

Ontario Ecology, Ethology and Evolution Colloquium



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Abstracts

Poster Presentations

1. Development of auditory sensitivity in the big brown bat (*Eptesicus fuscus*)

Doreen Möckel and Paul A. Faure

Bats have exceptional hearing which they use for passive orientation, alerting functions, and communication—just like other vertebrates. Additionally, echolocating bats use hearing for orientation and prey detection. In this study, we documented progressive change in auditory sensitivity by measuring change in the auditory brainstem response (ABR) of individual big brown bats (*Eptesicus fuscus*) over development. The ABR is a synchronous neural response evoked by acoustic stimulation and is thought to represent the summed activity of neurons in the auditory pathway between the cochlea and upper brainstem. We recorded the ABR and measured thresholds of hearing by presenting bats with different sound frequencies and amplitudes. Recording ABRs is a relatively non-invasive procedure, hence measurements can be conducted in either awake or lightly anaesthetised animals and repeated in the same individual to track the onset and development of hearing capabilities. We measured hearing thresholds in nine *E. fuscus* every 3 days, starting at postnatal day (PND) 10 and ending at PND 34 when pups neared adulthood. Between recordings, nursing pups were returning to their mother. During development, there was a dramatic shift in auditory sensitivity across frequencies between 4 and 100 kHz. Prior to PND 13-16 when young bats were still not flying, most pups were unable to hear frequencies above 48 kHz; however, sensitivity to higher ultrasonic frequencies increased with age. Notably, this change in ultrasound sensitivity occurred near the time when young bats start to fly and echolocate.

2. Assessing land use impacts in mussels in the Saint John River with mercury and stable isotopes

Ellie M. Weir, Emma L. Lippert, R. Allen Curry, Karen A. Kidd

The Saint John River (SJR) in New Brunswick supports diverse aquatic communities, a population of over 500,000 people, and many different industries. In recent years, the impacts of point and non-point sources of contamination have garnered increased attention in the SJR. Elevated mercury concentrations are of particular concern since mercury is known to bioaccumulate in tissues, biomagnify across trophic levels, and cause adverse health effects in fish and their consumers. The present study used mussels as bioindicators for mercury and stable carbon and nitrogen isotopes to evaluate nutrient inputs at 23 sites across 4 physiogeographic regions to assess spatial variability in contaminants and to identify specific sites which may pose a risk to wildlife. Foot tissue from Eastern elliptio and Eastern lampmussels was dissected, freeze dried and homogenized. Samples from similarly-sized individuals were analyzed for mercury on a DMA-80 and were sent to the University of New Brunswick for determination of stable isotopes. Significant differences in mercury were observed across physiogeographic regions (ANOVA, $p = 0.0131$), with sites downstream of the Mactaquac dam having notably high concentrations. At 7 sites, mercury levels exceeded the tissue residue guidelines for mink, a predator species of freshwater mussels. $\delta^{13}\text{C}$ decreases and $\delta^{15}\text{N}$ increases occurred in mussels from upstream to downstream along the SJR, with significant differences between regions for both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ (ANOVA, $p < 0.0001$). Overall, the spatial trends in both mercury and stable isotopes of the mussels likely reflected greater inputs from agricultural and urban land use in lower reaches of the river.

3. Female Participation in Pair Bonding Strongly Connected to Reproductive Success

Lydia Horton, Dr. David White, Hayden Davies

The goal of this study was to evaluate pair bonding from a female-centric point of view. Twelve female Brown-headed Cowbirds were video recorded to uncover the relationship between social behavior and reproductive success. Results showed that four specific aspects of sociality can accurately predict reproductive success. Highly successful females stayed for longer periods of time with their pair bond and developed more complex social interactions. They also maintained a farther distance from other females. Finally, females who were less successful aligned themselves away from males. The causal relationship of these variables is unknown, but the model suggests that highly successful females actively participate in pair bonding. Therefore, females must gain an advantage from pair bonding. This has implications for the ultimate cause of monogamy in cowbirds, and the evolution of pair bonding in other species.

5. Cryptic genetic variation in natural populations and its contribution to genetic assimilation in *Drosophila melanogaster*

Sarah Marzec and Ian Dworkin

Cryptic genetic variation (CGV) is standing genetic variation with little influence on organismal phenotypes under normal circumstances, yet can lead to heritable variation under rare/novel conditions. It remains unclear whether CGV is truly neutral under most conditions, or is maintained due to unmeasured pleiotropic phenotypic effects. CGV has also been linked to genetic assimilation, the evolutionary process whereby initially phenotypically plastic traits evolve to become constitutive. This was demonstrated 60 years ago when Waddington artificially selected on an environmentally sensitive change in *Drosophila* wing morphology initially observed at low frequency. After ~13 generations, not only had the frequency increased, but individuals from the selected lineage expressed these changes in wing morphology without the environmental stimulus. While much has been hypothesized about it, the underlying genetic architecture enabling CGV to contribute to genetic assimilation remains poorly understood.

To address these questions, I have repeated Waddington's experiment. I have generated replicate lineages for the increased frequency (penetrance) of the environmentally induced changes in wing morphology. From each replicate selection lineage, I have generated independent genetically assimilated populations. Using these lineages, I have examined potential pleiotropic and fitness consequences of the CGV in these populations. I will show that in aggregate, the alleles contributing to CGV for this phenotype influence at least one fitness component. Furthermore, by deep resequencing the ancestral population and all lineages at multiple time points during the selection process, I am investigating the relative contribution of CGV and *de novo* mutations to the genetic architecture for the assimilated phenotype.

6. How does *Carassius auratus* respond when exposed to conspecific chemical alarm cues aged for different time intervals?

Jake Kment and Istvan Imre

The interactions between predator and prey represent a dynamic relationship that is of great importance in the field of behavioural ecology. In response to predation, prey often exhibit behavioural defenses in order to increase its chances of survival. It would be adaptive for prey to eventually ignore increasingly older predation cues in the environment to balance the conflicting demands of predator avoidance with behaviors that are important to the survival and fitness of the organism, like foraging and reproduction. One previous study looked at behavioural responses of certain aquatic species to chemical alarm cues of varying ages, but it has not been investigated in *Carassius auratus* (goldfish). Here, we investigated anti-predator behaviours (time spent swimming, position in the water column, and shoaling index) of goldfish in response to conspecific chemical alarm cues aged for varying intervals. We predicted that the intensity of antipredator behaviour should decrease with increasing age of the conspecific alarm cue. Experimental animals were exposed to either deionized water (control treatment) or three experimental treatments (alarm cue aged for 0, 3 and 6 hours). We observed no significant differences between treatments for any of the behavioural measures considered, indicating that goldfish do not respond behaviourally to damage-released alarm cues of any age.

7. Behavioural Syndromes in the Invasive Round Goby

Cassandra Disanto, Adrienne McLean and Sigal Balshine

The round goby (*Neogobius melanostomus*) is an invasive fish species that has successfully invaded all of the Laurentian Great Lakes and has adversely affected native fish communities and their ecosystems. Invasion success may be facilitated by consistent differences in behavior between individuals within a population of animals (termed personality) by facilitating the persistence of the population under novel selective regimes. Invasion success may also be facilitated by correlations between personality traits (termed behavioural syndromes) through coupling of behaviours that are important during multiple stages of an invasion. I tested if round goby exhibit consistent individual differences in the five recognized personality domains using standardized tests used across a wide range of animal taxa: (i) willingness to exit an enclosure into a novel environment (a measure of exploration), (ii) change in activity in response to something startling and willingness to return to movement after being startled (both measures of boldness), (iii) willingness to move around an environment free of social and predator cues (a measure of activity), (iv) willingness to amicably interact with conspecifics (a measure of sociability), and (v) hostile interactions with conspecifics (a measure of aggression). I found evidence for personality in the round goby, as individuals were consistent over time in both their exploratory and social tendencies. I also found evidence that round goby exhibit a boldness-exploration syndrome. Insights from the study of personality and behavioural syndromes can provide a novel understanding of ecological invasions and how to manage them.

8. Are tree species organized non-randomly with respect to their associated mycorrhizae?

Riley Gridzak and Brandon Schamp

A focus in the field of community ecology has been on determining how various abiotic and biotic factors drive the organization of natural communities. Several processes can structure species assemblages, including; competition, abiotic filtering, and dispersal. However, the potential influence of mutualisms has received less attention. Mycorrhiza-plant associations are extremely common, and forests have been shown to harbor diverse networks of arbuscular mycorrhizae (AM) and ectomycorrhizae (EM). Evidence indicates that mycorrhizae are capable of providing protection from pathogens, increasing nutrient uptake, and initiating below-ground resource translocation. For this reason, we investigate whether tree species are organized non-randomly within and among forests with respect to associations with AM and EcM. We use a null model approach in conjunction with tree species abundance data from two datasets (A large dataset, 366 plots; and a small dataset, 48 plots), as well as data on which guild of mycorrhizae is associated with each tree species, to test whether AM or EcM are over- or under-represented in forest plots relative to what we might expect if these associations do not influence species organization. Tree species with AM tended to be over-represented relative to EcM in both data sets; however, this was contingent on which null model algorithm was used. When we considered species abundance, we tended to see a reverse of this pattern, with EcM over-represented. It appears clear that mycorrhizal associations with trees play a role in the assembly of forest communities; however, more research is required to understand how mycorrhizae interact with functional differences among tree species to organize tree species within and among forests.

9. Gene Expression Profiles in Honeybee Brains under the Food Search Box Protocol

Bandelet Morrison, Nadia Tsvetkov, Amro Zayed

Honeybees are central place foragers. Part of what allows the bees to improve their foraging skills is their ability to learn where food patches are relative to the hive, avoid predation risk and navigate new locations. The molecular mechanisms underlying this learning ability have been investigated by using Proboscis Extension Reflex (PER) and free-flight learning protocols. Examples of genes which are up-regulated in response to visual and olfactory learning in honeybees include Early Growth Response protein 1 (EGR1), cAMP response element binding protein (CREB), dopamine receptor 1 (dop1) and dopamine receptor 2 (dop2). However, very little attention has been given to changes in gene expression during spatial learning, a key feature of navigation in honeybees. Here, we utilize a newly developed learning protocol called the Food Search Box (FBS) paradigm to study spatial learning in the honeybee. By conducting time-course experiments in the context of FBS, we are investigating how gene expression changes over time in response to spatial learning.

10. Lord of the Fleas: Shedding Light on Nocturnal Hosts and Stress Hormones

Jasmine Veitch, Jeff Bowman, Albrecht Schulte-Hostedde

Parasites are often highly costly towards their hosts, depleting energy reserves and forcing redistribution of resources. A common response to parasite presence in some host species is an increase in stress hormones (e.g., glucocorticoids). These hormones have been proposed as biomarkers of physiological state and exposure to an adverse stressor. There is very little research on mammalian stress hormones and their variation with parasite presence, and therefore, the aim of this study is to determine how costs of parasitism are mediated through endocrine function in deer mice (*Peromyscus maniculatus*). Specifically, we tested whether host individuals respond to parasite presence by increasing glucocorticoid levels. Individuals were randomly assigned to a parasite removal treatment (application of Frontline Plus ®) or a control group. Fecal samples were collected from all host individuals, and glucocorticoids were measured using enzyme immunoassays. Glucocorticoid levels did increase with parasite presence, but not significantly. This suggests that deer mice may develop a tolerance to parasites as a strategy to reduce negative symptoms. Further research should examine the use of varying concentrations of insecticides in parasite removal and the effects of nest parasites.

11. Using genomics to test for multiple modes of sympatric speciation in the Cape Verde storm-petrel (*Hydrobates jabejabe*)

Emma Gillesse

Seabirds are excellent models for studying sympatric speciation, because they face few physical barriers to gene flow, and so do not fit the classical allopatric model of speciation. However, sympatric barriers may limit gene flow on both spatial and temporal scales. Cape Verde storm-petrels (*Hydrobates jabejabe*) are highly pelagic seabirds that breed year-round on multiple islets in the Cape Verde archipelago. We investigated the presence of genetic structuring across fine spatial and temporal scales in Cape Verde storm-petrels. Double digest restriction-site associated DNA sequencing (ddRADseq) was conducted on 149 individuals sampled across five islets in the Cape Verde archipelago, and at three time points throughout the year on the islets of Raso and Cima. We found evidence of low but significant genetic differentiation between the islets of Raso, Cima, and Boavista. No significant fine scale genetic structuring was found between individuals breeding in different months on the islet of Cima, and low but statistically significant differentiation was only found between the months of July and January on Raso. These results suggest that gene flow is limited across the archipelago, and that Cape Verde storm-petrels show some degree of spatial natal philopatry. In contrast, gene flow appears to occur among populations that breed at different times of the year. We propose that this may be due to variation in the timing of individuals' first breeding, and that Cape Verde storm-petrels show minimal temporal natal philopatry.

12. Assessing hybridization and population genomic structure of Glaucous Gull (*Larus hyperboreus*) in the Canadian Arctic

Emma Lachance Linklater, Vicki L. Friesen, Gregory J. Robertson, Sarah S. Sonsthagen

Climate change poses a significant threat to the future of arctic ecosystems. To effectively conserve arctic species, genetically differentiated populations must be defined for adaptive and neutral genetic variation to be appropriately managed. The aim of this study is to compare genetic differentiation within and among Canadian populations of Glaucous Gull (*Larus hyperboreus*), a circumpolar arctic gull species. Although the IUCN currently lists the Glaucous Gull as Least Concern, declines have been reported across their range in Arctic Canada. Glaucous Gull also hybridize readily with some white-headed gull species which may lead to introgression and outbreeding depression, especially as these species continue to expand north. Glaucous Gull is a valuable species, both biologically and culturally. As apex predators, Glaucous Gulls develop high levels of toxins in their tissue and are, therefore, excellent bioindicators of the long-range transport of contaminants in the Arctic. Glaucous Gulls also represent a traditional food to some First Nations and Inuit. Currently no finescale population genetic information exists for this species, and management units have not been demarcated. We are using next-generation sequencing to compare DNA from tissue samples collected from Glaucous Gulls across the breeding range. We will assess sequences for genetic diversity, evaluate the frequency of hybrids, and determine the extent of population differentiation (using STRUCTURE). Detailed information on population genetic structure and hybridization will help conservation practitioners effectively manage the long-term persistence of Glaucous Gull populations. A proactive management strategy for this species will benefit both Glaucous Gull and the entire arctic ecosystem.

