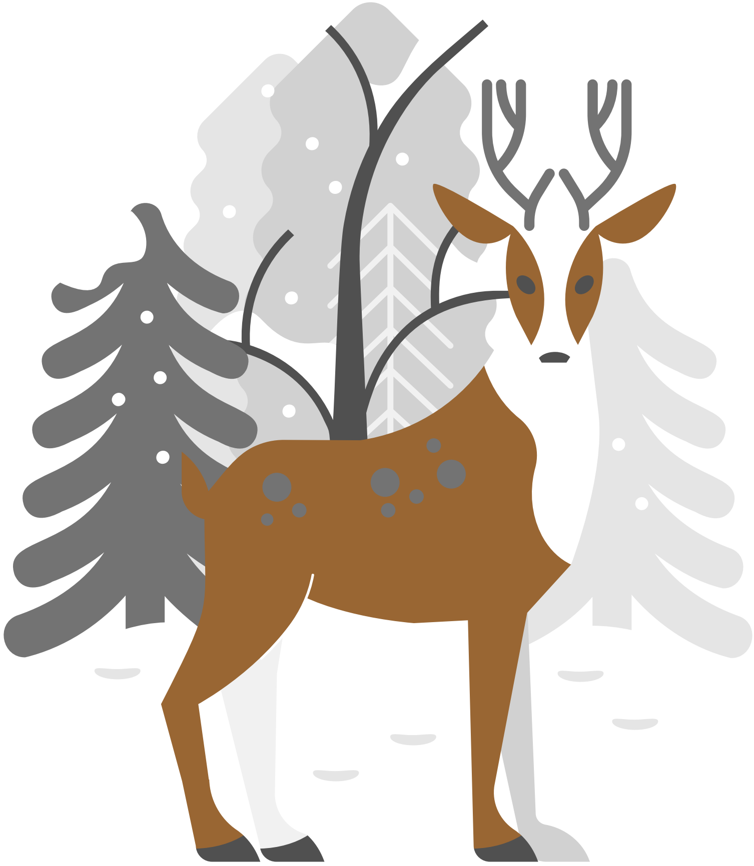
Ecology & Evolutionary Biology
UNIVERSITY OF TORONTO

EEB Undergraduate Research Fair

- Program Guide 2026 -



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Welcome

Thank you for joining us for the 2026 EEB Undergraduate Research Fair! We are so excited that you will be joining us for a showcase that highlights the incredible fourth-year research projects students have worked on during the Fall/Winter 2025-2026 term. The fair is a great way to experience the diversity of exciting undergraduate research in EEB, to hear about new scientific discoveries made by students, and interact with undergraduates and peers.

The students participating in the fair are competing for the *Corey A. Goldman Prize for Best Research Poster in Ecology and Evolutionary Biology*. The prize is named after former EEB Undergraduate Associate Chair Corey A. Goldman, and recognizes the top students within the department for excellence in their fourth-year independent research projects. Cash prizes will be awarded to the best research poster in each category.

Check out our website at https://eeb.utoronto.ca/education/undergraduate/research-courses-2/eeb-undergraduate-research-fair/!

Event Details

Date: Friday, March 27th, 2026
Time: 10:30am - 12:30pm
Location: Earth Sciences Library, Noranda (Second floor, 5 Bancroft Avenue)

Event Schedule

10:30am - 12:15pm	The Research Fair is open! Student researchers will be available to answer questions about their research.
12:15pm - 12:30pm	Brief closing remarks by Megan Frederickson and announcement of winners and honourable mentions.

Research Categories

Student	**Supervisor(s)**	**Project Title**
Category: Community & Ecosystem Ecology		
Judges: Micah Freedman & Zoie Diana		
Jon Agolli	Marie-Josee Fortin, Jonathan Ruppert	Predator Assemblages, Not Human Recreation, Drive Variation in Ground- and Low-Forest Bird Communities in Toronto's Tommy Thompson Park.
Makenna Brissette	Megan Frederickson	Microbial priority effects modulate community composition and host performance in the duckweed (*Lemna*) microbiome
Julia Cruz	Nathan Lujan	Niche Differentiation as a Driver of Freshwater Catfish Assemblage Structure (Siluriformes: Loricariidae)
Emma Zongaro	Tianna Peller	Spatial structure of consumer mortality regulates ecosystems connected by complex life cycles
Category: Evolutionary Ecology		
Judges: Tianna Peller & Jun-Long Huang		
Vanessa Lu	Megan Bontrager	Influence of spring warming patterns on temperature-induced reproductive responses in *Clarkia pulchella*
Nanor Pontigian	Megan Bontrager	From Winter Chills to Spring Blooms: Phenological Drivers of Germination and Flowering in *Camassia quamash* (Camas) Populations
Sarah Scott	Aneil Agrawal	Larval survival in sex-limited populations of *Drosophila melanogaster*
Lorien Simoes de Paiva	Megan Bontrager	Climate warming increases the risk of phenological mismatch for trout lily (*Erythronium americanum*) in cooler forests
Anna Whitehouse	Micah Freedman	Evaluating Geographic Range Size in Relation to Dispersal Ability in Milkweed Species
Category: Evolutionary Genetics & Modeling		
Judges: Tomomi Parins-Fukuchi & Jill Wheeler		
Tabris Cao	Matthew Osmond	Using ancestral recombination graphs to investigate the genetic basis of divergence in European crows
Jason He	Jacqueline Sztepanacz	Automated Measurement of Wing and Wing Spot Area of *Drosophila suzukii* and the First Estimates of Spot-Wing Ratio Variations and Heritability
Aatabi Shankar	Marla Sokolowski	Gene - Environment Interplay in *Drosophila melanogaster*: Mating Duration, Social Experience and the *foraging* gene
Jaico Yin	Stephen Wright	Investigating the Role of Independent Transitions to Self-Fertilization on Transposable Element Evolution
Cindy Yu	Nicole Mideo, Alison Hill	Modelling the impact of vaccine failure mode on the evolution of escape variants

