CHROMATIN REMODELLING COMPLEX COMPONENT ACTIN-RELATED PROTEIN 6 (ARP6) IN TEMPERATURE-REGULATED PLANT IMMUNITY IN *ARABIDOPSIS*

Shahmeen Farooqi*, Christina AM. Rossi and Christian Danve M. Castroverde
Department of Biology, Wilfrid Laurier University, Waterloo, ON N2L 3C5.

Plants possess two interconnected immune responses – pathogen-associated pattern-triggered immunity (PTI) and effector-triggered immunity (ETI) – which can be regulated by the defence hormone salicylic acid (SA). SA plays a critical role in activating immune responses to infection by various pathogens and pests, while also enhancing tolerance to different abiotic stresses. Transcription factors, CALMODULIN BINDING PROTEIN 60g (CBP60g) and SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1 (SARD1), promote SA biosynthesis; however temperature-sensitive CBP60g/SARD1 expression results in reduced SA production under moderately elevated temperatures associated with climate warming. The histone variant H2A.Z and its associated epigenetic regulators like ACTIN RELATED PROTEIN 6 (ARP6) are known to mediate temperature-related growth and development, wherein ARP6 facilitates H2A.Z incorporation into nucleosomes. However, their functional roles in temperature-sensitive immunity remains underexplored. To address this, our study investigated the potential role of ARP6 (a core component of the SWR1 chromatin remodelling complex) in temperature-modulated immunity in *Arabidopsis thaliana* plants. Using *arp6* mutants and wild-type Col-0 plants, we assessed disease progression, immune gene expression, and SA levels of these plants following infection with the model bacterial pathogen *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000 at ambient (23°C) and elevated temperature (28°C). Preliminary results showed that *arp6* mutants exhibit temperature-sensitive disease susceptibility to *Pst* DC3000, suggesting that ARP6 is not involved in temperature-modulated plant immunity. Our findings have clarified the possible role of chromatin remodelling and histone variants in temperature-mediated immune responses under warming conditions. Follow-up investigations with other histone variants and epigenetic factors will provide insights into plant resilience mechanisms.

049

A BACTERIAL VAGINOSIS MODEL: FOLLOWING DISEASE PROGRESSION

Morgane Brading*, Robin Slawson, and Joel Weadge
Department of Biology, Wilfrid Laurier University, Waterloo, ON.

Bacterial vaginosis (BV) is the most common vaginal dysbiotic condition of women of reproductive age. BV is characterized clinically by a vaginal flora not abundant in *Lactobacillus* spp.. It is a recurrent and persistent condition due to the overgrowth of commensal anaerobic bacteria such as *Gardnerella vaginalis*. Current BV studies are restricted to cell cultures, which can be costly and timely, and the temperamental nature of cell lines requires strict aseptic techniques and highly trained researchers. Furthermore, although studies have investigated the role of BV on clinical reproductive outcomes and the tolerance profiles of specific BV-associated bacteria (BVAB), none have highlighted the progression of the disease through time from complete *Lactobacilli* dominance to BVAB dominance. Thus, we present an in-vitro media-based BV model. A co-culture of *L. gasseri*, *L. jensenii*, *L. crispatus*, and *G. vaginalis* was successfully grown and monitored via pH readings, crystal violet biofilm assays, and Nugent scoring on days 3, 10, 16 and 26. This study determined that biofilm production showed only a significant difference on day 10 compared to other sample times, showing no significant increase in biofilm formation with increasing bacterial growth. The pH 7 broth media exhibited a drop in pH to 5 at day 0 and persisted at 4 for the remaining sampling days. Finally, Nugent score analysis via gram-staining will permit *G. vaginalis* growth to be assessed throughout the study period. Model optimization will enable cost-efficient research and a novel method for studying the condition.

050

DETERMINING THE CELLULAR LOCATION OF WSSF AND ITS ROLE IN PHENOTYPIC EXPRESSION OF ACETYLATED CELLULOSE BIOFILMS

Katrina Pegg*, Joel T. Weadge
Department of Biology, Wilfrid Laurier University, Waterloo, Ontario, Canada N2L 3C5