13. The genetic basis of complex traits: polymorphisms affecting wing shape and size in wild populations of *Drosophila melanogaster*

Katie Pelletier, Yuheng Huang, Will Pitchers, David Houle, John Pool, Ian Dworkin

Many traits of interest to biologists, including many diseases, have a highly polygenic genetic architecture with many alleles of small effect size contributing. However, many studies have focused on traits with a monogenic basis and alleles of large effect sizes. In addition, many identified effects of polymorphisms from lab studies cannot be recapitulated when looked at in larger populations, indicating that there is an interaction between the environment and genotype that is not accounted for. We are investigating the genetic architecture of *Drosophila melanogaster* wing shape and size using wild-caught populations of flies. First, we will test the effects of lab-identified SNPs in natural populations collected from Michigan to test for genotype x environment interactions. We will also map the variants contributing to divergence of two Sub-Saharan populations of *Drosophila* with variation in shape and size along an altitudinal cline. This will allow us to identify the polymorphisms involved in phenotypic divergence and also the effect sizes of these variants. This work will provide us with a broader understanding of the genetic architecture of *Drosophila* wing shape and size in natural contexts.

14. Distribution of mitochondrial introns in the *Cryptococcus neoformans* species complex

Yue Wang and Jianping Xu

Introns are prevalent in fungal mitochondrial genomes and they contribute significantly to mitochondrial genome size differences among species. However, there is relatively little information about their distributions among individuals within the same species. *Cryptococcus neoformans* is a human fungal pathogen that usually causes infections in the lungs or central nervous system. Using commercial monoclonal antibodies, strains collected from four regions in the United States were classified into three different serotypes (A, D and AD). In total, we have 325 samples of serotype A, 12 serotype D and 19 serotype AD with their mating type examined. Previous studies have identified ten introns present in the mitochondrial genome of model laboratory serotype D strains, JEC21 and JEC20, while in the serotype A strain H99, only one intron was detected. One objective of this study is to explore if serotype A and D strains from the clinical environment have these same intron distribution patterns. To examine this, mitogenomes of JEC21 and H99 were retrieved from the Stanford Genome Technology Center and the NCBI databases. Using BLAST, 9 exclusive introns were found in five genes in JEC21 including 3 introns in LsrRNA, 4 introns in COX1, 1 intron in NADH5 and 1 intron in COB1. Primers were designed based on the conserved intron-flanking regions of JEC21 and H99. PCR assays of these samples showed abundant variation in intron presence, absence and intron length at the five loci among strains. While most of the introns showed a biased distribution among the serotypes, there is limited geographic pattern. Further sequencing of selected introns and exons will be conducted to determine the potential mechanisms mediating intron distribution.

15. Effect of Flight Duration on β -hydroxybutyrate Concentration in Blood Plasma of *Eptesicus fuscus*

Byron, T.M.; McGuire, L.P.; Boyles, J.G.; Faure, P.A.

Insectivorous bats require changes in metabolism to compensate for high-energy activities, such as flight. Plasma metabolite analysis is one way of measuring refueling intensity. In this study, we measured plasma metabolite concentrations in the blood of captive big brown bats (*Eptesicus fuscus*). We collected blood samples in the lab from rested and exercised bats that were fasted. We quantified exercise activity as flight time. Our data indicate a correlation between exercise duration and plasma levels of β -hydroxybutyrate. Follow-up testing in the same animals suggested that β -hydroxybutyrate levels in plasma may also relate to increased food intake when bats are not fasted in captivity and/or they experience physiological changes in metabolism in the fall during preparation to overwinter via hibernation. We plan to re-measure plasma β -hydroxybutyrate levels in rested and exercised fasted bats from newly-caught, wild bats in spring 2019. The assessment of plasma β -hydroxybutyrate may provide new insights for assessing activity levels and/or torpor states of individual animals, thus furthering our understanding of bat metabolism and mammalian physiology in general.

16. Surviving the concrete jungle: The physiological consequences of anthropogenic food waste on raccoons (*Procyon lotor*) in urban environments

Christina Mozzon, Dr. Albrecht Schulte-Hostedde

Cities are expanding globally as more and more people migrate to urban areas. These novel habitats present challenging circumstances for urban wildlife because they are not matched with the habitats to which they have successfully evolved. Many species are not able to survive in urban habitats, but some thrive, in part driven by the consumption of human food waste. Little is known about the sub-lethal impacts of an urban diet on wildlife. Raccoons (*Procyon lotor*) are the ideal study species to conduct research on this topic as they are densely populated across North America and are commonly found in both natural and human-altered environments. They feed on all food available to them, including small mammals, fish, insects, and berries in natural habitats, and human food waste in urban areas. Therefore, we will examine the physiological consequences of urban life on raccoons, specifically focusing on the impacts of a diet of human food waste. We have been collecting data from three different groups of raccoons in Southern Ontario with varying levels of accessibility to garbage to determine if the animals' blood glucose and body mass will change with their diet. Stable isotope analysis will be used to quantify access to, or consumption of, human food by the raccoon. If impacts are evident, it will be important to assess the consequences for individuals' reproductive success and survival. Ultimately, evolutionary changes may be occurring to raccoons as they adapt to a new food resource.

17. Testing the effects of the social environment on female reproductive decisions and male competition

Christopher J. Fleet, David J. White, Hayden B. Davies

Altering relationships can destabilize how individuals react to each other and therefore the social environment. To test this, the present study aimed to use social networks to examine the effects of HVC lesions on the social behaviour of a captive gregarious songbird, *Molothrus ater* (Brown-headed cowbird), during the breeding season. A sample of cowbirds were taken that survived the 2017 (pre-lesion) - 2018 (post lesion) breeding seasons (males, $n = 15$, non-lesioned females, $n = 11$, lesioned females $n = 12$). It was predicted that lesions to this brain region would distort female preference for song, increasing female reactivity to songs and destabilizing competition between males. There were significantly more male-female interactions and males exhibited more variable behaviour after the lesions were introduced in 2018, suggesting that an individual's underlying neural circuitry may affect social behaviour of one's group and the social environment exerting its influence back on the behaviour of individuals.

18. Ploidy, Phenotypes and Mitochondrial genotypes of sexual progeny of the two human pathogenic fungi within *Cryptococcus* species complex

Man You and Jianping Xu

Cryptococcus neoformans species (CNS) and *Cryptococcus gattii* species (CGS) can cause life-threatening meningitis in both immunocompromised and immunocompetent individuals. Strains of CNS and CGS are haploid that either reproduce asexually by budding or sexually by mating. They possess a bipolar mating system, with either α mating type (MAT α) or a mating type (MATa). Mating may occur if cells of opposite mating types meet. In this study, we aimed to determine whether there is transgressive segregation in sexual progeny of CGS and CNS in different phenotypic traits. Phenotypes, including melanin production, growth at high temperature, minimum inhibitory concentrations (MICs) for fluconazole, and self-fertility of progeny were determined, as well as mitochondrial genotypes and mating types. We found that the progeny were diploid or aneuploid, with some of them were self-fertile. PCR analysis with primers specific for genes in the MATa and MAT α mating-type loci revealed that these progeny were heterozygous for the mating-type locus. Consistently with previous studies, most progeny inherited mitochondria from the MATa parent, and were intermediate between two parents in the tested phenotypic traits. Yet, a small fraction of progeny showed transgressive segregation, such as some progeny were observed that could grow at 42°C but none of the parents could. Therefore, our future steps will focus on: (1) the relationship between genetic divergence and phenotypic plasticity; (2) determination of the aneuploid chromosomes and nuclear genotypes; (3) the mitochondria-nuclear interactions among progeny; (4) the mechanisms/patterns that contribute to the observed transgressive segregation; (5) identification of the temperature-regulated genes.

19. Hot models: predicting the current and future distributions of two ambush bug species, *Phymata americana* and *pennsylvanica*

Vicki M. Zhang, David Punzalan, Locke Rowe

A fundamental question in ecology centers around species ranges and the limits of a physical niche space imposed by environmental variables. Species distribution models (SDM) provide the ability to identify the effect of environmental variables on species distributions and to forecast future environmentally-driven changes. One such SDM is Maxent, a machine-learning software that uses environmental raster grids to predict the probability of species presence within grids. In the present study, I use Maxent to identify the environmental variables maintaining the distribution of two closely-related ambush bug species found in parapatric distribution, *Phymata americana* and *Phymata pennsylvanica*. I also created binary suitability maps to predict the current and future ranges of both species given climate change scenarios. The model identified similar variables (temperature and precipitation) that contributed to predicting ambush bug ranges, but these variables have different means and consequently result in distinct ranges. To map future distributions, Representative Concentration Pathways (RCP) projecting various greenhouse gas emissions were used. Distributions narrow in latitude and longitude as RCP scenarios worsen for both *P. americana* and *P. pennsylvanica*, but *P. pennsylvanica* had relatively smaller-scale shifts at a lower RCP. These results provide evidence for specific environmental requirements for *P. americana* and *P. pennsylvanica* and highlight the effects of climate change on range shifts. Understanding how these abiotic factors affect ambush bug distributions will be fundamental for future research on their taxonomy and conservation.

20. The Evolution of Maneuverability in Hummingbirds

Roslyn Dakin, Paolo Segre, Andrew Straw, Douglas Altshuler

How does agility evolve? This question is challenging because natural movement has many degrees of freedom and can be influenced by multiple traits. We used computer vision to record thousands of translations, rotations, and turns from more than 200 hummingbirds from 25 species, revealing that distinct performance metrics are correlated and that species diverge in their maneuvering style. Our analysis demonstrates that the enhanced maneuverability of larger species is explained by their proportionately greater muscle capacity and lower wing loading. Fast acceleration maneuvers evolve by recruiting changes in muscle capacity, whereas fast rotations and sharp turns evolve by recruiting changes in wing morphology. Both species and individuals use turns that play to their strengths. These results demonstrate how both skill and biomechanical traits shape maneuvering behavior.

21. Mushroom-Insect Interactions: Living Together, Changing Together

Sarah Sandor, Jianping Xu

Fungi and insects are both found in ecosystems worldwide and as such, a range of complex fungi-insect interactions exist in nature. Mushroom-insect species interactions are of particular interest to study due to the transient nature of the mushroom fruiting body, which only forms during one short stage of the mushroom lifecycle to allow for spore dispersal. Despite the unpredictability of fruiting body formation, mushrooms are a common food source and egg-laying site for insects. However, few studies have examined large-scale insect association patterns encompassing a range of mushroom species and almost none have compared the evolutionary histories of both groups of organisms. This project involved conducting a broad ecological survey of wild mushrooms and the insects that were interacting with these fungi. About 370 mushrooms were collected from forests in Hamilton and the surrounding area and any insects or larvae found inside the mushrooms were removed. Mushroom and insect phylogenetic trees were constructed based on sequences of the barcoding genes (the internal transcribed spacer (ITS) region for mushrooms and the mitochondrial cytochrome oxidase 1 (CO1) gene for insects). Interestingly, several of the insects found living inside the mushrooms likely represent previously undocumented insect species. The next step of the project involves comparing the two phylogenetic trees to assess the distribution of insect-mushroom association and to look for evidence of host specificity and coevolution. This research will contribute greatly to our current understanding of mushroom-insect ecology and the evolutionary history of this interesting species interaction.

22. Living on the edge: Soil microedges provide an ecological niche for *Desmodium canadense* (Showy tick trefoil)

Jessica Kowalski, Dr. Hugh Henry

In heterogenous soils, variation among plant species in their preferences for growth in specific types of soil patches can promote increased species diversity. It has been suggested that some species may also be disproportionately abundant along the edges between patches (i.e. microedges). To examine the mechanism whereby microedges can serve as distinct ecological niches, one rare tallgrass prairie species observed anecdotally along patch edges (*Desmodium canadense*) was grown in either homogenized sandy loam, clay loam, or along the microedge, in the presence or absence of neighbours (*Andropogon gerardii* and *Solidago juncea*). Field and pot experiments were used to compare *D. canadense* establishment and competitive ability to *A. gerardii* and *S. juncea*, as well as to investigate changes in *D. canadense* root foraging strategies among the different treatments. *D. canadense* established better along the microedge in the presence of competitors than in their absence, a pattern which was not observed for *A. gerardii* and *S. juncea*. Shifts in the foraging strategies of *D. canadense* along the microedge also were observed. These results suggest that microedges provide an ecological niche for species to avoid intense competition effects yet still access beneficial soil patches, and thus, enhance their growth and survival.

23. Do we know the conditions to experimentally evolve male weapons? A test using *Drosophila melanogaster*

Audrey Wilson, Ruven Dukas, Ian Dworkin

Whether they are antlers, horns, or out of proportion limbs, male weapons are some of the most diverse traits seen in the animal kingdom. Male weaponry is often useful to the individuals that bear them because they can lead to advantages in obtaining desirable resources as well as mates. Three conditions have been hypothesized to result in the development of male weaponry; (i) there must be high competition between males for access to mates, (ii) resources on which matings occur must be organized such that males are able to defend them with only few being successful, and (iii) competition between males must be one-on-one battles. Although these conditions have been examined in many species by comparative means, it has yet to be tested if these conditions are sufficient to initiate the evolution of male weaponry. My research serves to address this issue by evolving the model organism *Drosophila melanogaster*, under different environments that represent varying levels to which the proposed conditions are met. My goal is to determine not only if the proposed conditions are sufficient for the evolution of male weaponry, but to also determine how this evolution occurs in terms of changes in morphology as well as mating and aggressive behaviours. This research has the potential to give insight into what is responsible for the extravagant structures seen throughout the animal kingdom and if our previous knowledge in this area is complete or if there are still missing pieces yet to be discovered.

24. Environmental Conditions Driving Allochronic Speciation in Seabirds

Sophie O. Raymond, Ryan P. Franckowiak, Rebecca S. Taylor, and Vicki L. Friesen

Allochronic speciation occurs when sympatric populations differentiate due to separation in breeding time. Band-rumped Storm-petrels (*Hydrobates spp.*) are a seabird species complex that shows variation in timing of breeding. Seasonal variation in prey availability is hypothesized to control timing of breeding in Band-rumped Storm-petrels, however, this relationship is poorly understood. To investigate this relationship, we examined the association between oceanographic conditions known to influence prey availability and breeding time of Band-rumped Storm-petrels. Oceanographic conditions during the breeding seasons of Band-rumped Storm-petrels were compared between the Azores Islands, where two species breed at different times and are thought to have undergone allochronic speciation, and the Cape Verde Islands, where one species breeds nearly year-round with two temporal peaks in breeding. Significant differences in sea surface temperature, chlorophyll-a concentration, and thermal fronts were observed between the two colonies and also between the warm and cool breeding seasons. This suggests both locations experience a high degree of seasonality, which presumably contributes to the observed divergence in breeding time. However, we also observed a significant interaction between location and season suggesting the two colonies may be experiencing different selective pressures. This could explain why Cape Verde has a protracted breeding season and exhibits an intermediate stage of divergence in timing of breeding. Cape Verde therefore provides a unique opportunity to study a colony of Band-rumped Storm-petrels potentially in an early stage of allochronic speciation and could contribute to our mechanistic understanding of speciation processes.

