



Ontario Ecology & Ethology Colloquium



Hosted by The University of Guelph
April 28 – 30, 2008

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Overview of Conference

	Monday	Tuesday	Wednesday
Time	Rozanski (room 101)	Rozanski (room 103)	Rozanski (room 102)
7:00 - 9:00 AM		Registration	
9:00 - 10:00 AM	Margo Wilson and Martin Daly Plenary		Locke Rowe Plenary
10:00 - 10:30 AM	30 Minute Break	30 Minute Break	30 Minute Break
10:30 - 10:45 AM	Conservation Genetics	Dispersal / Migration	Invasion / Herbivory
10:45 - 11:00 AM	Dennis Hedgecock	Karl Cottenie	Paul Caplat
11:00 - 11:15 AM	Lindsay Crawford	Astrid Schwalb	Steven Hill
11:15 - 11:30 AM	Heather Frearno	Noel Quinn	Andrew MacDonald
11:30 - 11:45 AM	Kelly McNichols	Lauren Hooten	Brandon Campitelli
11:45 - 12:00 AM	Elizabeth Boulding	Greg Mitchell	Min Ku Kim
12:00 - 1:00 PM	Lunch Break	Lunch Break	Lunch Break
1:00 - 2:00 PM	Rees Kassen Plenary		Scott MacDougall-Shackleton Plenary
2:00 2:15 PM	15 minute break	15 minute break	15 minute break
2:15 - 2:30 PM	Geometric Morphometrics Symposium	Animal Behaviour	Foraging / Diet
2:30 - 2:45 PM	Beren Robinson	Kenny Lee	James Morris-Pocock
2:45 - 3:00 PM	Tim Dickinson	Maria Diez-Leon	Liam McGuire
3:00 - 3:15 PM	Amanda Roe	Dara Orbach	Jeffrey Zeyl
3:15 - 3:30 PM	Sebastien Paquette	Rebecca Meagher	Marjorie Sorensen
3:30 - 3:45 PM	Harald Parzer	Jeff Stoltz	Michael Janssen
3:45 - 4:00 PM	15 minute break	15 minute break	Jennifer McCarter
4:00 - 4:15 PM	Geometric Morphometrics Symposium	Morph. / Devel.	Soil Ecology
4:15 - 4:30 PM	Miriam Zelditch	Kathleen Lucas	Ingrid Ng
4:30 - 4:45 PM	Dianne Sharpe	Erin Fraser	Terry Bell
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5:00 - 5:15 PM	Jessica Ward	Bhagwati Gupta	Cass Stabler
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5:00 - 7:00 PM	Registration		
7:00 - 8:00 PM	Ron Swaisgood Plenary	Poster Session and Mixer	
8:00 - 11:00 PM	Mixer - UC	in Atrium of the New Science Complex	

Monday, April 28 th

Opening Registration

- In the Atrium of Rozanski
- Presenters are encouraged to bring their oral presentations on either a USB key or CD and upload it to the laptop of the appropriate room.
- At this time you can also pick up your parking passes for the week

Opening Plenary Talk – room 101 Rozanski

7:00 – 8:00 PM

The big move: dispersal, habitat settlement, and conservation

Ron Swaisgood

UCLA

Behavioral ecological approaches have yet to be fully integrated into conservation biology, yet many behavioral processes are likely to influence the success of conservation programs. The subdiscipline of habitat selection, particularly how dispersing animals choose where to settle, provides a rich theoretical framework generating testable hypotheses that can guide many conservation actions. Here I review how some of these ideas may be incorporated into conservation programs. Perceptual and decision-making mechanisms in dispersers determine the distribution of members of a species on the landscape. Decisions made by dispersers sometimes run counter to goals set by conservation managers; for example, suitable habitat may be set aside but target species fail to settle there. Reintroduction and translocation programs suffer from high post-release mortality and long-distance, unpredictable dispersal behavior that exacerbates risks. These programs are essentially exercises in “forced dispersal.” Here I discuss several mechanisms known to influence dispersal and settlement, focusing on conspecific cueing and natal habitat preference induction (NHPI). The conspecific cueing (also called conspecific attraction) hypothesis posits that dispersers rely on the presence of conspecifics to assess habitat suitability. Similar to the concept of habitat imprinting, NHPI occurs when an animal’s experience in its natal habitat shapes its post-dispersal preference for habitat settlement. If dispersers continue to wander, exposing themselves to risks, until they find “someplace like home” or “someone like me,” conservation behaviorists should find solutions in shaping their pre-release experience or planting cues in the post-release environment that will accommodate these behavioral rules of thumb. I explore the possibility that these and other mechanisms can be manipulated to encourage animals to settle, quickly and safely, in appropriate protected habitat.

Opening Mixer

At the University Club

In room 5__ of The University Center

8:00 – 11:00 PM

Tuesday, April 29 th

Registration

Open from 8:00 – 9:00

In Rozanski Concourse

Morning Plenary Talk

9:00 – 10:00 AM

Human Impatience and Recklessness as Facultative Future Discounting

Margo Wilson and Martin Daly

McMaster University

People and other organisms generally prefer imminent goods over more distal future goods. But to what degree? Optimal discounting of the future entails facultative response to cues indicative of the relative utility of current versus future efforts, and varies across species, sexes, life stages, and circumstances. We have used this perspective on reproductive effort scheduling, pioneered by G.C. Williams, to generate hypotheses about human impatience and recklessness, and will present relevant data from both experimental and archival research.

30 minute morning break

- Coffee, water, and small pastries will be available
- In Rozanski Concourse

First Concurrent Session

Conservation Genetics (Room 101)

10:30 – 11:00 AM

Chance & Necessity in Highly Fecund Marine Life

Hedgecock, Dennis, University of Southern California

Most evolutionary biologists consider Natural Selection, particularly balancing selection, as the primary force behind the maintenance of biodiversity. In the 1980s, positive correlation between fitness-related traits, such as growth and survival, and allozyme heterozygosity in bivalve mollusc populations was taken by some as evidence that balancing selection maintained these protein polymorphisms. However, in the late 1990s, experimental work on the Pacific oyster revealed selection against recessive mutations as the more plausible alternative explanation for this correlation. Evidently, this oyster and, by inference, other highly fecund marine fish and shellfish generate a large load of deleterious recessive mutations, simply as a by-product of having to produce tens of millions of eggs (Necessity). Selection against homozygotes for these mutations likely causes the correlation of fitness with allozyme heterozygosity in natural populations. Why doesn't selection eliminate these mutations or drive them to low levels? A large part of the answer is "Chance," in the form of sweepstakes reproductive success, which is made possible, again, by high fecundity and which reduces effective population size (N_e), increasing genetic drift and inbreeding in marine populations. Genetic drift may allow even highly deleterious mutations to persist longer than expected in marine

populations; these mutations may also be introduced at frequencies greater than $1/2N$, through a process known as clustered mutation. Inbreeding depression, resulting from mutational load at the genomic level, coupled with sweepstakes reproductive success, may thus account for much of the standing variation in fitness (growth & survival) in marine fish and shellfish. Since many deleterious mutations are expressed in early life stages, these findings have implications for understanding the recruitment problem in fisheries.

11:00 – 11:15 AM

Genetic structure analysis of an endangered population of the Mormon metalmark butterfly (*Apodemia mormo*) using amplified fragment length polymorphism (AFLP)

Crawford*, Lindsay A., Keyghobadi, Nusha. Department of Biology. University of Western Ontario.

For many threatened invertebrate species, little is known regarding their population structure and dispersal behaviours, making it difficult to develop effective management strategies. The British Columbia population of the Mormon metalmark butterfly, *Apodemi mormo* (Felder, 1859) is an example of an at-risk species whose protection to date has been hindered by a general lack of knowledge surrounding the butterfly's basic habitat requirements, dispersal capabilities and population structure. Many conservationists now routinely use genetic techniques to provide insight into various aspects of a species' biology, in particular those aspects that may be difficult to study using traditional field methods. The objective of this study is to assess the genetic structure and diversity of the B.C. population of the Mormon metalmark using amplified fragment length polymorphisms generated from non-destructive samples of butterfly wing tissue. By examining the basic genetic structure of the population I will be able to identify potential source populations and critical habitat sites for protection, as well as estimate dispersal rates between habitat patches. This information will contribute to efforts to predict future population trends and develop a recovery strategy for this species. As well, both the successful development of AFLPs from wing tissue and the use of the technique to assess genetic structure in an endangered butterfly population will solidify the method as a valuable tool for conservation research.

11:15 – 11:30 AM

Identification of non-neutral single nucleotide polymorphisms in wild Atlantic salmon (*Salmo salar*) and their use in population identification for conservation

Freamo, Heather*; O'Reilly, Patrick; Boulding, Elizabeth
Department of Integrative Biology, University of Guelph

Inner Bay of Fundy (iBoF) salmon have declined during the last two decades, and in 2002 were designated by COSWEIC as endangered. Distinguishing iBoF from aquaculture and wild outer Bay of Fundy (oBoF) salmon would benefit current conservation programs for iBoF salmon. We propose to use genetic markers that are potentially under local selection to distinguish between iBoF and oBoF salmon. We developed non-neutral single nucleotide polymorphism (SNP) markers at the University of Guelph using various outlier detection programs, and then carried out the genotyping using Invader™ probe technology at a Department of Fisheries and Oceans laboratory in Dartmouth, NS. We will use these SNP loci as markers to a) estimate the proportion of genetic variation between and within populations, b) determine whether it is possible to use these SNPs to differentiate between iBoF and oBoF populations and c) further determine whether it is possible to use the SNPs to assign a salmon back to its natal river.

11:30 – 11:45 AM

Population dynamics of endangered species of freshwater mussels in the Sydenham River in Ontario.

McNichols, Kelly, A.*, Ackerman, Josef, D., Mackie, Gerald, L.
Department of Integrative biology. University of Guelph.

Freshwater mussels are among the most endangered groups of organisms in the world and particular declines have been observed in North America. There are 54 species of freshwater mussels in Canada and 34 of these occur in Ontario. Currently ten species have been listed as endangered by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). Information about current distribution, sex ratios, and proportion of gravid females is limited and is required to facilitate the recovery of these species. Our goal was to identify a suitable collection technique from which to determine the sex ratios and proportion of gravid females for endangered mussel species in the Sydenham River in

Ontario. Mussel species included: northern riffleshell (*Epioblasma torulosa rangiana*), snuffbox (*Epioblasma triquetra*), and rayed bean (*Villosa fabalis*). Two different collection techniques (quadrats and raccooning) were compared at six sites in the Sydenham River and no significant differences were observed in the number of mussels collected per person hour of searching. Using the individuals collected via raccooning, sex ratios and the proportion of gravid females were determined for a number of sites. Results indicated that there are site specific differences in the sex ratios, which tend to be skewed towards males, and proportion of gravid females (10-40%). This information is vital for the conservation of freshwater mussels in Ontario. It will allow us to determine which sites may be considered healthy in the Sydenham River and identify potential sites where augmentation or reintroduction may be successful.

11:45 AM – 12:00 PM

Conservation genomics of Atlantic salmon: SNPs associated with QTLs for adaptive trait differences in parr from four trans-Atlantic backcrosses

Boulding*¹, Elizabeth G., Culling¹, Mark, Glebe², Brian, Berg³, Paul R., Lien^{3,4}, Sigbjørn, Moen^{3,5}, Thomas
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The genetic basis of local adaptation by juvenile Atlantic salmon (*Salmo salar*) to their natal rivers is poorly understood. We created four large (N=300) backcross families by crossing trans-Atlantic F1 male siblings to a female from either the European or the North American parental populations. These four full-sib families showed segregation for alleles that were unique to each of the original parental strains. We genotyped these large full-sib families for 129 SNPs (single nucleotide polymorphisms) within expressed sequence tag loci (ESTs) that were well spaced throughout a new Atlantic salmon linkage map. The high polymorphism and low rates of cross-over in our hybrid males gave us a statistically powerful way to detect associations between SNP markers on a particular chromosome arm and quantitative trait loci (QTLs) for 30 morphological, two crypsis, and six life history traits. We found significant associations between particular SNPs and QTLs for early and late juvenile growth rate, condition factor, parr mark number and contrast, and 19/30 morphological traits that quantified body shape and fin position. Most parr traits had one or two major QTLs which explained 20-40% of the phenotypic variance and showed experiment-wise significance. Our work adds to the evidence that much of the variation in growth rate, shape, and colour observed among Atlantic salmon parr from different streams that vary in flow rate and substrate pattern and colour, is genetic. Future work with an even higher density of SNP markers may enable us to understand the molecular basis of adaptive trait differences among parr populations from different rivers.

Dispersal and Migration (room 103)

10:30 – 10:45 AM

Cryptic dispersal in zooplankton: insight from a metacommunity perspective

Cottenie*, Karl
 Department of Integrative Biology, University of Guelph

Dispersal is a key structuring force in structuring communities. The cryptic nature of the extent, rates, and mechanisms of freshwater zooplankton dispersal, however, has puzzled limnologists for the last 200 years. My main goal is to reassess this problem from a metacommunity perspective. I compared observational results from empirical metacommunity systems, spanning the range of highly connected to isolated, with a heuristic theoretical model and experiment that relates different metacommunity types to dispersal rates and environmental heterogeneity within a metacommunity. Both the experimental and observational results show that species sorting is the main determinant of zooplankton communities, or that dispersal is in general not limiting in freshwater zooplankton communities with some evidence for dispersal limitation and mass effects. Thus dispersal in zooplankton is not only cryptic because it is difficult to observe the dispersing stages, but it is also difficult to observe the results in community structure because it is efficient enough, relative to environmental heterogeneity, to result in strong species sorting dynamics.

10:15 – 10:30 AM

Freshwater mussel larval dispersal in rivers – a transport model and its empirical evaluation in the field

Schwalb*, Astrid.N., Garvie Marcus, Ackerman, Josef D.
Department of Integrative Biology, University of Guelph

Despite the importance of dispersal for many ecological processes such as population connectivity and (re)colonization of habitat, little is known about the extent of dispersal in freshwater mussels. We examined dispersal of larvae (glochidia) of a common mussel species *Actinonaias ligamentina*, which need to attach to a host fish in order to develop into juveniles. We parameterized an existing turbulent transport model with measurements in the field (e.g., flow speed) and in the laboratory (settling velocity of glochidia) and compared those with field experiments of release and recapture of stained glochidia. The number of suspended glochidia generally decreased logarithmically with distance, and a small proportion of glochidia were still found to be suspended 96 m downstream, suggesting that infestation of host fish may occur several tens to hundreds of meters downstream of the adults' location, even at relatively low flow conditions (mean flow speed = 15cm/s). Results indicate that dispersal distances increase with flow speed, but the number of suspended glochidia at a certain distance can vary considerably due to stochastic effects of turbulence, especially at shorter distances. Individual runs could therefore deviate considerably from model predictions, but overall there was a good correlation between measured data and model prediction ($R^2 = 0.82$, $p = 0.01$). The physically-based model will be useful to examine the passive transport of juvenile mussels and dispersal propagules of other organisms in streams, which will help to determine the effect of dispersal on connectivity and dynamics of populations, their spatial and temporal patterns, and their colonization potential.

11:00 – 11:15 AM

The influence of bathymetry on the external fertilization success of broadcast spawning freshwater mussels

Quinn*, Noel, P., and Ackerman, Josef, D., Department of Integrative Biology, University of Guelph, Ontario, Canada, N1G-2W1.

One of the critical life strategies for many benthic sessile invertebrates is broadcast spawning, and how eggs and sperm contact each other and escape from the benthic boundary layer into the water column. Turbulent sweeps and ejections, which are high speed fluid bursts towards and away from the bed respectively, are strongly controlled by bathymetry, but have not been considered in biological systems. The hypothesis that turbulence has a primary influence on external fertilization and gamete dispersal through topographic forcing near the bottom was examined in dreissenid mussels. This was addressed by determining whether there are fluid regions above the benthos where ejections (or sweeps) enhance (or inhibit) fertilization. Interestingly, fertilization success in both *Dreissena polymorpha* and *Dreissena bugensis* were 10-15% higher at sperm concentrations <1000 sperm/ml in static tests compared to other broadcast spawning organisms. Experiments were conducted in a recirculating flow chamber to examine the effect of velocity and turbulence generation (using Particle Image Velocimetry) and distance from spawning males on fertilization success. The generation of small-scale turbulence structures (higher ejection rates) by mussel patches on the bottom resulted in enhanced fertilization (6% increase) compared to a uniform distribution of mussels. Field trials conducted in Lake Erie illustrate a similar pattern. Topographic forcing appears to have an important role in the reproductive ecology of benthic organisms.

11:15 – 11:30 AM

Identifying critical areas for migratory bats: a case study using Long Point, Ontario

Hooton*, Lauren A., Fenton, M. Brock
Department of Biology, University of Western Ontario

Little is known about migratory bat species, making the design of effective conservation and management plans difficult. Recent research has shown that bats appear to be migrating through Long Point, Ontario, an important stopover site for migrating birds. I hypothesized that Long Point is a critical area for migrating bats, predicting higher activity levels on Long Point than in the surrounding area, as well as higher genetic diversity. I used acoustic monitoring of echolocation calls to measure activity levels of bats on Long Point and in the surrounding area. I also captured little brown bats (*Myotis lucifugus*) on Long Point, at a hibernaculum in eastern Ontario, and at several

maternity colonies. Activity levels on Long Point were highest during the spring and fall migration periods, and were much higher overall than at any location in the surrounding area. The lack of activity in the surrounding area suggests that Long Point is a specifically targeted area for migrating bats. Preliminary genetic analysis suggests that genetic diversity is greater on Long Point than at the hibernaculum, which is very surprising given that the hibernaculum is well known for attracting thousands of bats from all over southern Ontario. My research has highlighted the importance of Long Point as a habitat for migrating bats. By using a similar approach, further areas of importance to migratory bats may be identified. Once sites are identified, they may be incorporated into conservation and research planning for more in-depth study of elusive migratory bats.