Post-synthesis modifications of exopolysaccharides in both Gram-positive and Gram-negative bacteria lend unique properties to biofilms for colonization of certain niches. The *wss* operon (and specifically the WssF terminal acetyltransferase protein) is a great model system for observation of these biofilm modification pathways and is the focus of this research. Uncovering more information about the specific location of the WssF terminal acetyltransferase *in vivo* will aid our understanding of the role of this protein and its place in the Wss pathway. To detect the location of WssF, a plasmid construct was generated where GFP (green fluorescent protein) is arranged so that it is expressed as a fusion onto the C-terminus of the WssF protein. Following transformation and expression, cells positive for the WssF-GFP fusion were found to glow under ultraviolet light. Successfully expressed fusion protein was also verified using SDS-PAGE separation and Western immunoblots. Cell cultures containing expressed fusion protein were grown and fractionation processes were used to track the presence of the WssF-GFP fusion protein from the cytoplasm to the membrane. However, the GFP portion was lost between the membrane and the periplasm, as visualized based on size differences by SDS-PAGE. Identified GFP fragments in the periplasm indicate possible GFP degradation by proteases upon periplasm entry. Protocol modification with more stringent techniques and the use of protease inhibitors is currently being conducted to troubleshoot this process. Furthermore, the use of WssF activity assays will be used with each fraction to specifically verify its location in the absence of GFP.

051

LIGHTS, FISH, ACTION: INVESTIGATING THE EFFECTS OF LIGHT SETTINGS ON ATTRACTING DIFFERENT FISH SPECIES AND SIZES

Alyssa Dupuis*, Kristen Cyr, Isabelle Tormasi, Holly Mosco, Christina Semeniuk
Department of Integrative Biology, University of Windsor, Windsor, Ontario, Canada N9B 3P4

Studying nocturnal behaviours of fish presents challenges for researchers, as observing animals in aquatic systems is difficult in the absence of light. Tools, such as acoustic telemetry, or infrared cameras have helped overcome these challenges, yet are often expensive, collect data that is difficult to interpret, and provide limited insight into fine-scale behaviors, like prey preferences. Underwater lights with cameras are a cost-effective alternative that can directly observe fish behaviors. However, artificial lights may affect the natural behaviour of fish, and research is lacking in understanding how the use of lights may affect communities composed of individuals with varying abilities to perceive light intensity and colour. To address this knowledge gap, this study deployed fyke nets overnight under 3 replicated treatments of light conditions (white, red, or no lights) to compare differences in species, life history stages (i.e., adult vs. juvenile), and trophic levels (i.e., predator vs. prey) of fish captured in the Margaree River, Nova Scotia. Results indicated that different light colours influence fish community composition and trophic structure. Specifically, a greater number of adult predatory fish were captured in nets with no light, while a greater number of juvenile prey fish were captured using white light. Red light produced the most similar results to no light, as it captured a greater number of adult predators. Understanding the effects of artificial lighting on fish communities can help future studies collect data that better reflect natural nocturnal behaviors, improving conservation efforts and informing strategies that employ lights to help manage fish, like invasive species.

052

UNDERGRADUATE STUDENT KNOWLEDGE, ATTITUDES TOWARDS SCIENCE, PERCEPTIONS, AND EXPERIENCES WITH VACCINES AND RECREATIONAL IV DRIPS

Tiffany Huang* and Tanya Noel
Department of Integrative Biology, Faculty of Science, University of Windsor, Windsor, Ontario, Canada N9B 3P4

Public perceptions of medical and wellness interventions are shaped by many factors, some of which include personal experiences, scientific literacy, education, and social media influence. While vaccines have been well-studied and play an essential role in disease prevention, hesitancy persists, often due to misinformation and/or misconceptions. On the other hand, recreational IV drips have gained popularity as wellness treatments despite requiring injections and having limited scientific evidence supporting their efficacy (but many celebrity lifestyle endorsements). This study examines how undergraduate students at the University of Windsor perceive and experience both interventions, comparing the perspectives of students in Integrative Biology programs versus non-majors enrolled in biology courses. A survey will assess students' microbiology knowledge related to vaccines/immunity, their general attitude toward science, and trust in scientific information that guides their decisions on vaccines and recreational IV drips. It also explores students' personal experiences with both interventions. By identifying potential factors that contribute to vaccine hesitancy and the relative acceptance of recreational IV therapies, this study aims to inform future public health communication and educational initiatives. Findings may provide insights into improving science-based messaging to foster more informed health choices among young adults offer guidance for healthcare providers in enhancing patient communication strategies regarding medical and wellness interventions and improve education in microbiology/health sciences.

053

DOES STRUCTURAL ENRICHMENT AFFECT THE GROWTH AND BEHAVIOUR OF CAPTIVE-REARED CHINOOK SALMON?

