51st Ontario Ecology, Ethology, and Evolution Colloquium 2025

Navigating Earth's Ecosystems Today and Tomorrow

May 15th - 17th 2025

Programme & Schedule

Carleton University

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Opening Remarks

Dear attendees,

Welcome to the 2025 Ontario Ecology, Ethology, and Evolution Colloquium (OE3C) hosted by Carleton University! OE3C has been running for over 50 years. During this time it has become a staple conference for Ontario biologists. This conference is run “for students, by students.” Without the backing of an academic society, OE3C is only made possible through the imagination, commitment, and tenacity of self-assembling organizing committees, consisting of voluntary graduate students and postdoctoral researchers, as the conference bounces between Ontario institutes annually. We are excited to welcome you all for the 51st annual OE3C and the first to be hosted at Carleton in 20 years!

Cheers to a great conference!

Megan Raposo, Marrissa Miller, Katherine Di Iorio, and Isaac Finkelstein

OE3C 2025 Organizing Committee

Megan Raposo
Co-Chair

Marrissa Miller
Co-Chair

Isaac Finkelstein
Co-Chair

Katherine Di Iorio
Co-Chair (Financial)

AJ Deneka
Website Co-Chair

Charlotte Galloway
Website Co-Chair/Awards

Marcus Gauthier
Social Media

Caroline Grela
Abstracts and Awards

Émilie Gagnon
Social Media

Special thanks to our other volunteers who are not pictured: Mel Beaudin, Matthew Coffey, Maggie Hanna, Falisha Para, and Adam Storey.

Land Acknowledgment

As we begin the Ontario Ecology, Ethology, and Evolution Colloquium (OE3C), we wish to open with a meaningful and intentional land acknowledgment.

We gather here as a community of biologists, whose work is inherently tied to the land, water, and living systems that sustain all life. This land is not neutral ground. We are meeting on the traditional unceded territory of the Algonquin Anishinaabe Nation. These lands have long been home to vibrant Indigenous nations with rich ecological knowledge, deep-rooted cultural traditions, and enduring relationships with the natural world.

Too often, land acknowledgments become a rote gesture. At OE3C, we reject this approach. We commit to acknowledging and honouring the peoples whose lands we occupy not as an act of guilt or performance, but as an ongoing responsibility. This acknowledgment is not the end of the conversation, it is the beginning.

For those of us who are settlers, we recognize that our presence here continues to benefit from systems of colonialism that have dispossessed Indigenous peoples of land, language, and sovereignty. We commit to challenging the structures, within science and beyond, that uphold colonial violence.

Let this acknowledgment guide us not just during this conference, but in our work as biologists and as members of a shared world.

Statement of Equity, Diversity, and Inclusion

The OE3C 2025 Organizing Committee acknowledges the continual systemic barriers that affect the equitable development of members of our communities. Factors including age, sex, sexual orientation, gender identity, nationality, ethnicity, religion, socioeconomic status, physical and neurological differences, parental status, and others all continue to contribute to privileges and/or prejudices. These privileges and prejudices often determine who has the power to make decisions.

We are diverse by nature and inclusive by choice. Diversity is at the core of our vision, mission, and values in putting together and facilitating this conference. We are committed to the inclusion of people from all walks of life representing diverse cultures, backgrounds, and viewpoints. Representativeness is an aspect to be tackled head-on and embraced fully. We strive to foster a welcoming environment for all. While we know we cannot change the world in one conference, we recognize our capacity to promote and inspire change wherever possible.

The chairs of this conference established several awards to promote equity, diversity, and inclusion at this conference. We created a bursary to support a disabled student to travel to the conference, without the requirement to present, recognizing that presenting can pose barriers for students with disabilities. Additionally, $3000 was allocated as travel awards to support any student with financial need to present at this conference.

We hope that the environment and the discussions fostered during the OE3C 2025 will create a welcoming and safe space for all, and we encourage participants to reflect on our (collective and individual) positionality. The OE3C 2025 Organizing Committee looks forward to promoting Equity, Diversity, and Inclusion with you!

Acknowledgements

We would like to thank Sarah-Anne Szaboth, Jennifer Harris, and Salman Khan from the Carleton Biology Department for their invaluable support throughout the planning process of this conference, as well as their remarkable patience in responding to the innumerable emails we sent them. We would also like to thank Sarah Adams from Conference Services for her insights and assistance with planning the conference set-up. We are grateful to Sofia Parra for designing our conference logo, which perfectly captured the spirit of our event.

Sponsors

We would like to thank all of our sponsors for their generous support of OE3C. Without their donations and contributions, this event would not be possible. A special thanks to those societies and associations that have supported OE3C through conference awards and funds. The American Genetic Association graciously presented the 2025 Ontario Ecology, Ethology, and Evolution Colloquium with the special events award. The Canadian Society for Ecology and Evolution sponsored OE3C through their regional conference support funds. The Company of Biologists provided us with a Scientific Meeting Grant. The American Genetic Association award and the Company of Biologists Grant enabled OE3C to award four students with travel grants which are named in these societies' honour.

Additionally, we would like to wholeheartedly thank all the local companies and museums that were able to donate to our event. We are so grateful to be able to share some of our favorite spots around Ottawa with those registrants visiting from across Ontario. Thank you for your generosity and dedication to the community.

AGA American Genetic Association

Carleton University
Department of Biology

CSEE SCEE Canadian Society for Ecology and Evolution

AFS OC
American Fisheries Society
Ontario Chapter

The Canadian Section of The Wildlife Society
La Société de la Faune
Section Canadienne
Fostering Excellence in Wildlife Stewardship

The Company of Biologists 100

Canadian Herpetological Society
Société d'herpétologie du Canada

Ingenium

Comparative Cognition Society

ROM

canadian museum of nature
nature
musée canadien de la nature

Musée canadien de l'histoire
Canadian Museum of History

Canadian War Museum
Musée canadien de la guerre

moy moy
DESIGNS

Meow & Bark
DESIGNS
Handcrafted Gifts

mayfair theatre
since 1932

Rooster's Coffeehouse

The Merry Dairy

EST. 1998
EQUATOR
COFFEE ROASTERS

PGI
Pasticceria Gelateria Italiana 1979

THE MERRY DAIRY ™

Registration, Check-In, & Conference Locations

Upon arrival at OE3C 2025, please stop by the registration desk in the Galleria on the fourth floor of Nideyinàn (NN) to sign-in and pick up your conference name badge. If you arrive outside of the registration hours, please find a conference volunteer (wearing green) to ensure you receive your conference name badge. Your registration to OE3C 2025 includes access to all presentation and poster sessions, keynote talks, meals, social events, and excursions.

Day 1 - Thursday May 15th 2025

Location: Galleria in Nideyinàn (fourth floor)

Registration Hours: 9:00am to 3:30pm

Day 2 - Friday May 16th 2025

Location: Galleria in Nideyinàn (fourth floor)

Registration Hours: 8:00am to 9:00am

Day 3 - Saturday May 17th 2025

Location: Galleria in Nideyinàn (fourth floor)

Registration Hours: 8:00am to 9:00am

For a full campus map, please visit: https://carleton.ca/campus/map/

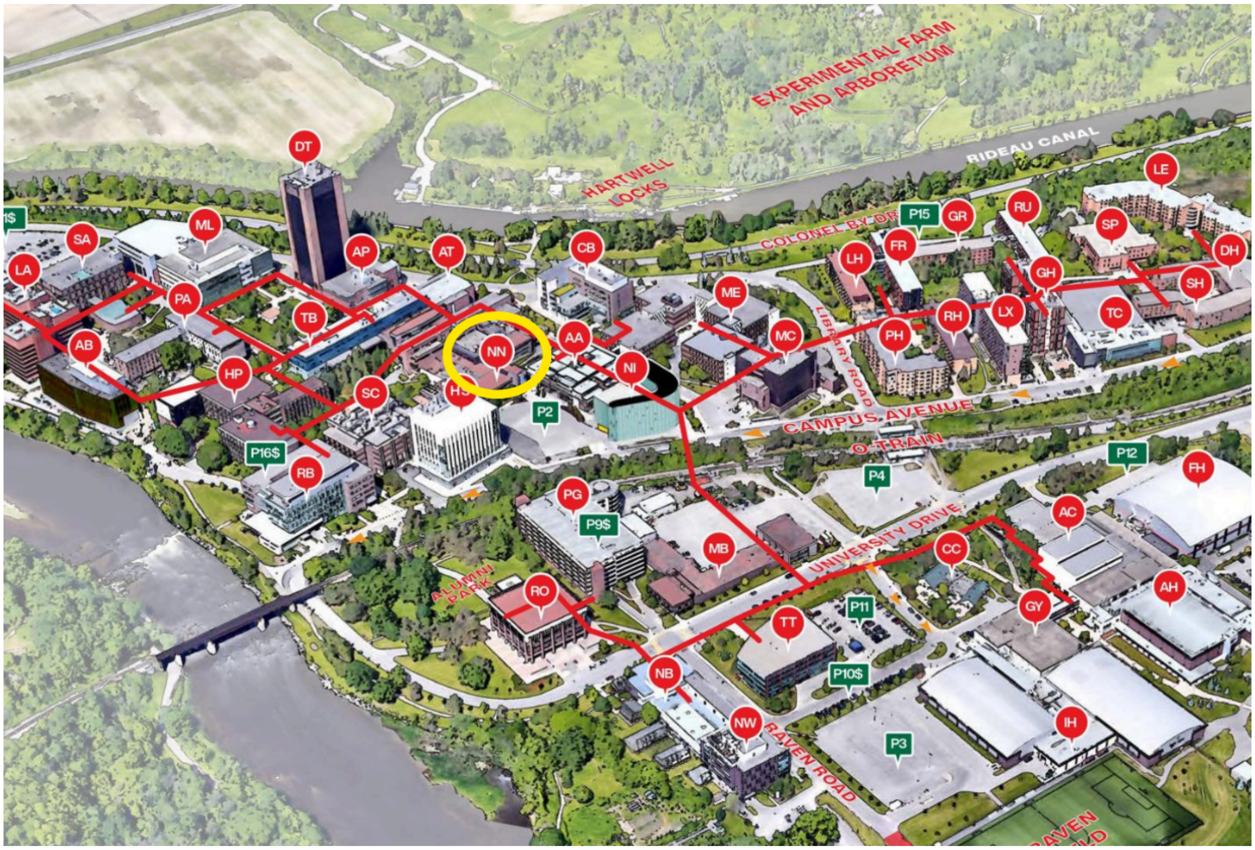
Carleton also has an underground tunnel system that connects all buildings on campus. For a full campus tunnel map, please visit: https://carleton.ca/finance-admin/campus-tunnel-map/
(Please note, Nideyinàn was formerly called the University Centre)

Visitor Parking

Please use the following Hotspot link or scan the QR code in the parking lot to validate your parking. Registrants may park in any Visitor Lot on May 15th to May 17th. Guests will be charged $11.00 per day in order to park their car. The code will start working at 7:00am and be good for the whole day. Please note that each day you are on campus you will need to pay for parking using the code provided.