11:30 – 11:45 AM

Factors limiting individual success during fall migration for three species of songbird breeding on Kent Island, New Brunswick, Canada: A research proposal

Mitchell*, Gregory, W., Norris, Ryan, D., Guglielmo, Christopher, G.

*Department of Integrative Biology. University of Guelph.

Factors limiting the individual success of organisms inhabiting seasonal environments may act within and across seasons. For migratory songbirds, our ability to understand these factors has been constrained by our inability to follow individuals throughout their annual cycle. Using a state-of-the-art automated telemetry system, light-sensing geo-locators, and stable isotopes, I will investigate the factors controlling individual success during fall migration. Research will take place on Kent Island, New Brunswick, Canada. Study species will include the Savannah sparrow (*Passerculus sandwichensis*), Swainson's thrush (*Catharus ustulatus*), and yellow warbler (*Dendroica petechia*). Individual success will be defined by (1) early departure during fall migration, (2) the ability to traverse an ecological barrier, and (3) a rapid southward migration. Hypotheses that will be examined to explain individual success include individual condition resulting from breeding events, breeding origin, breeding phenology, and meteorological events. We will employ a combination of observational and experimental approaches to test these hypotheses. Specifically, individual condition will be experimentally manipulated for each species by imposing nutritional stress through brood additions (adding eggs to nests, +2) and subtractions (taking eggs out of nests, -2), decreasing and increasing the condition of individuals (both parents and offspring), respectively. This research will provide one of the first examinations of how breeding season events are linked with events during fall migration, an important component towards understanding how and when migratory songbird populations are limited.

11:45 AM – 12:00 PM

Invasion Biology and Herbivory (room 102)

10:30 – 10:45 AM

Invasibility in a simulated tree population: importance of individual variability and timing of invasion

Caplat, Paul*, Anand, Madhur, Bauch, Chris T., Department of Environmental Biology, University of Guelph

The timing of introduction of a new species into an ecosystem can be critical in determining the invasibility (i.e., the sensitivity to invasion) of a resident population. Here, we use an individual-based model to test how the type of competition (symmetric vs. asymmetric) influences the success of invasion by producing oscillatory dynamics in a resident age-structured tree population. We focus on a case where two species (one resident, one invader introduced at low density) do not differ in terms of competitive abilities. By varying the time of introduction of the invader, we show that oscillations in the resident population favor invasion, by creating "invasibility windows" during which resource is available for the invader due to transiently depressed resident population density. Moreover, we show how stochasticity and age-structure affect the impact of the invasion on the resident population. We discuss these results in the context of current knowledge on forest dynamics and invasions, emphasizing the importance of variability in population dynamics.

10:15 – 10:30 AM

Phylogeny and invasion: relatedness of exotics to native family members influences the amount of damage from natural enemies.

Steven B. Hill* & Peter M. Kotanen

Department of Ecology and Evolutionary Biology, University of Toronto at Mississauga

The ecological and economic impacts of non-indigenous invasive species have been demonstrated worldwide. However, predicting which species are likely to become problematic is still beyond the ability of ecologists and evolutionary biologists. We explore phylogeny as a framework to fill this void. One barrier to invasion is enemies e.g. consumers and pathogens. If enemy host use is positively correlated with evolutionary relatedness of hosts, then invasion success may be mediated by the presence of close relatives in an exotic's invaded range. Specifically, exotics that have close relatives should accumulate enemies faster than exotics without; this will be manifested by increased damage on the former. We used common garden experiments and field surveys to test the hypothesis that damage decreases with phylogenetic relatedness of exotics to natives. Model selection indicated that phylogenetic relatedness of exotics to native family members was a better predictor than distance to their closest native relative. This result was apparent under experimental conditions, but not field surveys. Results from the experiment can be understood if innovations among plants that influence enemy host use are more likely to be conserved among recently diverged family members. The field survey results suggest that environmental variation in damage masks any phylogenetic signal, emphasizing the use of controlled conditions to increase statistical power. Our results have implications for understanding invasions in a phylogenetic context, and the role of escaping enemies as a mechanism for successful invasion.

11:00 – 11:15 AM

Natural enemies and fitness in Common Ragweed (*Ambrosia artemisiifolia*)

MacDonald*, A. Andrew M., Kotanen, Peter M.

How important is enemy escape in facilitating invasions? Many studies of invaders provide evidence for enemy release, without testing the assumption that natural enemies have important fitness effects across the life cycle. Ragweed (*Ambrosia artemisiifolia*) is attacked by both specialist and generalist consumers in its native North America, but enjoys enemy release in Eurasia. I tested the effects of competition, insect attack and conspecific density on ragweed fitness in the field during Summer 2007, using a factorial design (3 densities x competitors present/absent x enemies present/absent). In a second experiment, seed mortality is being examined in the context of two nested factors: control, rodents excluded, rodents and fungi excluded. Preliminary results suggest that high-density and competitor-free plots had the largest proportion of damaged leaves, while low-density, competitor-filled plots were safest. However, ragweed is tolerant; this damage did not translate into a loss of fecundity. In contrast, competition had a significant fitness cost: more plants died compared to those planted in open plots, and those surviving were much smaller and produced few to no seeds. ANOVA will be used to compare treatments, and a matrix population model will summarize the results into a complete survey of the life cycle. However, it can already be seen that aboveground insect damage does not significantly reduce fitness, making it unlikely that release from these consumers has caused ragweed's invasiveness in Europe.

11:15 – 11:30 AM

An Association between Leaf Variegation and Reduced Herbivore Damage

Campitelli*, Brandon E., I. Stehlik, J.R. Stinchcombe

Department of Ecology and Evolutionary Biology, University of Toronto

Leaf variegation refers to local regions of the upper surface of a leaf having reduced or obstructed chlorophyll which results in whitish spots. These lighter spots may compromise the photosynthetic efficiency of a leaf, and many competing hypotheses have been put forward to explain why this patterning may be adaptive. It has been suggested that variegation is either an adaptive response to environmental conditions or a defense mechanism against herbivore damage. This study focused on the hypothesis that variegation is a strategy employed to deter herbivory. To test whether leaf variegation reduces herbivore damage, we first assessed the frequency of variegated and non-variegated leaves in natural populations of the plant *Hydrophyllum virginianum*, and secondly, we measured herbivore damage for both variegated and non-variegated leaves. We found that variegated leaves were present at high frequencies within natural populations (range: 6- 31%) and that non-variegated leaves sustained nearly twice the amount of damage in comparison to variegated leaves. Therefore, leaf variegation appears to be beneficial by reducing herbivore damage to

leaves. These data are consistent with the fundamental prediction of the herbivory hypothesis for the benefits of leaf variegation.

11:30 – 11:45 AM

Using phylogenetically independent comparisons to explain interspecific variation in herbivore damage.

Kim*, Min Ku., Kotanen, Peter M.
Department of biology. University of Toronto at Mississauga.

Leaf characteristics of southern Ontario plants were measured and analyzed to test whether they predicted the amount of damage caused by invertebrate herbivores. Leaf toughness (g/mm^2), water content (% mass), nitrogen content (% composition), carbon content (% composition) and carbon : nitrogen ratio were measured for fully expanded leaves of 58 plant species. Damage also was measured, in two different ways: amount of leaf area damaged and proportion of leaves damaged. Phylogenetically uncorrected regression analysis showed a strong positive relationship between nitrogen content and both leaf area and the proportion of leaves damaged; in contrast, there was no relationship between damage and the other variables. However, such analyses can be misleading in comparative datasets, since they risk confounding the variables of interest with other unmeasured but phylogenetically conserved traits (e.g., toxins). When results were analyzed using Felsenstein's phylogenetically independent contrasts, significant positive correlations again were found between damage and nitrogen content; as well, a significant negative relationship was detected in most analyses between damage and carbon : nitrogen ratio. These results indicate that even after correcting for phylogenetic non-independence, food quality has an important effect on attack rates, but that leaf toughness may not be as good a predictor of herbivore damage as previously thought.

11:45 AM – 12:00 PM

Induced responses in *Ipomoea hederacea*: simulated mammalian herbivory induces resistance and susceptibility to insect herbivores

Simonsen, Anna, K., Stinchcombe*, John, R.
Department of Ecology and Evolutionary Biology. University of Toronto

Multispecies interactions between plants and natural enemies are ubiquitous, and often lead to diffuse interactions between plants and their herbivores. Nonspecific induced responses, where responses induced by one species affect other species, are one potential mechanism generating diffuse interactions. Using 57 inbred lines of the Ivy leaf morning glory, *Ipomoea hederacea*, in a greenhouse experiment, we examined whether simulated mammalian herbivory induced responses that could affect plant resistance to the generalist insect herbivore, *Spodoptera exigua*. Inbred lines were highly variable for induced responses, ranging from induced resistance to induced susceptibility, with the rank-order for resistance in inbred lines changing between clipping and control treatments. We failed to detect significant genetic correlations between induced responses and trichome density, or that clipping modified the negative relationship between trichome density and *Spodoptera exigua* consumption and biomass. Our results suggest that non-specific induced responses can mediate the diffuse evolutionary relationship between *I. hederacea* and its herbivores, and that genetic variation in induced responses are an important component of this interaction.

Lunch Break

- Break from 12:00 – 1:00 PM
- At this time a variety of sandwiches will be available in the Atrium of the New Science Complex
- Take this opportunity to preview the posters which will be on display tonight

Afternoon Plenary Talk – room 101
1:00 – 2:00 PM

The ecology and genetics of adaptive radiation: a microbial view
Rees Kassen
University of Ottawa

The history of life is punctuated by periods of unusually rapid evolutionary diversification called adaptive radiation. Darwin's finches in the Galapagos, cichlid fishes in African Rift and Nicaraguan crater lakes, and the emergence of mammals at the end of the Cretaceous are hallmark examples. Although we have learned much from these and other case studies about the putative mechanisms responsible for adaptive radiation convincing experimental tests of the theory are often lacking for the simple reason that it is usually impossible to 'rewind the tape of life', as Stephen Jay Gould was fond of saying, and run it again. This situation has changed dramatically in the last ten years with an increasing emphasis on the use of microbial populations to study evolution in the laboratory. One particular model system, the plant-associated bacterium *Pseudomonas fluorescens*, has proven particularly important for the insights it has provided into the ecology and genetics of adaptive radiation. I will discuss some of the recent work that we and our collaborators have been doing in this regard.

2:00 – 2:15

15 Minute Break

- Coffee and water are available in the Rozanski Concourse

Second Concurrent Session

Geometric Morphometrics Symposium (room 101)

2:15 – 2:45 PM

Geometric morphometric investigations into the evolution of developmental flexibility in Icelandic stickleback body form

Robinson, Beren W.
Dept. of Integrative Biology, University of Guelph, Guelph, ON., Canada

Until recently, evolutionary, functional and descriptive studies of phenotype were often limited to relatively simple traits by the challenges of identifying and quantifying more complex features. External body form is often a highly complex set of covarying features in 2- or 3-dimensional physical space characterized by the absolute and relative sizes and positions of subcomponents. Traditional approaches using linear measurements to quantifying feature size and position are being replaced by revolutionary approaches that assess the geometric locations of 2- or 3D coordinate information. Geometric morphometric methods can retain more shape information than traditional linear methods, increasing the ability to detect interesting shape variation; enhance visualization of variation in complex shapes; allow for efficient partitioning of size from shape information; allow for removal of artificial influences on shape; and generate shape information that can be analyzed using conventional statistical methods. Free software has dramatically automated geometric morphometrics and recent textbooks now illustrate many methods. I demonstrate the basic steps of data gathering and analysis using one common geometric morphometric approach involving the 'thin-plate-spline'. I use this method to study how developmental plasticity in response to salinity contributes to phenotypic evolution in Icelandic threespine stickleback during their evolutionary transition from ancestral marine to derived freshwater forms. Controversy about the role of developmental plasticity in adaptive evolution centers on whether it enhances or limits

evolutionary responses to selection. Here, I test predictions arising from two hypotheses about its positive effects on adaptive evolution in stickleback: the ‘Baldwin effect’ and Waddington’s ‘genetic assimilation’.

2:45 – 3:00 PM

Morphometrics in the systematics of unitary and metameric organisms - geometric and otherwise

Dickinson, Timothy A.
Natural History, Royal Ontario Museum
Ecology and Evolution, University of Toronto.

A revolution in morphometrics began more than 30 years ago as an accompaniment to revolutionary increases in access to computational power and digital data capture capabilities. This revolution was stimulated to a great extent by a series of polychromatic publications by Fred Bookstein and his collaborators. Interest in biological shape and shape change is, of course, much older but Bookstein’s work served to focus attention first on the importance of distinguishing shape from size variation, and then on the “landmarks” by means of which shape differences can be recognized. Landmarks and “pseudolandmarks” were inherent in traditional morphometrics, even in those cases in which landmarks may be seriously lacking. Nevertheless, a preoccupation with charismatic zoological structures may have initially hindered the recognition that there are biological shapes with few landmarks, or that lack landmarks altogether. Likewise, there may have been a typological prejudice early on that came from working with unitary organisms. My own experience, mainly with metameric organisms (plants) has given me a chance to observe, and participate in, this revolution in morphometrics as it relates to systematics at the species level and below, and to related questions in development. From this perspective I will compare methods, and survey some of the data capture approaches that are available.

3:00 – 3:15 PM

Delimitation of two sympatric *Dioryctria* species (Pyralidae: Phycitinae) using morphometrics, molecules, and larval host associations.

Roe,* Amanda D., Sperling, Felix A.H.
Dept. Biological Sciences, University of Alberta, Edmonton AB Canada

Cryptic sympatric species are often notoriously difficult to identify, and require the use of novel characters and methods to delimit these taxa. Members of the *Dioryctria schuetzeella* group (*D. reniculelloides* and *D. pseudotsugella*) (Pyralidae: Phycitinae) provide an excellent example of such species, due to their intermediate morphological forms, similar larval host plants, and a broadly sympatric distribution. Given these characteristics, we used a combination of morphometric, molecular, and ecological characters to test the delimitation of *D. reniculelloides* and *D. pseudotsugella*. Restricted gene flow was found between an eastern *D. reniculelloides* clade and a western *D. pseudotsugella* clade, which corresponded to clusters of morphometric variation and larval host plant association. The combination of morphometric traits, molecular variation, and larval host plant provided clear delineation of these two taxa, and demonstrates the importance of using a variety of traits to delimit species.

3:15 – 3:30 PM

Morphometrics and the conservation management of tortoises

Rioux Paquette*, Sébastien & Lapointe, François-Joseph
Département de Sciences Biologiques, Université de Montréal

Because of the continuous refinement and rising accessibility of molecular approaches, studies of genetic variation in wild populations have become a key element of the conservation biologist’s toolbox. For instance, they make the identification of distinct conservation units within species reasonably straightforward, and this knowledge is increasingly incorporated in conservation plans by wildlife managers. However, considering the sparse resources available for conservation initiatives in several parts of the world, we were interested in developing a cheaper alternative based on morphometric analysis. Here, we present the case of the radiated tortoise (*Astrochelys radiata*) from southern Madagascar, for which the reintroduction of confiscated individuals to their home range is a matter of concern. Previous work had found significant genetic differentiation at neutral loci in this species. Using 40 carapace characters measured in over 120 wild-ranging tortoises, we were able to detect significant morphometric differentiation among three groups of populations, and discriminant functions allowed for the correct assignment of 83% of sampled

tortoises to their original group. Traditional morphometric analyses were employed because most geometric morphometric approaches rely on standardized laboratory conditions for data collection and/or instrumentation unsuitable for field work. However, recent advances developed to investigate carapace shape variation in giant tortoises suggest that it should be possible to collect suitable data for geometric morphometric analyses in the future, even in field conditions.

3:30 – 3:45 PM

The evolution of insect genitalia: trade-offs, shapes and development.

Parzer*, Harald, Moczek, Armin.

Department of Biology, Indiana University

The evolution of male genitalia in insects is still considered as a “mystery of mysteries”: on one hand even closely related species exhibit highly diversified genitalia, which serve for many species as the only source for identification. On the other hand, genitalic variation within species is unexpectedly low, compared to the variation seen in other classes of traits. Therefore, it remains unclear how this low level of within species genitalic variation could fuel the extraordinary diversity of genitalia observed between species. To address the evolution of insect genitalia we are using species of the dung beetle genus *Onthophagus*, which recently established as a promising model system for integrating ecology, evolution and development. Here, we will present data which indicate that trade-offs between primary and secondary sexual characters might trigger rapid diversification between populations and species. However, shape and size evolve under different rates, indicating that most of the genitalic diversity observed between species is caused by changes in shape and not in size. To further elucidate the evolution of genitalia we are conducting a functional analysis of patterning genes (e.g. *distalless* and *abdominal B*), which will allow us to understand the evolution of genitalia by understanding its development.