Laura Middleton*[1], Dane Roberts[1], and Trevor Pitcher[1].
[1]Department of Biology, University of Windsor, Windsor, Ontario, Canada N9B 3P4

There are evident differences in morphology and behaviour when comparing wild and captive-reared fish. Structural enrichment may serve as an effective strategy to mitigate mismatches between captive and wild environments, potentially enhancing the success of captive-reared individuals upon reintroduction. To improve conservation efforts for species that rely on captive-rearing, such as Chinook salmon, we evaluated the effects of rearing juvenile Chinook salmon in structurally enriched environment versus a barren, non-enriched environment (control) to compare aspects of their growth and behaviour. We measured the growth rate and condition factor of the fish reared in each environment over a 49-day period. We assessed the behaviour of fish reared in enriched and non-enriched environments before and after exposure to a novel hatchery stressor (handling stress), focusing on ecologically relevant metrics for reintroduction. Specifically, we measured environmental preference (substrate habitat vs. barren habitat) and overall swimming activity (active swimming vs immobility). These results may inform rearing facilities of the potential benefits of enrichment in minimizing behavioural disparities between wild and hatchery-reared fish. By addressing these differences, enrichment strategies could contribute to conservation efforts by improving the post-release success of endangered species such as Chinook salmon.

054

PERCEPTIONS OF CLIMATE CHANGE LEARNING AMONG UNDERGRADUATE STUDENTS AND INSTRUCTORS

Linda Nguyen* and Tanya Noel.
Department of Integrative Biology, Faculty of Science, University of Windsor, Windsor, Ontario, Canada N9B 3P4

Despite growing recognition of climate change as a global priority, significant gaps remain in its integration across academic disciplines. Although science programs often address climate change, it is often not a central component of core curricula, leading to disparities in coverage across disciplines. This pilot study evaluates climate change education in selected programs at the University of Windsor, focusing on upper year undergraduates in programs offered by the Integrative Biology (IBio) and School of the Environment (SoE) departments. Through student surveys and interviews, we are examining students' perceptions of their learning and how climate change topics are incorporated and contextualised in courses. We hypothesized that IBio students will perceive lower climate change knowledge and curriculum integration than SoE students. SoE students may engage more with climate policy and real-world applications in Environmental Science courses, gaining greater awareness and integration of this knowledge into their lives. Survey and preliminary student interview analyses did reveal differences between the programs: SoE students reported greater inclusion of climate change, its impacts, and environmentally responsible habits in their courses, while IBio students did not report the same extent of climate change education. Instructor perspectives on challenges and opportunities related to integrating climate change content are also being explored. By identifying gaps and considering student and instructor viewpoints, the study may offer insights into how universities can strengthen climate change education, better equipping students with the knowledge, skills, and motivation to take meaningful action on climate change.

055

EXPLORING THE MECHANISMS OF *RHIZOBIUM LEGUMINOSARUM* BIOFILM FORMATION UNDER BACTERIOPHAGE SELECTIVE PRESSURES: AGRICULTURAL APPLICATIONS

Zahava Dworkin[1*], Zahra Salehimoghaddam[1], and Rebecca Doyle[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 2G1

Environmental stressors like drought and nitrogen deficiencies negatively impact soil microbiomes and reduce crop yields in Ontario agriculture. Chemical nitrogen fertilizers, a common solution, contribute to greenhouse gas emissions and hinder *Rhizobium leguminosarum*, a nitrogen-fixing microbe that forms root nodules on legumes. Replacing fertilizers with rhizobia inoculants could promote sustainable agriculture, but their effectiveness is limited by competition from native microbes. Co-inoculation with bacteriophages—viruses that infect bacteria—may enhance rhizobia's competitiveness. Some rhizobial strains produce biofilms as a defense against bacteriophages, which also protect them from environmental stressors like drought. This research explores whether bacteriophage-induced biofilms improve rhizobia survival and competitiveness. By analyzing biofilm production across rhizobial strains using plaque assays, crystal violet staining, growth curve analysis, and 16S rRNA sequencing, this study will determine whether biofilm formation results from pre-existing plasticity or novel genetic mutations. The goal is to harness bacteriophages as selective agents to enhance biofilm-producing rhizobia, improving their ability to outcompete native strains, enhance nitrogen fixation, and support plant growth.

