



# Ontario Ecology, Ethology, and Evolution Colloquium

2020 Digital Conference Program

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OE3C 2020 Planning Committee  
University of Guelph

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# Ecology Abstracts

## How to improve aquatic invertebrate metabarcoding?

### Evaluate your primers and skip size sorting

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DNA metabarcoding is an established tool for rapid biomonitoring, but it requires proper protocols and well-tested primer sets. If primers are biased, organisms will be undetected. Moreover, environmental bulk samples often include many different organisms that vary several orders of magnitude in biomass. Sorting of samples by specimen size is recommended to improve species detection but not well tested. We here designed two aquatic mock communities, one sorted by specimen biomass, and one unsorted. Both mock communities comprised of benthic macroinvertebrates, including mollusks, annelids, crustaceans, and insects that were collected with kick or dip net from four countries in Europe and North America. In order to evaluate primer sets, we amplified DNA barcodes (COI) with 31 primer sets, including two newly designed primers. Based on amplification success, we selected the most promising 20 primer sets for sequencing.

Our results show several primer sets, four of these including a newly designed primer, which recover more than 90% of the species in both mock communities, while some primers show rather poor performance. Our data also suggests that there is no significant difference between a sorted or and unsorted sample. Designing metabarcoding primer sets is challenging but necessary to improve species detection, leading to a better assessment of biodiversity. It is also important to optimize the metabarcoding workflow further, by testing the need for size sorting. We show that it is possible to eliminate size sorting for aquatic invertebrate metabarcoding and species detection can be improved by using well-designed degenerate primers.

# Improving extensive green roof functioning using invasion theory as a management tool x

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Green roofs have become an increasingly popular infrastructure development as a way to mitigate the negative impacts of urbanization and to enhance key ecosystem functions in cities. The majority of green roofs consist of Sedum-based plantings which are non-native to North America. Here, we propose a novel management method using principles of invasion biology to increase native biodiversity and species coexistence on extensive green roofs. Native species that invade the existing Sedum community are coined 'native invaders.' According to the "Resource Fluctuation Hypothesis", a plant community's susceptibility to invasion increases as the amount of unused resources increases. Using this invasion theory management tool, native invaders could overcome hurdles to successfully invade extensive green roof ecosystems. A positive link between plant diversity and ecosystem function has been well-established in ecological literature. We assess whether green roof functioning is improved by increasing native species diversity. We hypothesized that resource addition via irrigation and disturbance treatments will enhance native invader success, thereby increase roof cooling and stormwater management. We performed a full factorial experiment in the summer of 2018 and 2019 that manipulated disturbance, irrigation, and native invader diversity across eight sites at the University of Toronto Scarborough Campus. Results showed that irrigation significantly increased native invader success and decreased green roof mean summer temperature. The presence of Sedum and/or native invader vegetation increased both roof cooling and moisture retention, however evidence supporting diversity enhancing green roof functioning is lacking. Diversity effects on ecosystem function require co-existence mechanisms, thus requiring observation over longer temporal scale. It is worth noting that native invaders extended the blooming period of green roofs. This experiment demonstrates a low-cost method to increase native species diversity on extensive green roofs. Other ecosystem services such as improved aesthetics and habitat provisioning for pollinators should be evaluated in future research.

## **An environmentally-friendly alternative tracer particle for dispersal studies x**

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Physical models are used to study hydrodynamically-mediated dispersal when it is not possible or appropriate to release live organisms or their propagules. Large quantities of particles are required, which has historically limited the application of physical models to non-biodegradable plastics. We developed a novel biodegradable and non-toxic physical model (alginate microbeads) with modifiable size and density. We encapsulated two natural dyes to facilitate their detection via fluorescence and pH-induced colour change. The toxicity of the particles was tested through acute exposures (72 h) of dyed and undyed microbeads provided to quagga mussels (*Dreissena bugensis*). The microbeads are not acutely toxic and present a low risk to local species. We also assessed their degradability in a small-scale field study, which confirmed that the particles degrade under field conditions. Particles designed to simulate the physical characteristics of juvenile freshwater mussels (Unionidae) were released at a site with measurements of high-resolution riverbed elevation survey data. Microbead captures in drift nets and specially designed sedimentation traps revealed patterns of transport and entry into the riverbed. The decline in microbead capture rates with distance downstream correlated with negative exponential and power model predictions, which is consistent with dispersal studies on larval mussels and other taxa. The physical model developed in this study provides an environmentally-friendly technique to study the dispersal of aquatic organisms.

# **Black-Legged Tick (*Ixodes scapularis*) Impacts on Hematology and Ectoparasite Communities of *Peromyscus* Mice Across Southern Ontario**

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As the climate warms, the black-legged tick's (*Ixodes scapularis*) range expands further north in Ontario, Canada, reaching new host populations that have not previously interacted with this blood-feeding parasite. *Peromyscus* mice in these northern areas are unfamiliar and inexperienced to the effects of these ticks compared to their southern counterparts that have adapted to living with these organisms. The purpose of this study was to see if there is a difference in physiology between these two groups – deer mice living in areas where tick populations have established and deer mice living in black-legged tick-free environments – looking specifically to see if there is significant variation in hemoglobin levels, which can negatively impact how these mice function in their environment. Along with this, a comparison of the parasite community structure on these mice hosts was analyzed to see if ticks change the composition of these micro-environments. Blood samples were collected from individual mice from populations where black-legged ticks were either present or absent to assess haemoglobin levels. At the same time, ectoparasites were collected from these same mice to determine parasite loads and species diversity. Haemoglobin levels were found to be lower when tick loads were high and parasite diversity appeared to be higher when ticks were absent. Since black-legged ticks are carriers of many pathogens that can be passed on to humans, including Lyme's disease, it is important to understand their movement and distribution across Ontario as well as their interactions with their hosts (and co-occurring parasites) in their environments.



# Asian carps under climate change: modelling Bighead Carp populations in the Great Lakes

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Bighead Carp are a highly invasive, fast-growing and voracious species of fish that are abundant in the Mississippi River. There is a growing concern of their potential to expand northwards and enter the Canadian Great Lakes; however, they may encounter different environmental conditions that affect their growth and maturation. At higher latitudes, Bighead Carp have been observed to mature later in life and grow at a reduced rate. Under a changing climate, warmer temperatures are expected in the Great Lakes, potentially enabling the earlier maturation and faster growth seen at lower latitudes. This study presents a stage-based matrix population model that incorporates variable age of maturity, growth, survival, and fecundity parameters that shift with temperature to explore potential Bighead Carp invasions. Model simulations show that earlier maturation results in greater population growth; however, anticipated climate change may not be sufficient to induce early maturation in the near future. Alternatively, model outputs show that the fecundity of the initial individuals to arrive in the Great Lakes is the most influential to the rate of invasion.

# Hydrodynamic characteristics of juvenile unionid mussel habitats

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Freshwater unionid mussels are considered ecosystem engineers because of their suspension feeding and burrow activities. They are also among the most imperilled taxon due in part to their reliance on a vertebrate (mostly fish) host for development and dispersal. Unfortunately, little is known of their habitat features, which require protection and recovery to aid conservation efforts. We examined how hydrodynamic forces (e.g.,  $\tau_b$ , bed shear stress) at the reach and local scale affect the presence and distribution of juvenile mussels in the riverbed using: (1) high resolution riverbed elevation measurements; (2) vertical profiles of velocity using acoustic Doppler velocimetry; (3) analysis of pore water chemistry; and (4) an airlift system to excavate sediments in search of juvenile mussels. A total of 118 quadrats (14.3 cm diameter) were excavated in the Florence site in the Sydenham River in 2018 and 2019. Among these, 26 juvenile unionids (< 30 mm long) from five species were found in quadrats with  $0.07 \leq \tau_b \leq 0.77$  Pa and large amounts of sand and fine gravels (> 2 mm). Logistic regression ( $\tau_b$  and  $\tau_b^2$ ) indicated that the highest probability of juvenile presence was where  $\tau_b = 0.4$  Pa. Principal Component Analysis indicated that in addition to  $\tau_b$ , porewater dissolved oxygen, pH, specific conductivity and temperature were associated as habitat characteristic. These results provide new insights into the location of juvenile unionids in riverbeds, their habitat characteristics, as well guidelines for their conservation and reintroduction.