Code: OEEE25

Parking lot P16 is closest to the event locations. For list of parking lots and payment information, please visit: https://carleton.ca/parking/visitors/



(Nideyinàn — NN — circled in yellow)

Presentation Information

Oral Presentations: Presenters are asked to submit their presentations as a PowerPoint presentation to this Dropbox folder (linked here) by 5:00pm the evening before their presentation. Please submit using the following file name: TimeDay_FirstName_LastName (ex. 230Friday_Megan_Raposo.pptx).

Location: Oral presentations will be held in the Tory Building (TB) in room 240.

Poster Presentations: Presenters should bring their printed posters to the conference. Posters can be put the morning of their presentation during breakfast and remain up as directed.

Location: Poster presentations will be held in the Galleria on the fourth floor of Nideyinàn (NN).

Conference Schedule at a Glance

Thursday - May 15th

08:30……………………………………Excursion 1: Bird Walk at Mud Lake Conservation Area

09:00…………………………………………...Registration (NN - Galleria) (open until 15:30)

12:00……………………………………………...Excursion 2: Canadian Museum of Nature

15:00…………………………………………………………...Coffee Break (NN - Galleria)

15:30………………………………………………………..Opening Ceremonies (TB - 360)

16:00 …………………………………………………Keynote 1: Dr. Christina Caruso (TB - 360)

17:00………………………………………………………Catered Dinner (NN - Galleria)

18:30………………………………………………………………………..Trivia (TB - 360)

Friday - May 16th

08:00…………………………………………..Registration & Catered Breakfast (NN - Galleria)

09:00……………………………………………………..Keynote 2: Dr. Rassim Khelifa (TB - 360)

10:00……………………………………………………Poster Session #1 (NN - Galleria)

11:30……………………………………………………..Presentation Session #1 (TB - 240)

13:00………………………………………………………………...Lunch (NN - Galleria)

14:00……………………………………………………..Presentation Session #2 (TB - 240)

15:00…………………………………………………………...Coffee Break (NN - Galleria)

16:00…………………………………………………………………Lichen Talk (TB - 360)

17:00……………………………………………………………………....End of Day

Saturday - May 17th

08:00…………………………………………...Registration & Catered Breakfast (NN - Galleria)

09:00……………………………………………………Keynote 3: Dr. Tom Hossie (TB - 360)

10:00…………………………………………………………Poster Session #2 (NN - Galleria)

11:30……………………………………………………..Presentation Session #3 (TB - 240)

13:00……………………………………………………………………...Lunch (NN - Galleria)

14:00……………………………………………………..Presentation Session #4 (TB - 240)

15:00…………………………………………………………...Coffee Break (NN - Galleria)

16:00……………………………………………………..Presentation Session #5 (TB - 240)

17:00…………………………………………………………Catered Dinner (NN - Galleria)

Conference Excursions

We have two excursions taking place on Thursday, May 15th.

<u>Bird Walk at Mud Lake Conservation Area</u>: 8:30am to 11:00am

Mud Lake is a biodiversity hotspot right in the city of Ottawa! Join us for a guided tour of the area, with a chance to see a variety of bird, mammal, insect, and plant species!

For more information, see: https://ontarioconservationareas.ca/conservation-areas/mud-lake/

Mud Lake Excursion Instructions:

The bus to Mud Lake **will leave from Carleton campus at 8:30am** on Thursday, May 15th and will return to Carleton by 10:45am. The bus will be leaving from **Parking lot 7 at 8:30am**, so please make sure to be on time.

Canadian Museum of Nature Scavenger Hunt: 12:00pm to 2:00pm

Ottawa's Museum of Nature has fantastic displays of natural history, including huge skeletons of dinosaurs! Join us for a visit to the museum and a fun scavenger hunt of the exhibits.

For more information, see: https://nature.ca/en/

Canadian Museum of Nature Excursion Instructions:

We **will meet at the museum at 12:00pm** on Thursday, May 15th. The museum is accessible by city bus (7 - St. Laurent bus) from the Carleton campus. We will stay at the museum for around 2 hours before heading back to campus for the opening ceremonies.

Keynote Speakers

Ecology - Dr. Rassim Khelifa

HE/HIM/HIS
Concordia University

Dr. Khelifa studies community responses to climate change, anthropogenic impacts, sexual selection, and biodiversity conservation, with a primary focus on insects. He also has a broader interest in birds and plants. In addition to his scientific work, Dr. Khelifa is a strong advocate for equity, diversity, and inclusion in STEM. His primary focuses in this area include breaking language barriers for non-English-speaking scientists and promoting equitability in fieldwork.

Dr. Khelifa is currently an Assistant Professor in the Department of Biology at Concordia University. He holds two PhDs: one in Evolutionary Biology from the University of Zurich in Switzerland and another in Ecology from Université Mouloud Mammeri in Algeria. In addition to his academic role, he is a member of the IUCN/SSC Dragonfly Specialist Group, which assesses the conservation status of dragonfly species.

Ethology - Dr. Thomas Hossie

HE/HIM/HIS
Trent University

Dr. Hossie studies predator-prey interactions, exploring the ecological and evolutionary mechanisms that lie at the intersection of behavioral ecology and population biology. His research primarily focuses on amphibians and insects, using these taxa to address broader questions in this field. Currently, his work centers on the ecology of bisexual-unisexual salamander complexes.

Dr. Hossie is currently an Assistant Professor in Biology at Trent University. He completed his BSc and MSc at Trent University and his PhD at Carleton University. His PhD investigated the ecology and evolution of eyespots on caterpillars.

Understanding and conserving imperilled salamander complexes in a human-dominated world.

Global amphibian biodiversity is being lost at an alarming rate. For federally endangered species like the Jefferson and Small-mouthed salamander, conservation efforts are complicated by the presence of “unsexuals” – an all-female lineage of salamanders with a hybrid nuclear genome whose reproduction depends on stealing sperm produced by the males of other species. These obligate reproductive parasites also compete with the sexual hosts on which they rely, which should make these assemblages prone to collapse. Yet, examinations of their mitochondrial DNA tell us that unisexuals have persisted alongside their sexual hosts for 2-5 million years. My research explores the ecological and evolutionary dynamics of unisexual complexes, while also seeking to find practical strategies to ensure their long-term persistence. Unisexuals present an interesting challenge for conservation biologists because they defy the biological species concept, but are clearly distinct, wild by nature, and must be managed alongside sympatric their imperilled sexual host species. Through an improved understanding of the key ecological and genetic processes we can enhance our ability to conserve this unique part of our natural heritage.

Evolution - Dr. Christina (Chris) Caruso

SHE/HER/HERS
University of Guelph

Dr. Caruso is a plant evolutionary ecologist. Over the course of her career she has studied the causes of natural selection on floral traits, the evolution of sexual systems in flowering plants, and the roles of selection and constraint in the evolution of plant functional traits. Currently, her work focuses on the response of native plant populations to pollinator decline.

Dr. Caruso is currently an Associate Professor at the University of Guelph. She completed her BA at Oberlin College (Ohio USA) and her PhD at the University of Illinois. In addition to her academic role she serves as the Editor-in-Chief of the International Journal of Plant Sciences, a University of Chicago Press journal that celebrates its 150th birthday in 2025.

How will plant populations respond to anthropogenic pollinator decline?

As human activity changes the global environment, plant and animal populations will not persist unless rapid phenotypic change results in adaptation. Understanding how populations could adapt to human-mediated environmental change via both phenotypic plasticity within a generation and phenotypic evolution across generations is important because these mechanisms do not have independent effects on the probability that a population persists. In this talk, I will explore the potential for plant populations to adapt to a specific type of anthropogenic environmental change—pollinator decline—via both plasticity in floral traits within a generation and the evolution of floral traits across generations, and then evaluate whether this adaptation is likely to stabilize or destabilize the plant-pollinator mutualism.

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Poster Abstracts

Contemporary Statistical Methods in Dispersal Ecology

Allan Roberts[1]

[1] *Department of Biology, McMaster University, Hamilton*

This poster will present a survey of statistical methods that have been used in recent publications in the field of dispersal ecology, with a focus on methods that are used for dispersal kernel estimation. Both terrestrial and marine systems will be considered. A particular subtopic that will be looked at is dispersal by multiple vectors, including examples of diplochory. Attention will also be given to statistical methods that are used to handle scale and distance on a landscape. There are several ways that distances can be handled in a statistical model; for example, an explanatory variable may be based either on distance or density. Nearest distance to a type of landscape feature might be used as a variable, or one might use density of a feature within a radius or raster cell. This poster will also present statistical illustrations based on simulated data. Discussion will connect the topic of dispersal kernel estimation to current concepts in community ecology.

Effects of Introduced Salmonids on Native Lake Trout *Salvelinus namaycush* in Lake Huron: Evaluating Niche Overlap Using Stable Isotopes

Jacob Lasci[1]

[1] *Western University, London*

The Lake Huron fish community is comprised of many non-native species, including the piscivorous Pacific salmonids chinook salmon *Oncorhynchus tshawtscha*, coho salmon *Oncorhynchus kisutch*, and rainbow trout *Oncorhynchus mykiss*. The only abundant native piscivorous salmonid is the lake trout *Salvelinus namaycush*. Since 1980, there has been a steady decline in the biomass of the prey fishes these salmonids consume. Considering the collapse of alewife *Alosa pseudoharengus* in 2003, there has been growing concern that lake trout will be outcompeted by the non-native salmonids. Paramount to understanding this concern is determining the diet overlap between salmonids and how the overlap has shifted with changes in prey abundance. Here, stable isotope analyses ($\delta^{13}C$, $\delta^{15}N$) from lipid-extracted muscle tissues were compared among salmonids revealing large percentages of lake-wide isotopic niche overlap. Comparisons of these isotopes from salmonid scale samples taken before and after the alewife collapse revealed a shift in the diets of chinook salmon that now overlap with lake trout. Given the strong competitiveness of chinook salmon, this result is concerning for the management of the native lake trout.