056

THE EFFECT OF INTERSTRAIN COMPETITION ON THE NODULE OCCUPANCY OF GREEN PEA PLANTS

Sofiyyah Oladipupo[1*], Emily Perry[1], and Rebecca Doyle[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 2G1

Rhizobia, nitrogen-fixing bacteria commonly used in biofertilizers, form beneficial relationships with legumes such as peas, alfalfa, and clover. These bacteria infect plant roots, forming nodules and supplying nitrogen (N) to their hosts. However, the growth benefits conferred by rhizobia, known as partner quality, vary significantly among strains. While high-quality strains enhance plant growth in greenhouse conditions, they often struggle to establish nodules in field environments due to competition with other strains, a challenge known as the rhizobium competition problem. This issue limits the widespread adoption of beneficial strains as biofertilizers, despite their potential to replace chemical fertilizers. This study aims to address this gap by evaluating the effects of inter-strain competition among four field-collected rhizobia isolates. First, partner quality was assessed through single-strain inoculations in pea plants. Second, host responses to co-inoculation were examined by measuring leaf count, plant height, chlorophyll content, and shoot biomass. Third, inter-strain interactions were analyzed by determining final nodule occupancies. The experimental results show that one isolate consistently promoted the best plant growth under both single- and co-inoculation conditions, while other strains had minimal effects when co-inoculated with this high-quality strain. These findings suggest that inter-strain competition does not necessarily reduce the benefits provided by a superior isolate. However, further investigation is needed to determine whether nodule occupancy by the high-quality strain is affected. This study provides insight into rhizobia interactions, contributing to the development of more effective biofertilizer applications in agriculture.

057

A GENETIC APPROACH TO UNDERSTANDING PHAGE-RHIZOBIUM INTERACTIONS

Hanin Al-Ezzi[1*], Zahra Salehimoghaddam[1], and Rebecca Doyle[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4K1

Rhizobium leguminosarum are essential proteobacteria that form symbiotic relationships with legumes by infecting roots and establishing nodules for biological nitrogen fixation. While rhizobial inoculants are designed to enhance nitrogen fixation and crop yields, they often struggle to outcompete native strains in soil. Native rhizobia, though well-adapted to local environments, do not always contribute effectively to nitrogen fixation, leading to inconsistent crop growth. This study explores the use of bacteriophage (aka phage), viruses that infect bacteria, to selectively modulate rhizobial populations, promoting high-performing inoculant strains over less beneficial native strains. The first objective is to isolate and characterize 18 *R. leguminosarum* phages through genome sequencing and bioinformatics analyses. Using Illumina short-read sequencing and annotation tools (e.g., VIBRANT, PHASEST), we aim to identify genetic signatures associated with phage infectivity and host specificity. The second objective involves sequencing and annotating the genomes of 19 *R. leguminosarum* strains to uncover genetic elements linked to phage resistance. Integrating these genomic insights with phage resistance assays will determine which rhizobial strains are susceptible to specific phages. If phages can be used to selectively reduce uncooperative rhizobial populations, they could improve the effectiveness of rhizobial inoculants, enhancing nitrogen fixation while reducing reliance on chemical fertilizers. Understanding the genetic diversity of *R. leguminosarum* phages and their hosts provides critical insights into rhizobial population dynamics and their potential applications in sustainable agriculture.

058

RESILIENCE IN SYMBIOSIS: HOW RHIZOBIA SURVIVING PHAGE ATTACKS ENHANCE PLANT GROWTH

Olivia Robillard[1*], Zahra Salehimoghaddam[1], and Rebecca Doyle[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 2G1

As the demand for sustainable agriculture grows, eco-friendly alternatives to chemical fertilizers are pressing. Rhizobia, soil microbes that convert atmospheric nitrogen into ammonia through biological nitrogen fixation (BNF), offer a natural solution but face competition from other soil microbes that limits their effectiveness. Bacteriophages (phages), viruses that infect bacteria, have been proposed to enhance rhizobial competitiveness by selecting for resilient strains, stimulating biofilm formation, and reducing microbial competition. This study examines whether phage exposure improves rhizobial competitiveness and nodulation efficiency in pea plants using a single-strain inoculation experiment. Plants were individually inoculated with strains that were susceptible to phage (parents) and evolutionary derivatives of these strains that could survive phage infection (survivors). The results showed that plants exhibited consistent leaf growth, with no significant differences between parents and survivors, though shoot biomass varied slightly among strains. Nodule counts were generally high but small, indicating a strong but potentially inefficient symbiotic relationship as a consequence of phage survival. However, root biomass was lower in inoculated plants compared to controls, possibly due to the energy cost of nodule formation. These findings suggest that while phage survival may negatively impact plant-microbe symbiosis, its effects on nitrogen fixation efficiency and plant growth require further study. Investigating phage-rhizobia coevolution could provide deeper insights into their interactions and long-term agricultural benefits.