Student	Supervisor(s)	Project Title
Category: Global Change Ecology		
Judges: Danielle de Carle & Jill Sanderson		
Lauren DeLoyde	Megan Bontrager	Spring temperature regimes shape early development in a winter annual wildflower
Alexia Kallmes	Marie-Josee Fortin	Assessing the Haliburton Forest Health using Functional Traits
Maura McGregor	Chelsea Rochman	Does Chronic Microplastic Exposure Induce Gastrointestinal Tract Inflammation and Liver Vacuolization in Yellow Perch (*Perca flavescens*)?
Nola Roberts	Chelsea Rochman	Assessing the effects of microplastic exposure on freshwater fish prey consumption and diet composition in a whole ecosystem experiment
Gabe van Driesum	Marie-Josee Fortin	How Different Modes of Habitat Loss Fragment Blanding's Turtle (Emydoidea blandingii) Networks in Ontario
Category: Trait Evolution & Macroevolution		
Judges: Alison Hill & Takuji Usui		
David Carter	Maxwell Shafer	Mass Extinctions and Nocturnal Behavior: an Analysis of the Cryptic Activity Patterns of Arthropods
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Alana Lee	Rowan Sage	Unraveling the C4 Tree of Life; A Species-level Construction of C4 Ancestry
Vedant Gattani	Luke Mahler	To Blend in or Stand Out? Constraint versus conspicuousness in the evolution of color and pattern in *Anolis* lizards
Nathaniel Zongaro	Micah Freedman	The Ecological and Evolutionary Correlates of Conspicuousness in Lepidoptera

Poster Abstracts

Category: Community & Ecosystem Ecology

Judges: Micah Freedman & Zoie Diana

Jon Agolli (Supervisors: Marie-Josee Fortin, Jonathan Ruppert)

Predator Assemblages, Not Human Recreation, Drive Variation in Ground- and Low-Forest Bird Communities in Toronto's Tommy Thompson Park.

Abstract: In recent years, ground- and low-forest feeding bird species at Toronto’s Tommy Thompson Park have experienced documented declines in abundance during the spring migration period. This trend was thought to be associated with increased predation pressure and human recreational activity. Identifying which of these factors most strongly influences bird community structure at TTP is essential to understanding and managing ongoing changes in this important urban stopover habitat. Using camera traps and automated recording units, we quantified bird, predator, and human activity across two sites differing in human recreational use within TTP. Bird community composition differed between sites and was more strongly associated with predator assemblages than with human activity levels, while short-term variation in human presence showed little influence on bird communities. These results suggest that interactions with predator communities, rather than human recreation activities, are the primary drivers of spatial variation in ground- and low-forest feeding bird communities at TTP. Identifying the ecological relationships shaping urban bird community composition can help inform management strategies that support migratory birds, while maintaining public access to urban green spaces.

Makenna Brissette (Supervisor: Megan Frederickson)

Microbial priority effects modulate community composition and host performance in the duckweed (*Lemna*) microbiome

Abstract: Priority effects arise when early-arriving species alter host conditions and resource availability, thereby redirecting subsequent community assembly and function. By dictating the strength of host–microbe associations, priority effects can influence a microbiome’s capacity to deter pathogens or accommodate beneficial taxa. However, the mechanisms through which priority effects arise—and their consequences for microbiome composition and host function—remain poorly resolved in whole-system contexts where microbial, host, and environmental processes interact. This study examines how colonization order between a nitrogen-fixing mutualist (*Allorhizobium* sp.) and a plant pathogen (*Pseudomonas syringae pv. tabaci*) shapes microbiome composition and host performance in the duckweed *Lemna japonica*. Arrival order is manipulated across two host genotypes and two nitrogen regimes to test how host and environmental conditions modulate the strength of priority effects. Reciprocal home–away assays with experimentally evolved strains further evaluate whether microbial local adaptation reinforces early-arriver advantages. Host growth measurements are used to link community assembly to host performance. These experiments will clarify the conditions under which simple pairwise microbial interactions generate stable priority effects and identify the host, environmental, and microbial factors that shape priority effects in plant microbiomes. In doing so, this work contributes to understanding how microbiome assembly processes may be leveraged to support plant health and resilience to environmental change.