25. Effect of winter temperatures on microhabitat use by urban white-tailed deer (*Odocoileus virginianus*).

Anjalika Balasuriya, Momina Asad, Dr. Christoph Richter, Dr. Monika Havelka

White-tailed deer (*Odocoileus virginianus*) are ecological generalists that are distributed over a broad range of habitats across North and South America. They have become very successful in occupying urban green spaces and have had significant impacts on urban forests. As part of a long-term monitoring project that examines the effects of deer populations on vegetation at an urban park (The Riverwood Conservancy) in Mississauga, Ontario, we used camera traps to record the presence of deer in an urban woodlot over a three month period (January 2019 to March 2019). We hypothesized that deer use the woodlot as a refuge during periods of cold weather and, thus, there will be a temperature difference on days where white-tailed deer were sighted versus days where deer were not. Our results indicate that the days in which deer were observed (via camera trap) were statistically colder than days in which no deer were observed ($P < 0.01$). For every increase in average air temperature by 1°C, the odds of seeing a deer decreased by 0.85 times. This study provides information about seasonal use of microclimates by deer, which may have implications for urban forest ecology. Future work can include analyzing other types of weather conditions and the intersection of these factors on the presence of white-tailed deer and, therefore, their impact on urban environments.

Oral Presentations

Behavior I

26. Costs and benefits of clutch synchronization in joint-female nests

Blane Landsborough, Dr. James Quinn

Breeding males receive clear benefits from joint-laid clutches, in which multiple females lay eggs in the same nest. However, it is unclear why dominant female Pukeko (*Porphyrio melanotus melanotus*) allow other females to lay eggs in their nest. We explore whether the synchronization of clutches within kin-groups provides an alternative way to increase clutch size with a shorter laying period. We hypothesize that this will provide dominant females with greater inclusive fitness compared to the prolonged laying of a single clutch. To test this hypothesis, we manipulated joint-female clutches to create ten with exaggerated asynchronous hatching to mimic prolonged laying and nine with natural hatching synchrony as a control. We tracked hatching success, offspring growth, and offspring survival and used 'mock' measures of inclusive fitness, treating asynchronous young as if they were the dominant's offspring, for comparison between treatments. This research provides insight into how hatching synchrony affects reproductive success in joint-laid clutches, shedding light on the evolution of communal breeding in polygynandrous birds.

27. The relationship between spatial memory and elevation in a non-food hoarding great tit (*Parus major*)

Ethan Hermer, Ben Murphy, Alexis Chaine, Julie Morand-Ferron

Cognition is a suite of abilities involved in the collection, processing, storage and use of information. Learning and memory have been shown to increase foraging efficiency, survival, and reproduction. However, learning and memory also come with costs and should only be maintained in contexts where it is adaptive. Harsh environments, or environments where food resources are low or rapidly changing, are hypothesized to favour cognitive abilities that increase the ability to locate, remember, and predict the availability of food. We studied the 'harsh environment' hypothesis in non-food hoarding great tits (*Parus major*) that live along an elevation gradient that positively correlates with harshness. Spatial memory ability is predicted to increase with elevation as it may allow great tits to remember and return to previously visited food patches as other food patches are depleted. We captured a total of 72 wild great tits from 3 high and 3 low elevation sites and tested their accuracy using a spatial memory task in an outdoor aviary. We compared the number of errors they made before finding a hidden food item across 6 trials, and predict that the higher elevation great tits will perform more accurately than low elevation great tits. This study is the first to compare intraspecific differences in spatial memory in a non-food hoarding species from environments that differ in harshness. It will further our understanding of the relationship between cognition and the environment, as well as its adaptive significance.

28. No-evidence for adaptation effects of voice-pitch on attractiveness judgements

Jessica Ostrega, Anthony C. Little, Marie M. Armstrong, David R. Feinberg

Prior work has demonstrated that exposure or adaptation to voices can induce aftereffects and suggests that we use opponent coding to process voices. After exposure to high and/or low pitched voices, those voices begin to sound more normal. Studies on facial attractiveness show that these aftereffects also alter how attractive people look. After exposure to unattractive faces, unattractive faces become more normal, and more attractive, whereas attractive faces become less normal and less attractive. As voices are processed in a similar fashion to faces, we tested if adaptation to high- or low-pitch (the primary correlate of voice attractiveness) influences attractiveness of voices. Using identical stimuli and paradigm as prior work showing adaptation effects of voice pitch on normality judgments, we tested for adaptation effects of high and low-pitched voices for both male and female vocalizers. We replicated findings that there are sex differences in preferences for voice pitch, but we found no adaptation effects. This demonstrates that adaptation is not automatic, obligatory or the default in voice perception based on attractiveness preference. Our results highlight the need for rigorous replication studies in psychology.

29. Avian incubation: how previous hatchling success and ambient temperature can affect behaviour

Tanya T. Shoot, Sophie C. Edwards, R. Jeff Martin, Susan D. Healy, David F. Sherry, & Mark J. Daley

A stable nest environment is imperative for hatchling survival. Birds can vary nest structure and incubation behaviour to regulate nest temperature for successful offspring. I used a modeling approach to test the hypothesis that incubation behaviour can be adapted over short-term exposure to varying ambient temperature, and within a lab environment. I predict that birds will successfully adapt their behaviour to previous hatchling success and the ambient environment in the lab as has been seen in the field. I examined an extensive data set of nest temperatures and behaviour collected on zebra finch (*Taeniopygia guttata*) pairs that incubated at either 30°C or 14°C. Temperature loggers recorded in-nest temperature. Zebra finch pairs incubated in one of the two temperature conditions, then completed a second breeding attempt in the same temperature condition, or switched conditions. Incubation behaviour was video recorded. I used a Hidden Markov Model (HMM) to infer incubation behaviour from a subset of known behaviour and temperature data. Video records were compared to HMM predictions. Results show that the current ambient temperature and previous reproductive success significantly affect incubation duration. Further, birds that were previously successful incubated in a significantly more consistent manner than the unsuccessful birds. This research shows birds can adapt their incubation behaviour in a short period, and in the lab. The role of previous offspring success and current temperature are strong forces in driving these adaptive behaviours.

30. Physiological and behavioural effects of hypoxia and air exposure on an intertidally caring fish

Noah Houpt, Brittney Borowiec, Aneesh Bose, Nick Brown, Graham Scott, Sigal Balshine

Parental care in animals is costly. Nest site selection, a form of prenatal parental care, can lead to a trade-off between what is optimal for the offspring and the parent. Such a trade-off may occur in plainfin midshipman (*Porichthys notatus*) fish, which rear its young in abiotically dynamic intertidal zones along the West coast of North America. During their breeding season, parental males are often exposed to oxygen limiting conditions, including aquatic hypoxia and air exposure. We investigated the physiological and behavioural costs and mitigating strategies demonstrated by parental midshipman males in response to normoxia (9.1 mg/L dissolved oxygen content), declining oxygen levels (-0.8 mg/L dissolved oxygen content per hour), or air exposure for six hours. Air exposed fish showed greater physiological disturbance than normoxia and hypoxia exposed fish based on plasma and tissue metabolite measures, although glycogen content did not vary with exposure. Swim bladder oxygen content decreased during air exposure, suggesting that midshipman males may mitigate oxygen deprivation by drawing on endogenous O₂ stores. Additionally, midshipman performed surface respiration more frequently when exposed to hypoxia than when exposed to normoxia. Exposure to intertidal conditions is costly to midshipman fish, and these animals rely on a suite of physiological and behavioural coping mechanisms mitigate some of the costs of providing parental care in their dynamic environment.

31. Connecting female cognitive strategies to motivation and accuracy when prospecting for nests

Hayden Davies and David J. White

For female brown-headed cowbirds, *Molothrus ater*, one challenge in securing reproductive success involves locating and determining suitable nests to parasitize. Previous studies in highly controlled settings have provided critical insights into female cowbirds nest prospecting preferences as well as cognitive strategies they use when determining which nest to parasitize. Here, using automated tracking devices on nests in large semi-natural aviaries, we examined the decision processes underlying nest selection decisions. We collected a comprehensive dataset of female prospecting behaviour while experimentally manipulating the qualities of mock nests. We found females used varying strategies when prospecting for nests and these strategies influenced their accuracy at laying, as well as, how much time they spent prospecting and how they influenced other females within their group. These findings provide unique insights into how female cognitive strategies influence their behaviour and reproductive success.

Conservation I

32. Secondary invasion? Interacting effects of the emerald ash borer (*Agrilus planipennis*) and ecological integrity on invasive shrub establishment

Jennifer Baron, Dr. Benjamin Rubin

The emerald ash borer (*Agrilus planipennis*; EAB) is an invasive wood-boring beetle that causes high levels of ash (*Fraxinus* spp.) mortality in eastern North American forests. While the immediate impacts of the EAB are well studied, the indirect and long-term consequences are less well understood. Secondary invasions occur when one invasive species facilitates the entry or establishment of another invasive species. While limited previous work shows evidence of EAB-facilitated secondary invasion, further description of this process is needed. Forest responses to insect invasions may be influenced by ecological integrity^{3/4}the degree to which ecosystem composition, structure, and function deviate from their natural or historical range of variation. Here we investigate the effect of the EAB on understory vegetation diversity and invasive shrub establishment and, for the first time, assess its interaction with an index of ecological integrity. We quantify these impacts by comparing understory vegetation communities in EAB-induced canopy gaps, other canopy gaps, and regions without a canopy gap at sites near London, ON. We hypothesize that the EAB facilitates invasive shrub establishment through the rapid and synchronous creation of canopy gaps, and that plots with lower ecological integrity are more susceptible to non-native plant invasions following EAB infestation. Preliminary results suggest that the EAB may facilitate the establishment of European buckthorn (*Rhamnus cathartica*), an invasive shrub, at some sites. Continued research expands on these preliminary results and contributes to an understanding of the indirect and long-term impacts invasive insects have on forest structure and function.

33. Accumulation rates of marine debris on an important marine turtle nesting beach in Costa Rica

Melina Damian, Anna Harris, Costa Rica; Gail Fraser, Josaphine Aussage

Marine debris pollution is a prominent environmental concern for coastlines worldwide, this not only poses a threat for wildlife but can negatively impact the economy of communities whose livelihoods depend on ecotourism. Playa Norte beach, in northeastern Costa Rica, is an important nesting ground for four marine turtle species all identified on the IUCN Red List. Playa Norte beach is highly polluted but has low human occupancy suggesting that marine debris deposition is primarily influenced by external factors. In this study, we conducted accumulation rate surveys from March 2016 to January 2018 following the NOAA Marine Debris Protocol on Playa Norte beach. Macro-debris (debris larger than 2.5 cm) was categorized by size and material type. The quantity, concentration (number of debris items per m²) and type of marine debris will be presented and examined with local environmental variables. This study will contribute towards understanding the drivers of marine debris pollution for at-risk nesting marine turtles; and can inform managers and the local community on possible strategies that could be used to prevent and reduce marine pollution, thereby aiding in ecotourism derived economies.

34. How a changing climate in the tropics affects songbirds during their fat-fuelled migrations

Lisa Horn and Bridget Stutchbury

Migratory songbird declines are a major conservation concern, and global climate change is emerging as a new threat which has already impacted migration timing and population dynamics. Many of Canada's migratory songbirds spend 6-8 months of their annual cycle in the tropics, and in some regions hot, dry conditions are expected to occur more frequently as climate change accelerates. The amount of moisture in overwintering habitats has been found to determine food availability and, subsequently, body condition in several migratory songbird species. Drier and hotter environments in the tropics may affect the ability of migrants to prepare for, and execute, their spring migration. Studies of the relationship between climatic effects and arrival condition of migratory songbirds are scarce at more northerly latitudes, particularly in eastern Canada. I am investigating the strength of carry-over effects from climatic and habitat conditions in the tropics on bird body condition and migration timing at a northern stopover site. To assess how songbirds have historically responded to changes in habitat moisture and climatic conditions in their non-breeding habitats I am using over three decades of bird banding data from Long Point Bird Observatory in Ontario, satellite-derived imagery as a proxy for habitat quality, and climatic data. I predict that migrants will arrive later and in reduced body condition in years characterized by an intensified late-winter dry season during the critical pre-migratory period. Preliminary analyses suggest that carry-over effects of dry non-breeding seasons do not carry over to the later stages of migration.

35. Reserving suitable nesting sites for common terns in a mixed-species colony: An investigation of habitat quality and reproductive success

Molly Bradford

In mixed species colonies common among colonial nesting birds, species that arrive later to the breeding grounds, and smaller bodied species, may be vulnerable to competitive exclusion from suitable nesting habitat by larger or earlier arriving species. In this study, plastic sheeting was used to cover areas of sandy habitat on the tops of man-made islands in Windermere Basin, to deter Caspian Terns (CATE; *Hydroprogne caspia*) from nesting, and reserve this space for Common Terns (COTE; *Sterna hirundo*). The use of plastic sheeting to cover nesting substrate was not successful in deterring CATE nesting, and as a result many COTEs nested on the sloped and rocky sides of the islands, which is less preferred. Habitat quality can strongly influence reproductive success, however no significant difference was seen for hatching success among COTEs nesting on sand compared to rock. Low statistical power may be attributed to small sample sizes. Where COTEs were able to nest on sand, the cause of death of several chicks was due to suspected head trauma from aggressive adults. In the rocky habitat, chicks were found dead that had become caught between rocks and were unable to escape. The only COTEs confirmed to have fledged were from nests in suitable habitat. High disappearance of chicks, and difficulty locating nests throughout the study may be the product of high vegetative growth later in the nesting season. This study is a part of ongoing monitoring and management work conducted by McMaster University.