059

MICROBIALLY-MEDIATED IMPACTS OF CONTAMINANTS PRESENT IN RECLAIMED WATER AND BIOSOLIDS ON GREEN PEA GROWTH

Emily Cacchione[1*], Isabella Ippolito[1], Harmanpreet Sidhu[2], Greg Slater[2], and Rebecca Doyle[1]
[1]Department of Biology, McMaster University, Hamilton, Ontario, Canada L8S 4K1
[2]School of Earth, Environment, and Society, McMaster University, Hamilton, Ontario, Canada L8S 4K1

The global rise in antibiotic use has increased selective pressures on bacteria, leading to the accumulation and spread of antibiotic resistance genes (ARGs) in microbial populations. ARGs have been detected in biosolids, reclaimed water, both of which are increasingly being used as alternatives to chemical fertilizers and fresh water, respectively. The accumulation of ARGs and other contaminants within agricultural systems raises concerns about their potential impacts on soil microbiomes and plant health. However, research on both the direct and indirect effects of contaminant exposure on crop growth remains limited. This study investigates how contaminants present within biosolids and reclaimed water influence the soil microbiome and plant growth. Pea, lettuce, and radish plants were exposed to environmentally relevant and elevated contaminant levels through biosolid or reclaimed water amendments. Soil samples were analyzed using 16S rRNA amplicon sequencing prior to and after contaminant exposure, and soil slurries were cross-inoculated onto pea plants to assess microbiome-mediated effects on plant growth, measured by plant height, leaf chlorophyll content, and biomass. Results showed no significant plant growth differences following cross-inoculation, suggesting that contaminants in biosolids and reclaimed water did not disrupt the established microbiome or that the microbiome adapted to buffer plants from potential negative effects. These findings indicate that biosolids and reclaimed water may serve as sustainable nutrient sources for agriculture without significantly altering plant-microbiome interactions.

060

AMPLIFYING BIRDNET’S SPECIES IDENTIFICATION: IS CONFIDENCE SCORE RELATED TO SONG CHARACTERISTICS?

Vaidehi Patel* and Jennifer Foote
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4

Rapid and accurate species identification is made possible by automated bird song identification technologies like BirdNET, which have completely changed biodiversity monitoring. The accuracy and possible limitations of the software were evaluated in this study by examining the correlation between BirdNET confidence scores and several acoustics characteristics of bird songs. We made Automated recordings at 206 sites in the Hiawatha Highlands for a total of 1,030 hours in May and June. Ten different species were identified using BIRDNET and 360 (positive and negative) detection of each species were sampled across confidence score bins and examined. We selected 10 high quality songs for each species and analyzed maximum and minimum frequency, bandwidth and song length using Raven Pro. We found that, with the exception of one species (Blackburnian Warbler), with a confidence score of <0.3, BIRDNET consistently recognized species with a probability of 95%. Confidence scores (at p=0.99) were not significantly correlated with song attributes ($p > 0.05$). While our results differ somewhat from earlier research on particular species, they are consistent with results from Western Canada. It is interesting that our detection accuracy of Brown Creeper was higher compared to Western Canada. This could be because BIRDNET’s reference data included a higher representation of Eastern subspecies. These results imply that although BIRDNET offers true species identifications, some positive detections might be missed by a universal confidence threshold (0.70), For wider relevance, future studies should refine confidence criteria and include song measurements from more species.

061

BEHAVIOURAL RESPONSE OF ERPOBDELLA OBSCURA TO NA, MG, K AND CA

Kendra Favaro* and William Dew
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4

Aquatic animals use a wide range of sensory systems to obtain information about their environment, with olfaction playing a crucial role. The olfactory system is essential to aquatic animals, and aids in survival, predation, kinship, mating, and foraging in vertebrates and invertebrates alike. While extensive research has been conducted on vertebrate chemosensory mechanisms and avoidance responses to contaminants that are commonly found in aquatic systems, very little research has been conducted on invertebrate species. This study investigates the chemosensory responses of *Erpobdella obscura*, a freshwater ribbon leech that was the subject for a series of behavioural trials using four metals salts: magnesium nitrate ($Mg(NO_3)_2$), sodium nitrate ($NaNO_3$), calcium nitrate ($Ca(NO_3)_2$) , and potassium nitrate (KNO_3) at concentrations of 1 mM, 5 mM, 10 mM, and 50 mM. The objective was to understand if the response was due to charge, specific elemental properties, or a nitrate specific effect. Behavioural trials were conducted using a 3D-printed box maze that tracked the position of the leech and assessed avoidance responses. Results from this study show a strong avoidance to KNO_3 and $Ca(NO_3)_2$ ($p < 0.05$) indicating that avoidance to these chemicals is not solely driven by ionic charge due to the monovalent and divalent nature of these compounds respectively. These findings highlight the ability of aquatic invertebrates to recognize chemical cues that may be physiologically stressful to them and gives a broader understanding of invertebrate chemosensory mechanisms.