Julia Cruz (Supervisor: Nathan Lujan)

Niche Differentiation as a Driver of Freshwater Catfish Assemblage Structure (Siluriformes: Loricariidae)

Abstract: Many processes influence why species occur in specific assemblages. One possibility is niche differentiation, where species adjust their ecological niches to minimize resource competition. Species may broaden their niches (niche expansion), contract their niches (niche-packing), specialize on certain resources (niche specialization), or share resources (niche overlap). With over 1100 species inhabiting the Neotropics, the Loricariidae are a diverse family of armored, suckermouth catfish that often consume detritus, algae, or wood. Although Neotropical freshwater ecosystems contain large pools of organic matter, sustaining highly diverse consumer assemblages may create resource limitation and drive niche differentiation. To test whether niche differentiation structures Loricariid assemblages, we collected 3-dimensional measurements of the mandibles to plot species as points in morphospace representing their niches. We quantified trait variation in 8,421 empirical assemblages using volume and distance metrics, and compared these values to random assemblages to test if assembly patterns are driven by niche differentiation rather than chance. We found that coexisting species are spaced closer together and clustered in morphospace, illustrating assemblages of generalists or species occupying similar niches. These results indicate that assembly is shaped by environmental filtering, where habitat conditions select what species persist in an environment, and/or evolutionary biogeographic constraints, where limits on dispersal or establishment restrict lineages to specific regions. Overall, this study underpins the use of 3-D morphological data to quantify the ecological niche, and reveal how basal resources support species-rich consumer assemblages and food webs.

Emma Zongaro (Supervisor: Tianna Peller)

Spatial structure of consumer mortality regulates ecosystems connected by complex life cycles

Abstract: Many organisms undergo ontogenetic habitat shifts, linking distinct habitats across different life stages. Yet ecological theory integrating complex life cycles typically treats mortality as a net loss of biomass, ignoring nutrient recycling. In reality, consumers with ontogenetic habitat shifts provide important nutrient subsidies that can affect community dynamics in multiple habitats. Specifically, the carcasses of consumers can represent spatially structured nutrient subsidies; adults may die in either their adult habitat or in their natal habitat during breeding migrations. Variation in species' life histories can influence where nutrients are recycled and thus, may affect the dynamics of individual habitats and entire meta-ecosystems. We developed a mathematical model to investigate how the location of adult consumer mortality affects the dynamics of natal and adult habitats, as well as the whole meta-ecosystem. We found that when the natal and adult ecosystems are ecologically equivalent in their process rates, equilibrium stock of the whole meta-ecosystem is maximized when adult consumers primarily die in the natal habitat. However, spatial heterogeneity in process rates can mediate this effect. Spatial heterogeneity in process rates predictably shifts the optimal location of nutrient recycling and can reverse the pattern or generate parabolic relationships between recycling location and total stocks. These results demonstrate that the effects of ontogenetic nutrient subsidies depend critically on habitat-specific ecological rates. Ultimately, ecosystem dynamics depend on life history variation in adult consumers with complex life cycles and the degree of spatial heterogeneity in the local processes of the adult and juvenile habitats.

Category: Evolutionary Ecology

Judges: Tianna Peller & Jun-Long Huang

Vanessa Lu (Supervisor: Megan Bontrager)

Influence of spring warming patterns on temperature-induced reproductive responses in *Clarkia pulchella*

Abstract: Phenology, or the timing of biological events, is central for plant fitness, allowing individuals to align life-history transitions with favourable environmental conditions. For plant species, phenology is often triggered by the accumulation of warmth during spring, and may be mediated by the timing and rate of increasing temperature. Understanding plant responses to variations in seasonal temperature patterns is essential for predicting how populations may experience potential shifts in phenological responses. This study investigates the plasticity of flowering time in response to the velocity of spring-summer seasonal transition, for the winter annual wildflower Clarkia pulchella. In this study, we sourced seeds from eight populations spanning the latitudinal range of C. pulchella, and planted them in growth chambers. Temperature treatments simulated gradual or rapid spring-to-summer transitions, characteristic of northern and southern portions of the range, respectively. Gradual and rapid transitions were simulated under both ambient temperatures matching current range conditions, and heightened temperatures characteristic of climate warming. We recorded the timing of key reproductive stages, including the onset of vertical growth, budding, and first flowering, in addition to size measurements at budding and flowering. Additionally, we examined the geographic and phenological data for over 1200 herbarium specimens to expand the temporal, geographic, and climatic scope of the growth chamber work. Preliminary results suggest that populations vary in their responses to treatments, but generally show heightened plasticity to treatments simulating warming. This research provides insight into how variation in seasonal flowering impacts the transition into flowering, a phenological stage that is consequential for individual reproductive success, and expands our understanding of how species may persist under changing climate conditions.

Nanor Pontigian (Supervisor: Megan Bontrager)

From Winter Chills to Spring Blooms: Phenological Drivers of Germination and Flowering in *Camassia quamash* (Camas) Populations

Abstract: Plant phenology is an important aspect of plant survival and long-term population maintenance. With ongoing ecosystem changes driven by agricultural homogenization and climate change, species are expected to experience substantial environmental shifts that impact phenology. *Camassia quamash* is an ecologically and culturally significant species for many Indigenous communities and is currently facing population declines across its range. It is therefore important to understand whether the species exhibits intraspecific variation, particularly local adaptation to climate, that may enable it to persist under changing environmental conditions. Germination trials tested cold stratification requirements of *C. quamash* across four populations and one population of *Camassia leichtlinii*, along with monitoring emergence timing. Results indicate that increased chilling reduces days to germination across all populations; however, responses are population-specific, with varying magnitudes. Both *C. quamash* populations and the *C. leichtlinii* population from British Columbia show the highest sensitivity to cold stratification, followed by Conrad Meadows, Columbia Hills, and Camas

Meadows. Similarly, longer chilling reduces days to emergence across most populations, though effects are weaker in some. Separately, flowering phenology of *Camassia quamash* was examined using citizen science data from iNaturalist to assess how climatic trends, particularly conditions during the previous summer and winter, influence transitions to reproductive stages. Warmer previous summers and winters are associated with earlier transitions to reproductive stages, suggesting that climatic conditions play a key role in reproductive timing across the species' range.