Investigating Associations between Genome Size and Climate in the Potato Clade

Delaney Grace McTavish-McHugh[1] & Edeline Gagnon[1]

[1]*Department of Integrative Biology, University of Guelph, Guelph*

Genome size, the total amount of genetic material found within an organism, varies widely across angiosperms, but the causes of this variety aren't fully understood. Plant genome sizes vary mostly due to random duplication or deletion of genetic material in noncoding regions. Differences in genome size have been associated with environmental filtering in particular plant clades. Specifically, plants with small genomes are common in both mild (i.e. temperate, wet) and extreme climates, while larger genomes are rarer in hot, cold, or dry conditions. Genome sizes in the Potato clade have not been broadly studied, but the clade's members survive in a wide variety of habitats and climates, making it a suitable candidate clade to study whether a plant species' environment is associated with genome size. My research will provide a dataset of genome size estimates for members of the Potato clade collected through flow cytometry and sequence-based methods. If genome size variation is associated with climatic conditions (temperature, precipitation etc.), genome size could be a factor in environmental filtering of this ecologically diverse plant clade.

Evaluating Population Genetic Clustering Methods Under Different Migration and Sampling Scenarios

Bianca R. Tassi[1] & Catherine I. Cullingham[1]

[1]*Department of Biology, Carleton University, Ottawa*

Accurately identifying genetic populations is important as it aids in species identification, understanding disease spread-risk, and resource management. The software, STRUCTURE, is currently the standard in estimating the most likely number of populations (K). POPCLUSTER, a newer software, has a more efficient algorithm for handling large genomic data, and it is more accurate in handling small or highly unbalanced sampling. It does this by introducing a scaling parameter taking values 0 to 4 (no scaling to very strong scaling). However, there is limited understanding of how/when to use the scaling parameter to ensure an accurate clustering solution. Therefore, our project will test the scaling parameter by simulating three populations under an island model of migration at three different migration scenarios, and four different sampling schemes, that include equal sampling, and strong skews. We will estimate K using best practices in STRUCTURE, and POPCLUSTER, and then compare estimated K to the simulated K to assess the performance and level of agreement between the programs. Empirical data sets will also be used in simulations to compare to the simulated data. This comparative analysis will contribute to refining best-practices in estimating genetic populations based on the software, type of data, and parameters inputted.

Collision Course: How Well Can We Predict Building Collision Risk for Birds?

Joshua S. Cadieux[1], Stasha Lysyk[1], Krista L. De Groot[2], Barbara Frei[1,2], Rachel T. Buxton[1] & Roslyn Dakin[1]

[1] *Department of Biology, Carleton University, Ottawa*

[2] *Environment and Climate Change Canada, Science and Technology Branch, Wildlife Research Division*

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

Using Behaviour to Better Understand the Relationship Between Phoretic Mites and Burying Beetles

Shannon Marginson[1], Anjalie St-Louis-Hodgins[1], & Dr. Frances Bonier[1]

[1]*Department of Biology, Queen's University, Kingston*

Interspecific interactions shape ecological communities and drive evolutionary processes. These interactions range from mutualisms, where both species benefit, to antagonisms, where one benefits at the other's expense. However, these relationships' fitness outcomes can be unclear or context-dependent. Grooming, a fundamental behaviour across many species, might provide insights into the nature of interspecific interactions. Insects, including beetles, frequently engage in grooming, which might reflect the long-term, net fitness benefits of these relationships. Our study investigates how burying beetles (*Nicrophorus orbicollis*) behaviours change in response to phoretic mites (*Poecilochirus* spp.), their long-standing symbionts. While previous research

presents conflicting evidence, no study has assessed whether these beetles appear to actively resist, tolerate, or facilitate mite colonization. Using controlled behavioural trials, we tracked grooming, escape, and other behaviours before and after mite exposure. Mite-exposed beetles significantly increased both grooming and escape behaviours, while reducing others, compared to controls. This shift supports the hypothesis that beetles perceive mites as parasites rather than neutral or beneficial passengers. These findings contribute to growing evidence that the fitness effects of phoretic mites on burying beetles can be dynamic, but suggest that, over evolutionary timescales, mites have likely been detrimental to beetle fitness.

Effects of Pollinator Decline on the Evolution of Seed Production via Autonomous Selfing

Alise Catherine Griffiths[1] & Christina Marie Caruso[1]

[1]*Department of Integrative Biology, University of Guelph, Guelph*

Human-mediated pollinator decline can reduce the quantity and quality of pollination services to plants. To ensure seed production despite reduced pollinator services, plants with mixed mating systems may evolve floral traits that increase autonomous self-pollination. To test whether pollinator decline causes the evolution of increased autonomous selfing, *Mimulus guttatus* from six experimental populations that had evolved for three generations in either high or low pollination environments were grown in a pollinator-free greenhouse where any seed production would be caused by autonomous self-pollination. We found that *M. guttatus* that had evolved in a low pollination environment that mimicked pollinator decline produced 25% more seeds per fruit and 28% more seeds per plant relative to *M. guttatus* that had evolved in a high pollination environment. Our results indicate that plants with mixed mating systems can respond to pollinator decline by rapidly evolving traits that increase autonomous self-pollination. The resultant increase in the production of selfed seeds could provide reproductive assurance in the face of pollinator decline.

Can the steel slag microbiomes mediate plant growth responses to this material?

Quincy Lee Clark[1] & Pedro Madeira Antunes[1]

[1]*Department of Biology, Algoma University, Sault Ste. Marie*

Steel slag is the primary by-product of steel manufacturing and refining. This material is commonly used as a soil amendment to adjust pH and provide minerals beneficial for plant growth. However, we observed that plants growing in slag piles had roots colonized by fungi, suggesting that both biotic and abiotic factors might contribute to plant growth in these environments. To investigate this hypothesis, we conducted a controlled-environment experiment assessing the growth response of a model plant, *Lactuca sativa*, to increasing concentrations of slag with and without slag microbial communities. Specifically, we cultivated plants in substrates containing 1%, 10%, and 100% slag, either sterile or non-sterile (n = 6). Plants grew

significantly taller in non-sterile slag (mean ± SEM: 3.4 ± 0.20 cm) compared to sterile slag (2.8 ± 0.11 cm; $F_{1,35} = 20.8$, $p < 0.001$). Additionally, there was a significant interaction between sterility and slag concentration affecting plant height ($F_{2,35} = 4.1$, $p < 0.03$), with plants at 100% slag showing the greatest benefit from the presence of slag microbes. These results suggest that microbial communities within steel slag may enhance plant growth, highlighting potential applications for the slag microbiome.

Stress in the Spotlight: Impacts on Learning and Memory in a Cichlid Fish

Catalina Costiuc[1]

[1]*McMaster University, Hamilton*

Despite a commonly held belief to the contrary, fish are capable of forming long-term memories. However, what factors affect memory retention and how long memories can be held for have not yet been investigated in fishes. Increased stress has been shown to inhibit learning and memory in many other animals, but the effects of stress on memory formation and retention in fish have not been studied. Here we used *Neolamprologus pulcher*, an African cichlid species, to establish a memory timeline and determine the impacts of stress on memory. Fish were randomly assigned to either a control group or a stressed treatment group (which encountered repeated chasing) prior to learning a foraging task. Fish learned to move a single disc off of a food tray and then learned that lifting a particular-coloured disc would result in a food reward while lifting the other disc colour would not. It took control fish an average of 28 trials to learn the foraging task, while stressed fish appeared to be slower to learn this associative task, taking an average of 34 trials, but this difference did not quite reach significance. Once the fish learned the task, their memory for the task was tested after 12, 24, 48, and 96 days. Stress did not appear to affect memory, with approximately 80% of fish, regardless of treatment, remembering the task for 12 days, and 20% of the fish tested remembering even after 96 days. This research debunks the impression that fish are not capable of anything beyond short-term memory and expands our understanding of fish cognition.

City Slickers Outperform Country Cousins: Comparing Sibling Cannibalism and Survivorship in Urban and Rural Populations of the Invasive Australian Redback Spider

Sakura Fujii[1], Jenny Nguyen[1], Lauren Pearo[1], Samia Saif[1], Maydianne CB Andrade & Isaiah CH Box

[1]*Department of Biological Sciences, University of Toronto Scarborough*

Urban populations often show distinct phenotypic differences relative to congeners from natural habitats. Some of these traits may increase urban survivorship but also invasive potential. We studied the invasive Australian redback spider (*Latrodectus hasselti*), which thrives in urban

environments and spreads via human-mediated transport. We compared the offspring of females collected from rural and urban populations within its natural range, predicting that urban spiderlings would show higher survivorship, partially mediated by higher rates of sibling cannibalism. We reared spiderlings from each population alone or in groups for one week, then moved them to separate cages. The occurrence and cause of death was monitored. We found no significant population effects on sibling cannibalism. However, despite the occurrence of cannibalism, group-living hatchlings had significantly higher survival during their first week. Urban hatchlings showed higher survivorship after three weeks, a result that was driven by a subset of family lines with significantly higher survivorship than average. Our results suggest that sibling cannibalism may arise from behavioural plasticity rather than parental habitat origin, but also that urban spiders may have heritable traits that confer increased fitness, regardless of cannibalism. These effects could elevate the success of redbacks that spread to urban habitats.

Comparative observational analysis of plant-pollinator interactions on two large green roofs in Toronto

Hargun Rekhi[1], Scott MacIvor[1,2]

[1]*School of the Environment, University of Toronto, St. George*

[2]*Department of Biological Sciences, University of Toronto, Scarborough*

Green roofs are planted to improve building cooling and water capture, but also recreation and nature access for building users, as well as biodiversity provisioning. The Cooper Koo YMCA and the Central YMCA green roofs, located at Cherry Street and Grosvenor Street, respectively, are among the largest community-accessible extensive green roofs in downtown Toronto. This research paper is the first recorded applied qualitative observational study of flowering plant and pollinator populations at these sites. Vacuum sampling, pan traps and flowering species surveys were conducted over six weeks between July to September 2024. 30 plant species were observed across the two sites, 13 of these were unique to Cherry, 8 were exclusive to Grosvenor, and 9 plants were common on both green roofs. 158 specimens were pinned, 85 belonged to Cherry and 73 to Grosvenor. At Grosvenor, 12 genera, comprised of 8 bees and 4 wasps, were identified. 14 genera, with 3 flies, 7 bees and 4 wasps, were observed at Cherry. Pollinator diversity and abundance were greater at Cherry due to its locality and higher flowering species richness. A sex ratio and pollinator composition value analysis revealed that Cherry also had a higher proportion of solitary species compared to Grosvenor. Bipartite network analysis indicates a robust plant-pollinator network on the two green roofs. Spontaneous and intentionally planted species both received visitations, with an almost equal pollination frequency being observed at Grosvenor. Although not generalizable, the findings illustrate descriptive trends which can be used as a best practice guide for green-roof infrastructure and supply feedback on policy-driven changes to the built environment. Green roofs are an invaluable addition to Toronto's urban tapestry and can facilitate biodiversity conservation when combined with diverse plant compositions that optimize these spaces as a pollinator landscape resource.