36. Hamilton Harbour round goby population characteristics and trapping method bias

Caitlyn Synnshyn, Sigal Balshine

The round goby is a prolific and problematic invasive species originating from the Ponto-Caspian region in Europe. The Hamilton Harbour round goby population steadily declined between 2002 and 2008. Despite this, round gobies continue to persist in even the most contaminated sites around the Hamilton Harbour. Male round gobies exhibit alternative reproductive tactics, an important life history trait that is seldom considered in the population dynamics of invasive species. Abundance, size, sex ratios, and alternative reproductive ratios are analyzed across clean and contaminated sites. Size distributions of each sex and reproductive status (non-reproductive, reproductive, and alternative tactic) are described. Additionally, different fish capture methods can have biases in terms of catch rates, species caught, and even the sex, sizes and behaviour of individuals caught. Biases caused by variation of use within a single gear type may also occur, however the implications of this variation on population estimates and characteristics are generally not considered. Minnow traps are a gear type that comes in different makes and can be filled with various bait types or left unbaited. Round goby capture rates between traps baited with corn and traps left unbaited, as well as sex, reproductive status, and size differences are compared. Understanding the biological characteristics selected for by each trapping method is important when comparing abundance and range expansion results across studies and laboratories. Differences need to be considered by managers and conservation agencies to adapt management techniques and ensure population inferences are as accurate as possible.

37. Using genomic tools to answer conservation questions in the northern fulmar

Lila Colston-Nepali, Vicki Friesen, Jennifer Provencher, Mark Mallory

Human activities and climate change are the largest threats to Arctic ecosystems. Canada has an international responsibility to protect species that inhabit or breed in its Arctic territories, including several seabirds. Population genetics may help conservation practitioners appropriately manage threatened species, by providing indications of genetic diversity within and between populations. The northern fulmar (*Fulmarus glacialis*) is a seabird that breeds in colonies throughout the North Atlantic and North Pacific Oceans. Though not currently considered at risk, fulmars face increased levels of toxins and ingested plastics. Furthermore, approximately 1% of the global population is killed annually through unintentional capture in commercial fishing activities, and fulmar survival appears to be negatively affected by climatic changes. For these reasons, we are comparing genetic variation within and among colonies of fulmars in the North Atlantic to aid development of management plans. Using restriction site-associated DNA sequencing (RADseq), an advanced DNA sequencing technology which provides thousands of genome-wide markers, we are assessing genomic variation in fulmars to determine if colonies are genetically different. Furthermore, because northern fulmars are migratory, mortality often occurs away from the breeding colony, and the impact of these sources of mortality on specific colonies is unknown. Therefore, we further aim to create panels of colony-specific genetic markers for population assignment.

Evolution/Ecology I

38. How does condition dependence for sexually dimorphic traits evolve during rapid adaptation?

Maria Pesevski, Ian Dworkin

Sexual dimorphism, the phenotypic difference between males and females, is among the most captivating phenomena in biology. Sexual dimorphism is of particular interest to evolutionary biologists as it provides resolution to sexual conflict. Condition dependence, the relationship between access to resources and the organism's resource utilization efficiency that leads to the ultimate size of the organism, is essentially universal. Considerable evidence has demonstrated that traits expressing the greatest degree of sexual size dimorphism (SSD) are the most condition dependent. It remains unclear how condition dependence of sexual dimorphism evolves under different evolutionary scenarios and, in particular, under rapid evolutionary change in a new environment. In order to examine this, we used populations of *Drosophila melanogaster* from Sub-Saharan Africa that vary substantially with altitude. The high-altitude population has undergone rapid evolution during its adaptation to the high-altitude environment. These adaptations include a substantial increase in size and wing-body ratio. We raised flies from these two populations under multiple nutritional treatments to manipulate condition. We examined wing size, shape and larval weight. We measured cell densities across the wing to assess the proximate mechanisms contributing to the size and shape changes. Our preliminary data suggests that despite substantial changes in size and shape between high and low altitude populations, sexual dimorphism for these traits does not vary greatly. We aim to test whether condition dependence of sexual dimorphism varies between the two populations in order to show how condition dependence of sexual dimorphism is influenced by rapid evolution.

39. Long-term persistence of a species beyond its natural range

Regan Cross, Christopher G. Eckert

Species should be able to continuously adapt to conditions at their geographic range edge and disperse into the habitat beyond, yet most do not. Experimental planting of species within and beyond their range directly tests the mechanisms causing stable range limits, however experimental populations are rarely followed for more than one generation, providing little 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 individuals was comparable to within-range populations, suggesting that the northern range edge is limited by dispersal rather than niche constraints. Compared to sites within the range, the beyond-range population experienced high seedling recruitment in the two seasons following the transplant. In 2017 and 2018, we quantified abundance and individual fitness at the source populations and within- and beyond-range transplant sites. Approximately 12 generations after the original planting, beyond-range individuals remained as abundant and reproductively successful as within-range individuals, providing compelling support for a role of dispersal in limiting the northern range edge for this species. Long-term experiments provide robust conclusions in the face of environmental stochasticity, and allow for a better understanding of how species respond to novel habitats.

40. Impacts of altered metapopulation dynamics and dispersal limitation on the northern range limit of a Pacific coastal dune plant

Michael Dungey, Dr. Chris G Eckert

It is widely thought that the limits to species geographic distributions are niche limits expressed at a large spatial scale. However, recent meta-analysis of experiments that have moved species beyond their geographic range limits suggests that these limits are caused by constraints on dispersal rather than low population fitness caused by niche constraints. Altered metapopulation dynamics, through high dispersal costs and increasing spatial isolation of suitable habitat patches, can restrain habitat colonization and subsequently impose range limits. In this experiment, I will examine whether metapopulation dynamics and/or dispersal limitation cause the stable northern range limit in a Pacific coastal dune plant, *Camissoniopsis cheiranthifolia* (Onagraceae). Previous experiments have shown negligible local adaptation and similar fitness between within and beyond range transplants, suggesting dispersal limitation. With high habitat heterogeneity and frequent environmental disturbance of the coastal back dunes where *C. cheiranthifolia* resides, the system is an ideal setting for examining potential metapopulation range limitation. Hypotheses will be tested through high spatial-scale remote sensing habitat suitability analysis of the species latitudinal range, species distribution modelling to identify patterns in habitat heterogeneity as populations extend north, and ground-truthing field surveys to measure habitat patch occupancy and fitness's. Greenhouse experiments using within-range seed sources will also be conducted to examine potential trade-offs in *C. cheiranthifolia* seed dispersal potential and germination success. Understanding how metapopulation dynamics influence distribution, particularly as many at-risk Canadian plant species have northern distributional limits, will be critical for species conservation under increasing pressures for northern range expansion under climate change.

41. Melanin pigmentation predicts survival of *Daphnia melanica* following UV-B radiation exposure

Julia Muuse, Brooks Miner

Melanin pigmentation is frequently observed in organisms found in habitats with high levels of ultraviolet radiation (UVR). It has been hypothesized to be photoprotective, particularly when deposited in the outermost tissue of an organism, such as the carapace of the microcrustacean *Daphnia*. Because UVR that reaches living cells can lead to DNA damage and potential death, it could be a potent selective agent in natural populations. *Daphnia melanica* is a species of zooplankton found in high-elevation, high-UVR exposed lakes in the Sierra Nevada. In this study, we examined the concentration of melanin as a predictor of survival in *D. melanica* following experimental UV-B radiation exposure. We reared genotypes of *D. melanica* from four different Sierra Nevada lakes and measured melanin content upon maturity, followed by laboratory exposure to UV-B radiation. Our results show that individuals with higher levels of melanin were more likely to survive following UV-B exposure, demonstrating the photoprotective effect of carapace melanin pigmentation for this species.

42. Is within-brood variation in progeny dispersal a bet-hedging strategy against habitat heterogeneity?

Jory Griffith, Regan Cross & Christopher G. Eckert

Climate change, biological invasion, and habitat fragmentation have spurred a resurgence of interest in the ecology and evolution of dispersal because it directly impacts the movement of individuals and their genes in time and space. Past studies have focused on the mean dispersal traits of species and populations to understand how dispersal evolves in response to environmental change. However, dispersal traits often vary among the offspring within an individual brood, and this may be an adaptation to environmental variance in space and time. We tested whether within-brood dispersal variation has evolved as a strategy to bet hedge against spatial habitat heterogeneity. We used the coastal dune endemic *Abronia umbellata*, which disperses its seeds within winged anthocarps carried by wind. This species also exhibits a mating system shift from outcrossing in southern populations to selfing in northern populations. This allowed us to test the hypothesis that selection favors increased mean and variance in dispersal in outcrossing populations as bet-hedging against variation in pollinator service. We measured the mass-corrected wingedness of 10 anthocarps from 30 focal plants sampled in each of 14 populations distributed across much of the species' geographic distribution. We also measured the heterogeneity of suitable habitat around each focal individual. As predicted, outcrossing populations had both higher mean dispersal and higher within-brood variation in dispersal. Unexpectedly, within-brood dispersal variation exhibited a complex cubic polynomial relation with habitat heterogeneity, suggesting that habitat may influence within-brood dispersal variation but in a more complex way than previously imagined.

43. Evolution of three herbicide defence strategies: Trade-offs between glyphosate escape, resistance, and tolerance in *Amaranthus palmeri*

Zachary Teitel and Christina M. Caruso

In response to the application of herbicides, weeds can evolve multiple defensive strategies, including escape, resistance, and tolerance. Because evolving all three of these strategies is redundant, there should be trade-offs between the expression of escape, resistance, and tolerance. For example, populations that express high levels of herbicide resistance should express low levels of escape and tolerance. To test for trade-offs, I measured the expression of escape, resistance, and tolerance to glyphosate herbicide in 22 populations of the agricultural weed *Amaranthus palmeri*. Escape was measured as days from planting to emergence, with later emergence indicating a higher probability of escape; resistance was measured as the number of undamaged leaves following glyphosate treatment, with more undamaged leaves indicating higher resistance; and tolerance was measured as the fitness of glyphosate unsprayed weeds subtracted from glyphosate sprayed weeds, with no difference indicating perfect tolerance, a negative difference indicating lower tolerance and a positive difference indicating overcompensation. Expression of all three defensive strategies were evident in every population, though only escape and resistance significantly varied across populations. The expression of escape was positively correlated with resistance. The expression of tolerance was not correlated with either escape or resistance. These results show evidence for trade-offs between some defence strategies, but not others. Knowing which strategies are or are not trading off is useful for determining the persistence of some defence strategies over others in a population.

Behaviour II

44. Odour-based discrimination of similarity and diversity at the major histocompatibility complex in songbirds

L. Grieves, G. B. Gloor, M. A. Bernards, E. A. MacDougall-Shackleton

The major histocompatibility complex (MHC) is the most polymorphic region of the vertebrate genome. Individuals with more MHC alleles can respond to a broader suite of pathogens, suggesting that selection should favour the ability to assess the MHC genotype of potential mates. Indeed, MHC-based mate choice, particularly preferences for MHC-dissimilar or MHC-diverse partners, appears widespread among vertebrates. Mammals, fish, and seabirds assess MHC through odour cues. However, despite the prominence of songbirds in mate choice studies, the mechanisms by which this group might assess MHC remain speculative. Motivated by the discovery that chemical similarity in the preen oil of song sparrows (*Melospiza melodia*) predicts similarity at MHC class II, we examined preen oil odour preferences for MHC dissimilarity and diversity. We presented breeding-condition song sparrows with preen oil from opposite-sex conspecifics using a two-choice Y-maze design. We compared time spent with odour from MHC-dissimilar versus similar birds, and MHC-diverse versus less diverse birds. Both sexes spent more time with odour from more MHC-diverse than less-diverse birds, and males spent more time with odour from MHC-dissimilar females. We conclude that song sparrows, and presumably other passerines, can use preen oil odour to discriminate MHC similarity and diversity of potential mates.

45. Learning how they let go: Lamellar autotomy performance in live damselfly larvae

Gavin Hossack and Beren Robinson

Autotomy is a surprising antipredator trait because it is common in animals despite self-amputation of a body part harming the individual. Selection can favor autotomy when the benefits of increased chance of escape from a grasping predator exceed such harm. In arthropods, autotomy performance is regulated by traits that biomechanically influence the breaking plane at appendage joints. Modeling predicts an optimal breaking force for a population under specific predation risk and autotomy cost conditions. In dead larval damselflies, joint size is positively correlated with peak joint breaking force, yet variation in joint width persists in natural populations. Using live larvae, we tested for effects of joint size on autotomy performance (time to breakage), and whether behaviour compensates for effects of joint size variation on autotomy performance. We recorded behavioural activity leading to autotomy in live larval damselflies whose caudal lamella was held by a simulated predator but were otherwise allowed to freely move. After accounting for body size, individuals with larger joints took longer to autotomize as expected. However, variation in behavioural activity up to lamellar autotomy was unrelated to joint size and so did not appear to compensate for larger joints. Extending the consequences of lamellar joint size on autotomy performance in live individuals strengthens the idea that selection can act on joint traits that influence autotomy performance. Furthermore, the absence of behavioural compensation may simplify expectations of how lamellar autotomy evolves.

46. Kin recognition and co-operative foraging in *Drosophila melanogaster* larvae

Lucas Khodaei & Tristan A.F. Long

A long-standing goal for biologists and social scientists is to understand the factors that lead to the evolution and maintenance of co-operative behaviour between conspecifics. To that end, the fruit fly, *Drosophila melanogaster*, is becoming an increasingly popular model species to study sociality, however, most of the research to date has focused on adult behaviours. In this study, we set out to examine group feeding behaviour by larvae, and to determine whether the degree of relatedness between individuals mediates the expression of this co-operation. In a series of assays, we manipulated the average degree of relatedness in groups of third-instar larvae that were faced with resource scarcity, and measured the size, frequency and composition of feeding clusters, as well as the fitness benefits associated with co-operation. We found that larvae *D. melanogaster* are capable of kin recognition (something that has not been previously described in this species), as clusters were more numerous, larger, and involved more larvae, when more closely-related kin were present in the social environment. These findings are discussed in the context of the correlated fitness-associated benefits of co-operation, the potential mechanisms by which individuals recognize kin, and how that kinship plays a central role in facilitating the manifestation of this co-operative behaviour.