Animal Behaviour (room 103)

2:15 – 2:30 PM

Title: The effect of Flight Stimulation on Male Aggression and Fight Memory in *Teleogryllus oceanicus*

Lee, Kenny and Wang, Bunny

Department of Biology, University of Toronto at Mississauga

In many species, competition among males for mating opportunities has often resulted in the evolution of violent male-male aggression. Such competition among males has resulted in the phenomena known as the “loser effect”, where the losing individual has a higher probability of losing future fights, and the “winner effect”, where winner has a higher probability of winning future fights. It has been demonstrated that the stimulation of flight in male field crickets (Orthoptera, Gryllidae, Gryllinae) can eliminate both of these effects, but it had not yet been determined the extent to which crickets remember their fight history. We tested whether male Pacific field crickets (*Teleogryllus oceanicus*) remember the outcome (win or lose) of only their most recent fight or if they were influenced by both recent and early fights. Our experiment was designed so that we could test the effect of flight stimulation among crickets with four different fight histories: Winners (won two fights), recent winners (lost early fight but won recent fight), recent losers (won early fight but lost recent fight) and losers (lost two fights). Our study showed that in *T. oceanicus* the stimulation of flight reset aggression levels of crickets to that of a naïve male irrespective of their early fight history. Since these results suggest that crickets only retain memory of only their most recent fight, we conclude that the “loser effect” and “winner effect” is not an accumulation of past fight histories, but simply a result of a cricket’s most recent fight.

2:30 – 2:45 PM

Can captive conditions make animals dysfunctional? Preliminary data from a mate choice experiment

Díez-León*, María, Mason, Georgia

Department of Animal and Poultry Science, University of Guelph

Research and conservation efforts (e.g. reintroductions) typically rely on captive animals behaving as wild animals. A successful wild animal copes well with stressors, including those imposed by a changing and complex environment. In species with female mate choice, stress-resistant males are therefore typically preferred, and may even sire more/better quality offspring. In contrast, many captive animals display abnormal repetitive behaviours (e.g. stereotypic pacing) recently hypothesised to be caused by brain dysfunction. Furthermore, captive animals are rarely able to choose their

mates, and often experience breeding problems. Our research aims to understand the effects of captivity on animals by testing if abnormal repetitive behaviours are i) caused by brain dysfunction and ii) reduce overall fitness. We are raising American mink (*Mustela vison*) from birth in either enriched or non-enriched environments. We are collecting data on behaviour, on brain function, and on physical characteristics, as well as on mate preference and parental competence. Our first results confirm that enriched environments decrease abnormal behaviours ($F_{1,97}=4.57$; $p<0.05$). In a mate choice set-up, enriched but not non-enriched females visited enriched males more often ($F_{12,27}=3.57$; $p<0.05$); however they did not copulate more ($F_{1,27}=2.49$; $p=0.140$) or for longer ($F_{1,27}=1.56$; $p=0.236$) with them. Data on offspring paternity are now needed to assess whether enriched males are more reproductively successful. Future work will assess maternal abilities, fluctuating asymmetry and brain function in our differentially reared mink. If captive environments do compromise adult and offspring fitness, this could help explain why captive wild animals may have poor breeding success, and also low survivorship if reintroduced into the wild.

2:45 – 3:00 PM

Why do bats crash?

Orbach*, Dara, N.

Department of Biology, University of Western Ontario.

Free-flying insectivorous bats occasionally collide with stationary objects (windows, lighthouses, buildings, television towers, etc.) that should be easily detected by echolocation and/or vision. As many anecdotal reports of bat collisions report well-illuminated conditions, colliding bats may not pay attention to their echolocation and attend to visual sensory input despite decreased visual sensitivity at amplified light levels. To determine the role of visual and acoustic cues in object avoidance, I will set up obstacle grids across the flight paths of Little Brown Bats (*Myotis lucifugus*) at nursery colonies and swarming sites in Southern Ontario. Using combinations of light levels (ambient light, 10 lux, and 50 lux) and obstacle fabrics with different visual appearances but similar echo properties, I will observe and videotape bat flights through the grids to determine whether vision or echolocation plays a greater role in obstacle avoidance. The obstacle fabric strips will be spaced 30 cm apart and will be opaque, reflective, or transparent. I will playback recordings of conspecific distress calls to attract and distract bats, and will record echolocation calls and examine call rate changes to determine if obstacles are acoustically detected. I predict that bat collision rates will increase as light intensities increase and will decrease as fabric visibility increases. I also predict that colliding bats will not detect the obstacles acoustically. A better comprehension of the interaction between visual and acoustic roles in bat orientation will enable me to make conservation suggestions that reduce bat mortality rates resulting from collisions.

3:00 – 3:15 PM

Extreme inactivity as an indicator of impaired fitness and welfare in captive mink (*Mustela vison*)

Meagher*, Rebecca K., Mason, Georgia J.

Department of Animal & Poultry Science, University of Guelph

In many species, there are individual differences in response to barren captive environments: some animals develop stereotypic (abnormal, repetitive) behaviour, while others become extremely inactive. To determine whether the latter is a maladaptive response to the sub-optimal environment, we examined the relationship between inactivity and reproductive performance in 350 individually-housed females from three breeding lines on a commercial fur farm. Behavioural phenotypes were determined via scanning for four days before mating commenced. Although most females were stereotypic, some spent up to 90% of the day inactive. Our reproductive measures were quality of nest-building (an aspect of maternal care), scored by observers around the time of parturition; litter size at birth; and infant mortality before weaning. The relationships between these measures and inactivity were analysed using general linear models. High levels of inactivity in the nestbox predicted small litter sizes at birth ($F_{1,330}=4.40$, $P=0.037$), and among multiparous females, higher kit mortality between birth and weaning ($F_{1,202}=4.04$, $P=0.046$). Some signs of a link between inactivity and poor nest quality were also found, although they were not consistent over time. Stereotypic behaviour was inversely correlated with inactivity, but was a less consistent predictor of reproductive performance. We are currently replicating this study; exploring the roles of depression-like states, fear, and/or excess body fat in our findings; and investigating whether different forms of inactivity have different reproductive correlates. In addition to helping to identify individuals likely to breed poorly, extreme inactivity may have implications for welfare if it reflects chronic fear or 'apathy'.

3:15 – 3:30 PM

Turned on or turned off: Female sexual signaling varies with mating & life history in redback spiders

Stoltz, J.A.* & Andrade, M.C.B.

Integrative Behaviour and Neuroscience Group, University of Toronto Scarborough

In many species, virgin females produce sex pheromones that attract males or trigger courtship, but pheromone production ceases after mating. This can significantly constrain the opportunity for polyandry in nature, but it is often unclear whether variation in pheromone production is a strategic part of a female reproductive strategy, or due to chemical manipulation by males. If females produce pheromones strategically, then the interplay between the costs and benefits of polyandry at different stages of a female's life history should affect the timing of advertisement of receptivity via pheromones. We predicted (1) cessation of pheromone production by females after mating in redback spiders (*Latrodectus hasselti*), as females can fertilize thousands of eggs after a single copulation, and (2) resumption of pheromone production following the breeding season (three months) as females may need to replenish sperm stores prior to overwintering. We assessed pheromone production by comparing male activity on extracts from webs of females of different reproductive status. Activity on extracts from webs of virgin females significantly exceeded activity on extracts of webs of juveniles, non-virgin females and solvent controls. Moreover, male response to web-bound chemicals produced by virgin females disappeared within a day of these females mating. Since redback males dismantle much of their mate's web during courtship these results suggest that the web rebuilt by females after mating would not trigger male courtship. As predicted, females recommenced pheromone production 3 months after mating, although the degree of male activity was not dependent on previous sperm use by the female. Our results are consistent with the idea that females strategically alter pheromonal advertisement, however, these results could also indicate chemical manipulation of female receptivity by males. Regardless, the pattern of pheromone production revealed here suggests the opportunity for polyandry is constrained to particular periods in the female's life history, and this may have significant effects on patterns of sperm competition and male strategies.

3:30 – 3:45 PM

Foraging and Diet Quality (room 102)

2:15 – 2:30 PM

Comparative phylogeography of brown and red-footed boobies: can foraging distribution restrict gene flow in pelagic seabirds?

Morris-Pocock*, James A., Anderson, David J., Steeves, Tammy E., Friesen, Vicki L. Department of Biology, Queen's University, Kingston, ON K7L 3N6, Canada,

Despite their high vagility and potentially high gene flow between populations, many seabird species exhibit considerable levels of population genetic and phylogeographic structure. This pattern is particularly surprising in tropical or sub-tropical species that encounter few physical barriers to gene flow and have not been greatly affected by the fragmenting effects of Pleistocene glaciations. One mechanism that could contribute to this differentiation is strong philopatry coupled with restricted foraging range. To test the hypothesis that foraging range can influence population differentiation, we compared population genetic and phylogeographic structure between brown boobies (*Sula leucogaster*), which forage relatively close to shore, and red-footed boobies (*S. sula*), which forage up to 200km away from the breeding colony. We sequenced 550 base pairs of the mitochondrial control region from 220 brown and 250 red-footed boobies from throughout their global ranges. Global population genetic structure is high within both species ($\Phi_{ST} = 0.88$ and 0.82 for brown and red-footed boobies respectively), and in both cases gene flow seems to be restricted by physical barriers such as the Isthmus of Panama. However, the extent of population differentiation within ocean basins differs markedly between the two species. While several red-footed booby haplotypes are distributed throughout the Indian, Pacific, and Atlantic Oceans, no haplotypes are shared between any two brown booby colonies. These, and other results based on coalescent theory, suggest that gene flow within ocean basins is much higher in red-footed boobies than in brown boobies, and perhaps, that gene flow is restricted by the limited foraging range of brown boobies.

2:30 – 2:45 PM

Feeding and mass change of little brown bats (*Myotis lucifugus*) during swarming: A plasma metabolite perspective

McGuire*, Liam P., Fenton, M. Brock, Guglielmo, Christopher G.
Department of Biology, University of Western Ontario.

In August and September, little brown bats (*Myotis lucifugus*) gather at hibernacula in large numbers to mate and to deposit fat in preparation for hibernation. Bats begin arriving in early August, and mating begins to occur near the end of August. Mating occurs inside the hibernaculum and therefore while mating, bats are not able to forage and deposit fat for hibernation. All bats must deposit substantial fat stores for hibernation, and for sub-adults fat deposition is critical for survival of their first winter. We predicted that in the weeks before mating begins, all age and sex classes would feed intensely. However, during the mating period we predicted adult bats would spend more time in the hibernaculum mating and less time feeding, while first year bats continued to feed intensely. We measured the level of feeding by plasma metabolite analysis. Plasma triglyceride concentration increases relative to the level of feeding. As predicted, feeding decreased throughout the swarming period, however there were no age or sex effects. Interestingly, despite feeding equally, body mass increased over the swarming period for adult bats, but decreased for first year bats. The difference may be due to adult bats conserving energy more efficiently through behavioural or physiological strategies.

2:45 – 3:00 PM

Variation in visual risk perception corresponds with foraging behaviour in brook charr

Zeyl*, Jeffrey, N., McLaughlin, Robert, L.
Department of Integrative Biology. University of Guelph.

In the field, recently-emerged brook charr (*Salvinus fontinalis*) tend to specialize at a sit-and-wait tactic for feeding on crustaceans or an active search tactic for feeding on insects. Field and laboratory studies have demonstrated that differences in foraging tactics are linked to how quickly an individual will exit from a tube or glass jar into a novel environment. I altered light to test whether variation in exit times reflected differences in visual perception of risk, and not fixed dispositions to move. Individual brook charr were captured from the field, transported to Hagen Aqualab, and placed in an erect, translucent tube in an aquarium with the exit from the tube facing the aquarium's far end. Time to exit the tube into the aquarium and activity level in the aquarium were measured for each individual under well (white light, ~20 lux) and dimly (red light, ~1 lux) lit conditions. Under well-lit conditions, times taken to exit the tube were longer for less active individuals than for more active individuals, as observed in earlier experiments. Under dimly lit conditions, time taken to exit the tube was unrelated to activity, due to a reduction in exit times by less active individuals. These responses to changes in light support the hypothesis that visual perception of risk differs among individuals.

3:00 – 3:15 PM

Carry-over effects in a pacific seabird: stable isotope evidence that non-breeding diet quality influences reproductive success

Sorensen*, Marjorie C., Hipfner, J Mark., Kyser, T Kurt., Norris, D Ryan.
Department of Integrative Biology. University of Guelph.

Although most seabird species exhibit extreme annual variation in individual reproductive success, virtually nothing is known about how diet quality during the non-breeding period influences subsequent reproductive success. We used stable-nitrogen and -carbon isotopes to evaluate the effects of non-breeding diet quality on the timing of breeding and egg size in a population of Cassin's auklets (*Ptychoramphus aleuticus*) breeding on Triangle Island, British Columbia. Adult feathers are grown during two different periods of the annual cycle, which allowed us to estimate diet quality from the previous fall and pre-breeding (early spring) period. We found that the estimated proportion of energetically superior copepod spp. in the pre-breeding diet tended to be higher in females that bred earlier and laid larger eggs whereas energetically poor juvenile rockfish spp. were dominant in the pre-breeding diets of females that bred later and laid smaller eggs. Pre-breeding diet quality was not related to body condition measured soon after laying, which suggests that all females may need to attain a threshold condition before they initiate breeding and successfully rear young. Our results suggest that changes in climatic conditions during the pre-breeding period may have severe

consequences for population growth rates through their influence on copepod abundance. Our work emphasizes the importance of determining how events are linked throughout the annual cycle for understanding the fitness and population dynamics of migratory animals.

3:15 – 3:30 PM

Diet quality, body condition and breeding chronology of Marbled Murrelets (*Brachyramphus marmoratus*) within the Georgia Basin

Janssen*, Michael, H, Arcese, Peter, Kyser, Kurt, T., Williams, Tony, D., Bertram, Douglas, F., Norris, Ryan, D. Department of Integrative Biology, University of Guelph.

The Marbled Murrelet (*Brachyramphus marmoratus*) is a small, threatened seabird that nests in old-growth forest and forages year-round in near-shore waters of the Northeast Pacific Ocean. Previous research has demonstrated correlations between historic trophic feeding level and breeding success, but whether trophic feeding level is causally linked to breeding success and what the mechanisms behind this relationship are, remain unknown. We captured 212 murrelets during the 2006 and 2007 breeding periods in Desolation Sound, British Columbia, to test the hypothesis that pre-breeding trophic feeding level is positively associated with timing of breeding. We used stable-carbon and –nitrogen isotopes from feathers and blood of captured murrelets to determine trophic feeding level, and a plasma protein to assess breeding condition of females. We found that early in the breeding season, murrelets in breeding condition fed at lower pre-breeding trophic level than murrelets who were not in breeding condition, indicating a relationship between timing of breeding and diet quality. This study is one of the first to identify a potential mechanism by which diet quality influences breeding success. Our results suggest that conservation of the Marbled Murrelet within the Georgia Basin should focus on maintaining the integrity of marine, as well as terrestrial habitats.

3:30 – 3:45 PM

Trophic Control of Waterfowl Abundance in the Prairie Pothole Region

McCarter*, Jennifer, Iles, Dave, Department of Integrative Biology, University of Guelph

The abundance of organisms at particular trophic levels may be controlled by predators or food. Most empirical evidence comes from fish in whole lake experiments where, due to lake size, replication is limited. I evaluated the relative influence of predators versus food on the size and abundance of consumers in prairie pothole food webs to infer the effects of top-down versus bottom-up trophic control of waterfowl populations. If trophic control is predominantly top-down, then variation in waterfowl abundance in response to removal of their predators should cascade to phytoplankton such that phytoplankton will decrease (given an even number of trophic levels) or increase (odd number of trophic levels) compared to controls. If waterfowl are not predator-limited, then there will be no such cascade. Waterfowl (*Anas* spp., *Aythya* spp. and *Oxyura jamaicensis*), other consumers (fishes: *Pimephales pomelas*, *Culaea inconstans*, and salamanders: *Ambystoma tigrinum*), aquatic invertebrates and phytoplankton were measured on 36 ponds from May-July, 2007 in NE North Dakota. Preliminary results support bottom-up trophic control of prairie pothole food webs; despite macro-invertebrates having smaller body size ($p=0.07$) in ponds with greater waterfowl abundance, there was little difference in invertebrate abundance ($p>0.05$) or phytoplankton abundance ($p>0.05$) between ponds with high and low waterfowl abundance. Further research is being conducted to investigate my hypothesis that omnivory in the prairie pothole food web may be dampening the effects of trophic control.

3:45 – 4:00

15 Minute break

Third Concurrent Session

Geometric Morphometrics Symposium (room 101)

4:00 – 4:30 PM

Modularity of the rodent mandible: Geometric analyses of morphological integration.

Miriam Leah Zelditch*¹, Aaron R. Wood¹, Donald L. Swiderski².

¹Museum of Paleontology, ²Kresge Hearing Research Institute, U. Michigan, Ann Arbor

Modules are internally coherent, semi-autonomous units of developmental structure or process. Modularity has emerged as a major theme in evolutionary developmental biology because modules are both a fundamental feature of organismal organization and necessary for evolution. The rodent mandible is a classic model system for studies of modularity because it forms from six developmental modules that must be tightly regulated, both temporally and spatially, to produce a functioning whole. Additionally, these mandibular modules must be coordinated with developing muscles, a coordination that likely arises early in development but which regulates mandibular morphogenesis later. Whether musculoskeletal interactions integrate or modularize the jaw is an open question, and another is whether the integration that does arise results from direct epigenetic interactions among traits or from genes (or environmental factors) that act in parallel within different modules. Such questions have been repeatedly addressed using traditional morphometric methods. Traditionally, integration and modularity have been operationally defined in terms of statistical correlations between traits. Geometric methods present two major problems for analyzing modularity (1) we analyze landmark (and semi-landmark) configurations, not traits, and (2) we examine covariances, not correlations. I outline recent advances that make it possible to analyze modularity using geometric methods, and demonstrate their application to mandibles of deer mice (*Peromyscus maniculatus bairdii*) and eastern fox squirrels (*Sciurus niger*). Our results indicate a complex pattern of integration between teeth, muscles and bone as well as a structure better represented by a reticulated network than a nested hierarchy of semi-autonomous modules.