# Illustrating arthropod farmland biodiversity through metabaroding and distribution modeling

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The understanding of farmland arthropod biodiversity is hampered by the lack of temporal and spatial distribution information of species richness due to labour intensive and time-consuming field measurements. Expanding on traditional species distribution modeling techniques to model community structure could greatly enhance our capacity to monitor and predict ecosystem change at larger scales.

In summer 2017, we deployed a series of Malaise traps (SLAM type) across various agricultural plots with four crop types (alfalfa, soy, wheat, corn) at University research stations. Each plot hosted five traps at specific locations. Specimens were metabarcoded to provide weekly assessments of community composition. We used the resulting data to develop a species diversity mapping script for R. Multiple OTU tables representative of multiple collection events can be run simultaneously by the script. A custom binomial regression model was derived and used to forecast the community's structure across each sample site. The resulting predicts were expressed as heatmaps that can be exported from R in PDF format.

A collection of heatmaps was produced for each sample sites that together show that the changes to community distribution caused by time do not occur in a homogenous manner across the entire field. Rather they reveal the presence of a community that is dynamic across both the spatial and the temporal planes. It is rather difficult to identify all the species present in a location let alone to quantify their responses to environmental change. The combination of high-throughput DNA sequencing with the statistical modelling we developed makes it possible to scale up from data-rich but finite sets of point samples to spatially continuous biodiversity maps.

# Recovery of arbuscular mycorrhizal (AM) fungal communities in agricultural soils restored with prairie grassland plants

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Most vascular plant species form mutualistic relationships with root-inhabiting mycorrhizal fungi. Mycorrhizal fungi collect nutrients from soils with networks of hyphae, and transport nutrients into plant roots in exchange for carbohydrates. Most nutrients in terrestrial ecosystems taken up by plants are obtained through mycorrhizae, thus, mycorrhizal fungi play a central role in numerous ecological processes, such as nutrient cycling and primary productivity. AM fungal species richness and biomass is reduced in soils disturbed by human activities, with direct feedbacks on plant communities. But little is known about whether mycorrhizal fungi can recover from disturbance, or the successional patterns associated with recovery. We conducted a study on the most common type of mycorrhizal fungi, the arbuscular mycorrhizal (AM) fungi, in ecosystems recovering from agricultural disturbance. We characterized AM fungal communities at five farm sites in Southern Ontario where portions of farmland had been restored with prairie grassland plants. We sampled areas currently under cultivation to represent AM fungal communities before restoration, and we sampled the immediately adjacent restored prairies to represent communities undergoing recovery. Species richness was three times higher in communities undergoing recovery compared to communities in soils still under cultivation. Furthermore, communities undergoing recovery had doubled in biomass, in terms of mycorrhizal spore density in soils. The disturbance-tolerant *Glomus* genus was the dominant taxa in soils under cultivation. Two genera that have not previously been associated with early succession, the genera *Claroideoglomus* and *Diversispora*, were found abundantly in all restored prairies. These findings provide new insights into the recovery of AM fungi in remediated soils. And, this study puts emphasis on an ecologically important group of soil micro-organisms that have received less attention than above-ground communities in restored ecosystems.

Abbreviations: AM – Arbuscular mycorrhizal

# The Effects of Multiple Stressors on the Ecophysiology of Freshwater Mussels: Flow, Temperature and Turbidity <sup>x</sup>

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Freshwater mussels (Unionidae) are important constituents of aquatic systems because they are ecosystem engineers and provision water quality. Unfortunately, their habitats have been degraded through sedimentation and erosion as a result of land use changes, as well as altered hydrology and increased temperatures due to climate change. The goal of this research is to assess how the multiple stressors of flow, temperature and total suspended solids (TSS) affect the feeding of freshwater mussels. *Lampsilis siliquoidea* (n = 50; shell length = 11.00 ± 0.21 [mean ± SEM] cm) were acclimated to three water temperatures and examined at three levels of water velocity and TSS concentration in a split-split-plot design. In addition, treatments acclimated to 12.5 and 27.5 °C were examined at 20°C to determine acute temperature effects. Mussel feeding increased with flow and temperature, and decreased with increasing TSS concentration, as has been found in single-stressor studies. The interactions of the multiple stressors were, however, more complicated including both positive and negative multiplicative interactions. For example, in a worst-case scenario, increased water temperature and intensity of rain events would lead to a greater decrease in feeding than is predicted by individual stressors alone. The multistressor approach provides a more ecologically relevant way to examine organisms in nature as well as insight into ways to protect and recover their populations.

# Using stable isotopes to determine the effects of diet on metabolic fuel use in the yellow-rumped warbler (*Setophaga coronata coronata*)

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Previous correlative studies suggest that high protein diets in birds may increase the amount of protein they oxidize while flying, although an experimental wind tunnel study did not support this relationship. We tested this hypothesis that diet composition can affect nutrient oxidation in resting, fasted birds by directly tracing amino acid and carbohydrate oxidation with isotopically labelled substrates. We used technology that allows the analysis of stable carbon isotopes in breath CO<sub>2</sub> in real time, to measure nutrient oxidation in yellow-rumped warblers (*Setophaga coronata coronata*), fed a high carbohydrate or a high protein diet. As this technology was new, the study was divided into two parts: first, methods development was undertaken to determine the effects of the route of administration on tracer oxidation, and then diet was manipulated to study the effects of diet. During methods development, warblers were gavaged or subcutaneously injected with <sup>13</sup>C enriched glucose or leucine, and differences in instantaneous and cumulative oxidation rates were compared. Birds given the enriched tracer via gavage reached their maximum oxidation rate faster, oxidized approximately 3 nmol/s more, and arrived at their final cumulative oxidation faster than those given the same tracer via subcutaneous injection. During diet manipulations, warblers were kept on a 60% carbohydrate or 60% protein diet, and were subcutaneously injected with enriched glucose or leucine. Warblers kept on a high-carbohydrate diet reached their final cumulative oxidation values slightly quicker when given enriched leucine than those kept on a high-protein diet. This may be because of the nature of leucine in metabolism as a ketogenic amino acid. Our findings do not support the hypothesis that high protein diets increase the use of protein as a metabolic fuel during negative energy states, such as fasting or exercise.