Can Urbanization Lead to Convergent Evolution in a Common Plant Defence?

Hayden T. Fargo[1], Marc T.J. Johnson[1]

[1]*Department of Biology, University of Toronto Mississauga, Mississauga*

Evolution in response to urbanization has been well documented, with examples of parallel trait expression occurring across multiple urban–rural gradients. However, it is still undetermined whether populations of different species undergo convergent evolutionary change in response to similar urban environmental pressures. To test whether urban environments can drive convergent evolution between species, we evaluate whether shared expressions of a common herbivore defence (cyanogenesis) exist across urban–rural gradients in eight European cities. Using cyanogenic cline data on white clover (*Trifolium repens*) collected by the Global Urban Evolution Project (GLUE), along with our sampling of bird's-foot trefoil (*Lotus corniculatus*), we aim to compare how the expression of cyanogenesis between species may vary across gradients of urbanization within and between cities in Europe. Through this investigation, we aim to shed light on whether shared environmental pressures in urban areas are strong enough to drive convergent evolution between two species that have independently evolved a shared defensive trait.

Investigating Demographic and Morphological Differences Along an Invasion Gradient

Anna Farley[1], Chloé Souques[2], & Sigal Balshine[1]

[1]*Department of Psychology, Neuroscience and Behaviour, McMaster University, Hamilton;* [2]*Laboratoire d'Ecologie des Hydrosystèmes Naturels et Anthropisés – Université Claude Bernard Lyon 1, Ecole Nationale des Travaux Publics de l'Etat, Centre National de la Recherche Scientifique – France*

The round goby (*Neogobius melanostomus*) is an invasive species that poses a significant threat in the Great Lakes region due to its ability to outcompete native fish for resources and its role as a contaminant vector within the food web. The present study examines demographic and morphological characteristics along an invasion gradient in the Trent-Severn Waterway with the goal of assessing which phenotypic signatures may be driving range expansion of this species. We examined this invasion gradient by collecting specimens from two populations: one from an established population ("core") and one from an invasion front ("edge"). We used baited minnow traps to sample each population, and we then collected an assortment of data from each specimen, including external and internal measurements. Comparisons between the two populations revealed that fish at the edge were larger and that males at the edge had greater energy stores. Additionally, the population at the edge was significantly male-biased, while the core population had a much more balanced sex ratio. Our results suggest that differences in demography and morphology likely play an important role in the spread of this species.

Mutualistic Benefits Plants Receive from Mycorrhizal Fungi Decline in Response to Intraspecific Competition

Brooke Walker[1]& Hafiz Maherali[1]

[1] *Department of Integrative Biology, University of Guelph, Guelph*

The outcome of mutualistic symbioses depends on the balance of costs and benefits to each partner. Mutualisms arise when benefits outweigh costs, but their outcome often varies with biological context. Specifically, antagonistic biotic interactions, such as competition, may reduce the benefits of mutualistic symbioses. We conducted a meta-analysis to determine the effect of intra-specific competition on the magnitude of mutualistic response to root inhabiting arbuscular mycorrhizal (AM) fungi. Across studies, intra-specific competition reduced plant responses to AM fungi by an average of 47%. Additionally, the negative effect of competition on plant response to AM fungi was stronger as the intensity of intra-specific competition increased. These results suggest that competition reduces the benefit that plants obtain from mycorrhizal symbioses. More broadly, estimates of plant benefit from the mycorrhizal symbiosis may be inflated when antagonistic biotic interactions such as competition are excluded from experimental designs.

Impact Of Salinization Rate on Zooplankton Communities at Two Swedish Lakes

Erin Ford[1], Zorka Dulić[2], Shelley Arnott[1], Ingrid Sassenhagen[3], Jana Isanta-Navarro[4], Jose Luis Rodriguez Gill[5], Pablo Urrutia Cordero[6], & Silke Langenheder[7]

[1]Biology, Queen's University, Kingston; [2]Agriculture, University of Belgrade, Beograd, [3]Biological Oceanography, Leibniz Institute for Baltic Sea Research, Warnemünde, [4]Biology, University of Copenhagen, Copenhagen, [5]Experimental Lakes Area, International Institute for Sustainable Development, Winnipeg, [6]IMDEA Water, Madrid, [7]Ecology and Genetics, Uppsala University, Uppsala

The increasing salinization of freshwater systems is threatening planktonic communities globally. Studies have revealed variation in response to salinization among lakes. However, little is known about how the rate of salinization exposure impacts the ability for these communities to resist the effects of chloride. Zooplankton, some of which can rapidly evolve in response to stress, may respond differently to a gradual or abrupt exposure to a toxicant. To assess how differing rates of salinization impact zooplankton community diversity indices, we conducted field mesocosm experiments in 2 low-productivity lakes. Planktonic communities were exposed to 500 mgCl^-/L at an abrupt (all NaCl added on day 1) or gradual (NaCl added in 7 equal amounts every 3 days) rate. Zooplankton were sampled throughout the 36 day experiment. Total zooplankton abundance was reduced in salt treatments relative to control, but we didn't detect an

effect of salinization rate at either lake. While most community metrics were impacted by salt, salinization rate's impact diminished over time. This suggests that while salinization rate may have a short-term influence, it's not persistent through time. These findings add to the growing evidence that increasing salinization impairs zooplankton communities, which may support the improvement of road salt use guidelines.

Novel Organism and Technology-Agnostic Supervised Machine Learning Methods Rapidly and Accurately Classify Genotype Data of *Mus musculus* and *Ovis dalli* Populations

Athena Southworth[1], Spandana Chereddy[2], Gurjit Randhawa[2], & Kathleen A. Hill[1]

[1]Department of Biology, Western University, London; [2]School of Computer Science, University of Guelph, Guelph

Classifying an organism's genetic identity using supervised machine learning (ML) methods lets researchers identify organisms and populations in time with the current high rate of genomic data acquisition. Genotyping data, a datatype awaiting rapid classification for population-scale studies, identifies major homozygous (AA), minor homozygous (BB), or heterozygous (AB) alleles for many polymorphic genomic loci. ML applied to single-nucleotide polymorphism (SNP) genotype data can produce ultra-fast, accurate classifications of organisms according to strain, population and geographic region. Machine Learning with Digital Signal Processing (MLDSP) was used to conduct classification tests for array- and sequencing-based SNP genotype data. Proof-of-principle tests done on 840 mice (*Mus musculus*) genotyped at 493,290 loci/mouse classified by breeding strain including inbred, outbred, hybrid, and recombinant mice. 299 thinhorn sheep (*Ovis dalli*) sequenced at 9,536 loci/sheep with short-read SNP sequencing were classified by geographic region. Classification of mice was 98.1% accurate at most. Classification of sheep was 85.1% accurate at most, and the classes matched the geographic region distribution in Euclidean space. As a supervised ML tool, MLDSP applied to SNP genotyping data functions well given the prior knowledge and expectations of the data. Future MLDSP applications to genotype data are planned for classification using phenotype class labels.

Quantifying Flowering Bias in Observational Community Science Data

Matthew Coffey[1] & Andrew Simons[1]

[1]Department of Biology, Carleton University, Ottawa

There has been growing interest in the utility of observation-based community science platforms, like iNaturalist, as tools to study plant phenology. However, given community science data is generally comprised of casual observations rather than targeted field sampling, it is unknown the extent to which these observations may be biased toward specific plant life-stages. Here we perform two analyses to explore whether flowering individuals are overrepresented in iNaturalist observations. First, we scored observations of 656 eudicot species in Ottawa for flower presence.

On average, 60.6% of observations of each species showed flowers, but woody species (trees and shrubs) were significantly less likely to be observed in flower relative to forbs. In our second analysis, we explore whether observations are biased toward flowering. We expect that species with longer flowering periods should be observed in flower more frequently. We use phenological data from National Ecological Observatory Network (NEON) sites to define each species' flowering duration and then scored iNaturalist observations within a 50km radius of the NEON site for flowers. We then explore whether species are observed in flower more often than expected given their flowering duration. This analysis is ongoing; however, we will be able to share preliminary results at OE3C.

Impacts of Density and Spatial Complexity of Mating Environments on Male Harm Expression in *Drosophila melanogaster*

Kehinde Osijo[1]& Howard Rundle[1]

[1]*University of Ottawa, Ottawa*

Male harm occurs when traits in males that increase their reproductive success reduce female fitness as a side-effect. Male harm is common, generating selection in females counter its effects, which may in turn reduce male fitness. Such sexually antagonistic selection can drive a coevolutionary arms race that may be a driving factor in the evolution of both sexes. In *Drosophila melanogaster*, many lab studies have shown the existence of male harm, but recent work has shown that its expression can be drastically reduced, or even eliminated, when sexual interactions and mating occurs in an environment that is lower density and structurally more complex than traditional Drosophila rearing vials. Here I follow up on this to separately test the effect of fly density and structural complexity of the mating environment in mediating male harm. To do this, I performed two two-way factorial assays that manipulated male exposure and the factor of interest (fly density or structural complexity). Results showed that male harm did not differ between low vs. high fly density, but was significantly reduced (eliminated) by increased structural complexity. Structural complexity likely gives females with increased control over sexual interaction, providing choices as to where to forage and lay eggs, as well as refuges from unwanted male attention. This suggests that simple choices like the rearing environment used for common laboratory model systems have profound impacts on the importance we ascribe to fundamental evolutionary and behavioral phenomena.

Long Non-coding RNA Diversity in AMF Heterokaryons and Homokaryons

Fiona Hutchison[1], Jordana I.N. Oliveira, Ken Mugambi, & Nicolas Corradi

[1]*Department of Biology, University of Ottawa*, *Ottawa*

Arbuscular Mycorrhizal Fungi (AMF) form symbiotic relationships with most plant species, facilitating nutrient exchange. In *Rhizophagus irregularis*, the model AMF species, chromosome-level assembly has revealed significant variation in protein-coding genes, suggesting similar diversity may also affect regulatory RNAs, including long non-coding RNAs (lncRNAs). This study aimed to identify and classify lncRNAs across nine *R. irregularis* strains to improve understanding of AMF genomic regulation. We predicted the coding potential of transcripts we acquired through Kinnex PacBio sequencing by training well known *Candida* lncRNAs as reference. BLASTn was used to determine similarity of these putative *R. irregularis* lncRNAs with other organisms through comparisons with available lncRNAs datasets. On average we found 870 lncRNA genes for each strain, generating on average 1335 transcript isoforms with an average length of 699.63bp. We found that around 72% of lncRNA were shared across all strains, whereas 1.2% are strain specific. 56 of the AMF lncRNA showed at least 83% similarity with known lncRNA from fungi and other organisms. Our findings indicate an abundance of lncRNAs in AMF. We predict that these molecules play a role in strain-specific symbiotic interactions and gene regulation. This research is a steppingstone in our understanding of lncRNAs in AMF and their potential role in gene expression, with implications for agriculture and ecosystem management.