4:30 – 4:45 PM

Genetic and environmental contributions to the body shape of lake and stream stickleback: implications for gene flow and reproductive isolation

Sharpe, Diana M.T.*, Räsänen, Katja, Berner, Daniel, and Hendry, Andrew P.
Department of Biology, McGill University

Disentangling the relative contributions of genetic and environmental effects is important for understanding the factors that promote or constrain evolutionary diversification. Lake and stream populations of threespine stickleback (*Gasterosteus aculeatus*) show dramatic divergence in body shape in the wild; however, the genetic basis of these differences is poorly understood. In the Misty Lake system in British Columbia, one of the stream populations (inlet) shows strong divergence in body shape from the lake, whereas the other (outlet) does not. We have previously argued that natural selection has driven divergence in the inlet; whereas high gene flow has constrained adaptive divergence in the outlet. This interpretation implicitly assumes that the variation in body shape observed in the wild has a genetic basis. We tested that hypothesis here by raising the offspring of lake, inlet and outlet stickleback under common conditions in the laboratory. Variation in body shape among wild-caught and lab-reared stickleback from the three ecotypes was quantified using geometric morphometrics. We found that the most striking differences in body shape between wild lake and inlet fish were maintained under common garden rearing, as were the similarities in body shape between wild lake and outlet fish. Although we found substantial effects of rearing environment on body shape, these effects had little influence on the differences between the inlet and lake/outlet ecotypes. These findings are consistent with our previous interpretations regarding the role of natural selection and gene flow in this system, and suggest the possibility of several ecologically-dependent reproductive barriers between the lake and inlet.

4:45 – 5:00 PM

Correlated evolution of male and female morphology across populations of water striders (*Gerris* spp.)

Perry*, Jennifer C., Rowe, Locke
Department of Ecology and Evolutionary Biology, University of Toronto

Despite intense interest in sexual conflict, there are few uncontroversial examples of the sexual coevolution of traits involved in mating conflict. One well-documented example occurs in water striders: species in which males have exaggerated appendages for grasping females are also the species in which females have exaggerated anti-grasping structures. This species-level pattern is consistent with models of sexually antagonistic coevolution; however, there is currently little known about the extent of phenotypic divergence in these traits among populations. Moreover, theory predicts that local ecological factors should influence the outcome of sexual arms races, but there is little data available to address this hypothesis. In this study, we first assessed the extent of sexual covariation in body shape across populations of two water striders (*Gerris buenoi* and *G. incognitus*). We examined both new collections and museum specimens and employed a geometric morphometric analysis. We found that male and female body shape show tight covariance in *G. incognitus*, but not in *G. buenoi*. In contrast to the species-level pattern, populations with males that

possess exaggerated grasping traits occur with females that have reduced anti-grasping traits, and vice versa. Next, we tested whether geography is correlated with the extent of morphological divergence. Latitude explained nearly 50% of the variation across populations, suggesting that ecological factors may be important in sexual coevolution. Previous studies have shown that several ecological factors affect mating costs in water striders. Future work will investigate whether and how these factors are related to divergence in sexual armaments.

5:00 – 5:15 PM

Morphological divergence and speciation in the brook stickleback, *Culaea inconstans*.

Ward*, Jessica L., McLennan, Deborah A.
Department of Ecology and Evolutionary Biology, University of Toronto

In most species, morphology is shaped by a combination of random genetic mechanisms such as drift and mutation, and directional selection due to ecological factors. Using geometric morphometric methods, we evaluated the correlation between phenotypic diversification and available genetic and habitat data for two genetically differentiated, allopatric lineages of a widespread North American species, the brook stickleback (*Culaea inconstans*). Our results revealed differences in body shape broadly congruent with the distribution of two MtDNA lineages; a deep-bodied eastern form (Atlantic refugium) and a slim-bodied western form (Mississippian refugium). However, the two forms were not lineage-specific and Mississippian populations inhabiting the upper Great Lakes and associated drainages converged on the body shape of the Atlantic lineage. Apparent cladistic diversification may be an artifact of strong clinal variation associated with longitudinal and latitudinal gradients. Additionally, we found little evidence of diagnosable lake and river forms across North America. Taken together, the results suggest that much of the extant phenotypic diversity observed in *C. inconstans* is the result of continually varying natural selection and/or local gene flow across the range of the species, rather than an ancient genetic split or repeatable phenotypic responses correlated with habitat differences. In this case, integrating molecular approaches with analyses of phenotypic variation provided insight into the relative contributions of selection and drift to lineage differentiation and indicated that speciation hypotheses for brook stickleback based on molecular markers are not strongly corroborated by phenotypic data.

5:15 – 5:30 PM

Using Biomechanics and Ecology to Predict Evolution in a Genus of Livebearing Fish

Langerhans*, R. Brian
Museum of Comparative Zoology and Department of Organismic and Evolutionary Biology, Harvard University.

How predictable is evolution? Can we accurately predict the course of phenotypic evolution if we begin with a solid foundation of how organisms work (biomechanics) and how they interact with their environments (ecology)? Here, I illustrate the utility of using geometric morphometric methods to test the predictability of morphological evolution in a genus of livebearing fish (*Gambusia*, mosquitofishes). I first formulate predictions of phenotypic evolution based on biomechanical and ecological knowledge regarding the relationships between body morphology, locomotor performance, and fitness in alternative predator regimes for *Gambusia*. Divergent natural selection is predicted to favor particular body morphologies in different predatory environments, driving the repeated evolution of similar morphologies in similar environments. I test these predictions (as well as the assumptions of the generalized model) across multiple temporal scales in *Gambusia* fishes—microevolutionary divergence over the span of decades, incipient speciation over the course of 1000s of years, and macroevolutionary divergence across the genus. Using comparative and experimental data, results strongly match predictions at all scales. It appears that a general model grounded in the theoretical and empirical foundation of biomechanics and ecology can yield fairly accurate evolutionary predictions across both microevolutionary (< 100 years) and macroevolutionary (> 1,000,000 years) timescales.

Morphology and Developmental Biology (room 103)

4:00 – 4:15 PM

What do butterflies hear? The neuroethology of hearing in a tropical butterfly, *Morpho peleides*

Lucas*, Kathleen M. Department of Biology, Carleton University, Ottawa, Canada

Many butterflies of the large family Nymphalidae possess a sensory structure (Vogel's organ) that has been proposed to function in hearing. Although one species (*Hamadryas feronia*) has been demonstrated to use Vogel's organ to listen to sounds of conspecifics, most other butterflies lack the ability to produce sounds, and the function of the Vogel's organ remains unknown. We are testing the hypothesis that butterflies use their hearing to detect the flight sounds produced by predatory birds. *Morpho peleides*, a diurnal tropical butterfly known to be heavily preyed upon by birds, has a well-developed Vogel's Organ at the base of the forewing. It comprises a large (1573 x 918 μm) oval tympanal membrane associated with 3 chordotonal sensory organs. Extracellular recordings of the tympanal nerve indicate that the ear is sensitive to sounds between 500 Hz and 20 kHz, with a best frequency between 1-4 kHz (minimum threshold of 53 dB SPL). This sensitivity is in accordance with the frequency and intensity range of flight sounds recorded from avian predators. Further support of our hypothesis that butterflies are listening for birds comes from comparative studies of closely related species that have been removed from the selection pressure of avian predators.

4:15 – 4:30 PM

Using spectrophotometric techniques to detect pelage colour differences in live bats and study skins

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Animal colour plays an important role in many ecological interactions and is often measured using spectrophotometry. This technique subjects a study specimen to a controlled light source and measures reflectance at various wavelengths. Spectrophotometric techniques have been widely used on both live and dead birds, but infrequently on mammals. Fur is a complex surface that has the potential to fade and otherwise change colour as it ages. The objectives of this study were i) to determine whether it is appropriate to measure mammalian study skin colour as a proxy for live animals and ii) to assess the efficacy of spectrophotometric techniques to detect fur colour differences. We achieved these objectives by measuring individuals from two species of insectivorous bats known to have intraspecific colour differences, the Eastern Red Bat (*Lasiurus borealis*) and the Little Brown Bat (*Myotis lucifugus*). Study skins from both species differed significantly in colour from live animals (*L. borealis* – $p < 0.001$; *M. lucifugus* – $p < 0.001$, $p = 0.041$). There was no correlation between colour and study skin age ($p > 0.05$). Spectrophotometric data detected a significant difference between male and female *L. borealis* study skins ($p < 0.001$), but did not detect a difference between adult and subadult live *M. lucifugus* ($p > 0.05$).

4:30 – 4:45 PM

Morphology and echolocation characteristics of a bat community

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In southern Ontario, there are five residential insectivorous bat species that all belong to the family Vespertilionidae (*Myotis lucifugus*, *M. leibii*, *M. septentrionalis*, *Pipistrellus subflavus*, and *Eptesicus fuscus*). We tested each species' ability to aerial hawk and glean prey and, where each bat was successful, we analyzed the peak frequency, bandwidth and duration for each individual call. Weight and wing measurements taken to determine the wingspan, area, loading, and shape. Wingspan and area were significantly different for all species except between *M. lucifugus* and *M. leibii* as well as in between *M. leibii* and *P. subflavus*. There was no significant difference in the call duration for any phase of the attack sequence (search, approach, buzz) however significant differences were found in the search and approach phases for the other bandwidth and peak frequency. For both wing morphology and echolocation design there were areas of overlap between species, showing that although the community at a whole differs in ecomorphology, there were two pairs of species (*M. septentrionalis* and *M. lucifugus*; *M. leibii* and *P. subflavus*) that overlapped in various features. Based on this evidence we classify that the first two species as clutter-resistant bats able to both glean and hawk prey, the second pair as clutter-resistant aerial hawking species and *E. fuscus* is an open space aerial hawker. That some species appear to share the same general niche suggests future questions about how similar species co-exist (e.g., perhaps at the level of prey choice).

4:45 – 5:00 PM

Genetic analysis of vulval development in nematodes *C. elegans* and *C. briggsae*.

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The nematode *C. elegans* is an established model organism to dissect the genetic basis of animal development. The hermaphrodite vulva is formed by the progeny of three out of six vulval precursor cells that respond to evolutionarily conserved signal transduction pathways mediated by Wnt, Ras and Notch. We are taking genetic and genomic approaches to study how these pathways have evolved to regulate cell fates in other nematode species and to this end characterizing the phenotypes of vulvaless (Vul) and multivulva (Muv) class of mutants in *C. briggsae*, a species that is closely related to *C. elegans*. To date we have examined 24 mutants in some detail leading to the identification of 17 distinct loci. The molecular analysis of one of these, defined by *lin(sy5353)*, has revealed that it encodes an *Axin* family member. *Axin* is a known component of the canonical Wnt signaling pathway and negatively regulates cell proliferation. In *C. elegans*, mutations in the *Axin* homolog *pry-1* have been shown to cause a Muv phenotype. By contrast we have found that *C. briggsae pry-1* (*Cbr-pry-1*) animals exhibit a simultaneous Muv and Vul phenotypes. This “Muv-Vul” defect is caused by VPCs anterior to P6.p adopting an induced fate whereas those posterior to P6.p adopting a non-induced fate. Thus *Cbr-pry-1* phenotype differs from what has been observed in *C. elegans pry-1* mutants, suggesting a possible evolutionary change in Wnt signaling-mediated vulval cell fates. We are taking different approaches to study function of *Cbr-pry-1* and other Wnt pathway components in *C. briggsae* and their differences from *C. elegans*.

Soil Ecology (room 102)

4:00 – 4:15 PM

Effects of logging on lake zooplankton communities

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Logging has been shown to increase nutrient influx into nearby lakes, causing eutrophication. This is hypothesized to affect zooplankton communities via the lower trophic levels. One proposed method to mitigate the effects of logging on lake water quality is to leave unlogged a strip of trees around the lake – termed a riparian buffer. We use 17 headwater lakes (9 treatment, 8 control) in the Esker Lakes Research Area of northeastern Ontario to test: whether logging affects zooplankton communities, and if so, what riparian buffer width is needed to mitigate these effects. Catchments of the 9 treatment lakes were logged to varying riparian buffer widths (50, 70, or 120m), based on the current OMNR criteria for buffer width prescription. Catchments of the 8 control lakes were not logged. We collected two zooplankton samples from each of the 17 lakes both before (July 2002) and after (July 2005) the logging event (Feb. 2005) to determine zooplankton densities. We will use redundancy analysis to test for logging and buffer width effects. This study aims to determine the need for and the effectiveness of riparian buffers in mitigating the effects of logging on lake zooplankton communities.

4:15 – 4:30 PM

Seasonal responses of soil microbial biomass and extracellular enzyme activity to warming and nitrogen treatments in a temperate old field grassland

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Climate warming is predicted to increase the frequency of soil freeze-thaw cycles in northern ecosystems as a consequence of reduced snow accumulation. The soil freezing dynamics of northern temperate systems may be particularly sensitive to climate warming over winter, as air temperatures remain near freezing over much of this season. Rates of atmospheric nitrogen deposition are also expected to increase concurrently with climate warming in these systems. We examined the interactive effects of warming and nitrogen deposition on soil microbial biomass and extracellular enzyme activity across seasons in a temperate old field. We collected soil samples at six time points from March of 2007 to April of 2008: spring melt, early summer, late summer, late fall, mid-winter and the following spring melt. We measured microbial biomass using a modified chloroform fumigation method, the activities of cellulose-degrading enzymes using fluorescent MUB-tagged substrates, and the activities of lignin-degrading enzymes using L-DOPA and hydrogen peroxide as substrates. At each sampling point, the activity of most enzymes increased slightly in response to nitrogen additions, but enzymes were generally unresponsive to warming treatments. However, an exceptionally dry summer may have diminished treatment effects in this year. Total extracellular enzyme activity was

lower during the summer months than at time points in March and November of 2007, and February of 2008. Microbial biomass is currently being analyzed, but may be following a similar trend. This indicates that microbes are likely more active during the winter than has been traditionally thought, and are an important component of over-winter degradation and nutrient cycling.

4:30 – 4:45 PM

Interactive effects of winter warming and nitrogen deposition on temperate ecosystem soil nitrogen dynamics

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Human induced changes to the global nitrogen cycle exceed those to any other major biogeochemical cycle on Earth. Increases in atmospheric nitrogen deposition over the last several decades have led to concerns about the ability of ecosystems to assimilate and retain these additional inputs. Alongside increasing nitrogen deposition, climate warming is projected to significantly alter biogeochemical processes by reducing over winter snow cover and by changing soil temperature regimes. Ecosystem responses to the interactive effects of climate change and nitrogen deposition have not been thoroughly investigated; particularly for the late fall, winter, and early spring. I estimated soil nitrogen mineralization and leaching losses in an experiment designed to examine the effects of climate warming and atmospheric nitrogen deposition on a temperate ecosystem. I used ^{15}N to characterize the effects of warming on the partitioning of nitrogen among main ecosystem components. Warming treatments increased ammonium concentrations in lysimeter samples collected from warmed plots but had no effect on concentrations of nitrate and soluble organic nitrogen in Fall 2006. Spring melt in 2007 was characterized by higher concentrations of soluble nitrogen loss. Net nitrogen mineralization over the winter of 2007 was higher in ambient plots than in winter-warmed plots. The results of these experiments have important implications for understanding the effects of climate change and nitrogen pollution on ecosystem structure and function.

4:45 – 5:00 PM

The effects of manufactured spatial variability on vegetation community establishment: restoration of abandoned limestone quarries to alvar ecosystems

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Aggregate extraction in southern Ontario has left the landscape populated with abandoned quarries. This disturbance has degraded the landscape, natural habitat and vegetation communities have been removed. The Ontario Aggregate Resources Act delegates responsibilities for the restoration of abandoned quarry land to quarry operators. The Cliff Ecology Research Group (CERG), found that abandoned quarries exhibit similar environmental characteristics to alvar ecosystem (rare, naturally occurring limestone-pavement ecosystems) making them ideal restoration targets. In alvars, soil collects in cracks and divots in the limestone bedrock; alvar vegetation communities have adapted in these high-stress conditions. In September and October 2007, 144 vegetation plots were planted in three abandoned quarries in southern Ontario. Three spatial variability treatments (in the form of three soil depth classes - no change, complete homogenization, and increased variability) and two life stage treatments (seed addition and adult plug addition) were randomly applied to the plots. The plots will be surveyed from May 2008 to October 2008 for species richness, density, survivorship, and plant material ground cover. The data will be analyzed with the analysis of variance method and the thesis will be completed in April 2009. I predict that vegetation community response will increase with increased spatial variability and that communities established from seed will have increased response than communities established from adult plugs over all levels of variability. The success of restoration efforts in abandoned quarries will be improved with the understanding of how soil depth variability and life stage affect the establishment phase of alvar vegetation communities.