062

PHENOTYPIC VARIATION IN POLLEN GERMINATION AND TUBE GROWTH IN STIGMA LIPID MUTANTS OF TOBACCO (*NICOTIANA TABACUM*)

Alicia Bruni*, Richard Bourgault, Deborah Buhlers, and Isabel Molina
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4

Pollination is a critical biological process in plant reproduction and genetic diversity, requiring precise interactions between pollen and the stigma. In *Nicotiana tabacum*, a species with wet stigmas, lipids polyesters within stigma exudates are believed to play a vital role in pollen adherence, hydration, and pollen tube growth. To evaluate the specific contribution of lipid polyesters to these processes, we used three tobacco mutant lines with reduced lipid exudation compared to wild-type (WT) plants. Controlled pollination experiments were conducted, and pollen tube growth was visualized using aniline blue staining under a fluorescent microscope. Additionally, a subset of mutant plants were treated with oil to assess whether supplementation with neutral, non-polymeric triacylglycerol could restore normal pollen adherence and germination. Statistical analysis assessed differences among WT, untreated mutants, and oil-treated mutants. The results showed that mutants with reduced lipid polyesters experienced significantly lower pollen adhesion and tube growth compared to WT, while oil-treated mutants showed partial recovery of the WT phenotype. These findings highlight the important role of lipid polyesters in both stigma function and successful fertilization. Understanding the biochemical and physiological contributions of lipid polyesters may have broader implications for improving pollination efficiency in related crops and can address agricultural challenges related to plant reproduction.

063

RAPID IDENTIFICATION OF SPECIES AT RISK HABITAT USE WITH BIRDNET

Kristin Hillier* and Jennifer Foote
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4

Development proposals often have short time-lines for public consultation and review. However, identifying habitat use by species at risk in areas of proposed development can help shape land use changes in urban and suburban areas. New autonomous recording technologies have resulted in large, and often publically available, datasets that contain vocalizations of bird, mammal, amphibian, and insect communities. These recordings can be used to assess the community composition if recordings exist. New developments in machine learning have also made automated species detection a possibility, like the newly developed BirdNET. In Sault Ste Marie, ON, there was an announcement of a Hydro One route passing through a beloved recreational trails system within the city limits. We had made recordings just several months before during the breeding season of the songbird community. We ran these recordings through BirdNET for three species at risk, Eastern Wood Pewee, Wood Thrush, and Canada Warbler. We calculated confidence intervals for 90% probability of positive detections for these species and identified recording sites that met this criteria. Both Wood Thrush and Eastern Wood Pewee were locally abundant throughout the proposed route while Canada Warbler were found along a wetland area. We presented our data to the community and to Hydro One at their local consultation just 10 days after learning about it, revealing that big datasets can be rapidly used for identifying species at risk and informing local management plans using this approach.

064

INVESTIGATING THE ROLE OF SCREEN TIME AND AGE ON TEAR MENISCUS HEIGHT IN DRY EYE DISEASE

Bryanna Zimbaro*[1,2], Nikki Shaw[1]
[1]Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4
[2]FYidoctors, Sault Ste. Marie, Ontario, Canada P6A 3Z9

The tear film protects the front surface of the eye, maintaining ocular health by providing lubrication, removing debris, delivering oxygen to the cornea, and ensuring optical clarity. It consists of three layers: the outermost lipid layer prevents evaporation; the middle aqueous layer maintains hydration; and the innermost mucin layer ensures adherence of the tear film to the corneal surface. When the tear film becomes disrupted, it may lead to Dry Eye Disease (DED)—a common, multifactorial disease that causes discomfort. DED manifests itself in two forms: Aqueous Deficient Dry Eye (ADDE), which results from reduced tear production, and Evaporative Dry Eye (EDE), caused by rapid tear evaporation. Tear Meniscus Height (TMH) plays a crucial role in diagnosing DED, with values less than 0.20 mm considered aqueous deficient. This study aims to explore the relationship between age and screen time, an area with limited research. TMH was measured on 104 patients from FYidoctors in Sault Ste Marie, Ontario, where screen time, age, and their interaction were assessed using a multiple linear regression model. The results from the model showed that screen time and age were significantly related to TMH; ten percent of the variation in TMH was explained by screen time, age, and their interaction. Higher screen time was negatively associated with TMH; older respondents with lower screen time may have higher TMH values due to reflex tearing, where low-quality tears are overproduced due to irritation. Limiting screen time and taking frequent breaks, especially for young adults, may help improve TMH.