Investigating the Thermal Melanism Hypothesis in the Invasive Asian Lady Beetle (*Harmonia axyridis*)

Marcus Gauthier[1] & Tom Sherratt[1]
[1]*Department of Biology, Carleton University, Ottawa*

The Asian lady beetle, *Harmonia axyridis*, is a highly invasive species in North America, where it has displaced native lady beetles, disrupted local ecosystems, and become an agricultural and household pest. By analyzing thousands of citizen science observations of *H. axyridis* across North America, this research aims to map the distribution of melanic and non-melanic morphs and examine how the level of melanism correlates with environmental factors such as temperature and latitude. To streamline this analysis, a customized pipeline was developed to extract iNaturalist observations, remove image backgrounds, and quantify melanism as the percentage of the elytra covered by dark spots. This allowed for large-scale, standardized measurement of melanism across the species' range. Citizen science data has shown the northern limit of *H. axyridis* in North America, offering key insights into the invasion limits and ongoing range expansion of the species. By integrating citizen science data, field sampling, and laboratory analysis, this study provides new insights into the environmental, climatic, and ecological factors shaping the invasive success and adaptive evolution of *H. axyridis*.

Presentation Abstracts

The Good, the Bad, and the Mites: Unraveling the Relationship Between Burying Beetles and Phoretic Mites

Anjalie St-Louis-Hodgins[1], Shannon Marginson[1], & Dr. Frances Bonier[1]

[1]*Department of Biology, Queen's University, Kingston*

Ecosystems are delicate networks of species interactions that shape ecological and evolutionary processes. From mutualisms to antagonisms, these interactions often dictate who thrives and who fails. Yet, many relationships in nature are not fixed, they shift with environmental conditions and individual traits. Understanding when and why these shifts occur is essential for predicting ecological outcomes. The relationship between burying beetles (*Nicrophorus orbicollis*) and their phoretic mites (*Poecilochirus* spp.) exemplifies this complexity. Despite a long co-evolutionary history, whether these mites are harmful, neutral, or beneficial remains unresolved, with conflicting research suggesting a context-dependent relationship. Given this variability, how can we better assess these interactions and create a framework for understanding such fluctuating dynamics? To explore this, I conducted competition trials in which same-sex beetles competed for a shared resource at different temperatures. In the treatment trials, one beetle carried a pre-breeding mite load; in controls, neither had mites. The results hint at surprising shifts in competitive dynamics, revealing how context can influence competitive hierarchies. I also conducted grooming assays to assess how beetles respond to mites, offering insight into behavioural and evolutionary dynamics. This research takes a multi-perspective approach and highlights how behavioural and environmental factors interact to shape species relationships.

Helminth parasitism of rodent hosts in Algonquin Provincial Park, Ontario, Canada.

Sydney Miller[1] , Jeff Bowman[1] , Albrecht Schulte-Hostedde[1]

[1]*School of Natural Sciences, Laurentian University, Sudbury*

Helminths are gastrointestinal parasites that impose physiological costs on their hosts, influencing body condition, immune function, and overall fitness. This study examines helminth infections in three rodent species: deer mice (*Peromyscus maniculatus*), red-backed voles (*Myodes gapperi*), and woodland jumping mice (*Napaeozapus insignis*), in Algonquin Provincial Park, Ontario, Canada. We hypothesized that helminth diversity and infection intensity vary among host species and are influenced by individual traits such as age, sex, reproductive condition, and body mass. We predicted that larger, reproductively active individuals harbour greater parasite diversity and burden. Fecal samples were collected from each species and analyzed using the McMaster Technique to quantify helminth egg counts and assess infection intensity. Parasite diversity was measured using Simpson's Individual-Level Diversity Index, species richness, and total eggs per gram (EPG). Results revealed significant host-specific differences, with red-backed voles exhibiting the highest parasite burden, while parasite diversity was strongly linked to host traits. These findings underscore the importance of integrating multiple diversity metrics to understand parasite-host dynamics, offering broader ecological insights into how helminth infections shape small mammal communities.

Patterns of Parasitism in an Urban Population of White-Footed Mice (*Peromyscus leucopus*)

Albrecht I. Schulte-Hostedde[1], Sabrina Lepage[1], and Luigi Richardson[1]

[1]*School of Natural Sciences, Laurentian University, Sudbury*

Parasites are fundamental to ecosystems, playing a key role in trophic regulation in part through the costs they impose upon their hosts. The creation of novel habitats through urbanization can lead to changes in patterns of parasitism from host populations as well as expose human populations to potential zoonotic threats. We collected ectoparasites and morphological measurements from white-footed mice (*Peromyscus leucopus*) from areas of varying degrees of urbanization in the Greater Toronto Area. We assessed patterns of prevalence among the major groups of ectoparasites encountered (ticks, mites, lice, and botflies), and examined the effects of sex and age on the prevalence and diversity of these groups of parasites. The cost of parasitism was examined by relating body condition to parasite load. Finally, we used a proxy measure of urbanization (% impervious surface) to assess the effects of urbanization on parasite communities. The most prevalent parasite were mites, with few botflies and lice. Males had generally more diverse parasite communities than females, and urbanization had a significant effect on patterns of parasite prevalence and intensity. These findings help better our understanding of ectoparasite patterns of infestation and emergence and can help inform studies of disease ecology.

Vectors, Biotopes, and Seasonal Trends of Endemic Mosquito Arboviruses in Eastern Ontario, Canada (2017-2021)

Marc Avramov[1], Vanessa Gallo[1], Emilia Craiovan[2], Heidi Wood[3], Heather Coatsworth[3], Mahmood Iranpour[3], David R. Lapen[2], Catherine I. Cullingham[1], Antoinette Ludwig[4]

[1] *Department of Biology, Carleton University, Ottawa;* [2] *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa;* [3] *National Microbiology Laboratory, Public Health Agency*

of Canada, Winnipeg; [4] National Microbiology Laboratory Branch, Public Health Agency of Canada, St. Hyacinthe

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

The Effects of Air Pollution on Inherited Mutation Rate

Irtaqa Arif[1,2], Elysia Fuller Thomson[3], Matthew D. Adams[3], Marc T.J. Johnson[1], Rob W. Ness[1]

[1]Department of Biology, University of Toronto Mississauga, Mississauga; [2]Ecology & Evolutionary Biology, University of Toronto, Toronto; [3]Department of Geography, University of Toronto Mississauga, Mississauga

Urbanization results in increased levels of air pollution, which has been implicated in somatic and germline mutations in humans and other animals. However, air pollution's impact on somatic and inherited mutation rates in plants remains unexplored. Here, we investigate the effects of air pollution on plant mutation rates using whole genome sequence data analysis of plants grown across a pollution gradient in urban and non-urban locations. We answered the question: Does air pollution increase the inherited mutation rate in plants? Over the summer of 2022, replicated clones of cross-compatible white clovers were paired with air pollution samplers and distributed across Hamilton covering a gradient of pollution levels. We collected leaf tissue samples throughout the summer, performed cross-pollination and collected seeds. We then grew and sequenced the F1 progeny to identify *de novo* mutations correlating to measured levels of air pollution. A total of 422 verified inherited mutations were identified, the mean mutation rate was 1.103×10^{-8} (95% CI: 9.807×10^{-9}, 1.226×10^{-8}) per base pair. Preliminary analyses revealed that pollution levels did not influence mutation rate. By investigating this topic, we can better understand the impact of urban cities on the molecular level and how these can impact future generations.

Using Native Halophytes to Mitigate Road Salt Affected Soils in Southeastern Ontario: A Pilot Scale Phytoremediation Field Study

Amanda Chiasson[1], Lauren Nawroth[1], & Barbara Zeeb[2]

[1]*School of Environmental Studies, Queen's University, Kingston;* [2]*Department of Chemistry and Chemical Engineering, Royal Military College of Canada, Kingston*

In Canada, the application of road salt (i.e., NaCl) is a major source of anthropogenic salt to the environment. These salts travel through the soil and make their way into freshwater systems where they cause adverse impacts on aquatic life. Salt-tolerant plants (i.e., halophytes) are able to accumulate salt from the soil in their aboveground biomass, making them ideal candidates for mitigating the impact of road salt runoff. A pilot scale road-side field site was established in 2022 in southeastern Ontario, to determine the phytoremediation potential of multiple native halophyte species. From 2022-2024, plant and soil samples were collected, and plant biomass, plant Cl^- uptake and soil [Cl^-] were determined. Soil [Cl^-] across all plots decreased – almost to background levels (20 ppm) – from 336 ± 35 ppm Cl^- to 49 ± 12 ppm Cl^- between 2022 and 2024. The majority if this chloride loss was likely due to the migration of Cl^- through the soil away from the site. However, the two best performing species, *Sporobolus michauxianus* and *Panicum virgatum*, accumulated significant levels of Cl^- in their aboveground tissues and were responsible for the removal of ~15% and 20% of the Cl^- lost from their respective plots in 2024.

How I Fought My Mother (and siblings): Parent-Offspring Conflict and Sibling Rivalry in the Big Brown Bat (*Eptesicus fuscus*)

Tang Tang Guo**[1]**, Shane Seheult**[1]**, Sigal Balshine**[1]**, Paul Faure**[1]**

[1]*Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton*

Parent-offspring conflict occurs when parents and offspring disagree over allocation of parental resources. Conflict may also arise between siblings over resources, including food (i.e., sibling rivalry). We suggest big brown bats (*Eptesicus fuscus*) are a valuable model for studying both types of conflicts because: (1) In North America, *E. fuscus* birth singletons in the west and twins in the east, and (2) At Canada's only captive breeding colony of insectivorous bats, we can closely observe pup development and mother-pup interactions. We used growth rate (i.e., Δmass [g]) as a proxy for sibling rivalry and compared siblings (n = 18) across the first 30 days of life. Parent-offspring conflict was assessed by recording behaviours of pups (n = 26) and mothers (n = 13) for 5 minutes, first alone and then with a sibling, across six developmental timepoints. We also measured pup mass change (n = 9) during 90-minute nursing bouts across three timepoints. Same-sex and mixed-sex twins had similar Δgrowth rates. Mothers showed fewer guidance behaviours and initiated fewer interactions over time. Mass gain during nursing was lower in late development. Understanding these dynamics offers insight into resilience against stressors (i.e., reproduction and disease) and informs conservation of endangered bats.