Poster Session

Big mountains but small barriers: Population genetic structure of the Chinese wood frog (*Rana chensinensis*) in the Tsinling and Daba Mountain region

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Major landscape features such as mountain ridges have important impacts on population genetic structure and dispersal patterns of amphibians. The Tsinling Mountain range of northern China is one of the few major mountains on Earth that extend from east to west, and is the boundary between the Oriental and Palearctic zoogeographic provinces. We studied the population structure of the Chinese wood frog (*Rana chensinensis*) to test whether the Tsinling Mountains and the Daba Mountains impose major barriers to its gene flow. Using 13 polymorphic microsatellite DNA loci, 323 individuals from eight sites with geographical distances ranging from 2.6 to 422.8 kilometers were examined. Substantial genetic diversity was detected at all sites with an average of 17.4 alleles per locus and an expected heterozygosity ranging from 0.504 to 0.812. Additionally, there was a significant decrease in genetic diversity in two peripheral populations. Furthermore, the differentiation among the central populations was lower than expected, with pairwise F_{ST} values ranging from 0.0175 to 0.1625 with an average of 0.1048. Most importantly, the Tsinling Mountains and the Daba Mountains revealed no significant impact on the population genetic structure of the Chinese wood frog. AMOVA attributed most variation to the within-population component and most between-population variation can be explained by isolation by distance. High population connectivity and a large amount of juvenile dispersal may account for the low differentiation between populations. Additionally, the results suggest that Chinese wood frog may use mountain passes or river valleys as dispersal corridors to cross high mountain ridges.

The relation between song repertoire size and neophobia in song sparrows (*Melospiza melodia*).

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As a classic example of a sexually selected ornamental trait, song repertoire size of male song sparrows (*Melospiza melodia*) plays a key role in their reproductive success. Song repertoire size has been correlated with many aspects of male quality, and may be an indicator of early developmental conditions; males with good early development will have better neural development and learn more songs. Early development could also affect a variety of correlated behavioural traits such as boldness or neophobia. We investigated the possible relation between song repertoire size and neophobic behaviour. We captured sixteen male song sparrows from different sites in Ontario and recorded their songs in the laboratory. Neophobia was measured by observing the latency to approach and eat in the presence of novel objects, and the latency to approach and eat novel foods. The latency to approach novel objects and foods was not correlated within individuals. This suggests that either there is no consistent individual variation in neophobia, or that our behavioural tests were not sensitive to it. Song repertoire size, however, did correlate negatively with latency to approach food in control trials. This may indicate higher motivation to eat, higher general activity, or reduced stress in response to disturbance by the researcher for the males with larger repertoire size.

The indirect cannabinoid agonist URB597 improved Social recognition but not sociability in male CD-1 mice.

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The indirect cannabinoid agonist URB597 has been shown to affect a number of behaviours in rodents, including, activity, anxiety and social play in rats. In order to further investigate the involvement of the cannabinoid system in social aspects of behaviour, we conducted social recognition and sociability studies with CD-1 male mice using three doses of URB597 (0.05, 0.1, 0.4 mg/kg and vehicle). Social recognition was assessed in the mouse's home. The mice were habituated to two castrated conspecific mice over four 5-min trials, then, on a fifth trial they received a choice between a familiar and a novel castrated conspecific. Sociability was examined using a three chamber enclosed apparatus. After habituation to the apparatus, the mice were given a choice between investigating a novel object or an unfamiliar castrated conspecific. Social and non-social (e.g. activity) behavioural measures were recorded and scored.

Results show that URB579 at 0.1 mg/kg increased social recognition, while measures of locomotion and inactivity were not affected. In the sociability test the preferential investigation of the conspecific, which was shown by all mice, was not affected by URB597, nor were chamber entries or other scored behavioural measures. Overall, it appears that URB597's enhancing effects were more related to a mouse's recognition of a novel stimulus, particularly in its home environment, than to general effects on sociability.

Genealogical relationships of southern Ontario polyploid unisexual salamanders (genus *Ambystoma*) inferred from intergenomic exchanges and major rDNA cytotypes

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North American unisexual salamanders in the genus *Ambystoma* are common around the Great Lakes region of North America. They contain an almost identical mitochondrial genome across their distribution that is unlike that of any of the four species whose genomes may be included in their nuclei. Thus, sequence-based phylogenies of unisexual populations are confusing. We used chromosomal intergenomic exchanges and major rDNA cytotypes as combined cytogenetic markers to tentatively construct a genealogy of unisexual *Ambystoma* in southern Ontario. We employed GISH and sequential/simultaneous GISH/FISH-rDNA to reveal intergenomic exchanges and rDNA cytotypes in unisexual *A. laterale* × 2 *jeffersonianum* (LJJ) triploids and their tetraploid derivative *A. laterale* × 3 *jeffersonianum* (LJJJ). We identified 10 different patterns of intergenomic exchanges from 18 isolated populations and used them as primary cytogenetic markers. Major rDNA cytotypes served as independent and supplementary markers. Our results suggest that current LJJ and LJJJ populations in southern Ontario are likely derived from a few unisexual individuals. Intergenomic exchanges are common phenomena and widely distributed in the salamanders of the *A. laterale* × *A. jeffersonianum* unisexual complex. Integration of GISH and FISH can exhibit multiple unrelated chromosomal markers on the same chromosome spread and demonstrate lineage relationships in unisexual populations. Similar methods may be applied for studying the molecular cytogenetics of other unisexuals to improve our understanding of their genealogical relationships and historical dispersal.

Experimental study of adaptation to oxygen stress in *Drosophila melanogaster*

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Organismal responses to environmental stress can range from short term, acute changes in physiology, biochemistry, behaviour, and other traits, to long term adaptive changes arising across generations. The extent to which the latter, evolved responses parallel the former, acclimatory responses has received little attention in the literature. To explore this issue we conducted a laboratory evolution experiment in which replicate populations of *Drosophila melanogaster*, derived from a common laboratory stock, were independently evolved under different oxygen treatments, yielding three populations that experienced normoxia (21% oxygen; 'controls') and three that experience hyperoxia (40% oxygen) throughout their entire life cycles. After 11 generations in the hyperoxia treatment and x generations in the controls (control populations went extinct for unrelated reasons and had to be restarted from the stock), individuals were raised for one generation in a common, normoxic environment and assays were conducted to measure body size (wet weight of starved adults) and susceptibility to acute hypoxia. Hyperoxic populations were significantly more sensitive to hypoxia than control populations, demonstrating an evolved response to the hyperoxic treatment and suggesting a cost to adaptation. Body size also appeared to decrease in males in the hyperoxic populations, although caution is warranted because rearing density was not controlled in this assay. Our results demonstrate that an evolutionary response to oxygen stress can be studied over a relatively short time scales in this species and attest to the power of experimental evolution as a technique for studying adaptation to environmental stress.

DNA barcoding and the evolution of predator-prey strategies: new insights from Ontario Eastern Red Bats (*Lasiurus borealis*)

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**Department of Biology, University of Western Ontario, London Ontario, Canada

The evolution of insect hearing and bat echolocation is one of the most frequently cited examples of predator prey co-evolution. Many insect species have a simple ear composed of 1-3 sensory cells that react to the hunting calls of bats and elicit a behavioural avoidance flight response. A considerable body of literature has outlined the sensitivity of this relationship under different selective pressures. Some species have developed additional defensive characteristics including toxins that make them unpalatable and the emission of jamming signals thought to interfere with the echolocation ability of bats. In turn, bats may modify their sound production to shift outside the insect's range of hearing. Detailed studies of bat-moth interactions in a natural setting are often limited by the challenges inherent in determining exactly what bats are eating. Dietary analysis of bats has traditionally been carried out through collection of moth wings at feeding sites or direct identification of insect parts in guano or stomach contents. These techniques have identified a wide variety of prey but rarely beyond order. While this is suitable for profiling dietary composition and general resource partitioning among species, it lacks details required to test the efficiency of insect defenses in a natural setting. In this investigation, we test the ability of DNA barcodes to identify insect species from the guano of the Eastern Red Bats (*Lasiurus borealis*) captured during two successive years at Pinery Provincial Park in Ontario. We identified a large number of prey species using BOLD in one of the first applications of the barcode dataset to field ecology. Here we report on the novel insights into the diet and predator prey relationship of these species.

Social Behaviour in Gonadally Intact and Gonedectomized Male and Female Mice: Effects of an Estrogen Receptor Alpha Agonist.

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Affiliative and agonistic social interactions are mediated by gonadal hormones. Removal of the estrogen receptor alpha (ER α) gene reduces male aggression, either through developmental or activational effects of ER α . Additionally, little or no research has been performed on ER α 's effects on female territorial aggression. We assessed the effects of the ER α agonist PPT and gonadectomy on behavior of male and female mice in the intruder test. Individually housed mice interacted with a same-sex, gonadectomized intruder for 15 min interactions, and then we analyzed the videotapes of these interactions for 21 behaviors. We found the expected sex differences, that only the intact males attacked the intruders, but the overall aggression of males and females was not different when other types of agonistic (dominance related) behaviors were included. Females also shifted between behaviors less frequently and were more social than males. Gonadectomy reversed these differences. Castration decreased behavioral shifting, and increased social behavior, while ovariectomy increased behavioral shifting and decreased social behaviour. In both sexes, gonadectomy decreased sex-typical aggression (males: attacks, females: other dominance behaviours). ER α agonist PPT had few effects in gonadally intact mice, but increased sex-typical aggression in castrated and ovariectomized mice. This suggests that male and female aggression may also be mediated by the other ER (ER β). We show here that an ethological analysis allowed both the study of territorial aggression also in female mice and the assessment of gonadectomy and the role of ER α in male and female aggression. Supported by NSERC.

Do life histories and environmental factors affect molecular evolution of cytochrome oxidase I in the Echinodermata?

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Variation in rates of molecular evolution have been observed in many metazoan lineages, however few studies have explored the relationship between life history characteristics, environmental factors and rates of evolution in marine invertebrates. Although metabolic rate, body size and generation time seem to be correlated with rate variation in many vertebrate lineages, different factors may play a more important role in other organisms. While reproductive mode has the potential to affect a variety of micro- and macro-evolutionary processes in marine invertebrates, its effect on the rate of molecular evolution has not been widely examined. Moreover, ultraviolet light exposure, oxygen concentration and temperature can vary dramatically between marine habitats and may be linked to rate heterogeneity. In this study we will determine the relationship between sequence variation in an 841 base pair region of the cytochrome c oxidase I (COI) gene and several life history characteristics and environmental factors in the Echinodermata. Echinoderms are highly diverse, exhibit a range of reproductive modes within closely related groups and inhabit benthic zones from near-shore to deep-sea making them an excellent group for a comparative evolutionary study of this kind. Specimens will be obtained from a variety of geographic locations, depths and climates to facilitate comparisons for a variety of factors.

stability and turbidity. Understanding that vertical migration occurs in benthic algae in lakes will have important implications in how benthic communities are sampled, as well as how benthic primary production is measured.

Effects of melatonin on territorial aggression and hormone levels in song sparrows

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Western male song sparrows (*Melospiza melodia morphna*) are territorial during both the breeding (spring) and non-breeding seasons (autumn and winter). During the non-breeding season, however, plasma testosterone levels are non-detectable and castration does not decrease aggression. Interestingly, circulating levels of dehydroepiandrosterone (DHEA), a relatively inert androgen precursor, are detectable during the non-breeding season and may affect winter aggressive behaviour. In rodents, melatonin can increase aggression and adrenal DHEA synthesis. We thus examined whether song sparrow territorial behaviour and DHEA levels are regulated by melatonin. Wild non-breeding male song sparrows were given an empty or melatonin-filled silastic implant and released back onto their territories. To measure aggression, we used a simulated territorial intrusion (STI) at ~10 days after implantation. Subjects were recaptured and blood was collected for DHEA measurement. Subjects given melatonin showed reduced song and response latency, indicating that melatonin selectively increases song-related aggression. Melatonin also decreased DHEA levels in jugular, but not brachial plasma. These results suggest that melatonin regulates the metabolism of peripheral DHEA into active androgens within the brain to support aggression in the non-breeding season. Whether melatonin is also involved in dominant-subordinate aggression in social dominance hierarchies of the black-capped chickadee is currently being investigated.

What do non-stereotypic animals do in poor environments? A meta-analytic approach

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Stereotypic behaviour is invariant, repetitive, common and conspicuous in captive animals. Environments that cause or increase it are typically linked with poor welfare. However, within such environments, one often finds some individuals with very high level of stereotypies, but others with little or none. Paradoxically, those individuals that spontaneously develop high levels of stereotypies often fare better than their non-stereotypic peers. The aim of this study is therefore to analyze what animals in poor conditions do if non-stereotypic. Our hypothesis is that they are inactive, but alternatives could be that they show more normal behaviours, or instead other forms of abnormal behaviour. We are investigating this via a meta-analysis of existing datasets. Because of the level of detail required, we are focussing on the work of all relevant former students of Georgia Mason, so that information missing from theses/papers can be retrieved by questioning authors. If the 'inactivity' hypothesis is supported, this would suggest the importance of extreme inactivity as a welfare indicator. Consequently we would then investigate how to reduce inactivity to improve animal welfare. We know that environmental enrichment often reduces stereotypic behaviour, but does it also reduce inactivity? This second hypothesis would be tested via a second meta-analysis of published studies via the ISI Web of Knowledge. Overall this study will reveal how captive animals

Explaining the dichotomy in bat echolocation behaviour: low and high duty cycle echolocations.

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Two distinct approaches to echolocation are found in microchiropteran bats. While most bats use frequency modulated signals and separate pulse and echo in time (low duty-cycle), some bats (families Rhinolophidae, Hipposideridae and the mormoopid *Pteronotus parnellii*) use constant frequency signals and separate pulse and echo in frequency (high duty-cycle). Many explanations have been given for the advantages of using one approach over the other. My research is designed to result in a better understanding of what might have led to the diversity we see in the echolocation behaviour of bats. The hypothesis I intend to test is that detection of fluttering target is not an ability showing a gradual improvement while observing the transition from a low duty-cycle call to a high duty-cycle call. If the hypothesis proves to be right, the HDC behaviour is likely to have evolved rapidly, as an evolutionary "leap". Using synthetic calls of varying parameters and an electric insect that simulates wing movements, I am searching for acoustic cues in echoes that might translate into information for the bat. I will assess information, i.e. amplitude and frequency modulations, in

the echoes to identify prey detection efficacy of low versus high duty cycle signals with various approaches in signal processing. Given that the bats have access to this information, behavioural experiment involving field work will evaluate if the bats make use of these acoustic stimuli.

Good genes sexual selection in ancestral and novel environments

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Whether sexual selection reinforces or opposes natural selection is a controversial issue in evolutionary biology. Good genes models of sexual selection propose that natural and sexual selection act in concert because display traits are honest indicators of male genetic quality. Whether good genes mate choice occurs is unclear however, because experimental evidence is mixed. In particular, two of three recent experiments failed to find evidence that sexual selection promoted adaptation to a novel environment, a fundamental prediction of good genes. Here we outline our approach to test for good genes in an ancestral environment to which a population of *Drosophila melanogaster* is well adapted, and describe how we will explore its operation in various novel environments. In novel environments, genotype-by-environment interactions may initially disrupt a good genes process by weakening the necessary genetic correlations between male displays, female preferences, and offspring fitness. Twelve populations of *D. melanogaster*, all deriving from a common ancestor fixed for a different visible mutation will be used to test whether deleterious mutations for female productivity also tend to reduce male mating success. By raising these populations in a number of different environments, we will determine the degree to which novel environments disrupt this correlation, indicating that a good genes process is hampered. The influence of novel environments on the relationship between sexual and natural selection is fundamental to our understanding of adaptation to both new and changing environments.

Inferring the movement patterns of Western Cherry Fruit Fly, *Rhagoletis indifferens* (Diptera: Tephritidae), using molecular markers

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Population genetic studies of agricultural pests are important for understanding the dispersal of these pest species. For this reason, the use of genetic markers have become increasingly valuable tools in furthering our knowledge of the population structure, dispersal behaviours, and host plant usages of pest species that cannot be fully or easily determined by physical, behavioural, or demographic observations. The Western Cherry Fruit Fly (WCFF), *Rhagoletis indifferens*, is a major pest species of cherry growers but many aspects of this species' movement between orchards and between host plants remain unknown. Previous and ongoing studies of this species have concentrated on the behaviours of populations within orchards but have not addressed the dispersal of WCFF between orchards since direct studies of its movements continue to prove challenging due to its small size and cryptic behaviour. To date, neutral markers do not exist for *R. indifferens*, so I have developed microsatellites specific to this species. I will use these microsatellites to examine the genetic structure of populations of WCFF at a scale of <1 to 20 m. Determining the genetic structure at this scale will be valuable in implementing management schemes to control this orchard pest that are less dependent on pesticides, more cost effective and less environmentally damaging.

Source populations and reproductive mode of invasive *Cabomba caroliniana* in Canada

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Source population and mode of expansion can have important effects on the extent and rate of colonization by species to new environments. However, this information is often difficult to obtain. *Cabomba caroliniana*, or fanwort, is an invasive that has successfully colonized environments very different from its native range. Native to the southern United States and South America, this species has spread worldwide, including to the northern United States and a single population in Canada in Katchewanog Lake near Peterborough, Ontario. The mechanism of introduction is unknown, although most populations are assumed to be commercial introductions via the aquarium trade and spreading clonally. In this study, I will test the validity of these two assumptions by attempting to determine both source populations and mode of reproduction in the introduced range in this species. To do this I will use both flow cytometry and Amplified Fragment Length Polymorphisms (AFLPs) to analyze the genetic structure of populations from the native range, the introduced range and from a variety of aquarium suppliers. Populations that are more closely related are expected to be more similar genetically. If the species is reproducing asexually, populations are expected to contain

low genetic diversity compared to populations that are reproducing sexually. The results of this study will test the assumptions made about the spread of this species and its reproductive mode and provide information about the spread of invasive species in general, which could aid in the management of this species.