065

HOW DOES SOIL BIOTA AND FIRE DISTURBANCE AFFECT THE GROWTH RESPONSES OF BOREAL AND TEMPERATE ONTARIO TREE SPECIES?

Roxane Bergeron*[1], Joel Lucenay[1], Stephen Mayor[2], and Pedro M. Antunes[1]
[1]Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4
[2]Ontario Forest Research Institute, Sault Ste. Marie, Ontario, Canada, P6A 2E5

Canada's Boreal Forest is expected to experience rising temperatures and increased wildfire frequency under climate change. Soil biota play a critical role in plant establishment and seedling success, particularly in early successional landscapes. However, the potential northward migration of temperate tree species remains uncertain, as do the effects of novel soil biota associations on their establishment. To investigate these dynamics, we asked: (1) How do tree species respond to soil biota from their home forests versus foreign soil biota? (2) How does fire-disturbed boreal soil biota affect tree growth, and does the addition of temperate soil biota to burnt boreal soil alter this response? We conducted a greenhouse experiment growing three representative boreal and three temperate Ontario tree species in five soil biota inoculation treatments—temperate, boreal unburnt, boreal burnt, boreal burnt mixed with temperate, and a sterile control—measuring stem height over 154 days (n = 300). We found that tree growth responses to soil biota varied among species. Overall, boreal trees generally exhibited a more positive response to soil biota than temperate trees, but there was no significant difference in growth response across treatments.

066

DOES SEED REMOVAL BY GRANIVORES IN AN OLD FIELD PLANT COMMUNITY DIFFER AMONG PLANT SPECIES?

Hailey Frasier* and Brandon Schamp
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada, P6A 2G4

Granivores (seed-eating herbivores) may affect plant communities by altering species abundance or diversity. Seed consumption rate of plant species may vary depending on seed size and abundance, which can determine how easily the seeds are found and consumed. In this study, we set out seed depots of 24 plant species in an old field plant community to test how plant species identity and seed size affect seed removal. We also compared differences in seed removal rates when seeds were on soil to a previous study where seeds were not in substrate and just in a petri dish. Plant species were removed from the seed depots by granivores at significantly different rates, with seeds of varying species-level seed masses also differing in removal rates. When compared to a previous study, fewer seeds of all species were eaten when seeds were on soil, suggesting that search time for seeds is an important factor in granivore food choice and efficiency. Differences in traits among plant species (e.g. seed size, colour) may also be factors in seed removal when soil is present. Results suggest that species differences in seed removal may alter plant communities in a way which may enable coexistence.

067

THE INFLUENCE OF HARD VERSUS SOFT RELEASE METHODS ON EASTERN SAND DARTER (*AMMOCRYPTA PELLUCIDA*) BURROWING BEHAVIOUR IN RESPONSE TO A PREDATOR

Audrey Joan Verra*, Adam Gouge, and Christine Madliger
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada, P6A 2G4

Fishes are among the most endangered taxa in freshwater ecosystems. Reintroduction is one strategy for re-establishing populations, but it often involves transportation, which can introduce stress and behavioural changes. There are two release methods: hard (direct release) and soft release (includes acclimatization via enclosures). Soft release may aid in the recovery of natural behaviours, but its effects following transportation remain understudied, especially for small-bodied species. The Eastern Sand Darter (*Ammocrypta pellucida*), a species at risk, has been proposed for reintroduction to aid population recovery. However, little is known about how release methods influence their behaviour such as burrowing in sand, which is thought to aid in predator evasion. In this study, we examined whether soft release supports behaviours related to predator evasion compared to hard release methods. We assessed substrate preference (sand vs. rock) in a behavioural arena and used a lure (rainbow trout) to simulate a predator event. We calculated time spent on each substrate, burrowing frequency, and swimming behaviours before and after predator introduction. Results from this study show that release methods following transport did not significantly influence burrowing behaviour and substrate preference in response to a predator. Evasion was slightly lower in the hard release group, but not statistically significant. Hard release may be suitable for this species, but future work including a larger sample size and other endpoints should be done to verify the optimal release method.