Sarah Scott (Supervisor: Aneil Agrawal)

Larval survival in sex-limited populations of *Drosophila melanogaster*

Abstract: Experimental evolution can be used to evolve lines of male-limited and female-limited *Drosophila melanogaster* wherein the focal chromosome(s) only experience selection in males and females respectively. Previous studies show that limiting selection to one sex leads traits to evolve towards the optimum of the selected sex (Lund-Hansen et al. 2020). The evolution of these traits shows that they are constrained by a shared gene pool, and this constraint can be relaxed by forcing selection to undergo a specific pattern (Lund-Hansen et al. 2020). In a previous lab experiment, the fecundity of female-limited females was assessed by looking at the number of offspring produced. It was found that females in one treatment produced a greater proportion of total offspring without a significant difference in the total number of offspring, relative to male-limited females (Melo-Gavin). One possible explanation is that the experimental larvae have evolved to be extremely competitive to the point where they are harming each other, thus reducing the overall number of larvae. In this experiment, the survival of sex-limited larvae was assayed in two treatment groups: one at a low larval density, and one at a high larval density in combination with a competitor genotype. Once analysis is complete, we expect that the sex-limited larvae will survive at a different rate relative to the competitor genotype.

Lorien Simoes de Paiva (Supervisor: Megan Bontrager)

Climate warming increases the risk of phenological mismatch for trout lily (*Erythronium americanum*) in cooler forests

Abstract: In temperate deciduous forests, access to light for understory plant communities is largely determined by the leaf emergence timing of overstory trees. Aligning life history events with favorable light conditions is especially critical for spring ephemerals, a group of understory plant species which emerge and complete reproduction before tree canopies close in the spring. Under climate warming, spring ephemerals and trees may advance their lifecycle timing (phenology); however, these processes may shift at different rates, altering the light availability for understory plants. Phenological mismatch– the misalignment in phenology between canopies and spring ephemerals– can limit spring ephemeral growth. For example, when canopies close earlier than usual, spring ephemerals may not meet the annual energy requirements for successful reproduction. In this project, we investigated the effects of temperature on the reproductive phenology of a fast-blooming North American spring ephemeral, *Erythronium americanum* (trout lily). Using citizen science data from iNaturalist and climatic data from ClimateNA, we assessed the reproductive timing of *E. americanum* under spring average and anomalous temperatures across the range. We compared *E. americanum* reproductive timing to canopy leaf-out date, using data from the USA National Phenology Network, to understand phenological alignment between *E. americanum* and canopy trees. Results suggest that tree phenology is more sensitive to climate warming than *E. americanum*, particularly in colder sites. As such, colder deciduous forests are at greatest risk of phenological mismatch under future climate warming. Reductions in spring ephemeral growth may affect critical habitat and forage for early-emerging animals, threatening cascading impacts on deciduous forest ecosystems.

Anna Whitehouse (Supervisor: Micah Freedman)

Evaluating Geographic Range Size in Relation to Dispersal Ability in Milkweed Species

Abstract: The factors which govern species' geographic range sizes remains an open question in ecology. The *dispersal ability hypothesis*, which predicts a positive correlation between a species' long-distance dispersal (LDD) ability and its range size, is one of the hypotheses proposed to explain this phenomenon, although recent meta-analyses suggest the relationship between geographic range size and dispersal ability is highly variable. This project looks at dispersal and range size in milkweed (Apocynaceae: Ascelpiadoideae) species in order to determine: (1) whether seed morphology can be used as a proxy for LDD ability; (2) how geographic range measurement methods impact the geographic range size estimate returned; and (3) whether the seed morphological measurements which are predictive of a species' LDD ability are likewise predictive of a species' range size while accounting for co-variates. Drawing on field measurements of seed dispersal, we fit cumulative dispersal kernels to five milkweed species, and evaluated the ability of lab-measured dispersal proxies to predict LDD probability as described by each kernel. Next, we evaluated the similarity of species range size estimates derived from species distribution models (SDMs) versus extent of occurrence based on minimum convex polygons (MCPs). Finally, we investigated the relationship between measured proxies of dispersal ability and estimated range size in a phylogenetic generalised least-squares regression. Dispersal analyses suggest that the ratio of coma mass to seed mass is the best lab-measured proxy of LDD probability. Range analyses indicate that similar range estimates are obtained by MCP as by SDM. Finally, while accounting for phylogeny, morphological proxies were found to be better predictors of the dispersal-range size relationship than other covariates. Beyond adding to the literature on range size evolution, these results serve as proof-of-concept for a larger study of dispersal ability and range size across species in the genus *Asclepias* (subfamily Asclepiadoideae).