Declining ice duration and changing ice quality drive key ecological changes in Wisconsin lakes

Phoenix Sandrock, Joshua Culpepper, Arnab Shuvo, & Sapna Sharma

Ice conditions in lakes are changing worldwide. Shorter ice duration and changing ice quality are altering the structure and function of ice-covered lake ecosystems. However, lake ecosystem responses to ice loss remain poorly understood. Current research focuses on individual lakes and short time series. An analysis of under-ice ecology in diverse lakes over decades is necessary to understand how lakes will respond to changing ice conditions. We examined 11 lakes across Wisconsin, USA, varying in size from 0.6 ha to 3900 ha, from 1982 to 2023. Over the past 40 years, ice duration declined by 7.6 days on average. Shorter ice duration was associated with colder under-ice water temperatures, deeper photic depths, and lower chlorophyll a concentrations. Lower snow depths, a main driver of ice quality, also caused deeper photic depths and lower chlorophyll a concentrations. Changes in these key ecological parameters could alter lake ecosystem function over time, altering lake trophic status, driving shifts in algal and planktonic communities, and changing the timing of growth and breeding periods for aquatic organisms.

Lichens of Dinosaur Provincial Park, Alberta

AJ Deneka[1,2], Troy McMullin[1], and Myron Smith[2]
[1] Canadian Museum of Nature, Ottawa; [2] Carleton University, Ottawa

Lichens are composite organisms composed primarily of a fungus and one or more photosynthetic partners (algae and/or cyanobacteria). They have many ecological roles, including soil formation and stabilization, moisture retention, carbon and nitrogen fixation, and providing shelter, camouflage, and food for animals. Lichens can grow in habitats and on substrates unsuitable for vascular plants, and frequently compose a significant portion of the vegetation in extreme environments such as badlands. Badlands are a terrain type often associated with prairie ecosystems and characterized by extensive erosion, with steep slopes and little soil making them unsuitable for human development and agriculture. Despite their ecological importance, little is known about the lichens of the prairies and badlands of Alberta. Because Alberta's badlands have gone largely undisturbed while the surrounding prairies have been converted to farmland, they may be critical refugia for prairie species sensitive to anthropogenic disturbance. To contribute to our knowledge of prairie lichens, we conducted a lichen survey in Dinosaur Provincial Park (DPP), Alberta in 2024 which yielded 145 species. Newly reported are 28 species for Alberta and two for Canada (*Xanthoparmelia neochlorochroa* and *Lecania constricta*). Of the species previously known from the province, 90 are new to DPP and 11 are listed as "imperiled" or "critically imperiled" in Alberta. This study highlights the importance of

floristic surveys in providing baseline biodiversity data, crucial information necessary for successful conservation efforts in a changing climate.

Mounds of Opportunity or Missed Potential? Importance of Implementation in Conservation Policy and Management: A Case Study for Artificial Nesting Mounds in Eastern Ontario

Charlotte M. Galloway[1], Alexander Stone,[3] Christina M. Davy[1], & Amanda Martin[1,2]

[1]Carleton University, Ottawa, Canada; [2]Environment and Climate Change Canada, Ottawa;

[3]National Capital Commission, Ottawa, Canada

Conservation tools such as road underpasses, fencing, and artificial nesting mounds are commonly employed to reduce the impact of anthropogenic activity on wild turtle populations. However, the effectiveness of these tools depends on how they are implemented and can lead to negative implications if done inappropriately. This study investigated the effectiveness of artificial nesting mounds as management tools to increase recruitment for local turtle populations. Six nesting mounds were installed in the National Capital Region in the spring of 2024 as compensation for lost nesting habitat after mitigation fencing was installed along a known turtle crossing site. Nesting mounds were monitored using wildlife cameras from May to August. We quantified the use of mounds by nesting turtles, the number of successfully laid nests, and whether environmental parameters would allow successful nesting. We found that nesting mounds were rapidly and actively investigated as potential nesting sites by Snapping Turtles (*Chelydra serpentina*) and Painted Turtles (*Chrysemys picta*). Unfortunately, the aggregate composition used in the mounds presented a barrier to successful nesting, and turtles ultimately nested in the more suitable substrate adjacent to the mounds. This project highlights the importance of the implementation stage of conservation action and follow-up monitoring to evaluate outcomes.

The Limits and Costs of Plasticity in Response to Pollinator Decline and Drought

Caelen McCabe[1] & Christina M. Caruso[1]

[1]Department of Integrative Biology, University of Guelph, Guelph

Pollinator declines in North America have forced some wildflowers to plastically extend their floral longevity to increase the likelihood of pollen receipt. However, drought may limit this plasticity by reducing petal turgor pressure. Additionally, there could be a reproductive cost associated with extended longevity if floral maintenance costs exceed the reproductive benefits of extended longevity. To test how drought influences the limits and costs of this plasticity, *Lobelia siphilitica* plants were exposed to droughted or well-watered treatments just before the

onset of flowering. Floral longevity was measured in five flowers per plant, and the cost of longevity was assessed by comparing seed counts from flowers hand-pollinated on the first and fifth days of the female phase. Floral longevity under drought was 18% (~2.5 days) shorter compared to well-watered plants, indicating drought limits plasticity. However, there was no significant difference in seed production between early- and late-pollinated flowers across treatments, suggesting that the cost of extended longevity is unaffected by drought. These findings indicate that while drought limits plasticity in floral longevity, it does not affect the reproductive cost. Therefore, in water-limited environments, plasticity in floral longevity may be maladaptive, potentially reducing the likelihood of short-term population persistence as pollinators decline.

Territorial-sneaker games with non-uniform interactions and female mate choice

Sherratt[1] TN, Beatty[2] CD, Dewan[3] I, Di Iorio[1] K, Finkelstein[1] I, Loeffler-Henry[1] K, Miller[1] M, Para[1] F, Raposo M[1], Sherratt[4] F.

[1]Department of Biology, Carleton University, Ottawa; [2]Program for Conservation Genomics, Stanford University, Palo Alto, CA, USA; [3]Department of Evolutionary Theory, Max Planck Institute for Evolutionary Biology, 24306 Plön, Germany; [4]Department of Neuroscience, Carleton University, Ottawa

Territorial-sneaker polymorphisms are common in nature. To understand how they evolve in males, we developed a game theoretical model analogous to the classical Hawk-Dove model, but with two important differences. First, we allowed non-uniform interaction rates of strategies to account for the possibility that some interactions are more frequent than others. Second, we allowed females to exhibit a preference for one type of male and thereby choose mates adaptively. The model confirms that there is a broad range of conditions under which alternative mating strategies will arise. We applied the model to understand the genetic polymorphism in adult male Mnais damselflies (Zygoptera). Here, orange-winged adult males defend oviposition sites and mate with females when they arrive, while clear-winged 'sneaker' males are non-territorial and opportunistically mate with females. Intriguingly, in allopatry, the males of Mnais costalis and M. pruinosa both exhibit the same orange-clear winged polymorphism but where the species co-occur, males of M. costalis evolve orange wings while males of M. pruinosa have evolved clear wings. To understand this phenomenon, we extended our game-theoretical model to two interacting species. We show that when females of the rarer species change their male preferences to facilitate species discrimination, it can generate distinct morphs in the two species.

Ecological Drivers of Fruit Colour Evolution in *Solanum*: The Roles of Frugivory and Abiotic Environment

Olivia Demetrakopoulos[1], Edeline Gagnon[1]

[1]*Department of Integrative Biology, University of Guelph, Guelph, ON*

The dispersal syndrome hypothesis proposes that animal dispersers' preferences play a key role in selection and evolution of specific fruit traits, resulting in distinct "dispersal syndromes" across different plant taxa. However, distinguishing the selective pressures of frugivory from those of the abiotic environment is challenging, especially given that trait evolution is often constrained by phylogeny. This study examines the genus *Solanum*, a clade of c.1255 species, to assess how fruit traits are shaped by frugivory and abiotic factors, while accounting for phylogenetic relatedness. Fruit trait data were extracted from taxonomic literature and analyzed for inter-trait correlations and phylogenetic conservatism. Global patterns of fruit colour were then modeled using frugivory maps of birds, bats, and other mammals, alongside abiotic variables. Analyses revealed correlations that provide moderate support for the evolution of dispersal syndromes in *Solanum*. Among the traits examined, fruit colour was the least phylogenetically conserved, suggesting it is more evolutionarily labile and responsive to ecological selection. Modelling further showed that fruit colour is influenced by frugivory and temperature. These findings support the dispersal syndrome hypothesis but also suggest that frugivore-driven selection on fruit colour may be overridden by selection for traits that mitigate abiotic stress in cold environments.

Escape Artists and Eye Spots: Arthropod Predators as Selective Agents for High Inference Signals

Karl Loeffler-Henry

It has long been understood that prey often provide information to would-be predators in the form of chromatic signals that may dissuade attack. Much research in this area has assumed that avian predators are the primary selective agents for these antipredation signals. However, arthropod predators often far outnumber birds in many communities and impose significant selective pressure on other arthropods. Recent behavioral experiments have demonstrated that arthropods can select for antipredation signals in other arthropods. However, this work has largely been limited to signals that indicate that the prey is unpalatable. Learning to associate a conspicuous chromatic signal with an unpleasant taste does not intuitively appear to be a cognitively demanding task. We still know relatively little about the capacity of arthropod predators to respond to more cognitively demanding stimuli. Many insects utilize antipredation signals that convey more complex information to would-be predators than just the presence of chemical defense. These signals include indicators of extreme escape ability and eye spots that

are thought to dissuade predation by making the prey appear intimidating. Here, we test if visual arthropod predators can select for these signals in other arthropods. Our results demonstrate that in both cases, arthropod predators show a behavioral response that is remarkably similar to that exhibited by avian predators, calling into question basic assumptions about the cognitive capabilities of invertebrate predators.

Evolution of Territoriality in Odonates: A Phylogenetic Analysis

Finkelstein[1] I, Beatty[2] C.D., Kang[3,4]C, Loeffler-Henry[1] K, Sherratt[1] T.N.