The effects of density on the reproductive success of alternative mating tactics in male wood frogs (*Rana sylvatica*)

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Alternative mating tactics are a form of resource polymorphism where males diverge in their morphology or behaviour to compete for females. Anurans have been classified as utilizing a reversible conditional strategy where the same individual can employ multiple tactics. Demographic and ecological variables have been suggested to be important factors affecting the fitness of conditional strategies; however, few studies have tested their effects on the reproductive success of alternative tactics. We will test how density affects the reproductive success of conditional mating tactics in wood frogs, in southern Ontario, from 2008 to 2009. This will be accomplished by drift fencing four ponds and creating high and low-density treatment plots. Approximately 500 frogs will be captured, marked, toe-clipped and measured each year. Males and females will then be randomly assigned to a plot and male behaviour classified using scan sampling. Egg masses will be collected and parentage will be assessed using four polymorphic microsatellite DNA loci. The proportion of eggs sired by a male will be used as a measure of his reproductive fitness. We hypothesize that under high-density situations a calling male's reproductive success will decrease due to a greater abundance of satellite males and the greater probability of multiple paternity. This study will be a significant progression in our understanding of how density-dependent effects maintain male polymorphisms in animals and will aid in generating more sophisticated conditional strategy models.

The evolutionary ecology of heterospecific aggression

Peiman*, Kathryn S., and Robinson, Beren W.
Department of Integrative Biology, University of Guelph

The ecology and evolution of interference traits that influence species interactions is poorly understood. Interference traits are used in direct interactions between individuals for resources. Heterospecific aggression (HA) is one of the most common interference traits in animals, and like conspecific aggression, varies across age, sex, size, individual, population and species. However, the conditions under which HA will evolve, and its ecological consequences in terms of niche shifts and community structure, are not well studied. HA is often considered to be non-adaptive, reflecting misdirected conspecific aggression, although this conclusion is often based on poorly designed tests. We propose that HA may evolve adaptively under selection when two species compete for a shared, limited, and defensible resource. A stronger test of this hypothesis involves comparing HA in allopatric populations to populations sympatric with a competitor. We also outline a set of mutually exclusive predictions that can be used to disentangle the causal mechanisms that relate resource or habitat use to variation in HA, and summarize the available literature in order to evaluate our progress at understanding the ecology and evolution of HA. Our review found that 90% of taxa tested displayed HA; that HA was equal to or greater than conspecific aggression in 40% of the taxa studied; and that HA had changed from allopatry to sympatry in 10 of 13 studies. In view of this evidence, the evolution of HA and its role in species interactions (including invasive animals), niche use and adaptive divergence needs to be more fully considered.

Estrogens, Learning and Memory in Mice: Rapid Effects of Estrogen Receptor Alpha and Beta Agonists

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Estrogens affect learning and memory, although results are inconsistent. Estrogens have been shown to improve, impair or having no effect on learning/memory. These varying results may be due to the activation of different estrogen receptors (ER), ER α and ER β . Previous behavioural estrogen research has concentrated on the long term, genomic effects of estrogens, occurring >24hrs after estrogen treatment. Within the last decade, estrogens have been shown to have rapid, short-term effects (<1-2hrs) on neuronal plasticity, including effects on neuronal morphology and electrophysiology. However, there is little research on whether these rapid changes in neuronal plasticity have behavioral consequences. Therefore, we investigated the actions of an ER α agonist (PPT) and an ER β agonist (DPN) on 3 learning/memory paradigms, known to be estrogen-sensitive. Two month old female, ovariectomized, CD1 mice

were treated with PPT or DPN. The mice were then tested in social recognition (ability to recognize conspecific individuals), object recognition, or object placement paradigms. The paradigms were adjusted such that they were completed within 40min of the drug injections. PPT rapidly improved both social and object recognition compared to the vehicle control. DPN did not improve performance on either type of recognition task. In fact, DPN may impair social and/or object recognition. This data indicates that ER α and ER β may have differential effects on learning/memory within minutes of estrogen administration. Supported by NSERC.

Adaptation or phylogenetic constraint?: Anti-predator mechanism dynamics of sea cucumbers on coral reefs

Riopel*, Chad
Department of Integrative Biology, University of Guelph

Anti-predator mechanisms facilitate the survival of potential prey species in high predation environments, and may thus represent adaptation if they evolved for that purpose. Comparative phylogenetic methods are available to test for adaptation of anti-predator mechanism use across a group of related species, provided that they exist in high predation environments and their phylogenetic histories are known. Sea cucumbers (Holothuroidea) that inhabit coral reefs appear to be an excellent study system since they meet the two aforementioned criteria. Through a compilation of published life-history data and subsequent phylogenetic analyses, my MSc thesis will address the following questions: Are the distributions of anti-predator mechanism use by reef-dwelling sea cucumber species an adaptation to predation exposure? Is large body size an adaptation to predation exposure? Several possible laboratory experiments may be also be conducted in order to determine if trade-offs of effectiveness have evolved between pre-attack and post-attack anti-predator mechanisms across species. Understanding whether the dynamics of anti-predation mechanism dynamics appears to result from adaptation or phylogenetic constraint across such a wide array of species will be an important contribution to our understanding of predator-prey interactions, impacting ecology and evolution.

Population genetics of blue-footed boobies: does variation in mitochondrial DNA support subspecies designations of this charismatic species?

Taylor*, Scott A., Anderson, David J., Zavalaga, Carlos B., Friesen, Vicki L.
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Blue-footed boobies (*Sula nebouxii*) are often referred to as the most charismatic of the seven extant booby species, yet population genetic studies of blue-footed boobies are distinctly absent from the literature. In recent years interest in seabird population structure, genetic differentiation and speciation has peaked as various populations and species are threatened by climate change, fisheries and pollution. Examinations of other booby species using mitochondrial markers have detected highly structured populations, despite the high mobility of seabirds. Results from these studies indicate that the morphological variation we observe in many booby species correlates with variation in neutral molecular markers, and that each species exists as a number of evolutionary significant units. Two subspecies of blue-footed boobies are currently recognized: *S. n. excisa*, which is endemic to the Galapagos archipelago; and *S. n. nebouxii*, which is found along the west coast of South America from Mexico to northern Peru. Here we examine an approximately 550 base pair segment from the mitochondrial control region in 155 blue-footed boobies from eight colonies from throughout their range. We include three colonies from Mexico, one from Ecuador and one from northern Peru (*S. n. nebouxii*), along with three colonies from the Galapagos (*S. n. excisa*). We find that the subspecies classifications are not reflected in neutral genetic variation, and that blue-footed booby populations are only weakly genetically structured. We also present the first genetic evidence of a hybridization event between blue-footed boobies and Peruvian boobies.

To old to care? Resistance to environmental enrichment in individuals with a long history of stereotypic behaviour

Tilly*, Sarah-Lee C., Mason, Georgia J.
Department of animal Poultry Science, University of Guelph.
Department of Animals, Science & Society, University of Utrecht

When captive animals show stereotypic behaviour (e.g. pacing), environmental enrichment (e.g. adding more complexity or opportunities to perform natural behaviour to their enclosures) usually reduces it. However, this is not always the case: in some species, it is known that if stereotypic individuals are kept in barren cages for a very long time, their abnormal behaviour stops being ameliorated by environmental enrichment. This could implicate that older

animals no longer find the enrichments 'enriching': that is, they no longer improve welfare. For example, older individuals could suffer from anhedonia, and a tendency to interpret neutral or positive events, such as adding enrichment to the home cage, as negative. Alternatively, older animals could value the enrichments just as much as younger ones – but be too 'fixed' in their stereotypic behaviour to change it. The aim is to find out which of these ideas is correct. If environmental enrichments no longer improve welfare for older individuals, it is to be expected that older animals will be less willing to 'pay' to visit and use enrichment than younger individuals. Therefore, using C57BL/6 mice as a model, it will be investigated how much older and younger individuals value environmental enrichment (in terms of the maximum weight they will push to get through a door to reach it); and whether the degree to which they value enrichment predicts the impact it has on their stereotypic behaviour. This research will help us understand what effect environmental enrichment has on laboratory mouse welfare.

Abdominal dragging as a grooming response in *Gryllus texensis*

Vincent, Crystal M.*, Bertram, Susan M.
Department of Biology, Carleton University

Females of the parasitoid fly *Ormia ochracea* (Diptera: Tachinidae) acoustically orient to the Texas field cricket, *Gryllus texensis*. The fly lays her larvae on and around the cricket; larvae burrow inside the cricket and proceed to feed and grow within the cricket host. Infested crickets die within seven to ten days, usually immediately following emergence of the parasitoid larvae. It is estimated that between 10 to 17 % of crickets are infested with *O. ochracea* larvae in the wild. Given that parasitism results in cricket death, crickets should be strongly selected to avoid the lethal effects of being parasitized. Here we investigate the efficacy of abdominal dragging by *G. texensis* in dispelling attached *O. ochracea* larvae. Preliminary results suggest that crickets that drag their abdomen are more likely to become parasitized. These results imply that crickets drag their abdomens for reasons other than removal of *O. ochracea* larvae.

Wednesday, April 30th

Morning Plenary Talk

9:00 – 10:00 AM

Sexually Antagonistic Selection and its Consequences in Striders: Some Remaining Questions.

Lock Rowe

University of Toronto

Sexual conflict, although an idea with considerable history, has recently become a very active area of research. I will begin by defining sexual conflict, sexually antagonistic selection and sexually antagonistic coevolution. Sexually antagonistic selection and the resulting coevolution of interacting traits in the sexes, tends to lead to similar patterns as those expected from more commonly studied mechanisms of sexual selection. Patterns that result from sexually antagonistic coevolution, including the exaggeration of traits, the correlation of traits with condition, and intersexual genetic correlations are shared with most other models of sexual selection. These results suggest that "pattern" studies

will not be able to distinguish sexually antagonistic coevolution from other mechanisms of sexual selection. Instead, sexually antagonistic selection needs to be studied directly. These approaches can include functional, economic and selection studies. I use these approaches in studies of water striders to distinguish sexually antagonistic coevolution from other coevolutionary models. I will then turn to three data newer data sets on striders that don't quite fit.

10:00 – 10:30 AM

30 Minute Break – Coffee, water and pastries will be available

Fourth Concurrent Session

Social Living in Fish (room 101)

10:30 – 10:45 AM

Role of familiarity in the formation of shoals in juvenile fishes: a comparison of two sympatric species

Lee-Jenkins, Stacey S.Y., Godin, Jean-Guy J.
Department of Biology, Carleton University.

The composition of fish shoals in nature is based on non-random associations between individuals. Fishes are known to shoal preferentially with individuals of similar body length, with conspecifics, and sometimes with socially familiar individuals. The role of familiarity (a preferred social association with individuals with whom one has previously interacted) in fish behavioural ecology has recently received considerable attention. However, evidence for this social preference phenomenon remains somewhat ambiguous and controversial. Using a laboratory binomial shoal-choice test, we compared the role of familiarity in shoal-choice decisions in two sympatric species of fishes, juvenile banded killifish (*Fundulus diaphanus*) and juvenile bluegill sunfish (*Lepomis macrochirus*). Our study subjects were collected from the shallow, sandy, littoral zone of Patterson Lake, Ontario, Canada. Groups of socially familiar and unfamiliar conspecifics were created in the laboratory. Both species exhibited strong shoaling behaviour in the field and laboratory. However, juvenile banded killifish demonstrated a strong preference for familiar shoal mates, whereas juvenile bluegill sunfish exhibited no preference for either familiar or unfamiliar shoal mates. Bluegill sunfish are known to possess the ability to recognise individuals; therefore, the lack of familiar shoal-mate preference here is likely an active choice. The different role of familiarity in shoal-mate choice between juvenile banded killifish and juvenile bluegill sunfish could be due to their different ecologies and life history strategies.

10:15 – 10:30 AM

The stress response of a highly social African cichlid.

Mileva*, Viktoria R., Gilmour, Kathleen M., Balshine, Sigal.
Department of Psychology, Neuroscience and Behaviour, McMaster University

In many group-living species dominant individuals repress subordinates for long periods of time. This chronic stress can lead to depression of growth, reproduction and immune function, which in turn can decrease fitness. However in many cooperatively breeding species dominants exhibit more stress than subordinates. In this study, we investigated the relationship between social status and stress in cooperatively breeding groups of the African cichlid, *Neolamprologus pulcher*. We explored the effects of social status on levels of circulating plasma cortisol both at baseline and following an acute netting stressor. Although cortisol levels varied between study years, breeders (dominants) tended to have higher cortisol concentrations than helpers (subordinates). We found generally higher cortisol concentrations in helpers who performed more aggressive and submissive acts relative to those that did not. Our findings also show an increase in plasma cortisol following an acute stressor in all fish. Interestingly, no differences were found between dominants and subordinates in their response to acute stress. These data support the hypothesis that breeders tend to have higher cortisol concentrations at baseline. By combining behavioural and physiological data with molecular data in future studies, we hope to fully elucidate the stress responses of this species.

11:00 – 11:15 AM

Feast or famine: growth regulation in a fish social hierarchy

Wong*, Marian YL., Munday, Philip L., Buston, Peter M., Jones, Geoff P.
Department of Psychology, Neuroscience & Behaviour, McMaster University.

Understanding the structure and stability of hierarchical societies requires insights into why and how subordinates of many social animals often remain smaller than dominants. Subordinate growth regulation has typically been viewed as a non-adaptive consequence of food exclusion by dominants, or more recently, as an adaptive consequence of conflict over rank within size-based hierarchies. We conducted manipulative experiments using the group-forming goby, *Paragobiodon xanthosomus*, to determine the relative effects of non-adaptive versus adaptive subordinate growth regulation. In addition, we determine whether and by what mechanism subordinates adaptively restrain their own growth. Supplemental feeding of subordinates and dominant removal had positive and additive effects on subordinate growth rates, demonstrating that both food and social factors respectively promote subordinate growth regulation. Supplemental feeding of just one subordinate within natural hierarchies resulted in subordinates either i) reducing food intake without dominant aggression or ii) continuing feeding but being evicted from the group, once they reached a size threshold that instigates conflict with their dominants. Our results suggest that subordinates are capable of regulating their own growth by reducing their food intake when they approach a size where they risk conflict with dominants. Dieting therefore appears to be a behavioural mechanism by which subordinates ensure they remain smaller than their dominants.

11:15 – 11:30 AM

Effects of sex and status on liver investment patterns in the cichlid fish from Lake Tanganyika, *Neolamprologus pulcher*.

Sopinka*, Natalie M., Fitzpatrick, John L., Desjardins, Julie A., Stiver, Kelly S., Marsh-Rollo, Susan E., Balshine, Sigal
Department of Psychology, Neuroscience and Behaviour, McMaster University

Livers function to store and mobilize the energy reserves needed for both somatic growth and reproductive investment. In group-living fish, dominant individuals have pronounced growth and reproduction compared to subordinates who often show suppressed growth and reproduction. The physiological mechanisms contributing to this suppression have not been fully investigated before. To this end we examined liver and gonads in 167 wild groups of the cooperatively breeding African cichlid, *Neolamprologus pulcher*. As expected females had larger gonadal investment than males and dominants had larger gonads (controlling for body size compared to subordinates). Males and females did not differ in liver size (once we controlled for body size) but subordinates (of both sexes) had relatively larger livers than dominants. Feeding rates were negatively correlated with liver investment. Across the lunar reproductive cycle male and female liver investment was highest at full moon just prior to spawning, followed by decreases in liver size (controlling for body size) with increases observed again following fry emergence (new moon). Male and female breeders from large social groups had smaller livers, but workload and other social behaviours did not impact liver investment. Liver and gonadal investment were not related. Our results show that liver investment patterns are related to status-specific behaviour, and support the notion that subordinates may strategically shunt energy into liver to ensure continued social acceptance, avoid dominant eviction, and ensure the availability of a ready energy storage supply when an opportunities to ascend in status arise.

11:30 – 11:45 AM

Neuropeptides and social living in a cichlid fish.

Marsh-Rollo*, Susan E., Balshine, Sigal
Department of Psychology, Neuroscience and Behaviour, McMaster University

The neuropeptides, arginine vasopressin (AVP) (found in most mammals), or arginine vasotocin (AVT) (found in most non-mammals), are linked to both aggressive and affiliative behaviour. We used the cooperatively breeding African cichlid fish, *Neolamprologus pulcher*, to examine differences in AVT neuron number and size in dominant and subordinate individuals and in relation to aggressive and non-aggressive social behaviour. AVT neurons were concentrated in the preoptic area (POA) – a part of the brain typically associated with the control of social and reproductive behaviours. Dominant individuals had more neurons than subordinates and this was true of both males

and females. Dominants had larger neurons (more AVT secretion) than subordinates. Differences in AVT neuron size and number and linked behaviour will be discussed.

11:45 AM – 12:00 PM

Dominance establishment elevates male and female androgens in a highly social cichlid fish

Taves*, Matthew D., Desjardins, Julie K., Mishra, Sandeep, Balshine, Sigal.
Department of Psychology, Neuroscience and Behaviour. McMaster University

In most vertebrates, aggression and dominance are facilitated by high circulating testosterone. Fish, however, have two androgens (testosterone, T and 11-ketotestosterone, 11KT) that influence aggression and dominance. To date, very few studies have compared effects of aggressive contests and dominance establishment on androgens levels in both males and females of the same species. To investigate sex differences in androgens we staged 14 female and 10 male size-matched, limited-resource contests and examined androgen levels in emerging dominants and subordinates. Newly established dominant females had higher plasma T but similar 11KT to subordinate females. In contrast, newly established dominant males had higher 11KT but similar T to subordinate males. Females had higher T than males but no sex difference was found in 11KT. In all fish 11KT was positively correlated with relative gonad investment. These findings provide the strongest support to date that different androgens play an equivalent role in the effects of female versus male dominance establishment.