## **Diet: it's all about location, location, location! How urbanization influences isotopic signatures and oxidative stress in eastern chipmunks (*Tamias striatus*)**

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Urban habitats provide wildlife with reliable access to human food waste that is vastly different in nutrient content compared to natural food resources. Human food subsidies may influence the physiology of eastern chipmunks (*Tamias striatus*) living in urban habitats because this diet is atypical. I tested whether chipmunks in urban habitats are consuming more corn-based foods, high-protein foods, and antioxidant-rich foods than their natural counterparts by studying carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) signatures in hair and the concentrations of antioxidants in feces, respectively. I predicted chipmunks in urban habitats would have higher carbon and nitrogen signatures, and excrete more antioxidants compared to their natural counterparts because of the increased access to human food waste. We collected hair and fecal samples from individual chipmunks across 20 different locations throughout Sudbury, Ontario that varied in their degree of urbanization. To quantify urbanization, we surveyed all study sites over a three day period to score the level of human activity. Chipmunks from more urban habitats had higher nitrogen signatures than those from natural habitats, indicating that chipmunks from urban habitats are consuming a diet higher in protein, compared to their natural counterparts. There was no effect of urbanization on carbon signatures, and thus there was no significant difference in the consumption of corn-based foods. We also found females consume more antioxidants in urban habitats than their counterparts in natural habitats. As a consequence, chipmunks in urban environments may be at a higher risk for metabolic diseases because they are mostly consuming an anthropogenic diet. Additionally, my results may be pertinent for understanding how other species may consume human food waste and how the nutrient content of that diet may vary, depending on the degree of urbanization of a given area.

# Temporal changes in functional and taxonomic b-diversity of the Laurentian Great Lakes freshwater fish communities x

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The addition of non-native species and loss of native species has modified the composition of communities globally. Although changes in b-diversity over time have been well documented, there is a need for studies incorporating multiple time periods, more than one dimension of biodiversity, and inclusion of nestedness and turnover components to understand the underlying mechanisms structuring community composition and assembly. Here, we examined temporal changes in functional dissimilarity of fish communities of the Laurentian Great Lakes and compared these changes to those of taxonomic dissimilarity by decade from 1870 to 2010. We used Jaccard-derived functional dissimilarity index to quantify changes in functional b-diversity within communities, between all possible pairs of communities, and across all communities through time. Similar to patterns in taxonomic dissimilarity, each community differentiated over time, with Lake Superior changing the most (~24%) and Lake Ontario the least (~14%) compared to the historical community of 1870. However, while communities have become taxonomically homogenized, functional differentiation has occurred between communities over time. This is likely due to historically high functional similarity between the communities. The higher taxonomic turnover relative to functional turnover indicates that the species being replaced are functionally redundant, and this could be the result of the relatively harsh environmental conditions of the Laurentian Great Lakes region and/or the glacial history of the region. The biotic differentiation observed is likely due to the addition of non-native species with functional traits unique to the region or the loss of functionally redundant native species. This study is the first to comprehensively examine changes in patterns of taxonomic and functional b-diversity between the historical and present-day community, as well as continuously examine the dynamics between those two points in time.



# Baylisascaris larval migrans in wild rodents and lagomorphs in Ontario: A 30-year retrospective analysis x

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The larval stage of the raccoon roundworm, *Baylisascaris procyonis*, is known to infect a wide variety of birds and mammals. Following ingestion of infective eggs from the environment, these accidental hosts can develop severe, potentially fatal, neurological disease. We investigated the incidence of lesions consistent with *Baylisascaris* sp. larval migration in lagomorphs and rodents submitted to the Ontario node of the Canadian Wildlife Health Cooperative (CWHC) over a 30-year period. Examining the case reports for 837 animals submitted from 1989-2018, we identified animals with histological lesions typical of neural larva migrans (NLM) including the presence of inflammation and malacia of brain tissue, and in some cases, characteristic nematode larvae. Thirteen species of rodents and three species of lagomorph were submitted to the CWHC. Lesions consistent with *Baylisascaris* NLM were observed in 17% of submissions, representing 44% of those whose primary diagnosis was infectious in nature. Neural larva migrans were observed in 64% of submitted groundhogs (*Marmota monax*) which was the highest prevalence of lesions among examined species. Although *Peromyscus* sp. mice are believed to be the primary paratenic host for *B. procyonis*, only 10 animals were included in our dataset, none of which were positive for NLM. Therefore, the CWHC database may be better suited for surveillance of some species over others, resulting in potential gaps in knowledge overall. Nevertheless, determining the commonly affected species in Ontario will not only assist wildlife veterinarians, pathologists, and rehabilitation centers triage and diagnose individuals effectively, but also guide future work in identifying species important to the ecology of *Baylisascaris* sp. in Ontario.

# Forest and Conifer Amount around Stopover Sites Matter to Migrating Songbirds—Not in the Ways We Think

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Stopover sites, locations where migrating birds stop to feed, are crucial for their survival during migration. The study of stopover sites provides insight into the mechanisms causing changes in migratory bird populations, through affecting survival or subsequent breeding. These mechanisms can then be used to identify important stopover sites for conservation. Landscape composition may be an important factor in stopover site selection by birds. We examined the relationship between bird density at stopover sites and (1) the amount of surrounding forest, and (2) the proportion of that forest that was coniferous. In autumn 2018, autonomous recording units (ARUs) were set up at 37 stopover sites in Eastern Ontario, Canada, to monitor populations of nocturnal songbird migrants during daytime. A Generalized Additive Model (GAM) was applied to the number of bird calls per minute (a proxy for bird density) against the % of the surrounding landscape in forest and the % of that forest in conifer. We evaluated the landscape variables at multiple scales between 0.5-km and 15-km radius, and we accounted for time-of-day and date. Surprisingly, we found that the number of bird calls per minute declined with both increasing % of landscape in forest (at a 2-km scale) and increasing % of forest in conifer (at a 6-km scale). The selection of stopover sites surrounded by less forest suggests that nocturnal songbird migrants prioritize landscape complementation for diverse food resources, e.g. insect prey in crop fields. The selection of sites surrounded by less conifer suggests that they prefer food resources associated with deciduous forests. Our results suggest that conservation of sites surrounded by low forest, mainly deciduous, at relevant scales could aid survival of migrating songbirds en route to their wintering grounds.

# **The Woes of Winter Warming: The Impact of Winter Length on the Reproductive Cycle in Pumpkinseed Sunfish (*Lepomis gibbosus*)**

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The increased unpredictability of contemporary seasonal temperature cycles is disrupting the phenology of organismal life histories. In freshwater, this disruption is exacerbated at Northern temperate latitudes where seasonal water temperature oscillations are most pronounced. At these latitudes, the IPCC has projected that winter will be disproportionately impacted by global climate change. Though the role of winter in the context of aquatic ecology is still unresolved, the truncation of cold, ice-covered periods will likely have drastic downstream impacts on temperate and Arctic freshwater biota. Here, we investigated the impact of winter length on reproductive preparation and allocation in wild-caught pumpkinseed sunfish (*Lepomis gibbosus*) under simulated winter and spring conditions. We supplemented laboratory work with two years of monthly field collections (April-September) prior to and following spawning from the same pumpkinseed population. Though pumpkinseed are warm-water fish, we predicted that the misalignment of temperature and photoperiod cues associated with shorter winters would result in decreased reproductive preparation and allocation. This prediction was supported by both laboratory and field data; under simulated short winters, both reproductive preparation and allocation in males and females was consistently lower than in control and long winter treatment. In the field, fish sampled during the year with more rapid spring warming exhibited delayed reproductive preparation and reduced allocation. These results suggest that, even in warm-water fishes, rapid decreases in winter length may be associated with decreased reproductive output and recruitment. Such outcomes will be critical when forecasting fisheries stock trajectories and understanding the impacts of climate change on freshwater systems.