Category: Evolutionary Genetics & Modeling

Judges: Tomomi Parins-Fukuchi & Jill Wheeler

Tabris Cao (Supervisor: Matthew Osmond)

Using ancestral recombination graphs to investigate the genetic basis of divergence in European crows

Abstract: Ancestral recombination graphs (ARGs) capture the complete shared genetic history of recombining genomes, allowing improved inferences about spatial ancestry. By locating genetic ancestors at many trees across the genome, we can visualize the full variation in an individual's geographic ancestry through time. Here, we apply this approach to a classic hybrid zone between carrion and hooded crows (*Corvus corone* and *Corvus cornix*), species that diverged during Pleistocene glacial cycles and today meet in multiple contact zones. Despite over 99% sequence identity, these species maintain distinct plumage phenotypes through assortative mating and selection at a few large-effect loci, while experiencing asymmetric gene flow that has largely swamped the carrion crow genome with hooded crow ancestry. From whole-genome data of 135 crows including hybrid individuals (Gwee et al. 2025), we construct ARGs using Relate (Speidel et al. 2019) and locate genetic ancestors assuming Brownian motion down each tree (Osmond & Coop 2024). The resulting ancestor locations provide a direct visualization of the asymmetric gene flow and barriers to introgression that characterize this charismatic hybrid zone.

Jason He (Supervisor: Jacqueline Sztepanacz)

Automated Measurement of Wing and Wing Spot Area of *Drosophila suzukii* and the First Estimates of Spot-Wing Ratio Variations and Heritability

Abstract: *Drosophila suzukii*, the Spotted Wing Drosophila, is a globally invasive pest species. The melanized spot on the male wing is a sexual dimorphic trait, suggesting adaptive importance. However, the adaptive significance of this trait is poorly understood, partly because manual measurement of wing and spot areas for large datasets is time-intensive. While automated image analysis tools do exist, none are specifically designed for this precise morphometric task for *D. suzukii*. To address these problems, we developed a fully automated software based on computer vision methods to reliably measure wing area, spot area, and spot-wing ratio. We validated this tool by applying it to a half-sibling breeding design dataset. We provide the first estimates of phenotypic variance, additive genetic variance and heritability of the spot-wing ratio. The heritability was estimated at 0.22, with significant additive genetic and maternal variance components. This work presents an efficient phenotyping method for the sexual dimorphic wing spot in *D. suzukii* and a starting place for understanding its evolution.

Aatabi Shankar (Supervisor: Marla Sokolowski)

Gene - Environment Interplay in *Drosophila melanogaster*: Mating Duration, Social Experience and the *foraging* gene

Abstract: The pleiotropic *foraging* (*for*) gene is known to influence a suite of behavioural differences in *Drosophila melanogaster* while exhibiting plasticity. Relatively little, however, is known about the phenotypic plasticity of the for gene in response to male social environments and mating duration. This study explores whether there are differences in mating duration between rover and sitter allelic variants of the for gene and if these differences vary under different social environments. Additionally, we considered if the females' allelic variant contributed to mating duration differences and if the phenotypic differences could be mapped to a specific promoter of the *for* gene. We conducted mating assays involving one naïve male and one virgin female. Mating duration was measured in rover and sitter variants under two social environment precondition treatment groups provided to a male focal fly. Treatment groups comprise single-raised naïve males, and group-reared naïve males and were provided before the mating assay. We found a significant three-way interaction indicating that strain effects depend on both partner genotype and the social environment. Group reared effects depend on the male strain while single reared effects depend on both sexes. Significant differences in mating duration between social environments also indicate a female effect. There was no significant effect of genetic variation in the promoter-4 region on mating duration. Through future experiments, we hope to conduct assays mapping other promoter regions and explore other mating phenotypes.

Jaico Yin (Supervisor: Stephen Wright)

Investigating the Role of Independent Transitions to Self-Fertilization on Transposable Element Evolution

Abstract: Transposable elements (TEs) are major drivers of genetic variation and mutation in plant genomes. These “selfish” DNA sequences can insert into host genomes, disrupting functional genes and altering genome structure. Although TE abundance varies widely across plant taxa, the mechanisms underlying variation among closely related species remain poorly understood. Theoretical models predict that self-fertilization may reduce TE activity over evolutionary time due to increased homozygosity and more efficient purging of deleterious insertions. To investigate this hypothesis, we analyzed existing genome assemblies of *Capsella orientalis* and *Capsella rubella*. While *C. rubella* represents a recent transition to self-fertilization, *C. orientalis* is an older selfing lineage, providing a natural framework to examine how time since mating system evolution influences TE dynamics. Using EDTA, we annotated and compared transposable elements in both genomes. While *C. orientalis* contains more recently transposed intact elements, *C. rubella* shows a higher overall TE abundance. Additionally, Helitron elements, which are widely distributed and enriched in some gene-dense regions, constitute a larger proportion of intact TEs in *C. rubella* than in *C. orientalis*. Experimental work is ongoing to directly measure transposition rates using long-read sequencing of seedlings and detection of de novo TE insertions absent from parental genomes. We also evaluated the structural variant detection tool SVDSS using existing long-read sequencing data to refine approaches for identifying TE insertions. Our results provide a methodological foundation for directly measuring TE transposition rates in plant genomes and offer insights to how evolutionary changes in mating system may shape TE abundance in genome evolution in Brassicaceae.