[1] *Department of Biology, Carleton University, Ottawa;* [2]*Program for Conservation Genomics, Stanford University, Palo Alto, CA, USA;* [3]*Department of Animal Science and Technology, Konkuk University, Seoul, South Korea;* [4]*Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, South Korea*

Many, but not all, species of odonates (dragonflies and damselflies) exhibit territoriality. In species where it occurs, this territoriality is typically seen in males who defend oviposition sites from competitors and mate with females when they arrive. We describe the first systematic collation of the prevalence of territoriality in odonates. We follow it up with a phylogenetic analysis of the possible causes and consequences of territoriality. Our ancestral state reconstruction suggests that the common ancestor of all damselflies was non-territorial while the common ancestor of dragonflies was territorial. However, territoriality has been gained and lost several times throughout the phylogeny. Initial results indicate that, as expected, species with non-contact mate guarding tend to be territorial since this allows males to continue to defend their territories while ensuring paternity. However, contrary to our predictions, territoriality does not correlate with perching behaviour, which is energetically efficient and was predicted to have allowed more energy resources to be devoted to defending a territory. Additionally, territoriality does not correlate with exophytic oviposition, which is the faster oviposition method and was predicted to make territorial defence more cost-effective. Collectively, our results encourage a reassessment of our understanding of the ecological and evolutionary consequences of territoriality.

Natural Selection for Genetic Resistance to Domestic Anticoagulant Rodenticides in Ontario’s House mice

Luigi Richardson[1], Catherine Cullingham[2], Albrecht Schulte-Hostedde[1]

[1]*Laurentian University, Sudbury,* [2] *Carleton University, Ottawa*

Genetic resistance to anticoagulant rodenticides is a world-wide phenomenon, never investigated in Canada’s commensal rodents. In-vivo resistance was examined in the 1980s, but studies of the genetic basis of this resistance are entirely absent in Canada. Genetic analysis can allow us to track the evolution of resistance and how selective pressures and population connectivity can

influence its presence and spread. We sequenced exon 3 of the VKORC1 (vitamin K epoxide reductase, rodenticide resistance gene) of House mouse samples obtained from Pest management professionals in Southwestern, Central and Eastern Ontario. We found extremely high prevalence of 2 non-synonymous single nucleotide polymorphisms previously found in Europe, the Middle East and USA, known to cause extreme resistance to first and some second-generation anticoagulants. We conclude that uncoordinated rodenticide usage has selected for extreme resistance throughout Ontario, but strains and zygosity vary geographically. Therefore, chemical control of the House mouse with domestic products is likely completely impractical across the province. This knowledge will assist professional pest management operators in choosing the right chemicals for their House mouse control operations.

Examining the effects of traits on tree community productivity during drought

Magalie Galarneau[1]

[1]Department of Biology, University of Waterloo, Waterloo

The positive relationship between species richness and productivity found in forests around the world may be explained by two mechanisms: complementarity effects and selection effects. Both mechanisms rely on traits, whereby the diversity of traits (under complementarity effects) or the presence of specific trait values (under selection effects) increase productivity. However, the assumption that traits underpin the species richness-productivity relationship has not been tested. By using an experimental design of temperate tree communities with a fixed species richness but varying in trait diversity, this study tested which traits are responsible for the species richness-productivity relationship in temperate tree communities, and whether they act via the complementarity or the selection effect. In addition, two types of water stress were applied to the tree communities to examine the effects of environmental stress on the species richness-productivity relationship and its underlying traits.

In the Shadow of Selection: Investigating the Role of Epistasis, Age, and Sex on Mutation Accumulation

Ronni Prince[1], Imran Sayyed[1], & Adam Chippindale[1]

[1]Biology, Queen's University, Kingston

Aging presents an evolutionary paradox: while natural selection favours traits that enhance survival and reproductive success, senescence – the physiological decline associated with age – persists. The mutation accumulation theory posits that late-acting deleterious mutations can persist in populations because the force of natural selection weakens with age. Although widely accepted, this theory traditionally assumes additive effects of mutations. However, emerging

evidence highlights the importance of non-additive interactions (epistasis) in shaping the mutation accumulation process. Despite these advances, empirical tests for non-additivity within this framework remain limited, especially regarding sex-specific effects as well as changes with age. In this study, we utilized *Drosophila melanogaster* lines that have been accumulating mutations for over 30 generations. Specifically, we compared sex-specific fitness at early and late life stages and examined differences between lines with accumulated mutations across the entire genome versus those limited to the autosomal genome. Our research aims to disentangle the complex interactions between accumulated mutations, revealing how they influence aging through age- and sex-specific effects. The findings of this study have the potential to refine our understanding of the evolutionary mechanisms underlying aging, offering new insights into the interplay between genetic architecture, epistasis and senescence.

Genomic Assessment of the Validity of a Recently Described Butterfly Species, the Asher's Azure (*Celastrina asheri*)

Fangming Teng[1,2], Jason Weir[1,2]

[1]Department of Biological Sciences, University of Toronto Scarborough, Toronto; [2]Department of Ecology and Evolutionary Biology, University of Toronto, Toronto

Celastrina asheri, a new azure species in the northwestern United States and southwestern Canada, was described in 2022 based on phenotypic differences from *Celastrina echo and Celastrina lucia*. It is sympatric with *C. echo* in the northeastern portion of *C. echo*'s range, and narrowly sympatric with *C. lucia* along the Rocky Mountains. No study has investigated *C. asheri* genetically, leaving uncertainty about whether they represent a distinct species or merely a color morph of *C. echo* or a southern range extension of *C. lucia*. In this project, we analyzed the whole-genome data of *C. asheri*, allopatric and sympatric populations of *C. echo*, and *C. lucia*. We found that *C. asheri* is a valid species that is genetically distinct from *C. echo* and *C. lucia,* despite some evidence of introgression from *C. lucia*. Additionally, there is evidence of gene flow between *C. asheri* and sympatric *C. echo*, but the two species remain distinct in regions outside the Rocky Mountain. The *C. echo* population at the Rocky Mountain (*C. echo nigrescens*), appears to represent a hybrid species between *C. echo*, *C. lucia,* and *C. asheri*.

Bergmann’s rule in non-avian reptiles revisited: Turtles still follow it, but lizards and snakes don’t reverse it

Erin Huang[1] & Njal Rollinson[1]

[1] Department of Ecology & Evolutionary Biology, University of Toronto

Bergmann's rule is an intraspecific pattern of increasing body size with increasing latitude or decreasing environmental temperature. Mammals and birds broadly follow Bergmann's rule, but whether reptiles generally follow the rule is unclear. In an influential paper, Ashton & Feldman (2003) attempted to clarify body size trends of reptiles by conducting an analysis of 38 species of chelonians and 139 species of squamates, concluding that chelonians follow Bergmann's rule and squamates reverse it. However, the authors used a vote-counting analysis, which is an inadequate method which does not account for the magnitude of effects or sample sizes. We revisit this classic study using formal meta-analytic techniques. Our systematic review identified a total of 24 papers across 26 species and 66 effect sizes of the relationship between body size and latitude for reptiles. We confirm that chelonians follow Bergmann's rule, but we find that squamates do not reverse the rule. Rather, lizards and snakes showed variable temperature/latitude–size responses, and the mean effect sizes were centred around zero. The difference between turtles and squamates in body size responses to temperature/latitude may be attributed to differences in body plan. Due to their shell and voluminous body, chelonians have an increased capacity for thermal inertia. Thus, physiologies that modify heating and cooling rates may be effective for chelonians, such that body size may coevolve with the thermal environment. However, squamates have narrow and elongated body plans that restrict their heat retention capacity, where specialised physiologies that modify heating and cooling rates would be ineffective. The present study clarifies reptile body size clines and provides insight into their underlying mechanisms.

Narwhal Migration and Foraging Behaviours in Baffin Bay: A Multi-Elemental Approach Using Stable Isotopes and Trace Metals

Shanie Brault Nikolajew[1], Peter Crockford[2], Petrus Le Roux[3], Cortney Watt[4], Justine Hudson[4], Zoe Landry[1,5], Danielle Fraser[2,5,6,7] & Clément Bataille[1,8]

Earth Sciences, Carleton University, Ottawa; [3]Department of Geological Sciences, University of Cape Town, Cape Town, 7700, South Africa; [4] Fisheries and Oceans Canada, Winnipeg; [5] Palaeobiology, Canadian Museum of Nature, Ottawa; [6] Department of Paleobiology, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA; [7] Department of Biology, Carleton University, Ottawa; [8] Department of Biology, University of Ottawa, Ottawa[1]Department of Earth and Environmental Sciences, University of Ottawa, Ottawa, ON, K1N 6N5; [2]Department of

Arctic marine ecosystems are changing rapidly due to anthropogenically-driven climate change and increased human presence in the Arctic. Faced with rapid degradation of marine habitats, many marine mammal species have modified their mobility and diet in response to the ongoing environmental changes. The narwhal (*Monodon monoceros*), with its restricted range, selective diet, and strong dependence on sea ice, may be particularly vulnerable to these environmental shifts and could experience behavioral shifts. Therefore, there is a need to improve our understanding of narwhal ecology in order to detect any potential alterations in their behavior in response to ongoing climate change. In this study, we investigate the use of several isotopic and elemental proxies to reconstruct narwhal diet and mobility over time, offering novel insights into whether narwhal migratory and foraging strategies have shifted in response to environmental change.

Narwhal tusks are continuously growing teeth, preserving geochemical signatures that potentially offer a chronological record of individual movement and foraging behaviors over multiple decades. Several isotopes vary spatiotemporally in seawater and are incorporated into marine mammal tissues. Oxygen isotopes ($\delta^{18}O$) reflect seawater temperature and proximity to sea ice, while carbon isotopes ($\delta^{13}C$) vary with net primary productivity, differentiating coastal from offshore habitats. Other geochemical markers are more directly linked to foraging ecology, such as nitrogen isotopes ($\delta^{15}N$), and to a lesser extent carbon isotopes ($\delta^{13}C$). These isotopes fractionate with trophic level and can reflect shifts in dietary sources. Other non-traditional isotopic and elemental markers (^{143}Nd, $\delta^{138}Ba$, ^{206}Pb, and Hg concentrations) are thought to reflect water mass origin, salinity gradients, pollution exposure, and trophic structure. Together, these proxies could offer a comprehensive approach to reconstruct narwhal mobility and habitat use over time.

In this study, we test the potential of these different tracers for geolocation and foraging reconstruction by analyzing isotopes in two modern narwhal tusks from individuals of known sex, origin, migratory patterns, and of estimated age through growth layer group (GLG) counts. We collected 24 annual samples and 10 seasonal samples from each individual to generate multi-isotope profiles. We then compared the isotope profiles of each individual to existing isotope baselines within the foraging range to assess the geolocation and foraging information reflected in each of these tracers.