# **What is the value of community science? Participation in Bumble Bee Watch program increases awareness and skills and contributes to scientific data but user accuracy varies and room for improvement exists x**

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- Talk URL: <https://youtu.be/J1W2jzAludk>

Bumble Bee Watch is a community science program where participants submit photos of bumble bees from across Canada and the United States for expert verification, with the data used to help conservation efforts. It is important to understand the demographics, motivations, and outcomes of those who participate, as well as areas that are working well or could be improved. It is also important to understand who verifies the submissions, uses the data and their views on the program. Finally, a comparison between perceived accuracy of identification and actual accuracy, particularly for species of conservation concern, can be helpful to evaluate the need for expert review and to develop new identification resources. We present the results of a survey of participants and experts, with comparisons made to data submitted to Bumble Bee Watch. Most participate to contribute to scientific data collection, because of a worry about bees and a desire to help save them, to learn more about species nearby, and because of a personal interest. Many report increased awareness of species diversity and improvement in their identification skills. Respondents were happy with the program, particularly the website resources, the contribution to conservation efforts, the educational values, and obtaining identifications. Areas for improvement included app and website functionality, faster feedback, localized resources, and more communication. Perceived ease of identification was significantly different between experts and users and did not relate to actual accuracy of identification in most species. We compared user submitted names and final expert identifications and calculated that, for all species combined, the percent agreement (accuracy) between users and experts was significantly different at 53%, with individual species ranging from 0% to 100% agreement. Species at higher risk of extinction were more likely to be mis-identified than other species.

## Ethology Abstracts

### **No evidence for stress-mediated kin discrimination in the North American red squirrel (*Tamiasciurus hudsonicus*)** x

Alexander J Hare\*, Amy EM Newman, Ben Dantzer, Jeffrey E Lane, Stan Boutin, David W. Coltman, Andrew G McAdam

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A wide range of species have been found to differentiate kin from non-kin. However, the ability to recognize kin or the costs and benefits of discriminating kin from non-kin might depend on particular environmental or physiological conditions. This can result in context-dependent kin-discrimination, where differential treatment of kin and non-kin only occurs under certain conditions. North American red squirrels have been shown previously to discriminate the territorial calls of kin and non-kin. More recently, however it was hypothesized that kin discrimination might depend on the physiological state (acute stress) of the caller. Here we tested this hypothesis using a repeated-measures playback experiment in the Yukon Territory, controlling for both relatedness and the context in which the playback stimulus was collected (acute stress versus non-stressed callers). While squirrels were shown to register and respond to playbacks, the acute stress state in the sender had no effects on receiver behaviour. This experiment indicates that acute stress in the sender does not mediate kin discrimination in red squirrels, and we further found no evidence of kin discrimination through territorial rattles in red squirrels.

# A meta-analysis of the true effect sizes of winner and loser effects <sup>x</sup>

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The experience and outcomes of aggressive contests between two same-sex conspecifics can have profound effects on an individual's behaviour and success in subsequent contests, where winners are more likely to win repeated contests (winner effects), and losers are more likely to repeatedly lose (loser effects). Quantifying the magnitude of these effects is of great interest to biologists because fighting success can influence an individual's ability to acquire and hold resources, territory, and mates. However, many of the studies that have quantified these effects commit selection bias by pairing two animals in a fight and assigning the winner to a "winner" treatment, and loser to a "loser" treatment, rather than testing individuals randomly assigned to these treatments. Here, we performed a meta-analysis to quantify and compare the effect sizes of winner-loser effects in studies that commit selection bias and studies that used proper experimental methods to investigate if biased methods result in inflated estimations. We used Google Scholar to search for all primary studies on winner-loser effects and systematically extracted the results of 33 papers that met our selection criteria (measured fighting outcome of winners and losers against a naïve competitor). We found that although the persistence of winner-loser effects appears to be consistent across all studies, the estimated effect sizes of winner-loser effects does not significantly differ between those that used random- and self-selection protocols. We argue that although biased methodologies should be avoided, it may be that in this particular case that winner-loser effects are not strongly influenced by intrinsic biases.

## **Broiler chicks' motivational strength for different wood shavings and degrees of soiling x**

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Standard practice in rearing broiler (meat) chickens allows the birds' litter to accrue with excreta, feathers, and waste feed over the five to seven-week grow-out period. However, if improperly managed, litter can compromise the welfare of broiler chicks. To help prevent litter quality degradation, farms may opt to either replace litter or apply a chemical ammonia reductant. This experiment evaluated chicks' preferences for different litter management practices using a two-compartment consumer-demand test to determine the strength of preference. The experiment housed 40 three-week-old broiler chicks in six pens that consisted of a 'home' (H) and 'treatment' (T) compartment separated by a barrier with two unidirectional push-doors. H contained built up, soiled "home" shavings while T contained either a feed treatment (gold standard) or one of four litters (aspen wood shavings, pine & spruce wood shavings, soiled pine & spruce wood shavings, or ammonia reductant treated soiled pine & spruce wood shavings). To assess the chicks' motivation to access the different treatments, the push doors leading to T weighed 0% (doors were lifted), 10%, 20% or 30% of the chicks' body weight. The time spent in T, number of times birds pushed to access T, and the maximum weight birds pushed to access T were used to determine the strength of their preference for the different treatments. Chicks preferred feed over all litters and showed an equal relative preference for all litters. However, broiler chicks' preferences for litter management practices under commercial conditions must be further assessed along with the long-term effects of these practices on broiler health and welfare.

# Planar ears in a 3D world; Larviposition aiming behaviour of the acoustic parasitoid *Ormia ochracea* (Tachinid | Diptera) x

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Spatial sound localization is a complex behaviour requiring the integration of horizontal, vertical, and distance measurements to generate a point in three-dimensional space where the sound originated. The parasitoid fly *Ormia ochracea* localizes potential hosts by eavesdropping on host (calling field crickets) mating calls using a specialized hearing organ, however, the mechanics of this organ limits directional hearing to a single plane of measurement and the accuracy of larviposition, forceful expulsion of larvae from distal tip to sound source in front, requires three-dimensional localization. To test if three-dimensional sound localization was used during larviposition, female response to sound at three different sound intensities and three heights was recorded. There were significant differences in behaviour for both intensity and height; at higher sound intensities females initiated larviposition at a farther distance and female body position matched speaker height, indicating active aiming. We propose that by rotating their ears in the sound field, females gain vertical directional cues instead of strictly horizontal directional cues and sound intensity is used as a proxy for distance. The integration of these measurements allows *O. ochracea* to spatially localize sound despite the planar limitations of their hearing organs.



## Evolution Abstracts

### **Speciation in the lab - Reproductive isolation as a consequence of divergent selection regimes x**

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In this study we address whether three decades of divergent life history selection on development time has resulted in the evolution of reproductive isolation between the laboratory populations. Evolved differences in body size, an important sexually selected trait in *D. melanogaster*, and the increased ability of larger flies to cause and resist mate harm suggested the potential for sexual selection and sexual conflict as well as mechanical incompatibilities to create pre-zygotic barriers in this system. We tested for pre-mating reproductive isolation through individual female, male, and group mating choice assays in 3 replicates of population pairs undergoing divergent selection. Previous (unpublished) data suggests hybridization between the focal populations results in the production of viable, adult flies with intermediate developmental traits. We tested for the existence of post-zygotic isolation through a reproductive fitness assay of hybrid flies in comparison to the focal parental lines. While the signal of post-zygotic reproductive isolation is unlikely to evolve early in the speciation process of *D. melanogaster*, the length of divergent selection in this system is unmatched, and the possibility is acknowledged. Our results indicate that these populations do show assortative mate choice indicative of pre-zygotic reproductive isolation, and that there are only minimal trends suggesting the evolution of post-zygotic reproductive isolation. These results suggest to us that the evolution of reproductive isolation in hybrid zones between populations in recent allopatry are likely to be a consequence of pre-zygotic reproductive barriers than hybrid inviability. We believe that this study paves the way to use such replicated laboratory populations to study the potential of mutation order divergence to produce reproductive isolation in populations with tightly controlled niches.