47. Live fast, die young: Males that perceive competition alter the fitness of their mates

David Filice, Reuven Dukas

In many species, the reproductive interests of males and females conflict. Intense male-male competition for the opportunity to sire offspring has led to the evolution of selfish reproductive traits manifested via sperm competition that are harmful to the females they mate with. In the fruit fly, *Drosophila melanogaster*, males modulate their reproductive behaviours based on the perceived intensity of competition in their immediate environment. Specifically, males housed in social groups with other males (high competition) transfer a larger ejaculate during mating compared to males housed alone (low competition). Here, we set out to test if the difference in this investment has a significant effect on the fitness of the females that these males mate with. We briefly exposed females to males that were either housed alone or housed with a pair of rivals every other day for twenty days and then measured the lifetime longevity and fecundity of these females. We found that males who perceived more intense competition (housed with rivals) reduce the lifespan of the females that they mate with, and that this may be explained by a trade-off in female reproductive investment over time. These results highlight the complexity of sexual conflict and help explain the maintenance of variation in male mating strategies.

48. “General” cognitive abilities and risks associated with dimensionality reduction

Marc-Antoine Poirier, Julie Morand-Ferron and Vincent Careau

In the field of cognitive ecology, Principal Component Analyses (PCA) are frequently used to obtain individual scores for so-called "general" cognitive skills. This technique is somewhat similar to the estimation of the intelligence quotient (IQ) in humans, and is regularly presented as a measure of importance in animal cognition. Although the use of PCAs may be appropriate, an overview of its application in the literature raises several questions. We present an example based on data from a recent publication (Sauce et al., 2018; Proc R Soc B) estimating general cognitive abilities from PCA. We argue that the use of PCA in Sauce et al. (2018), and mainly the reduction of dimensionality, leads to erroneous conclusions. Our re-analysis suggests that the trends observed for "general" abilities are based here on only one of the five cognitive traits measured. We demonstrate how the analysis of individual traits, unlike the general scores, results in a better understanding of cognitive abilities and their genetic and environmental determinants. We suggest alternatives based on the use of mixed multivariate models and discuss the implications of dimensionality reduction on the study of cognitive traits in a context of evolutionary ecology.

49. Artificial selection on forced copulation success in *D. melanogaster*

Janice Yan, Carling Baxter, Reuven Dukas

Sexual conflict has been subjected to intensive research and it is taken as a given that males should be persistent at pursuing reluctant females. While it is often difficult to distinguish between male persistent sexual pursuit and aggressive coercion, we have focussed on a unique system in which we can exclusively study forced copulation. Male fruit flies aggressively pursue newly emerged, sexually immature females who, for a short period, can neither escape by flying nor prevent intromission. The females later produce a small number of offspring from such forced matings. Our analyses indicated significant genetic variation among males in sexual aggression. In our artificial selection study, we have generated lineages of sexually aggressive and sexually docile males, with the former having 3 times higher forced copulation rates. Males from the sexually aggressive lineages are more persistent at pursuing females and engage in more forceful mating attempts than males from the sexually docile lines. We are now in the process of studying the genomics of sexual aggression and its possible genetic correlations with other pertinent traits.

Conservation II

50. Getting one's ducks in a row: Conservation units of common eiders (*Somateria mollissima*) throughout North America

Russell R. Turner, Sarah A. Sonsthagen, Robert E. Wilson, Ryan P. Franckowiak, Philip Lavretsky, Marie-Josée Fortin and Vicki L. Friesen.

Anthropogenic climate change is producing a variety of consequences on ecosystems and biodiversity. Collectively these changes are negatively impacting species survival and are increasing rates of extinction. Species can, however, adjust to environmental changes through range shifts, phenotypic plasticity, or genetic adaptation. To ensure successful species conservation in the face of climate change, it is now crucial that a species' capacity for such change, as well as existing evolutionary differences among populations, are incorporated into species' management plans. Climate change will have a devastating impact on Arctic reliant species. Here, I evaluate the spatial genetic structure of a highly mobile Arctic breeding sea duck, the Common Eider (*Somateria mollissima*) by analyzing double-digest restriction site-associated DNA sequencing (ddRAD-seq) data from 320 ducks originating from 24 breeding populations spread across North America. I identify two evolutionarily significant units that show a clear west-east divide, which is suggestive of two distinct glacial refugia. I also identify five to six genetically distinct management units and detect three potentially adaptive units within North America. I also identify a pattern of isolation-by-distance across my entire study area and within the Eastern evolutionary significant unit. However, this pattern was not evident within the Western evolutionary significant unit. Taken together, my results reveal biologically appropriate population structuring that is vital to incorporate for the successful long-term management of the eider. This study contributes to the growing body of literature that has produced a broad spectrum of genetic diversity and divergence in avian populations that inhabit the Arctic that will help better manage their conservation.

51. Relative surface temperature measurements from satellites can be used to monitor terrestrial restoration projects

Jonas Hamberg, Stephen Murphy, Roydon Fraser, Derek Robinson

Monitoring restoration requires measuring ecosystem change. According to James Kay, an ecosystem's ability to degrade the useful work potential inherent in incoming energy (exergy) can be used as a measure of ecosystem development. As terrestrial ecosystems undergo succession after restoration, they grow both in biomass and in complexity. In turn this increases evapotranspiration, photosynthesis, and nutrient cycling which increases the ecosystems destruction of exergy, reducing the amount of energy re-emitted as heat from the ecosystem during the day.

For this research project, we tested if the relative temperature difference between paired restoration and a mature forest reference area decreased over 12 years, based on satellite thermal imagery. Starting in 2006, the restoration project is composed of actively seeded oak-woodland areas and passive (non-seeded) areas. The thermal data was compared with vegetation data to test if temperature decreases with an increase in species diversity (complexity) and ground cover (biomass).

Results show that both treatment areas were significantly warmer than the reference state in 2007 and then both decreased significantly between the beginning and end of the experiment (2018) with the active area being significantly cooler than the passive area. The percentage of ground covered by vegetation increased significantly for the passive area but not the active area. Plant species diversity, measured in Hill-number, increased significantly in both active and passive areas. This fits with the ecosystem-exergy theory. Overall, thermal imaging is shown to be a useful tool for monitoring ecosystem restoration areas, with relative temperatures decreasing with increasing ecosystem development.

52. Dispersal and fecundity across an invasion front in brown widow spiders

Anamaria Mihai, Monica A Mowery, Maydianne CB Andrade

Invasive species are problem throughout the world due to the negative impact they have on native species. They are often unintentionally introduced to a new region, and their ability to spread past the point of introduction can cause ecological damage. *Latrodectus geometricus* is a species of brown widow spider native to South Africa that has spread around the world through human-mediated transport. We investigate dispersal, size, and fecundity of *L. geometricus* to better understand how the species has been able to spread throughout the United States and Israel and if there are any differences among the populations established for different amounts of time. We hypothesized that successful invaders would show correlated traits that increase the likelihood of establishment and spread in new habitats, but these effects would be strongest in more recently-introduced populations. We predicted tradeoffs with high dispersal ability and fecundity linked to decreased offspring size, particularly in populations on the leading edge of invasion (recently introduced populations). We assessed these traits in the laboratory, using offspring of spiders collected from populations with different known times of introduction in the USA and Israel. We discuss our results in terms of insights for understanding traits that allow invasive invertebrate species to spread, which may allow anticipation of ecosystem damage following introductions.

53. Neophobia is affected by habitat urbanization in wild black-capped chickadees

Catherine Jarjour, Julian Evans, Julie Morand-Ferron

As human populations increase and city borders grow, many animals have to modify foraging behaviours in order to exploit evolutionarily novel urban food sources that could aid their survival. Neophobia, the fear of novelty, can lead to missed opportunities in these cases. Therefore we expect novelty to elicit different responses in urban and rural populations, a difference that is infrequently explored in free-ranging individuals in their natural habitat. Here we studied the novelty response of wild animals in ecologically-relevant conditions while controlling for individual characteristics. We predicted that urban black-capped chickadees (*Poecile atricapillus*) would be more likely to initially contact novelty than rural chickadees, and that subordinates and juveniles would be more likely to first contact novelty than dominants and adults, respectively. We ran replicated experiments using three novelty types on six sites and found that urban chickadees showed less neophobia than their rural counterparts, the latter initially contacting the familiar feeder before the novel feeder. There was no significant effect of an individual's dominance, age or sex on its first choice of feeder, nor was there an effect of novelty type. Overall, our results suggest that urban chickadees exhibit less neophobia than their rural counterparts, because they have generally learned to tolerate novelty in their habitat and/or they have adapted to live in an environment that rewards low neophobia.

54. Conservation genetics of geographically disjunct populations

Alyson Van Natto & Christopher G. Eckert

A species' genetic structure results from interactions between genetic drift, natural selection and gene flow and, therefore, strongly depends on the species' spatial distribution and can have a profound influence on the management of species at-risk. Species listed as "at-risk" in their geopolitical region, including approximately 75% of the terrestrial species at-risk in Canada, are often peripheral populations of a species that is much more common elsewhere, and a large proportion of these peripheral populations are geographically disjunct from the rest of the range. Currently, there is no consensus on the conservation value of disjunct populations. On one hand, they may be low in genetic variation and prone to extinction due to low fitness and demographic stochasticity. Alternatively, they could be genetically distinct and adapted to extreme range-edge environments and poised to play a key role in range expansion during climate change. *Abronia umbellata* is endemic to coastal dune habitat from San Quintin, Baja California, Mexico to Coos Bay, Oregon, U.S.A. but also occurs in several disjunct populations in Washington, U.S.A. and on Vancouver Island in British Columbia, Canada, where it is designated "at risk". We compared sequence variation at 10 single-copy genes for 125 individuals from 25 populations across the species range. As *A. umbellata* is listed as critically endangered in Canada, the results from our study will contribute to the recovery strategy of this precarious species. Moreover, studies like this will help us move towards biologically informed strategies for managing the many disjunct populations in southern Canada.

55. Has island colonization altered the mating system and population genetics of a coastal dune plant?

Hana Thompson, Alyson Van Natto & Christopher G. Eckert

Island colonization is expected to be accompanied by ecological and evolutionary changes with profound consequences for the genetic structure and diversity of island populations. Founder effect and reduced gene flow associated with colonization should render island populations less genetically diverse and more differentiated than their mainland counterparts. However, a scarcity of mates and/or pollinators on islands may select for self-fertilization which will, in turn, have similar genetic effects, potentially obscuring the direct effects of island colonization. We investigated the consequences of island colonization by comparing populations of the coastal dune endemic *Abronia umbellata* on three of the California Channel Islands vs. seven sites on the adjacent mainland in Southern California. We compared seed set (a strong correlate of the mating system) and sequence diversity at 298 SNPs from 9 single-copy genes. Contrary to expectations, island populations of *A. umbellata* exhibit low seed set typical of outcrossing and only a very modest reduction in genetic diversity. Although separated by open water, which should reduce gene flow, populations on Santa Cruz and Santa Rosa Islands were not strongly differentiated from mainland populations or each other. In contrast, San Nicolas Island populations were strongly differentiated from all other populations, possibly due to their geographic and geologic isolation. These findings highlight how the stochastic processes associated with island colonization can result in variable impacts on population genetic structure.

Community Ecology

56. Weed versus tallgrass prairie seedmix: Seed preferences of *Lumbricus terrestris* L exotic earthworms

Heather A. Cray, Stephen D. Murphy

Depending on seed and earthworm species identities, earthworms can be important seed predators which consume or bury large amounts of surface-applied seeds. As seeding is the most common practice for initiating tallgrass prairie restoration, earthworm-seed interactions likely contribute to restoration outcomes. This research represents the first feeding experiment focusing on tallgrass prairie restoration seed mixes. Nine native tallgrass prairie species frequently used in tallgrass prairie restoration and four common weed species were selected for this experiment. The results demonstrate that the widespread invasive *Lumbricus terrestris* earthworm has strong and consistent preferences for invasive plant, undesirable weed, and target restoration seed species. In terms of seed destruction, *L. terrestris* likely digested over 50% of the target tallgrass prairie seeds ingested in this study. As earthworm invasion of tallgrass prairie habitats is uneven but likely accelerating, understanding the effects of exotic earthworm granivory can contribute to more effective conservation and restoration.

57. Urbanization is associated with differences in age class structure in chickadees

Dovid Y. Kozlovsky, Catherine A. Jarjour, Julie Morand-Ferron

Urbanization has a tremendous impact on the environment from landscape features to distribution of food resources. Such drastic environmental changes can result in community, population, and individual differences between urban and non-urban animals. Urbanization has been associated with differential mortality and reproduction and therefore, differences in age structure may also be expected across urban gradients. Additionally, many traits studied along urban gradients also differ across age classes, and as such, age is an important factor to consider. Despite this, differences in age structure along urbanization gradients have only rarely been examined. Here, we use black-capped chickadee (*Parus atricapillus*) age, morphological, and feeder visitation data to address whether age structure, morphology, and age-related winter survival differ across a gradient of urban land use in and around Ottawa, ON. We found that urban environments were associated with significantly higher proportions of first year individuals and these proportions remained stable from late fall through all of winter. We did not, however, find evidence that age related differences explained variation in morphology. Instead variation in morphology was small and inconsistently associated with both urbanization and age. The results stand in contrast to results for two species of European birds. The present study calls for using broadly available but under-exploited data to better understand urbanization-related differences in age structure and its implications for population-level processes such as disease transmission and information flow.

58. Moss succession and biotic interactions following boreal wildfires in Canada's Northwest Territories

Julie Trus, Merritt Turetsky, Karl Cottenie

The fire-dependent ecosystem of the boreal forest is an integral part of Canadian identity. Mosses have many important functions in the boreal forest, ranging from their effects on the biophysical environment to community assemblage patterns in post-fire stands. While the contributions of mosses to boreal forest function are significant, they are also not well-studied in the context of post-fire plant succession. This study uses plant community data collected from plots along a time-since-fire gradient in the Northwest Territories to compare the biotic interactions of moss functional groups through time. Since key resources become increasingly limited with time following a forest fire, competition was predicted to be the main interaction of moss functional groups in young sites, neutral interactions were predicted to dominate in intermediate sites, and facilitative interactions were predicted to dominate in mature sites. Contrary to these predictions, significantly more neutral interactions were observed among moss functional groups in all three stages of post-fire succession. This generalization was true for interactions among functional groups of mosses, mosses and lichens, and mosses and vascular plants.