Our preliminary results show that $\delta^{18}O$, $\delta^{13}C$, and $\delta^{15}N$ differ between the two narwhal individuals. This likely reflects the distinct isotopic environmental baseline and foraging strategy of each individual belonging to different populations. Indeed, the $\delta^{18}O$ values of the Baffin Bay population are lower, reflecting their year-round location at higher latitudes and their longer residence in Baffin Bay open waters. The Hudson Bay population remains in southern coastal highly productive waters year-round, reflected in their higher $\delta^{13}C$ and $\delta^{18}O$ values. Elevated $\delta^{15}N$ values for the northern individual prior to 2003 indicate a diet dominated by higher-trophic level fish, consistent with the Baffin Bay population's winter reliance on Greenland halibut. Interestingly, its isotopic profile shifts after 2003 simultaneously with rapid and permanent losses of sea ice in the Canadian Archipelago and starts to resemble that of the southern population's diet with lower $\delta^{15}N$ values. This shift suggests that in response to climate change, the narwhals of the Baffin Bay population might be changing their foraging behavior, increasingly relying on bottom-dwelling prey as they spend more time in the ice-free coastal waters of the Canadian Archipelago.

These promising results suggest that multi-isotope profiling of modern and historical narwhals might provide key background data about the ecology of narwhal populations and their responses to loss of sea ice cover, progressive ocean warming, and other anthropogenic impacts.

Isotope Geolocation of the Defoliating Spruce Budworm in the Boreal Forest: Testing the transmission of isotopes from trees to insect wings

Brent Holmes[1], Felipe Dargent[2], Marrissa Miller[1,3], Naomi Wiseman-Beese[4], Megan Reich[1], Jean-Noel Candau[2], and Clement Bataille [1,4]

[1]Department of Biology, University of Ottawa, Ottawa, ON, Canada; [2]Great Lakes Forestry Centre, Canadian Forest Service, Natural Resources Canada, Sault Ste. Marie; [3]Department of Biology, Carleton University, Ottawa; [4]Department of Earth and Environmental Sciences, University of Ottawa, Ottawa

The eastern spruce budworm moth (*Choristoneura fumiferana*) is the most severe pest in North American boreal forests, substantially defoliating spruce and fir stands. Repeated outbreaks every 30-40 years, lead to adverse socio-economic effects, heightened risk of forest fires, increased CO_2 emissions, and diminished carbon capture capacity. Outbreaks are believed to stem from irregular migrations events of large swarms of gravid moths traveling long distances from their original sites to colonize new areas. Isotopes offer an effective approach for tracking the migration and population interconnectivity of insect species, but the relationships between the isotopic composition of spruce budworm moths and their host plants under different environmental conditions remains uncertain. We aim to explore the cycling of hydrogen, carbon, nitrogen, sulfur, and strontium isotopes from host trees to moths, to assess the possibility in applying those isotopes for provenance. In collaboration with National Resources Canada, we conducted field rearing experiments raising spruce budworms on selected trees across Eastern Canada, representing diverse environmental, climatic, and geological conditions. We measured hydrogen, carbon, nitrogen, sulfur, and strontium isotopes on the tissues of adult moths raised in field conditions as well as on their host tree; and found strong correlations between the tree and moth isotope composition. This demonstrates that several isotopes transmit from host trees to moths in a predictable manner, particularly sulfur and strontium. This research lays the foundation for utilizing multi-isotope geolocation to track the migration of spruce budworm throughout eastern Canada, advancing our comprehension of the pest's ecology and enhancing management approaches.

Assessing the Effects of Lead Exposure on the Flight Ability of Painted Lady Butterflies

Megan S. Reich[1], Gerard Talavera[2], Niclas Backström[3], Clement Bataille[4]

[1]Department of Biology, University of Ottawa, Ottawa; [2]Institut Botànic de Barcelona (CSIC), Barcelona, Spain; [3]Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden; [4]Department of Earth and Environmental Sciences, University of Ottawa, Ottawa

Lead is a ubiquitous component of the natural environment, but anthropogenic activities such as smelting, manufacturing, and the use of leaded gasoline have added this heavy metal to the biosphere, exposing both people and animals. While high doses of lead can cause mortality, low-level exposure often leads to sublethal effects. In insects, these effects can include poor mobility and orientation abilities. Migratory insects, which may have greater exposure to lead as they migrate through novel habitats, are particularly vulnerable because successful migration depends on effective flight. To investigate the sublethal effects of lead exposure in migratory butterflies, *Vanessa cardui* caterpillars were reared on host plants treated with control, low, or high lead concentrations reflecting environmental levels. We measured developmental timing, body size, and mass throughout the lifecycle, and assayed adult migratory flight ability on a flight mill. Lead concentrations were measured in host plant leaves, frass, exuviae, chrysalises, and adults. We found no effects of lead exposure on development or flight ability. Our results suggest that painted ladies mitigate lead toxicity by limiting gut absorption and shedding metal through exuviae. This study highlights the need to better understand species-specific responses to heavy metal exposure.

Lightning Talk Abstracts

Rock and Roost: Predator Avoidance Behaviour in Arboreal and Rock-Roosting Bats

Mika D. Tosoni-Eves[1], Erin E. Stukenholtz[1], Christina M. Davy[1]

[1]*Department of Biology, Carleton University, Ottawa*

Conservation of endangered species requires an understanding of their habitat and behaviours. Predation is a selective pressure that favours prey traits that reduce exposure to danger. We investigate predator avoidance behaviours of two endangered species of bat. The eastern small-footed bat (*Myotis leibii)* often roosts in rock crevices, whereas the little brown bat (*M. lucifugus*) roosts in trees or buildings. Due to their different roosting behaviors, they likely encounter terrestrial predators at different rates. We compared the responses of these two species to encounters with perceived predators through two experiments. We compared each species' boldness during interactions with a simulated predator, scoring behaviours such as biting, fleeing, and willingness to reapproach the "predator". We used a radial maze to test each species' willingness to spend time near the scent of a predator (eastern foxsnake, *Pantherophis vulpinus*). Both species were equally willing to reapproach a simulated "predator". Neither species avoided or preferred snake scent, but non-aggressive contacts between the "predator" and *M. leibii* were more frequent, suggesting they were more tolerant of the perceived predator than M. lucifugus. We speculate these differences reflect more frequent encounters between *M. leibii* and ground predators such as snakes.

Is Inflorescence Height a Target of Selection Under Pollinator Decline?

Emily T. Heagney[1], Christina M. Caruso[1]

[1]*Department of Integrative Biology, University of Guelph, Guelph.*

Global pollinators are experiencing decline which can strengthen selection for plant traits that enhance pollinator attraction. Previous research has found stronger direct selection for taller inflorescences under pollinator decline, but this effect on fitness may be due to an unmeasured trait correlated with height, rather than inflorescence height itself. To determine if inflorescence height is a target of selection under pollinator decline, we will manipulate both the height distribution and pollination environment for bumblebee-pollinated *Lobelia siphilitica*. We will manipulate height by elevating half of the plants and simulate pollinator decline by reducing pollinator access to inflorescences by 50%. If plants that were experimentally elevated and exposed to simulated pollinator decline produce more seeds, then we can conclude that inflorescence height is a target of direct selection. If height is a target of direct selection, then plants could adapt to pollinator decline through the evolution of taller, more attractive inflorescences.

The Genetic Diversity and Distinctiveness of Newly Discovered Bog Copper (*Tharsalea epixanthe*) Populations in Eastern Georgian Bay

Madison Connie Roberta Robinson[1]

[1]*Department of Biology, Western University, London*

The bog copper, *Tharsalea epixanthe*, is a small, poorly dispersing cranberry-specialist butterfly species found in eastern Canada and the northeastern USA. They exclusively feed on two cranberry species during their entire lifecycle and have only been documented in peatlands where these cranberries are found. Two years ago, four populations of bog coppers were discovered on remote islands in Georgian Bay that do not resemble typical peatlands. These islands are primarily barren rock with a few crevices containing small, densely packed cranberry patches with minimal water and soil. The question of how populations of the bog copper dispersed to, and established on, these remote Georgian Bay islands—across large expanses of water—remains unanswered. I will use microsatellite markers to determine the level of connectedness between the mainland and island populations of bog coppers on Georgian Bay by examining their genetic differentiation. I will also use these microsatellites to assess within-population diversity and compare the diversity of the island populations to that of the mainland populations. Low differentiation between the island and mainland populations would suggest recent colonization and/or ongoing gene flow between the islands and mainland, whereas high differentiation would imply ancestral colonization events with little current gene flow.

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

Shelby Atkinson[1], Melanie Beaudin[1], Root Gorelick[1], & Catherine Cullingham[1]

[1] *Department of Biology, Carleton University, Ottawa*

Opuntia fragilis, also known as the brittle prickly pear cactus, is one of four cactus species native to Canada. A disjunct population of *O. fragilis* located just outside Kaladar, Ontario, is notable for being found over 800 km away from its nearest neighbouring population. Many scientists have been intrigued by this population's isolation, but its isolation also makes the population vulnerable to extirpation. Kaladar *O. fragilis* cacti also flower very rarely and only produce imperfect flowers when they do. This suggests that the population could be clonal, which would contribute to the population's vulnerability. Our objective is to determine whether the population is clonal to provide insight into its ability to persist in Kaladar. To do so, we have performed microsatellite marker analysis on *O. fragilis* samples from Kaladar and other locales across North America. To date, we have tested 16 microsatellite primers designed for use in *Opuntia* species and have optimized and used 5 of these primers to assess genetic diversity. Our results show that there is no genetic variation among the Kaladar *O. fragilis* samples tested, which indicates the population may be clonal. This could make the population more vulnerable to extirpation and therefore, of possible conservation concern.

Selection For Environmentally-Associated Alleles Following Extreme Weather Events in an Alpine Butterfly Metapopulation

Laura Michele Bax[1]

[1]*Department of Biology, Western University, London*

Climate change has increased the occurrence of extreme weather events, but the genetic and evolutionary consequences of these events on populations are not well understood. Alpine insects are particularly affected by extreme weather because high-altitude environments already experience highly variable conditions that are exacerbated by climate change, and insects are ectotherms which rely on external environmental cues to regulate their behaviour and life cycle. Extreme weather conditions in a year can cause dramatic decreases in population size for insects, known as bottlenecks, which can affect genetic diversity of populations. The effects of bottlenecks on neutral genetic variation in populations of the alpine butterfly, *Parnassius smintheus*, have been well studied, but it is not known whether these bottlenecks also exert selection on the populations in response to environmental variables of extreme weather. I aim to determine whether there is evidence for selection acting during three population bottlenecks at a set of candidate loci associated with extreme environmental variables by measuring divergences in allele frequency across bottleneck events. I predict that loci which do show changes in frequency following population bottlenecks are under balancing selection, and thus show an oscillating pattern of frequencies across bottleneck events.