Assay details on following page

- All the flies in the experiments were sexed and collected as virgins prior to being housed together
- The individual mate choice assays provided a single focal fly two potential mates – one from each of the paired diverging populations. Mate choice, latency to mating and copulation duration were measured. 200 individuals were assayed, per sex/selection regime/replicate pair (~2400 total).
- The group mate choice assay housed 10 focal females with 24 males – 12 from each of the paired diverging populations. Proportion of homotypic mating was measured. 10 group vials assayed per selection regime/replicate (~60 vials)
- In our competitive fitness assays individual focal flies were housed with flies of both sexes marked with the recessive brown eye colour marker, and the proportion of red-eyed (wild type) offspring that ensued was measured. 30 individuals we assayed per sex/cross/replicate (~1080 total)

# Genomic signatures of reinforcement in sympatric populations of a sister-species pair of North American birds <sup>x</sup>

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Speciation results in the development of reproductive barriers between lineages, yet recently diverged species often hybridize in geographic regions where their ranges overlap. If hybrid offspring are unfit or inviable, selection may favour increased reproductive isolation between species. This process, known as reinforcement, can help facilitate the process of speciation and contribute to the maintenance of evolutionarily distinct lineages in sympatry. While reinforcement has been demonstrated in several animal species, its genomic effects are poorly known. Here, we use population-level whole-genome datasets to test for genomic signatures of reinforcement in alder and willow flycatcher (Tyrannidae), two bird species that are broadly sympatric in the southern Great Lakes region. We identify a large candidate region of a single autosomal chromosome that is potentially involved in reinforcement. This region shows elevated differentiation ( $F_{ST}$ ) between sympatric populations relative to baseline differentiation in allopatry, as well as signatures that it is under selection (reduced nucleotide diversity and Tajima's  $D$ ) in the sympatric willow flycatcher population. In addition, the best-fit demographic model from coalescent simulations suggests that interspecific gene flow did occur between species when sympatry was first established, but has since ceased, consistent with expectations of increasing reproductive isolation over time due to reinforcement. In contrast, these patterns were not observed in a very narrow region of range overlap in British Columbia where signatures of reinforcement are not expected, because gene flow from nearby allopatric populations may overwhelm any potential selection in sympatry. In British Columbia, there was no evidence that the candidate region is under selection, and substantial introgression between species continues to the present day. Overall, our results provide some of the first empirical genomic evidence of reinforcement for any species and suggest that the propensity for species to develop reinforcement may depend on their extent of geographic range overlap.

# Divergent Selection in Visual Opsins in Beloniformes

## Driven by Habitat and Behaviour <sup>x</sup>

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Beloniformes (i.e. needlefishes, halfbeaks, medakas, and flyingfishes) are surface-dwelling, schooling, epipelagic fishes that play an important role in oceanic food webs and fish farming. They are an extremely diverse family with intriguing morphological traits such as needle-like jaws or enlarged pectoral fins for “flight”. Belonids also contain marine-derived lineages; freshwater species that evolved from marine ancestors upon invasion of freshwaters. Shifting between freshwater and marine habitats fundamentally changes the requirements in visual perception in key vision genes (i.e. opsins). Marine waters are abundant in short, high-energy wavelengths due to low turbidity making these systems “blue-shifted”. Freshwater systems of the same depth are more turbid and attenuate blue light resulting in long, low-energy wavelengths of red light, thus freshwater habitats are “red-shifted”. However, constrained to the upper limits of the water column marine and freshwater belonids are exposed to the full light spectrum and rely on colour vision, whereas deep-dwelling fishes rely on dim-light vision due to reduced light availability. We use molecular approaches to analyze the rate of nucleotide substitutions in Beloniformes to assess the selective pressures on dim-light and colour vision genes by family and habitat. Our results indicate vast divergent selection among the colour opsins based on family and habitat, with greater positive selection in medium-wavelength (green-sensitive) opsins in freshwater belonids and in the needlefish family, and long-wavelength (red-sensitive) opsins in flyingfishes and sauries. Furthermore, the dim-light opsin rhodopsin was also found to be under significant shifts in selection based on diet in needlefishes which was unexpected for diurnal predators that forage under a broad daylight spectrum. Although belonging to the same order, these families differ in spatial distribution, diet, and physiology; factors that likely drive divergent selection in visual opsins.

## Functional characteristics of lichen mycobiont genomes

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Symbioses between organisms allow for the exploitation of ecological niches and have the potential to drive evolutionary change. Lichens are classic examples of symbiosis, yet we still do not understand the evolutionary drivers of the lichenizing life strategy of fungi, nor how this strategy has arisen and been maintained multiple times across fungal evolution. To begin to better understand the lichen symbiosis, we investigated fundamental traits of the nuclei and cells of lichenized fungi to identify what changes when a fungal lineage becomes lichenized. First, we designed and tested methodology for examining nuclear content in lichenized fungi, as no prior existing protocol tested has yielded reproducible results. We adapted an established Feulgen image analysis densitometry protocol to account for the unique response of lichens, particularly their generally small genome size and the tendency of the hyphal cell walls to bind with Schiff reagent. Next, we measured nuclear content and several key characteristics of the nuclei, cells, and extracellular matrix, including hyphal cell diameter, multinucleation, and presence of bacterial clusters. We examined these characteristics across a breadth of lichenized fungal taxa, to account for evolutionary history, structural type, and ecological tolerances. We found that lichenized fungal nuclear content ranges over a six-fold difference in size, and are on the smaller end of the range of known fungal genome sizes. We found that the presence of bacterial clusters is common, and they typically appear either adhered to hyphal strands or distributed in a jelly-like substance in the extracellular matrix. This newly generated knowledge of the nuclear content and functional characteristics of lichenized fungi at the cellular level, and the methods developed to generate this knowledge, will allow us to further generate interesting hypotheses about the nature of the lichen symbiosis and the evolutionary drivers of lichenization.

# Considering the Taxonomic Classification of *Escherichia coli*

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As new techniques have been introduced, specifically the possibility for sequencing complete genomes, methods for better defining bacterial species have been proposed. One of the most recent methods to identify species, using bioinformatic techniques, is to calculate the average nucleotide identity (ANI) between the genomes of different species. Another method for species classification that has been tested successfully is the similarity of DNA compositional signatures. However, in a recent assay, DNA signatures split the available *Escherichia coli* complete genomes into three different groups. To check if this result was consistent with such strains belonging to different species, we tested three other methods to see how the same *E. coli* strains would cluster. The three methods used were ANI, DNA signatures and 16S rRNA identity. All species delimitation methods clustered strains of *E. coli* slightly differently. However, one similarity among all three methods was that there were 24 strains that clustered out of the main group. Suggesting that these strains should not be classified as species of *E. coli*. Going forward, this research will now focus on further analysis of those genomes to decide if the DNA signature and ANI results are good indicators that the strains of *E. coli* should be reclassified into different species. These results will also aim to determine if there is a more appropriate threshold for DNA signature similarity in order to replace ANI for classification, as DNA similarity can be calculated much faster than ANI.