59. Competition and resource breadth shape niche variation and overlap in multiple dimensions

Raul Costa-Pereira, Márcio S. Araújo, Franco L. Souza, Travis Ingram

Competition plays a central role in the maintenance of biodiversity. A backbone of classic niche theory is that local coexistence of competitors is favoured by the contraction or divergence of species' niches. However, this effect should depend on the diversity of resources available in the local environment, particularly when resources vary in multiple ecological dimensions. Here, we investigated how available resource breadth (i.e., prey diversity) and competition together shape multidimensional niche variation (between and within individuals) and interspecific niche overlap in 42 populations of congeneric tropical frog species. We modelled realised niches in two key trophic dimensions (prey size and carbon stable isotopes) and sampled available food resources to quantify two-dimensional resource breadth. We found 14-fold variation in multidimensional population niche width across populations, most of which was accounted for by within-individual diet variation. This striking variation was predicted by an interaction whereby individual niche breadth increased with resource breadth and decreased with the number of congeneric competitors. These ecological gradients also interact to influence the degree of niche overlap between species, which surprisingly decreased with population total niche width, providing novel insights on how similar species can coexist in local communities. Together, our results emphasise that patterns of exploitation of resources in multiple dimensions are driven by both competitive interactions and extrinsic factors such as local resource breadth.

60. Habitat structure as a driver of arthropod communities

Bernal Arce, Andrew MacDougall

Plants provide structure that can drive the availability of space and shapes in a terrestrial habitat, which in turn can impact arthropod communities. The sensitivity to structure may differ between trophic groups. Effect may be strongest to predators if it limits their ability to catch prey which would affect their assemblage and recruitment into new habitats. This study manipulated the plant identity (chosen as analogs of increasing heterogeneity) and density (directly correlated to space availability) in 48 plots to evaluate their effects on the arthropod community in a realistic outdoor setting. The plants used were oats, soybeans, a mixture of these two, and a mixture of oats, soybeans, flax, and sunflowers. Ten control sites were sampled in the surrounding area: five in an open field and five in a nearby tree line. Arthropods were identified to family, and richness, abundance, and beta diversity were evaluated. Plant biomass was measured as an important co-variate with structure. Plots with sparse soybeans had higher predator and non-predator abundance ($p=0.003$ and $p=0.048$ respectively), and predator and non-predator richness ($p=0.003$ and $p=0.048$ respectively), than dense soybeans. Predator richness was significantly higher in the tree line control sites than in plots containing oats ($p=0.006$) or soybeans ($p=0.046$), while non-predator richness did not significantly change. Beta diversity, as measured by multiple site Bray-Curtis, was symmetrical among predators and non-predators across the eight treatment combinations. These results suggest that predator and non-predator arthropods track each others' responses to physical structures instead of having differing sensitivities.

61. Could urbanization affect the evolution of reproductive traits of the wildflower *Linaria vulgaris*?

Ariana Longley, Dr Christina Caruso

Urbanization-induced changes to the biotic environment can cause the divergent evolution of urban and rural plant populations. Two environmental changes that may affect evolution are pollinator limitation and habitat fragmentation. Decreased pollinator availability, by increasing competition for visitation, may result in selection for more attractive floral traits. Habitat fragmentation, by reducing population size and genetic variation, may lead to mate limitation and the breakdown of self-incompatibility. To test whether these environmental changes could influence the evolution of urban populations, we studied self-incompatible *Linaria vulgaris*. To test if urbanization intensifies selection on attractive floral traits, we measured selection on four traits in urban and rural populations. To test if urban populations are mate limited, we hand-pollinated plants with pollen from their own urban population and from other urban and rural populations. To test if urban populations experienced the breakdown of self-incompatibility, we self-pollinated plants. We did not find evidence that urbanization intensified selection on floral traits; there was significant selection via seeds/fruit on three traits, but selection did not differ between urban and rural *L. vulgaris* populations. However, there was evidence for mate limitation and the breakdown of self-incompatibility in urban *L. vulgaris* populations; the percentage of plants that did not produce a fruit was 5% higher for within-population crosses than between-population crosses, and ~13% of plants produced fruits when self-pollinated. This study suggests that floral traits will not diverge between urban and rural populations, but also that mate availability may be an under-appreciated limit on the reproduction of urban populations.

Population Genetics

62. Selection interference and haploid purging on plant Y chromosomes

Felix EG Beaudry, Spencer CH Barrett and Stephen I Wright

Recent studies estimate up to sixty percent of the genome of flowering plants is expressed in pollen, suggesting selection in the pollen phase may have a significant effect on the evolution of plant genomes. For example, purifying haploid selection may significantly slow or even arrest the degeneration of large non-recombining Y chromosomes. Here, we combine population genomics, transcriptomics and modelling to assess the extent to which haploid purifying selection can counter linked selection during Y chromosome degeneration. Specifically, we study the evolution of Y-linked pollen-expressed genes in the dioecious plant, *Rumex hastatulus*. We find evidence that both past and contemporary purifying selection is stronger for genes expressed in pollen. While pollen-expressed Y-linked genes tend to have higher constraints, past and present, than Y-linked genes without pollen expression, purifying selection is less effective on the Y than on the X chromosome regardless of pollen expression. We discuss how disproportionate degeneration of genes on the Y compared to those on the X chromosomes can cause populations with female-biased sex ratios in plants.

63. Fantastic yeasts and where to find them: Isolation of the pathogenic yeast *Cryptococcus neoformans* from Saudi Arabian soil, a novel niche

Himeshi Samarasinghe, Renad Alijohani, Carlene Jimenez, Jianping Xu

Cryptococcus deneoformans is an opportunist yeast pathogen and the causative agent of fatal meningoencephalitis in humans. Its geographical distribution is known to be largely contained to temperate climates. However, as of 2013, over 90% of all characterized cryptococcal isolates are of clinical origin, leaving environmental cryptococcal populations largely unexplored. Middle East remains one such underexplored area with no published study to date investigating the yeast diversity in soil. Here, we identified 76 *C. deneoformans* isolates from a survey of 562 soil samples collected from six Saudi Arabian cities. Multilocus sequence typing (MLST) revealed the presence of two major sequence types (ST), ST160 (n=63) and ST294 (n=9) along with four singleton STs, three of which were novel. 75 isolates belonged to mating type ‘alpha’ while one isolate was mating type ‘a’ suggesting that sexual reproduction between strains of opposite mating types is a possibility. In fact, ST613, one of the novel STs, appears to be a recombinant product between ST160 and ST294. Therefore, this population appears to be propagating via both asexual and sexual reproduction. Our analyses indicate that *C. deneoformans* was recently introduced to Saudi Arabia via anthropogenic activities. Due to its religious significance and thriving oil industry, Saudi Arabia has become one of the top five destinations for international migrant workers, resulting in frequent travel in and out of the country. Our study is the first to report the occurrence of *C. deneoformans* in a desert climate which represents a novel expansion to this species’ currently known ecological niche.

64. Using population genomics to disentangle the Leach's storm-petrel species complex (*Hydrobates* spp.)

Katie Birchard, Greg Robertson, Vicki Friesen

Understanding processes that drive population differentiation and speciation provides insight into how biodiversity arises, helps us identify the evolutionary history of a species, and aids natural resource managers when making conservation decisions. Seabirds represent useful systems for studying drivers of population differentiation. Despite their ability to overcome most geographic barriers and disperse long distances, many seabird species exhibit strong population genetic structure. We are assessing population differentiation within a pelagic seabird, the Leach's storm-petrel species complex (*Hydrobates* spp.; formerly *Oceanodroma*). This species complex covers a wide range in the northern Atlantic and Pacific oceans, and comprises three species (*H. leucorhoa*, *H. socorroensis*, and *H. cheimomnestes*) and two subspecies (*H. l. leucorhoa* and *H. l. chapmani*). Interestingly, *H. socorroensis* and *H. cheimomnestes* are proposed to be sister taxa that diverged in sympatry through allochronic speciation, or differences in breeding time. Because species classifications for Leach's storm-petrels are mostly based on morphological and vocal distinctions between populations, genomic work is needed to understand population differentiation and processes driving diversification of this species complex. Leach's storm-petrels also pose a conservation concern, as colonies in the Atlantic are rapidly declining and were recently classified as Vulnerable by the IUCN, but effects of this decline on genetic variation are unknown. Genomic work is needed to determine the number of Designatable Units required to maintain genetic diversity. Using high-throughput sequencing, we are assessing the level of population genetic differentiation and gene flow between both spatially and temporally isolated populations of Leach's storm-petrels across their entire range.

65. Examining phenological variation of an invasive plant using a developmental model

Eugene Sit, Christopher Eckert, Robert Colautti

My research examines the basis for flowering time variation in the invasive wetland plant *Lythrum salicaria* using a model of stem development. I present time series data from a common garden experiment at Queen's University Biological Station which captures genetic variation of phenology within and among populations distributed across a 1000km transect of eastern North America.

66. Uncovering the genetic basis of natural variation in sociability

Andrew M. Scott, Ian Dworkin, Reuven Dukas

Sociability, defined as the tendency of animals to engage in non-aggressive interactions with each other, is a highly ecologically relevant trait for which natural variation is observed throughout the animal kingdom, across populations within a species, and also among individuals within a population. This natural variation within populations, which is observed as sociability phenotypes in animals (including humans) ranging from solitary “introverted” behaviour to highly social “extroverted” behaviour, may have an important impact on potential fitness outcomes, however the genetic basis of this variation is not well understood. Using fruit flies as a genetic and behavioural model system, I have quantified natural genetic variation in sociability using inbred line screening, revealing that sociability has low-moderate heritability, has a minimal genetic correlation between the sexes, and exhibits genetic variation in phenotypic plasticity. In addition, I have undertaken a large-scale artificial selection project to uncover potential trade-offs with other behavioural and morphological traits, and to better understand the genetic architecture of sociability using evolve-and-resequence (E&R) techniques.

67. Negative selection in social insects

Arshad Imrit, Brock Harpur, Kathleen Dogantzis, Amro Zayed

Eusociality, characterized in part by cooperative brood care, and reproductive division of labor, evolved independently several times in insects. The evolution of eusociality has been hypothesized to lead to differences in the extent of both positive and negative selection. While population genomics studies of eusocial insects have so far focused on positive selection, there has been no study of the extent of negative selection in social insects, and its relationship to the evolution of caste-biased genes. To address this knowledge gap, my research will estimate the extent of negative selection in honey bees, bumble bees, and wasps, through analysis of published population genomic datasets. My study will compare the relationship between the strength of negative selection and caste-specific patterns of gene expression, and examine if the strength of negative selection correlates with the level of social complexity in this species triad.

68. Interannual variation in season length is linked to strong co-gradient plasticity of phenology in a montane annual plant

David J. Ensing & Christopher G. Eckert

Species are commonly distributed along latitudinal and elevational gradients of growing season length to which they might respond via phenotypic plasticity and/or adaptive genetic differentiation. However, the relative contribution of these processes and whether plasticity, if it occurs, facilitates expansion along season length gradients remains unclear but are important for predicting species fates during anthropogenic change. We quantified phenological trait variation in the montane annual *Rhinanthus minor* for 3 generations at 12 sites across 900 m of elevation in the Canadian Rocky Mountains and conducted a reciprocal transplant experiment for 2 generations among nine sites. We compared clines and interannual variation of phenological traits between natural and transplanted individuals. Season length declined by 37% along our elevational gradient and, as expected, plants emerged, reached first flower and made their first seed in 41% fewer growing degree days under shorter growing seasons. Although reciprocal transplants revealed modest genetic differentiation across elevation, trait clines were primarily due to striking co-gradient plasticity that paralleled genetic differentiation. Co-gradient plasticity likely evolved in response to considerable interannual variation in season length across our elevational transect, and should prepare *R. minor* to make adaptive changes to phenology in response to ongoing climate change predicted for montane environments.

Stress and Environment

69. Intertidal elevation and parental care in plainfin midshipman

Nicole Yee, Dr. Sigal Balshine, Nick Brown

The intertidal zone is ever-changing and poses challenges to the species that inhabit it—when the tide recedes, areas of the intertidal are left completely air-exposed. Environmental stressors, like temperature and air exposure, becomes increasingly severe with increasing intertidal elevation. Puzzlingly, several species of fish target the intertidal to lay their eggs as warm incubation temperatures and high oxygen diffusion may benefit developing eggs. The plainfin midshipman (*Porichthys notatus*) emerge from the deep waters of the Pacific Ocean to breed on the rocky intertidal shores of western North America. Male plainfin midshipman endure great hardship to guard their eggs, they remain in their nests for <60 days providing sole parental care to their broods. Recent work has quantified the physiological costs suffered by care-giving males; however, it remains unknown how these costs might affect differences in the amount and quality of parental care between intertidal elevations. I observed parental care of midshipman guarder males in situ at three intertidal elevations: ‘high,’ ‘middle,’ and ‘low’. I show that the frequency of parental care behaviours decreases with decreasing intertidal elevation. Despite higher physiological costs associated with higher elevations, my results suggest that this environment likely necessitates increased care. As an environment already characterized by extreme conditions, the effects of global climate change will likely be more pronounced in the intertidal zone. Thus, understanding how environmental severity impacts plainfin midshipman during their critical reproductive phase carries implications for how they, and intertidal-spawning species more broadly, will be impacted by climate change.

70. Tracking changes in stable isotope signatures and total mercury levels in aquatic environments in proximity to municipal wastewater treatment plants in Hamilton and Dundas

Katrina Cantera, Karen Kidd

Municipal wastewater effluent is considered to be the largest point source of pollution, by volume, to Canadian surface waters and the nutrients and contaminants it contains can impact water quality. Firstly, nutrient loading occurs downstream of wastewater outfalls and leads to eutrophication. Additionally, ecosystems receiving effluent experience high levels of contaminants, including mercury, a neurotoxin and endocrine disruptor, which can biomagnify in organisms at higher trophic levels. Both processes occur naturally, however human inputs, such as effluents, can accelerate and amplify these processes. I aim to assess how effluent alters carbon (C) and nitrogen (N) levels within ecosystems by measuring stable isotope values in fish and invertebrates. These values can be compared within and between sites to determine the impacts of effluent on nutrient levels. I expect to see elevated levels of C and N in areas receiving low-quality effluent. Total mercury (THg) levels will be measured in fish using a Direct Mercury Analyzer. I expect that fish receiving low-quality effluent will have higher THg content. This analysis will be done near WWTPs in Hamilton and Dundas. The Hamilton WWTP is being upgraded from secondary to advanced treatment, but is currently discharging a lower quality effluent. The Dundas WWTP has advanced treatment, but is unable to meet water quality standards. By analyzing these endpoints, I will determine how effluent alters the quality of aquatic ecosystems in Hamilton and Dundas. This may lead to initiatives that mitigate water quality concerns, ultimately improving human and environment health in the process.