Cindy Yu (Supervisors: Nicole Mideo, Alison Hill)

Modelling the impact of vaccine failure mode on the evolution of escape variants

Abstract: Vaccine escape variants, such as COVID-19’s Omicron strain, are a topic of much concern as they circumvent the efficacy of one of our most effective methods of disease control. Many mathematical models seek to understand how vaccination may affect the emergence of a vaccine escape variant. In many of these studies, vaccinated individuals are still susceptible to disease to some extent, though these studies often neglect the mode of vaccine failure. Vaccine failure mode refers to the way in which a vaccine is not effective, that is, whether every vaccinated individual has imperfect protection (leaky) or some individuals have perfect protection while others have none (all-or-nothing). Past research has shown that vaccine failure mode has profound impacts on the epidemiological outcomes of mathematical models. This study explored the emergence and spread of vaccine escape variants under leaky and all-or-nothing vaccine failure modes. To investigate the impact of failure mode on escape variants, this study used a compartmental Susceptible-Infected-Recovered (SIR) model to track transmission. All-or-nothing vaccines consistently produced fewer cumulative infections than their leaky counterparts in the presence of escape variants, though this difference was smaller than in variant-free scenarios. Escape variants had greater impact under all-or-nothing regimes, especially at intermediate vaccine efficacies. Overall, findings suggest that modelling choices regarding vaccine failure mode should be disclosed and treated as a source of uncertainty in future studies.

Category: Global Change Ecology

Judges: Danielle de Carle & Jill Sanderson

Lauren DeLoyde (Supervisor: Megan Bontrager)

Spring temperature regimes shape early development in a winter annual wildflower

Abstract: Climate change is altering not only mean temperatures but also the seasonal pace of warming. Differences in the speed of spring temperature increase and the degree of summer heat may influence early plant development in ways that vary among populations adapted to different climates. Early vegetative growth, which is often understudied, is particularly important in annual plants because it determines resource acquisition and developmental trajectories under seasonal time constraints.

I investigate how spring thermal ramp-up and summer temperature plateaus affect early vegetative growth in *Clarkia pulchella*, a winter annual distributed across broad climatic gradients in the interior Pacific Northwest. Using controlled growth chamber experiments that simulate realistic seasonal temperature regimes, I compare growth trajectories and developmental timing among populations originating from distinct seasonal climates. Specifically, I test whether (1) ramp speed and summer plateau temperature alter early growth rates and size accumulation, and (2) populations differ in their early growth sensitivity and plastic responses to these thermal regimes.

By isolating how the pace of seasonal warming shapes early development across populations, my research will evaluate whether population-level differences in plasticity reflect climatic history and may influence responses to ongoing warming. These results will contribute to understanding how seasonal temperature dynamics shape early life stages within species distributed across heterogeneous climates.

Alexia Kallmes (Supervisor: Marie-Josee Fortin)

Assessing the Haliburton Forest Health using Functional Traits

Abstract: Climate change is rapidly altering forest structure with unpredictable consequences. Human activity accelerates forest fragmentation, leaving forest stands vulnerable to environmental perturbations. Forest connectivity enables stands to disperse and exchange material, making tree dispersal and proximity integral to a forest's resilience. We map a section of the Haliburton Forest to assess forest stand health and assess whether tree age or species type influence the strength of material exchange among forest stands. We show that deciduous species compose the majority of each stand, and coniferous species the minority. Combined effects of human activity and higher temperatures may favour the survival of deciduous species and the decline of coniferous species. Understanding these relationships may inform forest management and lead to the maintenance of forest recovery and resilience.

Maura McGregor (Supervisor: Chelsea Rochman)

Does Chronic Microplastic Exposure Induce Gastrointestinal Tract Inflammation and Liver Vacuolization in Yellow Perch (*Perca flavescens*)?

Abstract: Microplastics (plastics <5mm) are a highly prevalent form of pollution that threatens both organism and ecosystem health. Laboratory based experiments have demonstrated that microplastic exposure can negatively impact aquatic organisms' physiology, such as gastrointestinal tract (GIT) abnormalities and metabolic interferences. However, the controlled nature of these experiments

restricts their ability to represent the complexity of natural environments. Therefore, a study was conducted at the International Institute for Sustainable Development - Experimental Lakes Area (IISD-ELA) in 2022, using in-lake mesocosms that received a one-time loading of microplastics. Young-of-year yellow perch (*Perca flavescens*) were sampled from the mesocosms following an exposure period of nine weeks, and their livers and GITs processed for histopathological analyses. A photomicroscope was used to image and examine the liver and GIT tissues for signs of stress. Specifically, we assessed the extent of (1) lipid and (2) glycogen vacuole accumulation in liver cells (hepatocytes) and (3) the intensity of inflammation within the GIT. Overall, glycogen and lipid vacuole presence in *P. flavenscens* liver tissues did not differ significantly between treatments. However, yellow perch GITs from mesocosms that were treated with non-additive plastic demonstrated an increase in inflammation. Given the world-wide abundance and pervasive presence of microplastics, it is imperative that we advance our understanding of their effects on organism and ecosystem health.1 This study provides an example of the impacts of microplastics on fish physiology under more realistic experimental conditions and strengthens our understanding of the consequences of plastic pollution in freshwater ecosystems that are highly species diverse and ecologically vital.