# An Improved Shine-Dalgarno Model Reveals Evolutionary Differences in Cyanobacteria and Chloroplast Translation Initiation

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Microorganisms require efficient translation to grow and replicate rapidly, and translation is often rate-limited by initiation. A prominent feature affecting translation initiation in prokaryotes is the Shine-Dalgarno (SD) sequence found in the 5' UTR of mRNAs, which pairs with the anti-SD sequence located at the 3' terminus of mature 16S rRNA (3' tail). Mechanistically, a good SD signal that facilitates ribosome recruitment requires optimal SD/anti-SD pairing potential and location. Nonetheless, there is much debate over SD function, especially in Cyanobacteria and in chloroplasts which presumably originated from endosymbiosis of ancient Cyanobacteria. Elucidating their utilization of SD sequences is important to understand whether 1) SD role in Cyanobacterial translation initiation has been reduced prior to chloroplast endosymbiosis, or 2) translation initiation in Cyanobacteria and in plastids has been subjected to different evolutionary pressures. The challenge lies in the identification of optimal SD signals because the 3' tail is often mis-annotated. To correct these errors, we employed an RNA-Seq-based approach to accurately characterize the 3' tail in 18 bacterial species. These results allowed us to propose a new model to better define optimal SD/anti-SD complementarity and locational constraints. To validate our newly proposed pairing location coined as DtoStart, we conducted Ribo-Seq analyses and showed, with single-nucleotide resolution, that increase in ribosome loading rate in SD-facilitated genes precisely aligned with DtoStart. Finally, we found that cyanophages well-mimic Cyanobacteria in SD usage because both have been under the same selection pressure for SD-facilitated translation initiation. In Cyanobacteria, optimal SD sequence significantly increases protein expression, and SD-less genes compensate by having weaker secondary structure at the 5' UTR. Whereas chloroplasts lost these characteristics because the need for SD-mediated initiation has been reduced in plastids as a result of host-symbiont coevolution.

## Ecology & Ethology Abstracts

### **The Stability of Individual Differences in Activity in Maturing Sea Lamprey (*Petromyzon marinus*)**

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- Talk URL: <https://youtu.be/zZQn0Zo1c-Q>

Conservation and resource managers need methods to control the spread and reproduction of invasive species. Trapping can be a useful control method if efficiency is high enough to reduce population size. An understanding of how consistent individual differences in behaviour influence trapping efficiency is needed because, in many species, differences in behaviour have been correlated with trapping vulnerability. A study performed on sea lamprey (*Petromyzon marinus*), an invasive species in the Great Lakes, found that trapping vulnerability was unrelated to consistent individual differences in activity, contrary to findings for many other species. One explanation for this finding is that initial differences in behaviour become unstable as sea lamprey mature. We tested if consistent individual differences in activity in the lab remained stable while maturing sea lamprey were released in the field, trapped, and rescored for activity in the lab. Activity was measured as the proportion of time spent moving during a lab trial. The activity of individuals declined over time, and individual ranks in activity were maintained to a moderate degree before and after trapping. These results are helping sea lamprey managers understand if trapping can be an effective method of control.



## **Should I stay or should I go? Experimentally testing for phenotypically-directed movement behaviour using sunfish ecotypes**

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Adaptive divergence of populations in sympatry is known to be resisted by gene flow between those populations. However, recent theory suggests that gene flow may also promote divergence under certain circumstances. For example, matching habitat choice can promote adaptive population divergence if individuals sort themselves among discrete habitat patches based on functional phenotypic differences, thereby potentially reducing gene flow. One way this could be achieved is through directed movement behaviour. Directed movement is a mechanistic response of an individual to select a site or habitat after departure from a natal site, as opposed to random movement. I employed a mark-transplant-recapture experiment using specialized sunfish ecotypes to test for phenotype matching behaviour and other mechanisms that may contribute to directed movement behaviour in the field. Sunfish ecotypes consume different prey in the shallow, inshore littoral and deeper, offshore pelagic lake habitats. Various morphological traits differ between ecotypes consistent with some degree of prey specialization because of functional trade-offs in feeding performance. Here I hypothesize that phenotype-habitat associations are formed by directed movement behaviour of adult and near-adult individuals. In addition, the mechanism by which they choose to leave and select new habitats is hypothesized to be due to phenotype matching behaviour. Results indicate that strong directed movement operates in the system on both site and habitat scales, although the effect of phenotype-matching on this behaviour seems to be subtle, combined with a strong homing response. Ecotypes also exhibit interesting differences in movement behaviour that may reflect heritable or learned differences. In addition to consequences for adaptive divergence, understanding what drives individual movement behaviour and habitat selection are necessary in conservation and management where identifying significant habitat is critical for population maintenance.

## **Intraspecific variation on predation rate in *Stratiolaelaps scimitus* (Womersley) (Acari: Mesostigmata) in response to short-term acclimation <sup>x</sup>**

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Extreme climate events, such as heat waves, are becoming more frequent and intense with temperatures that often exceed optimal ( $T_{opt}$ ) for many ectotherms, decreasing performance and survival. With increased exposure organisms can acclimate to these conditions through behavioral and physiological mechanisms. In our study, we used a reciprocal transplant experiment to determine how feeding rate and body size of an invertebrate predator (*Stratiolaelaps scimitus* (Womersley) consuming prey (*Carpoglyphus lactis* (Linnaeus))) changed with increased acclimation time (one, three, seven days, and a control) to a new temperature (16°C and 24°C). Our data revealed that increasing acclimation time of predators reared at 16°C and placed in 24°C lead to feeding rates similar to predator mites reared at 24°C, while predators reared at 24°C but placed at 16°C had feeding rates that were constant across acclimation times and similar to that of 16°C reared predators. On average, 24°C acclimated predators lost more weight when food deprived compared to predators acclimated at 16°C, but body size varied little between 16°C and 24°C mites post-feeding, regardless of acclimation time. These results suggest that recovery for predators after a heat stress event is possible when exposed for a longer duration. Climate warming has led to increasing mean temperatures, but short-term variability as well. Understanding the implications of these short-term warming events will aid in understanding and predicting future interactions amongst individuals.

## **Till Death Do Us Part: Mate mortality predicts breeding dispersal in Canada jays**

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- Talk URL: [https://youtu.be/jaiiG\\_fA7Yw](https://youtu.be/jaiiG_fA7Yw)

Dispersal in animals can be shaped by both environmental and social constraints. Among adults, breeding dispersal provides individuals the opportunity to acquire a new mate or territory. However, dispersing does not guarantee improvement in future reproductive success and the mechanisms behind breeding dispersal remain poorly understood in vertebrates. We examined the causes and patterns of breeding dispersal within a marked population of Canada jays (*Perisoreus canadensis*) that have been monitored since 1964 in Algonquin Provincial Park, Ontario. Across all years of the study, breeding dispersal occurred 97 times, which was 4% of all potential breeding events. We used generalized linear mixed models (GLMM) to examine the relative contribution of explanatory factors affecting breeding dispersal and dispersal distance and used linear models to quantify whether the frequency of dispersal events has changed over time. Dispersal tended to occur most frequently when an individual's partner disappeared, but this effect only occurred when the disappearing partner was older. Dispersal distances ranged from 500 m-35 km (mean  $\pm$  SD:  $2 \pm 4$ ), but no variables significantly influenced breeding dispersal distance. The number of dispersal events each year also significantly increased over time. Our results suggest that the primary motivation for dispersal in Canada Jays occurs when their mate dies, particularly when their mates are older. Thus, social factors rather than environmental factors seem to shape dispersal strategies in adults.