71. Investigating the chronic effects of environmental stressors on populations of wild bees using spatial analysis

Emily Agar, Dr. Alana Pindar, Dr. Dennis vanEngelsdorp, and Dr. Nigel Raine

The current state of wild bee populations is very much undocumented despite their unequivocal importance to the world's economy and ecosystems. Previous research suggests bee populations are decreasing due to many environmental stressors, particularly anthropogenic changes to the environment and climate change. Despite significant research on the acute effects of these stressors on pollinators, very little research currently exists on the chronic effects of these environmental stressors. My research aims to fill some of these gaps through spatially analyzing historical datasets of bee population dynamics and environmental stressors. An updated dataset based on previous research has resulted in a significant compilation of data on Pennsylvanian wild bee populations over the past 120 years. This provides a good metric in understanding the large-scale changes in bee populations both spatially and temporally. Historical government datasets, such as datasets on pesticide use and land use change, can then be compared spatio-temporally to this 120-year dataset. The long-term element of this analysis will provide a greater understanding of the chronic impacts of these stressors on pollinators. The results of this research will allow for more informed conservation strategies to be implemented in the future.

72. Exploring the role of insect defoliators (gypsy moth) in the restoration of industrially degraded landscapes

Michael J. McTavish, Emily Smenderovac, John Gunn, Stephen D. Murphy

Although insect defoliators are recognized as major agents of ecological change in North American forests, their impacts on the restoration of industrially degraded landscapes are largely unknown. We fed gypsy moth (*Lymantria dispar* L.) paper birch leaves (*Betula papyrifera* Marsh) collected from experimental forested catchment areas near an abandoned Cu/Ni smelter in Sudbury (Ontario, Canada) and measured gypsy moth feeding, frass properties, and the effects of frass on the growth of ticklegrass (*Agrostis scabra* Willd.). Gypsy moth larvae generally ate more and produced more frass on a diet of leaves from the more industrially degraded sites. Frass had an overall positive effect on plant growth and survivorship, although the smallest benefits came from frass derived from vegetation from the more heavily degraded sites. Our results suggest that defoliating insects may play a unique and important role in the recovery of degraded landscapes with poor-quality soils, metal contamination, and marginal vegetation growth. These landscapes may be particularly susceptible to: (a) more extensive defoliation; and (b) higher frass inputs. Some of these effects may pose additional challenges to the recovery of these landscapes (e.g., increased defoliation) while others may be beneficial (e.g., enhanced plant growth and soil development).

73. Resource limitation reduces tolerance to ultraviolet radiation via multiple mechanisms

Winona Platt, Brooks Miner

Freshwater zooplankton in clearwater habitats must persist under substantial UV radiation exposure. Various photoprotective pigments have been observed across zooplankton taxa, with carapace melanin pigmentation being the most common for the water flea *Daphnia*. Because melanin must be continually synthesized by the organism and deposited in the carapace with each molt cycle, melanin pigmentation has been presumed to be energetically costly to produce. We asked whether resource limitation affected both melanin pigmentation intensity and UV radiation tolerance in laboratory-reared *Daphnia melanica* descended from an alpine habitat in the Sierra Nevada. We raised individuals from birth to adulthood at six different algal feeding concentrations, followed by exposure to UV radiation. We measured three response variables: body size, melanin content, and survival following UV-B exposure. We found that feeding treatments significantly predicted both melanin content and survival following UV-B exposure. Additionally, melanin content significantly predicted survival following UV-B exposure. These additive effects indicate that resource limitation reduced UV radiation tolerance both indirectly, via reductions in melanin pigmentation and subsequent increases in UV exposure for the organism's tissues; and directly, presumably via physiological mechanisms.

74. Can honey bees detoxify Neonicotinoids?

Gursimran Bahia, Nadejda Tsvetkov, Avidah Khalili, Amro Zayed

Canadian honeybees have experienced high colony mortality in recent years with neonicotinoid usage on crops being a major contributing factor. In 2018, the Canadian Association of Professional Apicurists reported that the national winter loss of bee colonies was 32.6%. Neonicotinoids are a class of agricultural pesticides that are chemically similar to nicotine. They are highly agonistic to insect nicotinic acetylcholine receptors (nAChRs), compared to the mammalian nAChRs. Honey bees tend to be more sensitive to N-nitro neonicotinoids (imidacloprid, clothianidin, thiamethoxam) compared to the N-cyano class (thiacloprid) due to the latter being more easily metabolized by the honeybee. Here we examine if honey bees that survive exposure to the N-nitro neonicotinoid clothianidin have different levels of expression of specific detoxification enzymes (e.g. CYP9Q1-3, a family of cytochrome p450 monooxygenases responsible for metabolizing neonicotinoids) relative to honey bees that die after exposure to clothianidin. We compared the expression of CYP9Q genes of bees of different genotypes after feeding them a field realistic dose (4.6 ppb), as well as a LD50 dose (29 ppb) of clothianidin.

75. Why do naturally wide-ranging Carnivora pace in zoos?

Georgia Mason and Miranda Bandeli

Applying Comparative Methods to data from captive wild animals can identify traits predisposing animals to fare poorly in these conditions, which can then be used in to improve captive management. Past work demonstrated that wide-ranging Carnivora (with large median annual home ranges) are most prone to time-consuming stereotypic pacing in zoos, but the R^2 was low. Using an updated database of 27 species and Phylogenetic Least Squares Regressions, we investigated whether controlling for home range size plasticity (assessed via coefficient of variation) would improve the variance in pacing behaviour explained. It did ($F_{2,15} = 8.4$, $p = 0.6$, $R^2 = 0.47$). Controlling for home range size plasticity also revealed a weak relationship between large range sizes and increased captive infant mortality ($p = 0.048$, $t_{23} = 1.73$). We then investigated what might underlie the home-range effect, since being naturally wide-ranging co-varies with many attributes such as being large bodied, travelling long distances per day, and covering little of the annual home range daily. Travelling small fractions of the annual home range each day (i.e. being naturally semi-nomadic) strongly predicted pacing ($F_{1,17} = 30.15$, $t = -5.49$, $R^2 = 0.62$, $P < 0.0001$), but did not statistically account for annual range size effects which remained significant when both variables were in the same model ($t_{17} = 2.04$, $P = 0.029$). Factors predicting captive infant mortality are being analysed, but overall the Carnivora most prone to stereotypic pacing in zoos are naturally semi-nomadic species with large, relatively invariant annual home ranges: information that could improve the husbandry of polar bears and similar species.

Behaviour III

76. The developmental effects of information-acquisition on cognition and behavior: An experiment with passerine birds

Isabel Rojas-Ferrer, Julie Morand-Ferron

Animals display individual differences that could indicate differences in developmental trajectories. Though some individual variation can be explained through genetic inheritance, little is known about how the developmental context plays a role in the expression of cognitive and behavioral traits. To test this link, we exposed juvenile zebra finches (*Taenopygia guttata*) to three experimental conditions with differing information sources; i.e. an environment where (i) colour cues reliably predicted the presence of food (simple learning), (ii) a combination of two colour cues reliably predicted the presence of food (complex learning), or (iii) colours cues were non-informative (control). After exposing individuals to the treatment for 500 trials, individuals were subjected to three different personality assays, two of which are normally associated to information acquisition, and a learning task. We predicted that individuals exposed to a more complex learning environment would result in individuals with higher scores for personalities traits associated to information acquisition, and higher learning abilities. Our preliminary results indicate a significant effect of treatment, but no correlation to the personality traits measured. Furthermore, our results show a trend for higher learning accuracy in individuals exposed to environments with simple over complex learning suggesting that paying attention to more information throughout development may not necessarily favor learning ability.

77. Seasonal variation in estradiol transfer among male and female big brown bats

Lucas J. Greville, Tyler Pollock, Denys deCatanzaro, Paul A. Faure

A growing body of research suggests that unconjugated steroids are excreted in the urine of male mice and alter the reproductive physiology/behaviour of female conspecifics. These observations support the notion that steroids may act as pheromone in mammals. Using radioactive tracers, past research from our lab demonstrates that female big brown bats (*Eptesicus fuscus*) readily absorb both exogenous estradiol via cutaneous and intranasal exposure, with radioactivity measured throughout their neural, peripheral, and reproductive tissues 1 hour after exposure. Additional experiments using radioactive steroids have shown the reliable transfer of estradiol from male to female conspecifics in *E. fuscus* during the reproductive mating season. The current project aims to explore seasonal variation in estradiol transfer between male and female big brown bats at three time points: Autumn (coinciding to mating season), Spring (coincides with female ovulation and implantation), and Summer (coinciding with maternal colony formation and care). Using radioactive tracers, we observe seasonal variation in male estradiol transfer to a variety of female tissues including the frontal cortex, heart, liver, uterus, and blood serum, with a number of other tissues approaching statistically significant differences among seasons. Additionally, we present preliminary data demonstrating the presence of unconjugated bioactive estradiol in male urine across the various time points, supporting our hypothesis that urinary steroids are involved in the observed steroid transfer. Thus, the seasonal variation in estradiol transfer may influence sexual behaviours and reproductive physiology of female bats during reproductively relevant timepoints, as transferred steroids are found in both neural and reproductive tissues.

78. The effects of barren housing on mouse sociability and attractiveness

Aimee Adcock, Emma Nip, Aileen MacLellan, Basma Nazal, Georgia Mason

Compared to rodents raised in the 'shoebox' cages typical of research laboratories (standard housing: SH), those from environmentally enriched (EE) cages have improved cognition, are healthier, less anxious and aggressive, show fewer signs of depression, and perform less stereotypic behaviour (SB; repetitive movements such as route tracing). Such changes may affect other aspects of social behaviour in positive ways, making EE rodents both more sociable and socially attractive. We tested these two hypotheses in female mice (*Mus musculus*), and assessed whether any deficits reflect three housing-influenced attributes that could cause poor social functioning: SB; time spent inactive-but-awake (IBA)-- a potential sign of depressive-like states; and giving or receiving more agonism. To do this, we used a novel familiarisation paradigm to equally expose C57BL/6 focal mice to non-cagemate EE and SH stimulus mice, and then tested them in sociability and social preference tests. We found that EE focal mice were more sociable than SH, but only towards SH stimulus mice; while EE stimulus mice were more attractive to SH, but not to EE, focal mice. This is the first demonstration that mice can distinguish between individuals from physically different cages. Stimulus mouse SB, IBA, and agonism did not predict their sociability or social attractiveness. However, focal mice who received more agonism in their home cages (an issue for SH mice in particular) spent significantly more time near EE stimulus mice. This likely reflects a preference for less agonistic social partners, and suggests that agonism from female cagemates is aversive to mice.

79. Analysis of living social networks: Insights from a *Drosophila* model

Christine T Scharf and Graham J Thompson

Social structure can be highly organized yet vary with context. In our research, we vary the social demographic and genetic context of small populations of *Drosophila melanogaster* to test for changes to the number and nature of social interactions. Using a combination of video-captured behavioural trials and in silico network analysis, we have found three distinct patterns. First, at high density, flies interact more often and with more individuals, as expected, but do so in more well-connected groups of individuals or 'neighbourhoods'. Second, we found that females form clusters more often than males, and do so preferentially with those they have previously interacted. Finally, we found that age tends to render flies more social, such that they form more-dense networks. Taken together, our living social network analysis provides new insights into the hidden social life of an otherwise well-studied insect and, in the end, may have implications for the study of other, non-model taxa. We are currently testing the role for sex ratio bias and nlg genotypes on social network structure.

80. Identifying enriched housing conditions for zebrafish (*Danio rerio*) that vary along a scale of preference

JM Lavery, V Braithwaite, N Miller, GA Mason

Zebrafish (*Danio rerio*) are widely used in research and typically live in small, barren tanks. Environmental enrichment (EE) can improve their welfare and cognition, but the present literature on zebrafish EE preferences is limited to two studies lacking statistical power. Our objective was therefore to determine zebrafish preferences for 13 putative EE treatments. 20 groups of 8-10 adult zebrafish underwent 13 consecutive preference tests, with putative EEs (black/underwater image on walls; sloped/flat gravel; plastic grass/overhanging plants; visual contact with neighbouring groups) randomly installed on opposing sides of each group's tank. After three days of habituation, optimal sampling intervals (10-30 minutes) and preference stability were evaluated. Percent occupancy was recorded from both sides of each tank over the three days following preference stabilization and analyzed with one-sample t or Wilcoxon tests. Fish preferred gravel over barren conditions (sloped: 77.12%, $p < 0.001$; flat: 77.16%, $p < 0.001$) and plants (58.82%, $p = 0.001$); plants and gravel over plants or gravel alone (vs. plants: 67.77%, $p < 0.001$; vs. gravel: 69.71%, $p < 0.001$ [grass] and 66.92%, $p < 0.001$ [overhanging]); and four plants over two (58.68%, $p < 0.001$). They were indifferent to wall type (black: 53.75%, $p = 0.233$, underwater: 49.46%, $p = 0.897$), visual contact with neighbouring tanks (52.57%, $p = 0.286$), and between plant morphologies (50.00%, providing plants were present in equal numbers). Given the tests performed, EEs can be ranked from least preferred to most (plants < gravel < two plants + gravel < four plants + gravel), which may inform the degree of enrichment that researchers employ, depending on their research questions, resources, and/or personal ethics.

81. Sex-specific performance of an allocentric spatial memory task in brown-headed cowbirds

Nanxi Huang, Madeleine IR Brodbeck, Scott A MacDougall-Shackleton

Spatial memory is the encoding, consolidation, and retrieval of information relating to space. Spatial information within an environment can be categorized into geometric and featural cues. Brown-headed cowbirds (*Molothrus ater*), an obligate generalist brood parasite, exhibits sex-specific differences in spatial memory performance. However, it is unclear whether female cowbirds outperform their male counterparts by using more geometric or featural cues. We examine sex-specific differences in brown-headed cowbirds' reliance on geometric and featural cues when relocating a food reward. We investigated the allocentric spatial memory performance of three male and four female brown-headed cowbirds within a rectangular arena, in which the presence of geometric and featural cues were manipulated. Preliminary analyses show no significant difference in spatial memory performance between male and female cowbirds in the two testing conditions, regardless of the presence of geometric and featural cues. The results from this study reinforce the notion that differences in spatial memory performance between male and female brown-headed cowbirds vary depending on the type of task.