Nola Roberts (Supervisor: Chelsea Rochman)

Assessing the effects of microplastic exposure on freshwater fish prey consumption and diet composition in a whole ecosystem experiment

Abstract: Microplastics have been recognized as pervasive pollutants in aquatic ecosystems, yet their ecological effects on aquatic food webs at the whole-ecosystem scale remain poorly understood. To address this gap, a long-term whole-lake experiment is underway at the IISD Experimental Lakes Area, involving the controlled addition of polyethylene terephthalate, polystyrene, and polyethylene to Lake 378, with Lake 373 serving as a reference. This study examines how microplastic addition influences food web dynamics by comparing diet composition and mass in 2 species: lake trout and pearl dace. Microplastic exposure was hypothesized to reduce prey mass in lake trout diets, reflecting decreased feeding efficiency or altered prey availability, and composition was expected to differ between experimental and control lakes due to structural and spatial variability. Diet contents for both species were analyzed using standardized gastric lavage and gastrointestinal tract diet characterization protocols. Prey items were identified, dried, and weighed, and multivariate analyses (PERMANOVA and NMDS) were used to test for differences in diet composition, and a Gamma-distributed GLMM was used to investigate variability in total mass consumed between pre and post-plastic addition years, and between lakes. Lake trout exhibited total gut mass differentiation between lakes and across periods, with a lake × period interaction of gut masses increasing post addition, significantly in Lake 378. Diet composition differed significantly between lakes and between periods, although no strong lake × period interaction was detected. Pearl dace showed no significant difference in total mass or diet composition between lakes. While anticipated reductions in prey mass were not observed, this study represents one of the first whole-ecosystem investigations of microplastic impacts on freshwater food webs, highlighting the complexity of ecological responses to microplastics under natural conditions and offering a foundation for future research on trophic responses to plastic pollution.

Gabe van Driesum (Supervisor: Marie-Josee Fortin)

How Different Modes of Habitat Loss Fragment Blanding's Turtle (Emydoidea blandingii) Networks in Ontario

Abstract: Climate-driven drought and human land-use change increasingly threaten Ontario's wetlands, which provide essential habitat for semi-aquatic species. While both processes reduce total habitat area, their spatial patterns differ and impact ecological connectivity in distinct ways. This study models how varying configurations of wetland loss influence functional connectivity for Blanding's turtles (*Emydoidea blandingii*), a species of conservation concern which relies on overland movements. Using 15 m-resolution land-cover data and empirical dispersal kernels (500 m, 1 km, and 2 km), we estimated connectivity using the Probability of Connectivity (PC) framework implemented in the R package Makurhini. Four wetland loss scenarios were simulated, including random removal, edge-based contraction, large-to-small removal, and small-to-large removal, to identify which spatial processes pose the greatest risk to landscape integrity. A 15% reduction in wetland area decreased connectivity across all scenarios, but the magnitude depended on both dispersal distance and pattern of loss. Large-to-small removal drove the greatest PC decline at 500 m, while random removal produced the greatest declines at 1 and 2 km. A two-way ANOVA confirmed significant effects of treatment, dispersal distance, and their interaction on PC and PCintra (all $p < 0.001$). Edge-based contraction produced the least connectivity decline across all scenarios. These findings demonstrate that how wetland area is lost matters as much as how much is lost. Large wetland retention should be prioritized for species with limited dispersal, while network-wide connectivity becomes critical at broader movement scales, informing spatially explicit strategies to meet Canada's biodiversity protection goals.

Category: Trait Evolution & Macroevolution

Judges: Alison Hill & Takuji Usui

David Carter (Supervisor: Maxwell Shafer)

Mass Extinctions and Nocturnal Behavior: an Analysis of the Cryptic Activity Patterns of Arthropods

Abstract: Animals typically adopt a diurnal or nocturnal activity pattern in response to the daily light-cycle. However, the causes and consequences of these adaptations to the day-night cycle are not fully understood. This is especially the case for Arthropoda, the largest phylum of Animalia, which contains classes such as insects, arachnids, and crustaceans. Moreover, the ancestral circadian state of arthropods is currently unknown, and in order to deduce the ancestral circadian state, ancestral reconstructions must be performed using large-scale databases of daily activity patterns of extant species. While there have been efforts made to construct such databases, previous attempts are limited to smaller subsets of arthropoda, such as particular orders. Thus, there is a need for the development of a large-scale daily activity pattern database covering all arthropods. To address this, a machine-learning assisted systematic literature review was conducted to build a database on arthropod daily activity patterns, in order to facilitate ancestral state reconstructions of arthropod circadian rhythm states. The tools developed in this project have the potential to aid any sufficiently large literature review, and the potential results of this study may better inform conservation decisions in light of the "6th mass extinction event" that is currently occurring.