## Ecology & Evolution Abstracts

### **Raccoon vs. world: The eco-physiological consequences of urbanization on raccoons (*Procyon lotor*)**

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Cities are expanding globally, resulting in drastic changes to natural landscapes that present challenging circumstances to wildlife as they strive to adapt to these alterations. However, readily available food sources in urban areas have allowed certain species to prosper instead. Diets in urban environments primarily consist of anthropogenic food waste, but the physiological consequences associated with this type of food consumption have rarely been studied. We examined the impact of an urban diet on raccoon (*Procyon lotor*) fat and glucose metabolism, as well as body condition using mass-size residuals. Blood samples, hair, and morphometric measurements were collected from individuals throughout Southern Ontario and Quebec, across a natural-urban gradient. The level of urbanization associated with each site was quantified and given an 'urban score' using various landscape characteristics, such as buildings, roads, croplands, vegetation, and other man-made structures. Carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) stable isotope analysis was used to quantify access to, or consumption of, human food by the raccoon. Our preliminary results show that between natural and urban environments, there are no significant changes in fat or glucose metabolism. Since sampling occurred in the fall, the absence of change in fat and glucose metabolism is likely due to the animals building up fat stores to prepare for the winter season. Although there are no significant changes in male raccoon body condition, it is shown that female raccoons from urban environments are found to be in poorer body condition compared to those from natural areas. These results are likely due to male raccoons exhibiting a capital breeding strategy, while female raccoons would be considered income breeders. Overall, this research will provide a preliminary model that can help researchers understand the effects of urbanization on wildlife populations while allowing for the development of better management techniques so humans and animals can coexist.

## **Genomic analyses reveal strong population structure and admixture in black rat (*Rattus rattus*) population in India**

x

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- Talk URL: <https://youtu.be/DnEZbN2irD4>

Rodent constitutes 40% of mammalian diversity. The black rat, *Rattus rattus*, and the house mouse, *Mus musculus*, are the world's most widespread and destructive invasive rodent species. *R. rattus* revealed a long history of commensalism and were transported by humans during maritime operations. All previous studies on *R. rattus* heavily focus on mitochondrial DNA analyses and include very few samples from India. Considering India as the focal point of origin and spread of commensal black rat to the rest of the world, understanding population structure within India is of utmost importance. In this study, we sampled 34 *R. rattus* samples from east coast and west coast, regions that spread commensal rats out of the subcontinent. Few *R. rattus* were also sampled from central India including three mice to be used as outgroup species. Genomic DNA obtained from samples was subjected to Genotype-By-Sequencing (GBS) to scan their genome for SNPs. FASTQ files of *R. rattus* were analyzed along with the reference genome of *R. norvegicus* for SNP calling in TASSEL-GBS pipeline version 3. After filtering, resulting vcf file comprising of 27 *R. rattus* and 3 *M. musculus* samples were subjected to population genetics indices estimation and phylogenomic tree construction. Our first ever genomic study on *R. rattus* reveal strong population structure in contemporary *R. rattus* population within India. We identified two east and west coast specific clusters along with a few hybrid individuals. We argue the role of ~5000 years old Indus civilization in shaping the genome of the black rat during their transition from wild ecological niches to urban ecological niches with the advent of agriculture and city life. The resulting genomic data will be discussed in the light of archaeology and ecology of the Indian subcontinent.

## **Do species need to adapt to persist outside their ranges for multiple generations?**

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- Talk URL: <https://youtu.be/91wPBp0jS2c>

Biologists often infer long-term ecological and evolutionary processes from short-term experiments. For instance, many species exhibit stable limits to their geographic ranges and the most direct way to test mechanisms causing these limits is to experimentally plant species within and beyond their ranges. However, most experimental populations are only followed for a single generation, preventing insight into long-term demography and potential for local adaptation beyond the range. In 2005, we transplanted eight source populations of the Pacific coastal dune plant *Camissoniopsis cheiranthifolia* into four sites within and one site beyond its northern range limit. During the first generation, fitness of beyond-range transplants was often greater than within-range populations, suggesting that this range edge is limited by dispersal rather than niche constraints. More than 10 generations later, plant density and individual fitness remain high in descendent populations beyond the range. To determine whether experimental populations adapted to the extreme environment beyond the range, we performed a second transplant experiment in 2018 using individuals from all 8 original source populations and 5 original transplant sites, including the beyond-range site. All populations were planted at two sites within-range, one at the range edge, the original beyond-range site, and a site further beyond range. Lifetime fitness at both beyond-range sites was again high, but recruitment into the following generation was low at the far-beyond site. Individuals sourced from beyond range populations did not outperform individuals from within the range when planted beyond the range, suggesting a lack of local adaptation to conditions beyond the range. Taken together, our results provide strong evidence that dispersal limits the northern range of this species.

## Phylogenetic Signal of Sub-Arctic Beetle Communities

Samantha E. Majoros\*, Sarah J. Adamowicz

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- Talk URL: <https://youtu.be/keYbJCT-JaM>

Post-glacial dispersal and colonization processes have shaped community patterns in sub-Arctic regions such as Churchill, Manitoba, Canada. Important questions remain about the species that colonized this area, in particular the role of glacial history and biological traits in governing colonization patterns from refugial and southerly geographic regions. This study quantifies sub-Arctic beetle phylogenetic community structure using the net relatedness index (NRI) and nearest taxon index (NTI); calculated using publicly available data from BOLD; compares patterns across families with different traits (habitat, diet) using standard statistical analysis (ANOVA) as well as phylogenetic generalized least squares (PGLS) using a family-level beetle phylogeny; and compares phylogenetic community structure in Churchill with a region in southern Canada (Guelph, Ontario). The dominant pattern detected in our study was that aquatic families were much better represented in Churchill compared to terrestrial families, when compared against richness sampled from across Canada and Alaska. Individually, most families showed significant phylogenetic clustering in Churchill. Closely related species were likely found together due to the strong environmental filtering present in Arctic environments. There was no significant difference in phylogenetic structure between Churchill and Guelph, although the trend was towards stronger clustering in the North. Similarly, there was no difference in phylogenetic structure metrics calculated for aquatic vs. terrestrial beetle families, again with a trend towards stronger clustering in water beetles. By contrast, there was a significant relationship between diet and community structure. Predators showed significantly stronger clustering in Churchill compared to other feeding modes, perhaps due to phylogenetic conservatism of their overwintering ability or generalist diet of some clades within families. This study contributes to our understanding of the traits and processes structuring insect biodiversity and macroecological trends in the sub-Arctic.

## **Seasonally-induced cardiac remodeling and adaptive divergence of heart plasticity in Pumpkinseed (*Lepomis gibbosus*)**

Susan M. Procopio\*, Frédéric Laberge, Beren W. Robinson and Caleb Axelrod

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- Talk URL: <https://youtu.be/3yn5hPfvwRM>

Experimental work on temperature acclimation suggests that ectothermic fish preserve cardiac function during seasonal temperature change by means of reversible cardiac remodeling, which is required for effective performance in ecological tasks and can influence fitness. Heart plasticity may be energetically costly and thus subject to loss under relaxed selection. This study investigated whether Pumpkinseed (*Lepomis gibbosus*) spongy heart ventricles (without compact myocardium) can remodel in response to seasonal temperature change, and whether seasonal cardiac remodeling is reduced or lost in fish exposed to reduced temperature seasonality for multiple generations. We measured relative heart ventricle size and myocardial collagen content in Canadian and Spanish Pumpkinseed populations sampled across seasons from a location subject to high-temperature seasonality (amplitude = 30 °C) in Lindsay, ON. The Spanish Pumpkinseed were transplanted from a Canadian ancestral population into a low-temperature seasonality regime (amplitude = 15 °C) for over 100 years before being brought back in a semi-natural common garden environment along with two Canadian local populations. Canadian Pumpkinseed collected in the summer had smaller hearts than Canadian Pumpkinseed collected in any other season, evidencing seasonal cardiac remodeling in this species. Spanish Pumpkinseed demonstrated no significant variation in heart size across seasons, suggesting that Spanish Pumpkinseed have lost the ability to remodel the heart across seasons, as predicted. This is the first demonstration of cardiac remodeling in a fish species with a spongy ventricle. Further, these results suggest that cardiac remodeling is energetically costly and can be lost under relaxed selection over a time scale of approximately 25 generations.