82. Nocturnal incubators in communal nesting cuckoos: Risks and rewards

Jim Quinn

A single male smooth-billed ani is mostly responsible for the risky task of nocturnal incubation, night after night on the same communal nest. Meanwhile, other group members huddle together in a safe nocturnal roosting location of their choosing. Nocturnal incubating males are rewarded with greater fitness as measured by numbers of nestlings sired. In this socially monogamous joint-laying species, multiple females lay eggs in the same nest, and following a period that may involve egg tossing and burial (in the nest structure), group members share in the care of the eggs and chicks. The fitness advantage to the nocturnal incubator may be explained by either effective extra-pair mating behaviour by him, or by egg laying/ovicide tactics by him and his social mate. We examine these alternate hypotheses.

Evolutionary Biology

83. Sequencing and assembling the nuclear genome of the Antarctica psychrophilic green alga *Chlamydomonas* sp. UWO241: Unravelling the evolution of cold adaptation

Xi Zhang and David Smith

The Antarctic harbours a variety of algae that can withstand extreme cold but falter at warmer temperatures (psychrophiles), including the unicellular green alga *Chlamydomonas* sp. UWO241. Little is known, however, about the origins and evolution of psychrophilic algae, and their nuclear genomes remain largely unexplored. For my PhD, I propose to sequence and assemble the entire nuclear DNA of UWO241 using a next-generation sequencing (NGS) approach, and then employ these data to better understand the evolution of photopsychrophily. DNA sequencing technologies have undergone tremendous advancements in recent years, but assembling, annotating, and analyzing a nuclear genome is still a huge undertaking, especially for small laboratory groups, partly because many eukaryotic genomes are repeat rich and contain thousands of genes and introns. To characterize the UWO241 genome I will, firstly, develop an assembly pipeline for processing high-throughput DNA sequencing reads into genomic contigs. These contigs, alongside RNA-sequencing data, will then be fed into an annotation pipeline, which I will design based on the most up-to-date eukaryotic bioinformatics gene-profiling software. Computational analyses will be carried out on an in-house computer, which I have constructed for the Smith Lab, as well as on Western's supercomputing network SHARCNET. Lastly, I will perform a wide range comparative genomic analyses of the UWO241 genome with those of other model green algae, including *Chlamydomonas reinhardtii*. Preliminary data already suggest that the UWO241 genome is exceptional in many ways—including its size (>230 Mb) and gene copy number—and at least some of these features appear to have a fundamental role in surviving in the extreme cold.

84. Spatial patterns of substitutions in bacterial genomes

Daniella F. Lato and G. Brian Golding

Increasing evidence supports the notion that different regions of a genome have distinct molecular properties. This variation is abundant in bacterial genomes where essentiality and gene expression decrease with distance from the origin of replication, while at the same time mutation rate increases. There is limited research on how molecular trends such as substitution rates vary between the assortment of genomic structures, for example linear, circular, and multi-repliconic genomes. In this work, we mapped extant and ancestral substitutions to the phylogenies of *Escherichia coli*, *Bacillus subtilis*, *Streptomyces*, and *Sinorhizobium meliloti*, quantifying how many substitutions were at each coding and non-coding position of the genome. Previous studies indicate that the number of substitutions should increase with distance from the origin. Our analysis instead demonstrates the opposite, that the number of substitutions decreased when moving away from the origin of replication in six of the ten replicons analyzed. The replicons that did not follow this trend were pSymB of *S. meliloti* and the chromosome of *Streptomyces* where we found the number of substitutions increase with increasing distance from the origin. We explore how these substitution trends impact the functional categories of genes and their placement within a bacterial genome.

85. Insurrections of sex determination in the frog family Pipidae

Caroline M. S., Cauret, Marie-Theres T., Gansauge, Andrew S., Tupper, Benjamin L., S., Furman, Martin Knytl, Xue Song, Eli Greenbaum, Matthias Meyer, Ben J., Evans

Sexual reproduction allows genetic recombination to occur, which increases the efficacy of natural selection. In many species, separate male and female individuals, and their development, is triggered by diverse genetic and/or environmental mechanisms. In several groups with genetic sex determination, such as mammals and some insects, the sex chromosomes (the X and Y or alternatively the Z and W chromosomes) have large non-recombining regions and substantial differences in gene content and size. However, in other groups such as fishes and frogs, the sex chromosomes look cytologically very similar. Possible explanations for non-diverged sex chromosomes include (1) persistent recombination and (2) frequent change of the identity of the sex chromosomes. In frogs of genus *Xenopus*, the trigger for sex-determination is known to frequently change: at least three different systems exist in this genus. We screened various *Xenopus* species for DM-W, a trigger for sex-determination that emerged in this lineage, and identified the sex-chromosomes of three additional pipid frog species, including one from the genus *Xenopus*, and one species from each of the closely related amphibian genera *Hymenochirus* and *Pipa*. We recovered new evidence for additional variation in the genetic control of sexual differentiation. This includes an evolutionary transition between male and female heterogamy, a change in the genomic location of the sex-chromosomes, and in several species, multiple independent losses of a gene that triggers sex-determination.

86. The genomic architecture of sex-biased gene expression in *Xenopus*

Xue Ying Song, Benjamin L.S Furman, Martin Knytl, Ian Dworkin, Ben Evans

Most vertebrates have separate sexes, and sex-specific traits that are regulated by sex chromosomes and by genes with sex-biased expression patterns. In newly evolved sex chromosomes, genetic recombination can be suppressed on genomic regions linked to the master regulator of sex determination. Genes with sex-specific effects, such as genes with sexually antagonistic fitness effects (e.g., beneficial to females but harmful to males), are hypothesized to accumulate in the non-recombining regions of sex chromosomes because providing sex-specific or sex-biased modes of inheritance can resolve associated genomic conflict. But do sex-specific genes actually accumulate in newly evolved sex chromosome as predicted by theory? We will explore this question with an African frog species *Xenopus borealis*, whose sex chromosome evolved within the last 25my and have a large (~50Mbp) region of suppressed recombination, making it a relatively young sex chromosome system. We predict that sexual antagonistic genes will evolve in or translocate to in the non-recombining region of the sex chromosome. To test this, we examined the genomic location of transcripts with sex-biased patterns in liver tissues and gonadal tissues. We found that the sex-linked region of the sex chromosome has accumulated higher concentration of sex biased transcripts compared to the non-sex-linked region of the sex chromosome and the autosomes. We did not observe the same pattern in a closely related frog species, *Xenopus laevis*, which unlike *X. borealis*, lacks a large region of suppressed recombination on its sex chromosome. As a next step, we will examine the directionality of gene expression evolution using Brownian Motion model in a phylogenetic context with *X. laevis* and an outgroup, *Xenopus tropicalis*. Taken together, this work advances our understanding of sex chromosome evolution by providing an empirical evaluation of theoretical expectations.

87. The role of Pleistocene glacial/interglacial cycles on the phylogeography of the American mastodon.

Emil Karpinski, Dirk Hackenberger, Chris Widga, Daniel Fisher, Grant Zazula, Ross MacPhee, Hendrik Poinar

Ancient DNA studies have greatly enhanced our understanding of Pleistocene megafaunal ecology, identifying demographic changes not observable in the palaeontological record. However, phylogeographic studies of North American megafauna have largely focused on grazing species (e.g. mammoths, bison) that inhabited open grassland and steppe-tundra environments, omitting key forest and mixed-environment species such as the American mastodon (*Mammuth americanus*). Recent paleontological work has shown that mammoths and mastodons were differently affected by Pleistocene glaciations, suggesting that forest and grassland species were asymmetrically impacted by climatic shifts. The focus on animals from a single environmental context has resulted in a biased understanding of the roles of climate and human-induced factors on the population dynamics of American megafauna.

Here we apply a palaeogenomic approach to questions of the impact of Pleistocene glacial-interglacial cycles on American mastodon evolution and population histories. We generated 33 new complete mitochondrial genomes and identified two separate mitochondrial lineages in the Alaska-Yukon region. Molecular clock dating suggests that the median ages of the two Alaska-Yukon clades potentially fall within two separate interglacial periods. Our analysis also reveals comparatively low levels of genetic diversity in the larger Alaska-Yukon clade in comparison to samples from south of the ice-sheets. Both results support palaeoecological theories that propose *M. americanus* occupation of northern latitudes was restricted to warmer interglacials when forests and wetlands would have been abundant. Our data also suggest that mastodon colonization and extirpation in northern latitudes was possibly a recurring event that happened at least twice during the Pleistocene.

Evolution/Ecology II

88. Dissecting the genetic underpinnings of pathogen loads in the honey bee

Tanushree Tiwari, Clement Kent, Stephen Rose, Harshil Patel, Alivia Dey, Ida Conflitti, Amro Zayed and BeeOMICS consortium

The honey bee, *Apis mellifera* is a model organism for sociogenomics and is one of the most important managed pollinators. As such, recent threats to honey bee health are particularly alarming. The social honey bees live in highly crowded nests providing favorable conditions for the spread of infectious diseases. But honey bees have several social and individual mechanisms for protecting themselves against disease. The BeeOMICS consortium has sequenced the genomes of approximately 1,000 honey bee colonies in Canada, which were evaluated for a number of traits, including the abundance of several pathogens within each colony. I plan to carry out genome-wide association studies (GWAS) on colony pathogen loads to gain a deeper insight of the genetics of immunity in honey bees. This research will set the groundwork for breeding disease resistant honey bees using marker assisted selection.

89. Temporal and demographic variation in avian malarial infections among song sparrow (*Melospiza melodia*) populations in southern Ontario

Lydia Balogh, Leanne Grieves, Elizabeth MacDougall Shackleton

Avian malarial parasites (genera *Plasmodium*, *Haemoproteus* and *Leucocytozoon*) are unicellular organisms, transmitted by biting dipteran insects, that infect over 70% of bird species worldwide. Due to its pathogenic nature, avian malaria exerts strong selective pressures on hosts. The effects of avian malaria are often sublethal in areas where malaria is endemic. However, both observational and experimental studies have revealed strong associations between malaria infection and host mate choice, reproductive success, senescence and survival, suggesting that sublethal malarial infections have important regulatory effects on avian host populations. However, many of these studies are “snapshots” where data are collected for only a short period of time or within a single breeding season, with fewer studies investigating multi-year infection dynamics. To address this, we quantified the variation in avian malarial infections in three populations across Ontario, across three breeding seasons, at two times of year, and between the sexes within a single host species, the song sparrow (*Melospiza melodia*), a common and widespread North American passerine. We found significant differences in the likelihood of malaria infection across populations, years and seasons. Surprisingly, we also found evidence of host sex differences in the genera of malaria parasite song sparrows were infected with. Together, our results demonstrate that the prevalence and composition of avian malarial infections can be extremely variable, making sampling regimes and sampling duration key considerations when drawing conclusions about study results.

90. Experimental evidence of maternal haemosporidian infection effects on offspring quality in a wild passerine

Ivana Schoepf, Sarena Olson, Ignacio T. Moore and Frances Bonier

Vector-borne haemosporidians are among the most diverse and widespread endoparasites. Haemosporidian infections can affect their hosts in a number of ways, including reducing immune function and ability to provision the young. Costs of infections are, however, not uniform across taxa, and vary depending on whether hosts are naïve to the parasite or have co-evolved with it. Among co-evolved populations, in particular, the effects of haemosporidian infections at key life-history stages, such as during reproduction, remain unclear. Correlational and experimental research on maternal fitness and offspring quality in a range of vertebrate hosts has found positive, negative, and no effects of haemosporidian infections. However, previous studies have mostly been conducted in systems with chronically low infection levels, which may have masked the true costs of infection. We studied how malarial infection affects maternal reproduction and offspring quality in a free-ranging population of red-winged blackbirds (*Agelaius phoeniceus*) naturally experiencing unusually high incidences of parasitemia. At our field site in southeastern Ontario, where >90% of individuals are infected with 1 or more genera of haemosporidian parasites. To assess effects of infection on mothers' reproductive success and offspring growth, physiology, and immune function, we caught adult red-winged blackbird females before onset of egg-laying and experimentally manipulated their parasite burden by administering either an anti-malarial medication or a control solution. Our results provide experimental evidence that reduced haemosporidian burdens lead to higher reproductive success in adult females and affect offspring quality. Overall, our study supports the idea that haemosporidian infections decrease fitness in co-evolved populations.

91. Predicting bird community reservoir competence for West Nile virus using phylogenetic mixed effects models and eBird citizen science data

Morgan Kain and Ben Bolker

West Nile virus (WNV), a vector-borne pathogen of birds, is a model system for studying vector-borne disease transmission and virulence evolution, and has important wildlife and human health implications. While past research has focused on the survival and reservoir potential (competence) of many different bird species infected with WNV, the diversity of North American bird communities makes it difficult to make clear predictions for the spread of WNV in, and spillover potential (into the human population) from, a given bird community. As part of a broader effort to combine the existing knowledge base on WNV into an integrated eco-evolutionary model, we use phylogenetic relationships among 47 bird host species with measured infection profiles and mortality probabilities to improve estimates of virus load and survival in measured species and predict virus load and survival in host species that have not been tested in the lab. Using these predictions along with temperature, mosquito transmission ability, and mosquito biting preferences, we calculate aggregate community competence for WNV transmission of the bird communities in Texas, USA throughout the year using bird communities estimated using ebird, a citizen science database from the Cornell Laboratory of Ornithology. We find that temperature has the largest impact on WNV transmission, but that at a given temperature an increase in bird species richness decreases WNV transmission potential. Across Texas communities we find that Northern Cardinals are the most important amplifiers of infection and that Mourning Doves are the most important diluters of infection.

92. Contemporary gene flow is a major force in shaping the New Zealand *Aspergillus fumigatus* population

Greg Korfanty, Lisa Teng, Nicole Pum, Jianping Xu

Aspergillus fumigatus is a globally distributed opportunistic fungal pathogen capable of causing highly lethal invasive aspergillosis in immunocompromised individuals. Recent studies have indicated that the global population is consisted of multiple divergent genetic clusters but that most of these clusters are geographically broadly distributed. However, most of the analyzed samples have come from continental Eurasia and the Americas where the effects of ancient vs. recent factors are difficult to distinguish. Here we investigated environmental samples of *A. fumigatus* from New Zealand, a geographically very isolated population, and compared them with those from other parts of the world to analyze the relative roles of historical differentiation and recent gene flow in shaping *A. fumigatus* populations. Our data suggest that the New Zealand *A. fumigatus* population has genetic elements similar to those from other regions such as Europe, Africa, and North America. Additionally, susceptibility testing identified two triazole-resistant strains, one of which contained the globally distributed mutation TR34/L98H in the *cyp51A* gene. Our results suggest that contemporary gene flow, likely due to anthropogenic factors, is a major factor shaping the New Zealand *A. fumigatus* population.