Alice Dooley (Supervisor: Rowan Sage)

C2 Photosynthesis Evolution: A Parallel Increase In The Proportion Of Glycine Decarboxylase In The Bundle Sheath

Abstract: C4 photosynthesis is a complex phenotype that has evolved independently more than 60 times. C2 photosynthesis is hypothesized to have enabled this repeated evolution with its anatomical and metabolic modifications. One key modification is the evolution of a glycine decarboxylase (GDC) concentration gradient between the mesophyll and bundle sheath. To investigate how the GDC distribution evolves, I took advantage of the hypothesized extant intermediate species in six distantly related lineages. I worked on species from *Flaveria* (Asteroideae), *Euploca* (Heliotropiaceae) and *Homolepis* (Poaceae), and combined my data with additional lineages from the literature. I measured the photosynthetic efficiency at low CO2 concentrations to evaluate the strength of the C2 phenotype. I also quantified physiological trends in the GDC, and mitochondria distributions. I found a gradual increase in the apparent photosynthetic efficiency with the hypothesized stage of C2 intermediacy. I also found a gradual trend in the proportion of GDC in the bundle sheath. As photosynthetic efficiency increases, the proportion of GDC in the bundle sheath increases. This trajectory is repeated in all of the origins we examined, which suggests that the shift in GDC is a significant factor in the development of the C2 phenotype. The gradual shift in GDC in turn enables a suite of other modifications that open the morphological space for C4 evolution. This case of evolutionary determinism suggests that other complex traits may also depend on a series of previous modifications.

Alana Lee (Supervisor: Rowan Sage)

Unraveling the C4 Tree of Life; A Species-level Construction of C4 Ancestry

Abstract: Natural selection on photosynthesis has always been in the direction of achieving energy efficiency on a morphological, enzymatic, and molecular level. The evolution of photosynthetic enzymes has been, at its core, an optimization of thermodynamics; The fluctuation of temperature and CO2 over geological time has influenced random mutations in protein structure. As a result, in C4 photosynthesis, the main CO2 fixing enzyme, RuBisCO, has been increasingly optimized over time in terms of increased coordination and diversity. Although the core enzymatic machinery of C4 photosynthesis has been well characterized, phylogenetic relationships among C4 species remain poorly resolved. Here, I propose a global ancestral tree of C4 flora at the species level. Every C4 species has been collected from public data, standardized using Plants of the World Online, and fed through a bioinformatic pipeline to display species richness and independent origins on an ancestral tree. As a formidable example of convergent evolution, multiple independent origins arose from C3 plants adapting to increasingly arid, low latitude conditions during the late Oligocene epoch. In the past, errors in C4 data collection have ultimately blurred the distinctions between parallel, convergent, and inherited traits. This study aims to provide an evolutionary foundation on C4, to be one day integrated with future studies to delineate the biological mechanisms that underlie the origin, diversification, and repeated innovation of the C4 pathway.

Vedant Gattani (Supervisor: Luke Mahler)

To Blend in or Stand Out? Constraint versus conspicuousness in the evolution of color and pattern in *Anolis* lizards

Abstract: Colour and pattern play crucial roles in animal communication, camouflage, and mate recognition. The relationship between signaling traits and body colouration may be shaped by competing evolutionary pressures. While signaling traits may evolve independently from body colouration if selection favors signals that maximize contrast and conspicuousness to receivers, they may also covary with body colouration if shared genetic or developmental pathways constrain their independent evolution. Accordingly, I tested predictions derived from these alternative hypotheses: signals evolving to maximize contrast should differ from dorsal coloration more than expected by chance, whereas shared genetic or developmental constraints should produce greater similarity between signaling and dorsal traits than expected by chance. I tested these hypotheses in *Anolis* lizards, which exhibit remarkable diversity in both dorsal body colouration and the colour and pattern of their extendable throat fan, the dewlap. Using colour-standardized photographs, I quantified colour and pattern complexity in both the dewlap and dorsal regions using the image analysis software DEWPAT. I measured colour differences as Euclidean distances in a perceptually uniform 3-dimensional colour space, and summarized pattern features using a phylogenetically informed principal component analysis (pPCA) of complexity measures derived from DEWPAT. Results showed that, across species, both colour and complexity differences between dewlap and dorsum were significantly lower than expected under random association. However, the effect sizes detected between observed and permuted mean distance values for both colour and complexity were very small, indicating minimal biological significance. Collectively, these findings suggest that although dewlap and dorsal traits show statistical evidence of integration, the strength of this association is weak, reflecting substantial evolutionary flexibility in a complex signaling structure.

Nathaniel Zongaro (Supervisor: Micah Freedman)

The Ecological and Evolutionary Correlates of Conspicuousness in Lepidoptera

Abstract: Lepidoptera possess incredible colour variation across both the larval and adult stages. Analyzing which traits predict variation in colour advances our understanding of anti-predator defense, plant-insect interactions, and the principles of evolutionary ecology. Species traits related to diel activity, diet, and size are often hypothesized to correlate with the conspicuousness of animals, but are rarely tested together, or in a diverse set of species. We used 'recolorize' and 'pavo' to amass a dataset of adult and larval colouration data for 301 species of North American Lepidoptera across 22 families. We also collected data on dietary traits, diel activity, and size, testing hypotheses about variation in conspicuousness within and across life stages using phylogenetic generalized least squares regression. After accounting for phylogenetic relatedness, body size was the lone species trait that predicted conspicuousness in larval Lepidoptera; no trait predicted conspicuousness in adult Lepidoptera. Surprisingly, contrary to previous studies, neither diel activity nor diet explained variation in conspicuousness. Finally, both conspicuousness, and colouration, were both correlated between the larval and adult life stages — the first result of its kind in Lepidoptera. We suggest further work in developing alternate formulations of conspicuousness, while underscoring the importance of controlling for phylogeny and for multiple trait covariances in analyses of colouration.