Adaptive Radiation (room 103)

10:30 – 10:45 AM

Changes in gene regulation across species and tissues of polyploid clawed frogs (*Xenopus*) following whole genome duplication.

Anderson*, Dave, W, Evans, Ben, J.
McMaster University

Abstract:

Genetic redundancy created by gene duplication provides a window of opportunity for rapid changes in gene expression, which can alter phenotypes and promote speciation. African clawed frogs (genus *Xenopus*) offer a useful model for studying expression divergence after gene duplication because species in this group recently experienced whole genome duplication and, in many cases, still express both copies of many duplicate genes. Gene expression divergence between species may occur via *cis*- acting regulatory changes (e.g. loss or gain of a transcription factor binding site) or via *trans*- acting regulatory changes (e.g. increased expression of a transcription factor). We aim to dissect apart the relative contributions of *cis*- and *trans*- acting regulatory elements in expression divergence between species, duplicated genes, and different tissues. Using the RAG1-RAG2 heterodimer as a case study, we examined mechanisms of expression divergence between *X. laevis* and *X. borealis*. Since the protein products of these genes must interact before becoming physiologically active, we expect them to be exposed to similar functional selection pressures. Our results indicate that regulatory evolution of these interacting gene products varies across tissue types, and that compensatory *cis*- and *trans*- divergence act in opposite directions in some tissues. Our results highlight a key role of tissue-specific *trans*- factors in influencing the level of *cis*- divergence between species. We also provide a novel method for comparative regulation analysis in genes in which both duplicates are expressed.

10:15 – 10:30 AM

Field experimental test of competition between sympatric sunfish ecomorphs

Colborne, Scott F.* & Robinson, Beren W.
Department of Integrative Biology. University of Guelph.

Pumpkinseed sunfish (*Lepomis gibbosus*) are commonly found inhabiting the littoral habitat of many lakes where they feed on a variety of macrobenthic invertebrate prey. However, in some lakes, the ancestral littoral ecomorph coexists with a derived pelagic ecomorph that feeds extensively on zooplankton prey. Ecological and phenotypic polymorphism is common in fishes in postglacial lakes, and is thought to arise by a density-dependent process of increasing intraspecific competition in the face of weak interspecific competition for replaceable resources. Here, we stocked

different densities of both ecomorphs together in littoral enclosures placed in a south-central Ontario lake to test for the effects of density and prey type on fitness. At high density we predicted that increased competitive interactions over resources would reduce fitness compared to low density. By adding pelagic zooplankton prey to enclosures, we predicted that the negative effects of density would be relieved more for pelagic compared to littoral ecomorphs. Our results suggest a previously unknown trade off between density and diet in these sunfish: fitness decreased as density increased as expected, but there was also an unexpected increase in mortality particularly in littoral ecomorphs associated with exposure to pelagic prey. These results are consistent with some density-dependent effects on individual fitness but also suggest a potential cost to feeding on novel prey that may constraint diversification in this system.

11:00 – 11:15 AM

Analyzing nested variation in the body form of Lepomid sunfishes

Riopel*, Chad, Robinson, Beren W., Parsons, Kevin J.
Department of Integrative Biology, University of Guelph

Phylogenetic hierarchies are often composed of younger diverging lineages nested within older diverging lineages. Comparing phenotypic variation among several hierarchical levels can be used to test hypotheses about selection, phenotypic evolution and speciation. Such hierarchical comparisons have only been performed in threespine stickleback, and so here we use a hierarchical pattern of divergences between near-shore littoral and off-shore pelagic habitats to test for selection on the evolution of body form in *Lepomis* sunfish in lakes. We compare variation in external body form between fish from littoral and pelagic habitats at three levels: among ecomorphs within individual lake populations (intrapopulation), among populations of the same species in different lakes (interpopulation), and between bluegill and pumpkinseed sunfish species (interspecifically). Using geometric morphometric methods, we first demonstrate that interpopulation variation in mean body form of pumpkinseed sunfish varies with the presence of pelagic habitat. We then incorporate these results with existing data in order to test the similarity of phenotypic divergence between littoral and pelagic habitats at different hierarchical levels. Parallel relationships between certain body form traits (head length, caudal length and pectoral length) and habitat occur at all three levels suggesting that selection persistently acts at all levels to diversify these traits and so may contribute to species formation. For other traits (caudal depth and pectoral altitude), divergence between habitats is inconsistent at different hierarchical levels. Thus, nested biological variation in Lepomid body form reflects a history of deterministic selection and historical contingency, and also identifies traits that likely influence fitness.

11:15 – 11:30 AM

Do life history shapes sexual size dimorphism in anurans: a comparative analysis.

Han*, Xu and Fu, Jinzhong
Department of Integrative biology. University of Guelph.

The evolution of sexual size dimorphism (SSD) is hypothesized to be constrained by life history traits, and therefore, mating combat, length of breeding season, female fecundity and parental care are expected to be correlated with male and/or female body sizes. Using phylogenetic comparative methods, correlations between SSD and life history traits were examined in 545 anuran species. Data were analyzed with phylogenetic independent contrasts and a maximum likelihood method. A positive correlation was found between mating combat and body size. Egg size, clutch size and clutch volume were also positively correlated with female body size and SSD. Furthermore, body size and SSD were positively correlated in all anurans and in the family Bufonidae, but were negatively correlated in the family Dicroglossidae. Female fecundity may mainly influence the evolution of SSD, and the general pattern of SSD in anurans does not follow Rensch's rule, although SSD does so follow in the family Dicroglossidae.

11:30 – 11:45 AM

Natural selection on photosynthetic physiology varies with resource availability in a perennial grass.

Sherrard*, Mark E., Maherali, Hafiz
Department of Integrative Biology. University of Guelph.

Physiological variation is often correlated with environmental resource gradients, suggesting that this variation is the product of natural selection. For example, comparative studies have shown that high growth rate may be adaptive in high resource environments. However, few studies have directly measured the adaptive value of physiology in natural

plant populations by linking variation in physiological traits with fitness. Using three populations of *Bromus inermis* growing in contrasting soil environments, I tested whether high resources lead to stronger selection for traits that confer increased growth rate. At each site, I measured photosynthetic rate, CO₂-saturated photosynthetic capacity and chlorophyll concentration on 125 systematically sampled plants. I estimated phenotypic selection by regressing these physiological traits against two fitness metrics. In 2006, I found selection for increased photosynthesis at the two sites with high phosphorus availability, but not at the low phosphorus site. In 2007, there was selection for increased photosynthesis at all three sites early in the growing season. Later in the season, however, I only found selection for increased photosynthesis at the two sites with high phosphorus availability. These results indicate that selection on plant photosynthesis is spatially and temporally variable, and stronger in high resource environments.

11:45 AM – 12:00 PM

A preliminary survey and test of alternative evolutionary hypotheses about visual trait diversity among sunfish in the family *Centrarchidae*

Paige*, J.-M., Robinson, Beren W.
Department of Integrative Biology, University of Guelph.

For those species possessing it, vision can influence fitness through mate selection, by avoiding hybridization, finding food and avoiding predators. Eyes of aquatic animals must be able to see in a medium that can drastically affect visual signal transmission. Thus, we expect that variation in visual receptor traits will be associated in predictable ways with the photic environment because of functional effects on these important fitness related traits. For example, strong relationships may exist between retinal pigments and water colour. The fish of the Centrarchid family are ideal for studies of vision trait evolution because they exist in a range of fresh-water habitats; feed at different light intensities; include trophic specialists and generalists; and utilize all major feeding modes. In addition, their phylogenetic relationships and times since diversification are becoming well-understood. We have collected and analyzed vision traits from 19 species of Centrarchids collected from their native habitats. We report on variation in two vision traits here, visual pigment spectral sensitivity using microspectrophotometry and rod and cone patterning across the retina using light microscopy techniques. These will be used to assess evolutionary hypotheses about the origins of the visual receptor traits in a phylogenetic context in order to better understand the evolution of this complex organ.

Lunch Break

- Break from 12:00 – 1:00 PM
- At this time, pizza will be available in the Atrium of the New Science Complex

Afternoon Plenary Talk -
1:00 – 2:00 PM

For every season: brains! brains! brains! Seasonality of songbird reproduction.
Scott A. MacDougall-Shackleton
University of Western Ontario

Almost every habitat on the planet is seasonal, and animals time the occurrence of major life history events to occur at times of year that will maximize lifetime reproductive success. For example, reproduction is timed such that offspring are produced at times of year conducive to their survival. Songbirds typically use the annual change in photoperiod to time reproduction. In many species young are produced in spring when the insects that parents feed their young are abundant. Other species have more flexible or opportunistic breeding schedules. Large changes in the brain underlie these seasonal changes in reproductive physiology and behaviour. I will review comparative studies of how different species of birds respond to photoperiod to time reproduction, and how brain regions that control gonadal activity and singing behaviour change seasonally.

2:00 – 2:15

15 Minute Break

- Coffee and water are available in the Rozanski Concourse

Fifth Concurrent Session

DNA Barcoding (room 101)

2:15 – 2:30 PM

Inferring patterns of molecular evolution: the utility of DNA barcoding in analyzing sequence evolution among Amphipoda and Polychaeta

Carr*, Christina M., Hebert, Paul D.N.
Department of Integrative Biology, University of Guelph.

The generality and magnitude of the factors driving the pace of molecular evolution have been long debated. To be effective, study systems require enough lineages to be able to make broad scale comparisons as well as evidence of varied exposure to evolutionary agents. DNA barcoding provides rapid acquisition of nucleotide sequence libraries and holds enormous potential for comparative study of evolution in the mitochondrial gene cytochrome *c* oxidase I (COI). Alternate life histories expose lineages to different environmental conditions. This variation results in different exposure to environmental mutagens and thus selective pressures may vary. Benthic and pelagic zones are practical venues for comparison of evolutionary rates because agents such as oxygen levels and UV radiation vary considerably yet organisms have adapted to and become extremely successful in both realms. In this study we investigate variation in rates of COI in two marine invertebrates, Class Polychaeta and Order Amphipoda in Canadian arctic waters. Despite its critical function, there is marked variation in amino acid composition of COI across these taxa. Both metabolic rate and exposure to UV have been postulated as explanations for rate heterogeneity between organisms but have not been tested at this scale. The results of this study will provide insights into evolutionary history and have broad implications for understanding factors controlling rates of evolution.

2:30 – 2:45 PM

***Tetrahymena* and the molecular barcode: a new approach to species identification.**

Kher, Chandni P.* and Lynn, Denis H.
Department of Integrative Biology, University of Guelph.

A variety of different approaches have been used over the years to aid in the field of ciliate systematics. Recently, DNA barcoding using the cytochrome *c* oxidase subunit I (cox-1) gene of the mitochondria has gained popularity as a potential tool for species identification. The major objective of our project is to assess the overall feasibility of cox-1 barcoding by using it to elucidate the relationships between different species of *Tetrahymena*. We have confirmed that intraspecific sequence divergence is typically less than 1%; however, in the process we have uncovered a plethora of probably mislabeled and/or misidentified cultures. We have also used cox-1 barcodes in conjunction with nuclear small subunit rRNA gene sequences to aid in the first genetic redescription of *Tetrahymena rostrata* and have discovered what appears to be a *Tetrahymena*-like strain of the genus *Ichthyophthirius*. We have also used cox-1 sequences to provide the foundation for a population genetics analysis to determine whether there is biogeographic patterning in the distribution of *Tetrahymena* species. Results suggest that cox-1 barcoding is indeed an invaluable tool for protistologists, especially when used in conjunction with classical taxonomic techniques.

2:45 – 3:00 PM

Using DNA barcoding to re-evaluate the harvest management of Canada and cackling geese.

Kerr*, Kevin C. R., Gendron, Michel, Hebert, Paul D. N.

Department of Integrative biology. University of Guelph.

The Canada goose (*Branta canadensis*) is a familiar species throughout North America with a myriad of subspecies and clinal variants. In 2004, the American Ornithologists' Union decided there was sufficient evidence to separate the smaller tundra-breeding population as a unique species, the cackling goose (*B. hutchinsii*). Both species are hunted extensively across their fall migration routes. Identification keys were developed in the 1960s to allow wildlife officials to monitor the harvest rates of 'large' and 'small' Canada geese. However, the development of these keys predates the division of the two species and it is not known if the delimitation is reflective of species boundaries. DNA barcoding utilizes a short segment of the mitochondrial gene cytochrome *c* oxidase I (COI) as a genetic marker to identify different species. We have employed DNA barcodes to assess the ability of these keys to distinguish Canada and cackling geese. We sampled geese from breeding sites distributed throughout Canada and Alaska. Feather samples were obtained from birds identified to species on their breeding grounds. These samples were then barcoded to establish a reference library of COI sequences. Wing and tail feathers of harvested geese were volunteered from hunters across Canada. The identification of these samples was determined using the keys, then verified or rejected using DNA barcodes. Pending the results of this study, we hope to re-evaluate morphological characters and produce a key that accurately differentiates these species. If characters overlap significantly, then SNP analysis might be explored as a tool to accurately monitor the harvest of these two species.

3:00 – 3:15 PM

SeqCleanR: a tool for scanning, editing and identifying diagnostic characters in large homologous DNA sequence data sets prior to analysis of sequence variation

Taika von Königslöw*, Daniel Ashlock**, and Paul D.N. Hebert*

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Progress in DNA-sequencing techniques has led to vast improvements in the speed and accuracy in which DNA sequence data is recovered. However, uncertainty remains in the results obtained from DNA sequencing, especially when compiling large datasets from different sources. These uncertainties include systematic and random errors that are missed in the process of raw sequence editing. Since it has been demonstrated that even extremely low error rates can influence analysis of sequence variation, additional error correction would be useful to improve the accuracy of DNA sequences in molecular databases. The program, SeqCleanR, makes use of *profile hidden Markov models* to estimate the probability of variation at a site given the sequence diversity of the related sequences. This program can be used to summarize the information in large DNA sequence datasets by reporting such things as: potentially erroneous bases; sequences that have variation masked by ambiguous character information; IUPAC characters; sequences that are unlikely to belong to a given dataset; and, characters diagnostic to a dataset. This program is intended to help manage unwieldy datasets and provide another level of error detection and characterization prior to sequence analysis.

3:15 – 3:30 PM

Barcoding Microlepidoptera : enhanced species discovery and integrative taxonomy

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We barcoded ~17,200 specimens of Microlepidoptera representing 50 families, ~500 genera and ~1,400 species, encompassing ~ 23 % of the North American micromoth diversity. DNA barcodes were highly effective in species recognition, resulting in the separation/recovery of nearly all species sampled, and correlated closely with most existing species defined largely on the basis of morphological characters and hosts. Shorter barcode fragments ('mini-barcodes') were successfully recovered from 99 type specimens of *Coleophora* (Coleophoridae) ranging in age from 62 to 136 years old and matched remarkably well with barcode sequences obtained from recently collected specimens. We discuss and provide case studies for applications of DNA barcoding in Microlepidoptera that complement morphology-based taxonomy, such as association of sexes between specimens, identification of otherwise unidentifiable life stages, and effective sorting of large series of specimens, and corroboration of synonymies. We propose a framework that incorporates DNA barcoding with traditional character systems for an integrative approach to Microlepidoptera taxonomy that could significantly reduce the current impediment caused by an inadequate and fragmentary taxonomic foundation.

3:30 – 3:45 PM

How many barcodes does it take to identify a sphingid? Effect of sequence library size on subfamily, tribe, genus and species assignments

Wilson*¹, John J., Rougerie¹, Rodolphe, Janzen², Daniel H., Hallwachs², Winnie, Kitching³, Ian J., Vaglia⁴, Thierry, Haxaire⁵, Jean & Hebert¹, Paul D. N.

¹University of Guelph, ²University of Pennsylvania, ³Natural History Museum, London, ⁴Insectarium de Montreal,

⁵Muséum National d'Histoire Naturelle, Paris.

DNA barcoding is receiving growing acceptance as a means of providing unidentified specimens with a species name. Sequencing the 'DNA barcode' segment of the COI mtDNA gene and performing comparisons against a database of curated sequences has been successfully implemented for the identification of Lepidoptera specimens from Area de Conservacion Guanacaste, northwestern Costa Rica, and in many other animal groups around the world. However, the approach still being attacked on the following two fronts. Firstly, the successes reported in DNA barcoding studies are labelled as unrealistic due to biased and incomplete taxonomic sampling regimes. Secondly, DNA barcoding is predicted to fail due to an incomplete reference database against which to perform the identification analysis. These may appear as contradictory arguments; DNA barcoding is said to only work due to taxonomically incomplete datasets and DNA barcoding is said to fail due to taxonomically incomplete datasets, but both are often alluded to in a single study or opinion article. In this study we aim to counter these two concerns by first measuring the success of identifications through DNA barcodes with a complete dataset: the "Sphingidae of the world". Are test specimens correctly assigned or are they confused with other species? Second, we will determine if specimens can be assigned to a correct higher taxonomic group when conspecifics are absent in an incomplete dataset. In this regard we will investigate how the size of the reference database and how it is assembled (i.e. randomly or systematically) impact the success of taxonomic assignments using DNA barcodes.

Sexual Selection (room 103)

2:15 – 2:30 PM

Good-genes and the intersex correlation for fitness across environments.

Delcourt*, Matthieu, Mark, Blows, W., Howard, Rundle, D.
Department of Biology. University of Ottawa.