068

THE BEHAVIOURAL EFFECTS OF ARTIFICIAL LIGHT AT NIGHT IN BIRDS: A META-ANALYSIS

Washma Arshad* and Christine Madliger
Department of Biology, Algoma University, Sault Ste Marie, Ontario, Canada, P6A 2G4

Artificial light at night (ALAN) is increasing globally due to the expansion of anthropogenic activities in both terrestrial and aquatic environments. Although artificial light is beneficial for humans, its effects on other species are not fully understood. Excess light can interfere with organismal physiology, behaviour, and fitness, with potential consequences for whole ecosystems. As literature has amassed in avian species over the past 20 years, there is the opportunity to synthesize the effects of ALAN on key traits, such as behaviour. The objective of my study was to perform a meta-analysis to determine the types and extent of behaviours that can be affected by ALAN in birds. I used a structured search in Web of Science to establish a dataset of 245 journal articles. I collected information from each publication on the type of behaviour, species, year of publication, location of study, type of light, and effect on behaviour. I found that behaviourally focused research on ALAN has been steadily increasing over time. In addition, the majority of studies reported negative effects of ALAN on avian behaviour. Finally, certain behavioural traits were more extensively researched than others, with migration, vocalization, and sleep being the most prevalent. Further research is needed to establish the influence of ALAN on other behaviours, such as habitat selection and vigilance. My results reinforce the importance of considering ALAN as a threat for birds across multiple parts of their life cycles.

069

ASSESSING SWIMMING PERFORMANCE OF THE EASTERN SAND DARTER FOLLOWING HARD AND SOFT RELEASE TECHNIQUES

Anton Peter*, Adam Gouge, and Christine Madliger
Department of Biology, Algoma University, Sault Ste. Marie, Ontario, Canada P6A 2G4

Aquatic ecosystems are among the most threatened habitats worldwide, with habitat degradation and fragmentation significantly impacting freshwater fish populations. The Eastern Sand Darter (*Ammocrypta pellucida),* a small benthic fish listed as a species at risk in Canada, relies on sandy substrates and undisturbed flow conditions, making it highly vulnerable to habitat disturbances. Translocation is an emerging conservation strategy for this species, yet the effect of transport and success of different release techniques remains unclear. A proxy for swim performance was assessed in summer and fall by measuring swimming distance across three groups: control (not transported), hard release (immediately following transport), and soft release (following 24-hours in an in-river enclosure after transport). In summer, fish released in the soft release treatment swam significantly farther than those in the hard release group ($p = 0.003$), suggesting a potential benefit of a gentler release method. However, in fall, both release groups swam significantly farther than the control group ($p = 0.005$), with no significant difference between the two techniques. These findings indicate that the effectiveness of release methods may be season-dependent, with soft release showing greater benefits in summer. Understanding the influence of release strategies on post-translocation performance is crucial for conservation planning. This study emphasizes the significance of adjusting conservation efforts to seasonal circumstances in freshwater environments and contributes guidance on how to best reintroduce the Eastern Sand Darter.

070

AN ANALYSIS OF GLAUCOUS GULL (*LARUS HYPERBOREUS*) DIET FROM CORNWALLIS ISLAND, NUNAVUT

Lucy van Haaften*[1], Mark Mallory[2], Jennifer Provencher[3], and Sarah Jamieson[1]
[1]Department of Biology, Trent University, Peterborough, Ontario, Canada K9L 0G2
[2]Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada, B4P 2R6
[3]Science and Technology Branch, Environment and Climate Change Canada, Ottawa, Ontario, Canada K1A 0H3

Glaucous Gulls (*Larus hyperboreus*) are diet generalists that usually nest in coastal colonies with other seabird species, often preying upon their neighbours' eggs and young. On Cornwallis Island, Nunavut, a colony of Glaucous Gulls inhabits a small island within a lake, where they are the only seabird species nesting. Given this unique non-coastal habitat not shared with other birds, we wanted to determine whether their diet differs from other more typical nearby populations. To assess this, we collected 79 regurgitated Glaucous Gull pellets from this colony, dissected them, and identified prey items to the lowest possible taxonomic level. We found that this population was feeding predominantly on northern collared lemmings (*Dicrostonyx groenlandicus*), which is unusual for the species which usually feeds mostly on marine prey and young of other seabird species. Other prey items found include bivalve and gastropod shells, bird eggshells, and garbage from the nearby landfill. This study provides evidence for a specialized diet of Glaucous Gulls in this unique environment. Since this population feeds largely on terrestrial prey, this information could be used for future studies that compare the contaminants ingested by gulls that feed in terrestrial vs. marine environments.