## OE3C 2020 Plenary Speakers

### Obese humans and fat birds: what is the role of limited, unpredictable food? | Dr Melissa Bateson



Find out more about Dr. Bateson's work [here](#).

### A strike for ecosystem health: the round goby invasion of the Great Lakes | Dr. Sigal

#### Balshine

Dr. Balshine's research interests are centred on evolutionary behavioural ecology with a special focus on sociality, breeding system evolution and anthropogenic impacts on behaviour. Dr. Balshine received her B.Sc. in Zoology from the University of Toronto, a Ph.D. from the University of Cambridge and conducted post-doctoral research at Tel Aviv University, the Konrad Lorenz Institute for Ethology in Vienna and the University of East Anglia in Norwich. Dr.

Balshine joined the Department of Psychology, Neuroscience & Behaviour in 2000 and was granted tenure in 2006 and full professor status in 2011. She is also an associate member of the Department of Biology at McMaster University and is a member of the Animal Behaviour Society and the International Society for Behavioural Ecology. Find out more about Dr. Balshine's research [here](#).



## Insights from avian hybridization into the origin and maintenance of biodiversity | Dr. Scott Taylor



Dr. Taylor is an Assistant Professor in the Department of Ecology and Evolutionary Biology at the University of Colorado Boulder. Research in his lab is focused on using natural avian hybrid zones and recent avian radiations to understand the genetic bases of traits involved in reproductive isolation, population divergence, and speciation, and the impacts of anthropogenic change, including climate change, on species distributions, interactions, and evolution. He and his lab are fascinated by natural history and the intersections between art and science, and are committed to doing their part to increase diversity and make our community inclusive and supportive.

Scott completed his B.Sc. at the University of Guelph in Wildlife Biology, his Ph.D. at Queen's University, and was a Banting Postdoctoral Fellow at the Cornell Lab of Ornithology. He currently teaches ornithology and population genetics, as well as field courses in the Galápagos, Brazil, and the Rocky Mountains. Find out more about Dr. Taylor's work [here](#).

## OE3C 2020 Planning Committee

OE3C is a student-run, student-focused conference celebrating the very best ecological, ethological, and evolutionary research being done in Ontario and surrounding areas. The University of Guelph organizing committee is very proud to host the 50th annual OE3C online in 2020!

### Committee Co-chairs



#### Meagan King

Meagan is one of the OE3C co-chairs and also works on fundraising for the 2021 event. She is currently doing her post-doctoral research on wildlife health and welfare with Claire Jardine and Jane Parmley at the University of Guelph.

#### Alicia Halhed

Alicia completed her undergraduate degree at Trent University in 2019, majoring in Forensic Science with a minor in biology. She is currently a Bioinformatics MSc student at the University of Guelph studying microbial ecology in the Department of Integrative Biology. Her thesis research focuses on the metacommunity dynamics of microbiomes from two host species – the Canada Jay and the North American Red Squirrel.



## Committee Members



### Michelle Lavery

Michelle is a PhD Candidate in Integrative Biology, studying how degree of preference might change the effects of environment enrichment on the welfare, cognition, and brain development of laboratory zebrafish with Dr. Georgia Mason. She has previously completed an MSc in Biology at the University of New Brunswick, where she studied the winter ecology of Atlantic salmon. She's currently running this website and handling OE3C's twitter account!

### Aileen Maclellan

Aileen completed a BSc in Animal Biology at the University of Guelph, before beginning an MSc with Dr. Georgia Mason examining the effects of standard, barren housing the behaviour of laboratory mice. This laid the groundwork for her PhD, where she is investigating whether the stress of standard cages causes states consistent with clinical depression, and whether environmentally enriched cages protect mice from such effects.



### Lindsey Kitchenham



Lindsey is an M.Sc. student in Dr. Georgia Mason's Animal Behaviour and Welfare lab. She completed her H.B.Sc. in Psychology Brain and Cognition with a minor in Neuroscience here at the University of Guelph. Her research is aimed at understanding the neurobiological correlates of cage-induced stereotypic behaviours in laboratory mice by comparing the effects of barren (standard laboratory housing conditions) versus enriched housing on stereotypic behaviour severity/type and neuronal activity in the basal ganglia and the prefrontal cortex. She looks forward to continuing this work in her Ph.D.



## Xuezhen Ge

Xuezhen completed a BSc and MSc at Beijing Forestry University. Currently, she is a second-year PhD candidate working on climate change impacts on species distribution, supervised by Dr. Jonathan Newman in the Department of Integrative Biology at the University of Guelph. She uses species distribution models and investigates the roles of biotic interactions, climate variation, and evolutionary change in determining species distribution under climate change.

## Colin Bonner

Colin is a PhD student in the Integrative Biology department studying the ecological and evolutionary effects of climate change in the Swedish Arctic. His work focuses on how plants have migrated and shifted their phenology over the past century by comparing modern observational and experimental data to transect data from the turn of the century.



## Nathaniel Quarrell

Nathaniel is a Masters student in the Norris Lab expecting to graduate in 2020. He is currently studying how environmental factors effect the lower range limits of Canada Jays on Vancouver Island. His future interests lie in pursuing ecological epidemiology.

## Quinn Rausch

Quinn (they/them) is a PhD student at the Ontario Veterinary College studying animal welfare and behaviour. Specifically their research focuses on early puppy socialization and development. They completed a BScH in Animal Biology from the University of Guelph in 2018 and entered their PhD program with Dr. Lee Niel in September of 2019. They have a passion for ethology and joined the OE3C Organizing Committee to be able to give back to the local scientific community.



## Faculty Advisor



### Georgia Mason

Dr. Mason is a behavioural biologist who moved from Oxford to Canada in 2004 to take up a Canada Research Chair in Animal Welfare at the [University of Guelph](#). In May 2020, she became Director of the [Campbell Centre for the Study of Animal Welfare](#). She and her fabulous lab are interested in how animals adapt (or otherwise) to barren, unstimulating captive housing conditions. In other words, if animals are healthy, well-provisioned and protected from physical harm, is that all that they need for good welfare? Or do they still need to be able to perform activities like social interaction, foraging, or ranging? She also studies sentience, environmental enrichment, and states like 'boredom', to name a few.

## Abstract Review

The OE3C 2020 planning would like to extend thanks to the members of the University of Guelph community who assisted with the review of abstract submissions. We would like to acknowledge the following individuals for their assistance in abstract review.

Shannon French

Jonathon Kotwa

Angela Demarse

Gavin Hossack

Braden Judson

Nathaniel Quarrell

Matthew Furst

Sophia Stoltz

Hayley Wilson

Xuezhen Ge

Colin Bonner

Alex Sutton

Thanuja Fernando

Ashley Skillings

Aliana Hellmuth

Anna Solecki

Alicia Halhed

Lena Levison

Cassandra Carolino

Melanie Denomme

Robert Matson

Erin Ross

Ana Rentsch

Emily Leishman

Hannah Golightly

Midian Nascimento Dos Santos

Kristina O'Hanley

Rosie Whittle

Carol Tinga

Michelle Lavery

Aileen Maclellan

Lindsey Kitchenham

Meagan King

Nienke Van Staaveren

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Laura Frielingsdorf

Patrick Barclay

Angélica Oliveira

Aleta Pleasant

Jolene Giacinti

Quinn Rausch

## OE3C 2020 Sponsors

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