Mate preferences are common in sexual species such that females discriminate among potential mates based upon certain traits. Such preferences are assumed to be costly and their evolution within populations has therefore been the subject of much research. A longstanding theory, termed the good-genes hypothesis, posits that preferences for such traits evolve because they are indicative of high genetic quality in males. By mating with such males, females may gain an indirect benefit by passing the father's good genes on to their sons. However, the magnitude of this indirect benefit depends on the intersex genetic correlation for fitness (r_w), a measure of the extent to which genes for high fitness males will also produce high fitness females. Here we use quantitative genetic methods to estimate r_w in a population of Australian fruit flies (*Drosophila serrata*) when raised in two environments: the laboratory food to which they are well adapted and a novel corn-based food. Genetic variance for fitness was present in both environments but had opposite effects on average in the two sexes (r_w : yeast = -0.418; corn = -0.726; $P = 0.062$). Negative r_w values will hamper a good-genes process because sires producing higher fitness sons tend to produce lower fitness daughters and vice versa. Such sexually antagonistic fitness effects have been reported previously in a handful of other cases, suggesting they may be common. Their persistence in a novel environment may explain why sexual selection did not speed adaptation to this novel environment in a past experiment.

2:30 – 2:45 PM

Experienced (but not virgin and socially-naïve) female field crickets exert directional selection on males.

Judge, Kevin A.
Department of Biology, University of Toronto at Mississauga

A large and increasing number of factors have been shown to affect female mating behaviour, and thus to affect the strength and/or direction of selection that females exert on males. One of these factors is female social experience (including mating history), which has received relatively little attention. I used multivariate selection analysis to

estimate the linear and nonlinear selection gradients exerted by female field crickets (*Gryllus pennsylvanicus*) with different social backgrounds. Females were either: 1) virgins with no experience of conspecifics as adults or 2) experienced females from a large, mixed-sex population. I assessed relative fitness through either mating success (mated or not) or attractiveness (inverse of latency to copulate) and calculated selection gradients based on each fitness measure for four male traits: age, body size, residual head width and residual mass. Based on previous research, I predicted that older males would have higher relative fitness than younger males. I also tested the prediction that, virgin females would exert weaker selection than experienced females. Overall, this prediction was supported, and experienced females exerted significant positive directional selection on male age and residual head width. I also detected significant nonlinear selection by both virgins and experienced females, and these gradients differed between the two classes of female. I discuss these results in light of the prediction that virgin females should be less choosy than mated females. And, in the context of previous work on *G. pennsylvanicus*, the present study replicates an important earlier result that older males have a mating advantage.

2:45 – 3:00 PM

Polygyny despite male genital mutilation in the western black widow (*Latrodectus hesperus*)

MacLeod, Emily C., Modanu, Maria, Ruthiran, Russanthi, Andrade, Maydianne C. B.
Department of Ecology and Evolutionary Biology. University of Toronto Scarborough.

Spiders of the genus *Latrodectus* have a mating system often characterized by sexually cannibalistic, polyandrous females and monogynous males. Monogyny may arise because males in this genus lose a portion of their copulatory organ (apical sclerite) during mating, and this may reduce the likelihood of successful remating. We investigated the consequences of genital mutilation in males of the western black widow spider (*Latrodectus hesperus*) to examine whether such males can mate multiply, and whether they gain reproductive benefits from genital mutilation. To determine whether males can mate multiply, males were presented with four mating opportunities and we examined whether sperm transfer occurred successfully on each occasion. We found that males are able to mate multiple times, even after the loss of the apical sclerite and that these copulations can result in viable offspring. We also examined whether the apical sclerites function as sperm plugs by using a sterile male technique to assess paternity. Female black widows were inseminated by an irradiated male and a fertile male and paternity assessed by counting the proportion of hatched eggs in subsequently deposited egg sacs. Our preliminary data supports the hypothesis that the apical sclerites function as plugs, blocking males that mate with a non-virgin female from gaining any paternity. We discuss the implications of these results for the selection pressures driving the evolution of this mating system.

3:00 – 3:15 PM

The role of previous experience on contest outcome and patterns of selection in a jumping spider

Kasumovic, Michael M.; Punzalan, David; Elias, Damian O.; Mason, Andrew C.; Andrade, Maydianne C. B.

There are many phenotypic traits that are associated with competitive success. However, phenotypic determinants of contest outcome are not absolute as past contest experience can alter future competitive performance, and therefore, phenotype-fitness associations. As most examinations of experience effects focus on higher vertebrates, our primary goal in this study was to examine the role of multiple experiences in contest outcomes in a short lived invertebrate. As experience could potentially change phenotype-fitness associations, our secondary goal was to determine whether experience alters patterns of phenotypic selection as more experience is gained. To answer these questions, we used a jumping spider, *Phidippus clarus*, where males undergo intense intrasexual competitions for female access. Jumping spiders are interesting to study in this regard as they have excellent visual acuity and undergo stereotyped interactions where a winner can easily be identified. We fought males in three consecutive contests with different opponents to determine the role of experience in contest outcomes relative to other phenotypic traits. Here we show that both weight and experience significantly predicted contest outcomes, with weight being approximately 1.5 times more important than experience. As a result, despite the important role of experience in contests, the pattern of selection did not change between rounds. Overall, our results demonstrate that contest experience can be an important determinant in contest outcomes, even in short lived invertebrates, and that experience is unlikely to alter phenotype-fitness associations in this species.

3:15 – 3:30 PM

Male-biased parasitism by common helminths is not explained by sex differences in body size or spleen mass of breeding cormorants *Phalacrocorax auritus*.

Robinson*, Stacey A., Forbes, Mark R., Hebert, Craig E. McLaughlin, J. Daniel. Department of Biology, Carleton University.

In vertebrates, males are often more parasitised than conspecific females. This bias in parasitism might result from sex differences in parasite exposure and/or susceptibility to infection. Such information is important for testing hypotheses about allocation of resources to life histories of males and females and for testing hypotheses about factors thought to influence parasite fitness and parasite dynamics. We tested whether double-crested cormorants *Phalacrocorax auritus* exhibit male-biased parasitism by gut helminths. The prevalence of nematode *Contracaecum* spp. and trematode *Drepanocaphtalus spathans* infections was ~90% and 39%, respectively. Cestode, primarily *Paradilepis caballeroi* and acanthocephalan *Andracantha grandidi* infections were less common (< 10%). Male and female cormorants did not differ in prevalence of infection by any helminth species. However, males had twice the abundance and intensity of *Contracaecum* spp. infections and twice the intensity of *D. spathans* infections than found in females. For common parasites showing male-biased parasitism, degree of parasitism was also unrelated to body size or mass in either sex. Males and females did not differ in spleen mass and spleen mass was unrelated to abundance of common parasites. Furthermore, abundance of trematodes and nematodes was not correlated. At present, male biases in parasitism by nematodes and trematodes in cormorants are independent patterns that remain unexplained, but are most likely attributable to sex differences in exposure and/or immunological differences not yet assessed.

3:30 – 3:45 PM

Sexual selection in the sex-role reversed Mormon cricket (*Anabrus simplex*)

Robson*, L.
University of Toronto, Mississauga

Two morphs of Mormon crickets (*Anabrus simplex*) are found in south-western U.S.A. Solitary populations are found in low densities, demonstrating a typical mating system with male-male competition and female choosiness. Gregarious individuals march in dense bands wrought with cannibalism, demonstrating sex-role reversal where females compete for mates and males often reject females. Given this variation in mating system and population structure, we predict different selection on males and females in the two population types. Crickets from the two morphs were compared using a series of morphological traits related to general size, fighting ability or mate retention. Preliminary analyses show that males and females of the gregarious morph were significantly larger (as indicated by pronotum length) than their solitary conspecifics. All populations showed distinct sexual dimorphism; females of both morphs had proportionately wider heads and maxillae spans than males suggesting selection for fighting ability is stronger in females than males. The gregarious bands of sex-role reversed Mormon crickets provide a unique opportunity to examine the strength and direction of sexual selection in females. As a continuation of our research, we propose the use of a selection analysis comparing morphological traits between copulating and singleton females from the band populations. To determine the mechanism behind the selection, we will conduct female-female competition trials and male choice trials. By comparing the preferences of the competition and choice trials with those of the selection analysis, we hope to be able to identify the dominant mechanisms of sexual selection on females of the gregarious morph.

3:45 – 4:00

15 Minute break

Sixth Concurrent Session

Climate Change and Environmental Stress (room 101)

4:00 – 4:15 PM

Here Today, Gone tomorrow? Targeting Conservation Investment in the Face of Climate Change

Olson*, Leif T., Lindsay, Kathryn F., (Geomatics and Landscape Ecology Research Lab, Carleton University)

Abstract

To optimize the use of scarce resources, it is imperative to target conservation investment wisely. We present a novel methodology to evaluate the impact of potential climate-driven shifts in species distributions on the future conservation utility of a present-day reserve design. Using Breeding Bird Survey data for 150 species in the conterminous USA east of the 100th meridian and two predicted future species distributions models (generated by others, using modelled tree species information and two global circulation climate models). Using present-day distributions, we select sets of sites meeting a range of conservation targets; from 10 to 100 occurrences of each species in the reserve network. These sites cover 68 – 79 % of bird species in the two future scenarios. Underrepresented species fall into two principal groups, those associated with more northern tree species (Balsam Fir *Tsuga canadensis* or Paper Birch *Betula papyrifera*) and those linked to temperature variables. Changes in the geography of conservation priority are highlighted by an interpolated ‘conservation priority surface’, informing strategies for adaptive conservation management in response to climate change and encouraging the geographic targeting of conservation investment.

4:15 – 4:30 PM

Comparing tropical tree spatial patterns across populations and time

Leithead*, Mark D., Deeth, Lorna, Anand, Madhur.

* Department of Environmental Biology. University of Guelph.

A reoccurring issue in the analysis of spatial patterns is the inability to dissociate an observed pattern from the scale (distance, spatial lag, window-size) at which it is quantified, which often makes cross-year and/or cross species comparisons cumbersome. Here we introduce an approach to deal with this issue. We use spatial point data of *Quararibea asterolepis* (Bombacaceae) and *Ocotea whitei* (Lauraceae), two of the most common and best studied tropical tree species on Barro Colorado Island (BCI), Panama, from a 20-year dataset with a census every five years starting in 1985 to illustrate the method. We fit the data from seedlings and adults of each species to a Neyman-Scott Poisson cluster process to estimate the variance of points dispersed from cluster centers (σ^2), and the intensity of repulsion between cluster centers (ρ). We develop a method for comparing spatial patterns based on deviations from the most clustered pattern observed for each population determined by σ^2 and ρ . We then use our approach to examine changing tropical spatial patterns in response to El Niño events and the Janzen-Connell Hypothesis. We conclude that the approach presented can be a simplified and powerful method for testing hypotheses regarding changing spatial patterns.

4:30 – 4:45 PM

Endocrine Disruption and Altered Prey Responses in Round Gobies (*Neogobius melanostomus*) Exposed to Great Lakes Contaminants

Marentette*, Julie R., Gooderham, K. L., Hynes, H., Stosic, A., McMaster, M.E., Parrott, J.L., Slater, G.F. Wilson, J.Y., Balshine, S.

Department of Psychology, Neuroscience and Behaviour, McMaster University

Persistent contaminants in Great Lakes waterways are a problem for both human health and the integrity of aquatic ecosystems. A recent invasive fish, the round goby, is ideal for examining the consequences of *in situ* contaminant exposure because of its benthic nature, high site fidelity and diet of zebra mussels. The incorporation of the goby into Great Lakes foodwebs means that contaminants previously restricted to zebra mussel biomass are increasingly available to higher order carnivores. We have examined changes in behaviour and physiology of round gobies collected from both highly contaminated and relatively clean areas of Hamilton Harbour, a Canadian IJC Area of Concern with a long history of industrial and urban pollution. Contaminated gobies showed decreased activity levels, greater fin loss, higher frequencies of intersex males, heavier PCB body burdens and elevated liver monooxygenase (e.g., EROD) activity compared to cleaner gobies. Contaminated gobies were less likely to seek shelter following a simulated predation episode than fish from cleaner sites. Sex-specific variation in contaminant responses will affect predictions of natural population-level dynamics in polluted waters. An impaired ability to evade predators in contaminated fish may also accelerate bioaccumulation of toxins in higher trophic levels, including humans.

4:45 – 5:00 PM

The effects of hypoxia on cardiac function and development in rainbow trout (*Oncorhynchus mykiss*)

McGoey, Brechann V. *, Gillis, Todd E.

Department of Integrative Biology, University of Guelph.

*Currently at Department of Ecology and Evolutionary Biology, University of Toronto.

The physiological impacts of chronic hypoxia during the development of fish are not well understood. Rainbow trout (*Oncorhynchus mykiss*) embryos are subjected to variable oxygen levels in the natural environment because of eutrophication, climatic effects and seasonal fluctuations. Hypoxia has been found to induce tachycardia in rainbow trout larvae but bradycardia in mature rainbow trout. The objective of this experiment was to determine the impacts of chronic hypoxia (50% oxygen saturation) on the cardiac function of rainbow trout embryos. To achieve this, rainbow trout embryos were raised in two different treatments, normoxia and hypoxia, from 13 days post-fertilization (dpf) to 29 dpf. Nitrogen gas was used to displace oxygen in the hypoxic treatment heath trays. Embryos from the hypoxic treatment had statistically significant higher average heart rates than those in the normoxic treatment. Therefore, low oxygen levels can directly impact the cardiac function of rainbow trout embryos. Increased heart rates may lead to cardiac hypertrophy and possibly increased aerobic fitness.

Theoretical and Experimental Evolution (room 103)

4:00 – 4:15 PM

A three-player game theoretical analysis of the co-evolution of predators, pollinators, and flowers

Abbott*, Kevin R.

Department of Psychology, Neuroscience & Behaviour. McMaster University

Some pollination systems contain ambush predators that hunt pollinators from flowers. These predators may depress the reproductive success of flowers by deterring or killing pollinators. Thus, in addition to classic questions about predator-prey and pollinator-flower co-evolution, we can ask novel questions about what floral traits should evolve in the presence of predators and about how these floral traits should affect predator and pollinator behaviour. One floral trait that is likely to affect predator-prey interactions is colour. Two alternate floral colour strategies can be considered: one where the colour of the flower facilitates predator camouflage by matching the colour of the ambush predator (concealing strategy), and one where the floral colour contrasts with the predator's colour (revealing strategy). Concealing flowers may have a fitness advantage because pollinators are less likely to detect and avoid the presence of a predator. However, predators may prefer to hunt on concealing flowers and the increased frequency of predators and the decreased probability of the detection of predators may mean that pollinators are generally reluctant to visit concealing flowers. Therefore, it is unclear which floral strategy would be evolutionarily favoured. Here I describe the design and results of a three-player game theoretic model that explores the co-evolution of predator, pollinator and floral strategies. This model uses a signal detection framework for describing how pollinators decide whether or not a flower is safe as well as a habitat selection framework for determining how pollinators and predators distribute themselves between concealing and revealing flowers.

4:15 – 4:30 PM

Interactions in the bacterial world: an antibiotic resistance paradigm.

Boland, Timothy W., Sherratt*, Tom N., Kassen, Rees,

Department of Biology, Carleton University

The evolution of resistance to antibiotics in bacteria is an issue of growing concern. Interactions between genetically distinct bacterial populations may play an important role in mediating the evolution of this resistance, since non-resistant “cheats” have the potential to undermine the spread of traits that confer resistance. In the antibiotic setting, the plasmid pBR322 allows the bacterium *Escherichia coli* to produce β -lactamase (at a cost), an enzyme released into the periplasmic space that breaks down β -lactam antibiotics. Some enzyme also leaks out of the cell into the surrounding media through the outer membrane and so can be utilised by individuals that are not themselves producing the β -lactamase. Here we have investigated how the density and relative frequency of mixtures of *Escherichia coli* DH5 α , one resistant to β -lactam antibiotics (via the acquisition of the plasmid pBR322) and one sensitive to β -lactams (lacking any mechanism of resistance) influence the evolution of resistance on two different types of environmental media (liquid and solid), and under different antibiotic (ampicillin) concentrations. Our results indicate that there was a significant effect of both starting frequency and density on the evolution of resistance in both liquid and solid media, as

well as a clear effect of ampicillin concentrations. The implications of these combined density and frequency dependent effects for resistance evolution, as well as their interactive effects, are discussed.

4:30 – 4:45 PM

Selection for Desiccation Resistance: Ecological Speciation in *Drosophila melanogaster*

Kwan*, Lucia and Rundle, Howard
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Ecological speciation occurs when divergent natural selection between populations occupying different environments generates reproductive isolation as a side effect. Although laboratory experiments have demonstrated that it can occur, important questions remain concerning its frequency and the relative rates at which various forms of reproductive isolation evolve. Using 12 replicate populations that have independently evolved under alternative desiccation treatments (six control, 'C', and six desiccation-selected, 'D'), we are examining the evolution of both pre- and postmating isolation (only premating isolation results are available to date). Despite 57 generations of selection and well characterized evolutionary responses in both sexes, tests for assortative mating revealed that adaptation to desiccation failed to generate any detectable premating isolation between C and D populations. Nevertheless, two interesting patterns were apparent. First, females from all six D populations achieved more matings than did C females, irrespective of the type of male involved. This could be the result of an increased willingness (decreased resistance) of D females to mate, favoured by selection because few males survive the desiccation treatment and females must therefore mate quickly prior to this. Second, males from all six D populations achieved fewer matings than did C males, again irrespective of the type of female. This could be the result of inbreeding depression of male mating success in the D populations, or the evolution of unattractive males via sexual conflict. Experiments are currently underway to address these possibilities.

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Thank you for attending OEEC 2008. We hope you enjoyed the conference.